CPPTRAJ

Daniel R. Roe

October 16, 2026

https://github.com/Amber-MD/cpptraj

Contents

1 Introduction **8**
- 1.1 Manual Syntax Format . . . 9
- 1.2 Installation . . . 9
- 1.3 Examples . . . 9

2 Running Cpptraj **9**
- 2.1 Command Line Syntax . . . 10
- 2.2 Commands . . . 11
- 2.3 Getting Help . . . 12
- 2.4 Batch mode . . . 12
- 2.5 Interactive mode . . . 12
- 2.6 Trajectory Processing "Run" . . . 13
  - 2.6.1 Actions and multiple topologies . . . 13
- 2.7 Parallelization . . . 13
  - 2.7.1 MPI Trajectory Parallelization . . . 14
  - 2.7.2 OpenMP Parallelization . . . 14
  - 2.7.3 CUDA Parallelization . . . 15

3 General Concepts **16**
- 3.1 Units . . . 16
- 3.2 Atom Mask Selection Syntax . . . 16
- 3.3 Ranges . . . 19
- 3.4 Parameter/Reference Tagging . . . 19

4 Variables and Control Structures **19**
- 4.1 for . . . 20
- 4.2 set . . . 22
- 4.3 show . . . 23

5 Data Sets and Data Files **23**
5.1 Data Set Selection Syntax . . . 24
5.2 Data Set Math . . . 26

6 Data File Options **27**
6.1 Standard Data File Options . . . 28
6.2 Grace Data File Options . . . 31
6.3 Gnuplot Data File Options . . . 32
6.4 Amber REM Log Options . . . 32
6.5 Amber MDOUT Options . . . 33
6.6 Evecs File Options . . . 33
6.7 Vector psuedo-traj Options . . . 33
6.8 OpenDX file options . . . 33
6.9 CCP4 file options . . . 34
6.10 Charmm REPD log options . . . 34
6.11 Amber Constant pH Out options . . . 34
6.12 Amber prep file options . . . 34
6.13 Amber Library (OFF) file options . . . 35
6.14 Amber Parameter (main force field) file options . . . 35
6.15 Amber leaprc file options . . . 35
6.16 Coords file options . . . 35

7 System Build and Parameterization Commands **35**
7.1 build . . . 36
7.2 sequence . . . 42
7.3 source . . . 43

8 Coordinates (COORDS) Data Set Commands **44**
8.1 catcrd . . . 45
8.2 combinecrd . . . 45
8.3 crdaction . . . 46
8.4 crdout . . . 46
8.5 crdtransform . . . 46
8.6 createcrd . . . 47
8.7 emin . . . 47
8.8 extendedcomp . . . 49
8.9 graft . . . 49
8.10 loadcrd . . . 51
8.11 loadtraj . . . 51
8.12 permutedihedrals . . . 52
8.13 prepareforleap . . . 54
8.14 reference . . . 58
8.15 rotatedihedral . . . 59
8.16 sequence . . . 59
8.17 splitcoords . . . 59
8.18 zmatrix . . . 60

9 General Commands **61**
9.1 activeref . . . 61
9.2 calc . . . 62
9.3 clear . . . 62
9.4 create . . . 62
9.5 createset . . . 62
9.6 datafile . . . 63
9.7 datafilter . . . 63
9.8 dataset . . . 64
9.9 debug | prnlev . . . 68
9.10 ensextension . . . 68
9.11 exit | quit . . . 68
9.12 flatten . . . 68
9.13 go | run . . . 69
9.14 help . . . 69
9.15 list . . . 70
9.16 noexitonerror . . . 70
9.17 noprogress . . . 70
9.18 parallelanalysis . . . 70
9.19 parsedata . . . 71
9.20 precision . . . 72
9.21 random . . . 72
9.22 readdata . . . 73
9.23 readensembledata . . . 74
9.24 readinput . . . 74
9.25 removedata . . . 74
9.26 rst . . . 74
9.27 runanalysis . . . 75
9.28 select . . . 76
9.29 selectds . . . 76
9.30 sortensembledata . . . 76
9.31 usediskcache . . . 76
9.32 write | writedata . . . 76
9.33 System Commands . . . 77

10 Topology File Commands **77**
10.1 angleinfo | angles | printangles . . . 78
10.2 atominfo | atoms | printatoms . . . 79
10.3 bondinfo | bonds | printbonds . . . 79
10.4 bondparminfo . . . 80
10.5 change . . . 80
10.6 charge . . . 82
10.7 comparetop . . . 83
10.8 dihedralinfo | dihedrals | printdihedrals . . . 83
10.9 hmassrepartition . . . 84
10.10improperinfo | impropers | printimpropers . . . 84

10.11 mass . . . 85
10.12 molinfo . . . 85
10.13 parm . . . 86
10.13.1 *PDB format:* . . . 87
10.13.2 Charmm PSF: . . . 88
10.13.3 Gromacs Top . . . 88
10.14 parmbox . . . 88
10.15 parminfo . . . 88
10.16 parmstrip . . . 89
10.17 parmwrite . . . 89
10.17.1 Amber Topology . . . 89
10.17.2 Charmm PSF . . . 90
10.18 printub | ubinfo . . . 90
10.19 resinfo . . . 90
10.20 scaledihedralk . . . 91
10.21 solvent . . . 91
10.22 timap . . . 91
10.23 updateparameters . . . 96

11 Trajectory File Commands **97**
11.1 ensemble . . . 99
11.2 ensemblesize . . . 100
11.3 reference . . . 101
11.4 trajin . . . 102
11.4.1 *Options for Amber NetCDF, Amber NC Restart, Amber Restart:* . . . 104
11.4.2 *Options for CHARMM DCD:* . . . 104
11.4.3 Options for PDB files: . . . 105
11.5 trajout . . . 105
11.5.1 *Options for pdb format* . . . 107
11.5.2 *Options for Amber ASCII format:* . . . 109
11.5.3 *Options for Amber NetCDF format:* . . . 109
11.5.4 *Options for Amber Restart/NetCDF Restart format:* . . . 109
11.5.5 *Options for CHARMM COORdinates:* . . . 110
11.5.6 *Options for CHARMM DCD:* . . . 110
11.5.7 *Options for GROMACS TRX/XTC format:* . . . 110
11.5.8 *Options for mol2 format:* . . . 111
11.5.9 Options for SQM input format: . . . 111
11.5.10 Options for XYZ format: . . . 111

12 Action Commands **112**
12.1 addatom . . . 116
12.2 align . . . 117
12.3 angle . . . 118
12.4 areapermol . . . 118
12.5 atomiccorr . . . 119

12.6 atomicfluct | rmsf . . . 119
12.7 atommap . . . 121
12.8 autoimage . . . 123
12.9 average . . . 124
12.10avgbox . . . 125
12.11avgcoord . . . 126
12.12bounds . . . 126
12.13box . . . 127
12.14center . . . 128
12.15check | checkoverlap | checkstructure . . . 128
12.16checkchirality . . . 130
12.17closest | closestwaters . . . 131
12.18cluster . . . 132
12.19clusterdihedral . . . 132
12.20contacts . . . 134
12.21createcrd . . . 134
12.22createreservoir . . . 134
12.23density . . . 135
12.24diffusion . . . 136
12.25dihedral . . . 139
12.26dihedralrms | dihrms . . . 139
12.27dihedralscan . . . 140
12.28dipole . . . 140
12.29distance . . . 142
12.30drms | drmsd (distance RMSD) . . . 143
12.31dssp . . . 144
12.32enedecomp . . . 144
12.33energy . . . 145
12.34esander . . . 149
12.35filter . . . 150
12.36fixatomorder . . . 151
12.37fiximagedbonds . . . 152
12.38gist (Grid Inhomogeneous Solvation Theory) . . . 152
12.39grid . . . 165
12.40hbond . . . 169
12.41image . . . 174
12.42jcoupling . . . 175
12.43keep . . . 176
12.44lessplit . . . 177
12.45lie . . . 178
12.46lipidorder . . . 178
12.47lipidscd . . . 179
12.48makestructure . . . 180
12.49mask . . . 183
12.50matrix . . . 184
12.51mindist/maxdist . . . 186

12.52minimage . . . 186
12.53molsurf . . . 187
12.54multidihedral . . . 188
12.55multipucker . . . 189
12.56multivector . . . 190
12.57nastruct . . . 191
12.58nativecontacts . . . 197
12.59outtraj . . . 201
12.60pairdist . . . 201
12.61pairwise . . . 202
12.62principal . . . 203
12.63projection . . . 204
12.64pucker . . . 205
12.65radgyr | rog . . . 206
12.66radial | rdf . . . 207
12.67randomizeions . . . 209
12.68remap . . . 209
12.69replicatecell . . . 210
12.70rms | rmsd . . . 211
12.71rms2d | 2drms . . . 214
12.72rmsavgcorr . . . 214
12.73rmsf | atomicfluct . . . 214
12.74rotate . . . 214
12.75rotdif . . . 216
12.76runavg | runningaverage . . . 216
12.77scale . . . 216
12.78secstruct . . . 216
12.79setvelocity . . . 220
12.80spam . . . 221
12.81stfcdiffusion . . . 222
12.82strip . . . 223
12.83surf . . . 224
12.84surftension . . . 225
12.85symmrmsd . . . 226
12.86temperature . . . 227
12.87time . . . 228
12.88tordiff . . . 229
12.89trans | translate . . . 230
12.90unstrip . . . 230
12.91unwrap . . . 231
12.92vector . . . 232
12.93velocityautocorr . . . 234
12.94volmap . . . 235
12.95volume . . . 237
12.96watershell . . . 237
12.97xtalsymm . . . 238

13 Analysis Commands **239**
13.1 autocorr . . . 242
13.2 avg . . . 243
13.3 calcdiffusion . . . 244
13.4 calcstate . . . 245
13.5 cluster . . . 248
13.6 cphstats . . . 261
13.7 corr | correlationcoe . . . 262
13.8 crank | crankshaft . . . 263
13.9 crdfluct . . . 263
13.10 crosscorr . . . 264
13.11 curvefit . . . 264
13.12 diagmatrix . . . 265
13.13 divergence . . . 268
13.14 evalplateau . . . 268
13.15 fft . . . 269
13.16 hausdorff . . . 269
13.17 hist | histogram . . . 271
13.18 integrate . . . 273
13.19 ired . . . 273
13.20 kde . . . 275
13.21 lifetime . . . 276
13.22 lowestcurve . . . 279
13.23 meltcurve . . . 279
13.24 modes . . . 279
13.25 multicurve . . . 282
13.26 multihist . . . 283
13.27 phipsi . . . 284
13.28 projectdata . . . 285
13.29 regress . . . 285
13.30 remlog . . . 286
13.31 rms2d | 2drms . . . 287
13.32 rmsavgcorr . . . 288
13.33 rotdif . . . 290
13.34 runningavg . . . 293
13.35 slope . . . 294
13.36 spline . . . 294
13.37 statistics | stat . . . 295
13.37.1 Torsion Analysis . . . 296
13.37.2 Distance Analysis . . . 296
13.37.3 Pucker Analysis . . . 296
13.38 ti . . . 297
13.39 tica . . . 298
13.40 timecorr . . . 299
13.41 vectormath . . . 300
13.42 wavelet . . . 301

14 Analysis Examples **305**
14.1 Cartesian covariance matrix calculation and projection (PCA) . . 305
14.2 Dihedral covariance matrix calculation and projection for backbone phi/psi (PCA) 305

1 Introduction

Cpptraj[1] (the successor to *ptraj*) is the main program in Amber for processing coordinate trajectories and data files. *Cpptraj* has a wide range of functionality, and makes use of OpenMP/MPI to speed up many calculations, including processing ensembles of trajectories and/or conducting multiple analyses in parallel with MPI.[2]

Here are several notable features of *cpptraj*:

1. Trajectories with different topologies can be processed in the same run.
2. Several actions/analyses in *cpptraj* are OpenMP parallelized; see section 2.7.2 for more details.
3. In addition to processing single trajectories, can read, process, and write ensembles of trajectories at the same time (from e.g. REMD).
4. Trajectory and ensemble reads can be MPI parallelized.
5. As of version 7.0 has the ability to fully build and parameterize systems for MD simulations, including the addition of solvent and ions (similar to the LEaP program from AmberTools).
6. Almost any file read or written by *cpptraj* can be compressed (with the exception of the NetCDF trajectory format). So for example gzipped/bzipped topology files can be read, and data files can be written out as gzip/bzip2 files. Compression is detected automatically when reading, and is determined by the filename extension (.gz and .bz2 respectively) on writing.
7. The format of output data files can be specified by extension. For example, data files can be written in xmgrace format if the filename given has a '.agr' extension. A trajectory can be written in DCD format if the '.dcd' extension is used.
8. Multiple output trajectories can be specified, and can be written during action processing (as opposed to only after) via the ***outtraj*** command. In addition, output files can be directed to write only specific frames from the input trajectories.
9. Multiple reference structures can be specified. Specific frames from trajectories may be used as a reference structure.
10. The ***rmsd*** action allows specification of a separate mask for the reference structure. In addition, per-residue RMSD can be calculated easily.

11. Actions that modify coordinates and topology such as the ***strip***/***closest*** actions can often write an accompanying fully-functional stripped topology file.

12. Users usually are able to fine-tune the output format of data files declared in actions using the "**out**" keyword (for example, the precision of the numbers can be changed). In addition, users can control which data sets are written to which files (e.g. if two actions specify the same data file with the 'out' keyword, data from both actions will be written to that data file).

13. Users can manipulate data sets using mathematical expressions (with some limitations), see 5.2 on page 26 for details.

14. There is some support for creating internal loops over e.g. mask expressions and setting internal variables (see ***for***, ***set***, and ***show*** commands).

See the README.md file in the *cpptraj* home directory for information on how to build, authors, and so on.

1.1 Manual Syntax Format

The syntax presented in this manual uses the following conventions:

<> Denotes a variable.

[] Denotes something is optional.

{|} Denotes several choices separated by the '|' character; one of the choices must be specified.

... Denotes the preceding option can be repeated.

Everything else is as printed.

1.2 Installation

See instructions in the CPPTRAJ GitHub repository README.md file under 'Installation & Testing': `https://github.com/Amber-MD/cpptraj`

1.3 Examples

Some examples of running CPPTRAJ are available in the **examples** subdirectory. There are also many tests in the **test** subdirectory which can serve as simple examples.

2 Running Cpptraj

Cpptraj can be run in either "interactive mode" or in "batch mode".

2.1 Command Line Syntax

```
cpptraj [-p <Top0>] [-i <Input0>] [-y <trajin>] [-x <trajout>]
        [-ya <args>] [-xa <args>] [<file>]
        [-c <reference>] [-d <datain>] [-w <dataout>] [-o <output>]
        [-h | --help] [-V | --version] [--defines] [-debug <#>]
        [--interactive] [--log <logfile>] [-tl]
        [-ms <mask>] [-mr <mask>] [--mask <mask>] [--resmask <mask>]
        [--rng {marsaglia|stdlib|mt|pcg32|xo128}] [--charge <mask>]
* denotes a flag may be specified multiple times.
```

-p <Top0>* Load <Top0> as a topology file.

-i <Input0>* Read input from <Input0>.

-y <trajin>* Read from trajectory file <trajin>; same as input 'trajin <trajin>'.

-x <trajout>* Write trajectory file <trajout>; same as input 'trajout <trajout>'.

-ya <args>* Input trajectory file arguments.

-xa <args>* Output trajectory file arguments.

<file>* A topology, input trajectory, or file containing cpptraj input.

-c <reference>* Read <reference> as reference coordinates; same as input 'reference <reference>'.

-d <datain>* Read data in from file <datain> ('readdata <datain>').

-w <dataout> Write data from <datain> as file <dataout> ('writedata <dataout>).

-o <output> Write CPPTRAJ STDOUT output to file <output>.

-h | –help Print command line help and exit.

-V | –version Print version and exit.

–defines Print compiler defines and exit.

-debug <#> Set global debug level to <#>; same as input 'debug <#>'.

–interactive Force interactive mode.

–log <logfile> Record commands to <logfile> (interactive mode only). Default is 'cpptraj.log'.

-tl Print length of trajectories specified with '-y' to STDOUT. The total number of frames is written out as 'Frames: <X>'

-ms <**mask**> `Print selected atom numbers to STDOUT. Selected atoms are written out as 'Selected= 1 2 3 ...'`

-mr <**mask**> : `Print selected residue numbers to STDOUT. Selected residues are written out as 'Selected= 1 2 3 ...'`

–mask <**mask**> `Print detailed atom selection to STDOUT.`

–resmask <**mask**> `Print detailed residue selection to STDOUT.`

--rng <**type**> `Change default random number generator.`

--charge <**mask**> `Print total charge (in e-) of atoms selected by <mask> to STDOUT.`

Note that unlike *ptraj*, in *cpptraj* it is not required that a topology file be specified on the command line as long as one is specified in the input file with the 'parm' keyword. Multiple topology/input files can be specified by use of multiple '-p' and '-i' flags. All topology and coordinate flags will be processed before any input flags.

2.2 Commands

Input to *cpptraj* is in the form of commands, which can be categorized in to 2 types: immediate and queued. Immediate commands are executed as soon as they are encountered. Queued commands are initialized when they are encountered, but are not executed until a Run is executed via a ***run*** or ***go*** command. Actions, Analyses, and Trajectory commands (except ***reference***) are queued commands; however, they can also be run immediately via commands such as ***crdaction***, ***runanalysis***, ***loadcrd***, etc. See 8 on page 44 for more details.

Commands fall into seven categories:

General (Immediate) These commands are executed immediately when entered.

System (Immediate) These are unix system commands (e.g. 'ls', 'pwd', etc).

Coords (Immediate) These commands are used to manipulate COORDS data sets; see 8 on page 44 for more details.

Trajectory (Queued) These commands prepare cpptraj for reading or writing trajectories during a Run.

Topology (Immediate) These commands are used to read, write, and modify topology information.

Action (Queued) These commands specify actions that will be performed on coordinate frames read in from trajectories during a Run.

Analysis (Queued) These commands specify analyses that will be performed on data that has been either generated from a Run or read in from an external source.

Control (Immediate) These commands set up control blocks that can be used to e.g. loop over a set of commands.

In addition to normal commands, *cpptraj* now has the ability to perform certain basic math operations, even on data sets. See 5.2 on page 26 for more details.

Commands in *cpptraj* can be read in from an input file or from the interactive command prompt. A '#' anywhere on a line denotes a comment; anything after '#' will be ignored no matter where it occurs. A '\' allows the continuation of one line to another. For example, the input:

```
# Sample input
trajin mdcrd # This is a trajectory
rms first out rmsd.dat \
    :1-10
```

Translates to:

```
trajin mdcrd
rms first out rmsd.dat :1-10
```

2.3 Getting Help

If in interactive mode, the 'help' command can be used to list recognized commands and topics; topics (such as mask syntax) start with uppercase letters. 'help <command>' can be used to get the associated keywords as well as an abbreviated description of the command. Most commands have a corresponding test which also serves as an example of how to use the command. See $AMBERHOME/AmberTools/test/cpptraj/README for more details.

2.4 Batch mode

In "batch" mode, cpptraj is executed from the command line with one or more input files containing commands to be processed or STDIN. The syntax of <input file> is similar to that of *ptraj*. Keywords specifying different commands are given one per line. Lines beginning with '#' are ignored as comments. Lines can also be continued through use of the '\' character. This is the only allowed mode for cpptraj.MPI.

2.5 Interactive mode

In "interactive mode" users can enter commands in a UNIX-like shell. Interactive mode is useful for running short and simple analyses or for trying out new kinds of analyses. If *cpptraj* is run with '–interactive', no arguments, or no specified input file:

```
cpptraj
cpptraj --interactive
cpptraj <parm file>
cpptraj -p <parm file>
```

this brings up the interactive interface. This interface supports command history (via the up and down arrows) and tab completion for commands and file names. If no log file name has been given (with '–log <logfile>'), all commands used in interactive mode will be logged to a file named 'cpptraj.log', which can subsequently be used as input if desired. When starting cpptraj, command histories will be read from any existing logs.

2.6 Trajectory Processing "Run"

Like *ptraj*, a trajectory processing "Run" is one of the main ways to run *cpptraj*. First the Run is set up via commands read in from an input file or the interactive prompt. Trajectories are then read in one frame at a time (or in the case of ensemble processing all frames from a given step are read). Actions are performed on the coordinates stored in the frame, after which any output coordinates are written. At the end of the run, any data sets generated are written, and any queued Analyses are performed.

2.6.1 Actions and multiple topologies

Since *cpptraj* supports multiple topology files, during a Run actions are set up every time the topology changes in order to recalculate things like what atoms are in a mask etc. Actions that are not valid for the current topology are skipped for that topology. So for example given two topology files with 100 residues, if the first topology file processed includes a ligand named MOL and the second one does not, the action:

```
distance :80 :MOL out D_80-to-MOL.dat
```

will be valid for the first topology but not for the second, so it will be skipped as long as the second topology is active.

2.7 Parallelization

Cpptraj has many levels of parallelization that can be enabled via the '-mpi', '-openmp', and/or '-cuda' configure flags for MPI, OpenMP, and CUDA parallelization respectively. At the highest level, trajectory and ensemble reads are parallelized with MPI. In addition, certain time consuming actions have been parallelized with OpenMP and/or CUDA.

Note that any combination of the '-openmp', '-cuda', and '-mpi' flags may be used to generate a hybrid MPI/OpenMP/CUDA binary; however this may require additional runtime setup (e.g. setting OMP_NUM_THREADS for OpenMP) to work properly and not oversubscribe cores.

2.7.1 MPI Trajectory Parallelization

Cpptraj has two levels of MPI parallelization for reading input trajectories. The first is for '***trajin***' trajectory input, where the trajectory read is divided as evenly as possible among all input frames (across-trajectory parallelism). For example, if given two trajectories of 1000 frames each and 4 MPI processes, process 0 reads frames 1-500 of trajectory 1, process 1 reads frames 501-1000 of trajectory 1, process 2 reads frames 1-500 of trajectory 2, and process 3 reads frames 501-1000 of trajectory 2. Most Actions will work with across-trajectory parallelization with the exception of the following: ***'clusterdihedral'***, ***'contacts'***, ***'createreservoir'***, ***'lipidorder'***, ***'pairwise'***, ***'stfcdiffusion'***, ***'tordiff'***, ***'unwrap'***, and ***'xtalsymm'***. The ***'diffusion'*** Action will only work with across-trajectory parallelism if no imaging is to be performed.

In addition to across-trajectory parallelism, the ***'gist'*** command will also MPI-parallelize the entropy calculation that occurs after trajectory processing.

The second is for ***'ensemble'*** trajectory input, where the reading/processing/writing of each member of the ensemble is divided up among MPI processes. The number of MPI processes must be a multiple of the ensemble size. If the number of processes is greater than the ensemble size then the processing of each ensemble member will be divided among MPI processes (i.e. across-trajectory parallelism will be used). For example, given an ensemble of 4 trajectories and 8 processes, processes 0 and 1 are assigned to the first ensemble trajectory, processes 2 and 3 are assigned to the second ensemble trajectory, and so on. When using ensemble mode in parallel it is recommended that the ***ensemblesize*** command be used prior to any ensemble command as this will make set up far more efficient.

Note that most Analyses are not MPI-parallelized, with the exception of the ***calcdiffusion*** Analysis (13.3 on page 244).

In order to use the MPI version, Amber/*cpptraj* should be configured with the '-mpi' flag. You can tell if *cpptraj* has been compiled with MPI as it will print 'MPI' in the title, and/or by calling 'cpptraj —defines' and looking for '-DMPI'.

2.7.2 OpenMP Parallelization

Some of the more time-consuming actions/analyses in *cpptraj* have been parallelized with OpenMP to take advantage of machines with multiple cores. In order to use OpenMP parallelization Amber/*cpptraj* should be configured with the '-openmp' flag. You can easily tell if *cpptraj* has been compiled with OpenMP as it will print 'OpenMP' in the title, and/or by calling 'cpptraj —defines' and looking for '-D_OPENMP'. The following actions/analyses have been OpenMP parallelized:

```
2drms/rms2d
atomiccorr
calcdiffusion
checkstructure
closest
```

```
cluster (pair-wise distance calculation and sieved frame restore only)
diffusion
dssp/secstruct
energy
gist (non-bonded calculation)
hbond
kde
lipidscd
mask (distance-based masks only)
matrix (coordinate covariance matrices only)
minimage
radial
replicatecell
rotdif
rmsavgcorr
spam
surf
surftension (3-D Gaussian filter only)
tordiff
unwrap
velocityautocorr
volmap
watershell
wavelet
```

By default OpenMP *cpptraj* will use all available cores. The number of OpenMP threads can be controlled by setting the OMP_NUM_THREADS environment variable.

2.7.3 CUDA Parallelization

Some time-consuming actions in cpptraj have been parallelized with CUDA to take advantage of machines with NVIDIA GPUs. In order to use CUDA parallelization Amber/cpptraj should be configured with the '-cuda' flag. You can easily tell if cpptraj has been compiled with CUDA as it will print 'CUDA' and details on the current graphics device in the title, and/or by calling 'cpptraj —defines' and looking for '-DCUDA'. The following actions have been CUDA parallelized:

```
closest
watershell
gist
radial
```

3 General Concepts

3.1 Units

Cpptraj uses the AKMA system of units. The execption is time, which is typically expressed in ps (except where noted).

Variable	Unit
Length	Angstrom
Energy	kcal/mol
Mass	AMU
Charge	electron
Time	ps (typically)
Force	kcal/mol*Angstrom

3.2 Atom Mask Selection Syntax

The mask syntax is similar to *ptraj*. Note that the characters ':', '@', and '*' are reserved for masks and should not be used in output file or data set names. All masks are case-sensitive. Either names or numbers can be used. Masks can contain ranges (denoted with '-') and comma separated lists. The logical operands '&' (and), '|' (or), and '!' (not) are also supported.

The syntax for elementary selections is the following:

@{atom numlist} e.g. '@12,17', '@54-85', '@12,54-85,90'

@{atom namelist} e.g. '@CA', '@CA,C,O,N,H'

@%{atom type name} e.g. '@%CT'

@/{atom_element_name} e.g. '@/N'

:{residue numlist} e.g. ':1-10', ':1,3,5', ':1-3,5,7-9'

:{residue namelist} e.g. ':LYS', ':ARG,ALA,GLY'

::{chain id} e.g. '::B', '::A,D'. Requires chain ID information be present in the topology.

:;{pdb residue number} e.g. ':;2-4,8'. Requires a PDB loaded as topology, or Amber topology with embedded PDB information (see **??** on page ??).

^{molecule numlist} e.g. '^1-10', ':23,84,111'

<**mask**><**distance operator**><**distance**> Selection by distance, see below.

Several wildcard characters are supported:

'*' Zero or more characters.

'=' Same as '*'

'?' One character.

The wildcards can also be used with numbers or other mask characters, e.g. ':?0' means ":10,20,30,40,50,60,70,80,90", ':*' means all residues and '@*' means all atoms. If the atom name (or type name) contains a wildcard character like an asterisk, it can be explictly selected by escaping (i.e. preceding) the wildcard character with a backslash '\'. So for example:

```
atoms @C?*
```

would select atoms named C5, C4*, C422, etc., but:

```
atoms @C?\*
```

would only select C4* out of the above 3 atoms.

Compound expressions of the following type are allowed:

```
:{residue numlist | namelist}@{atom namelist | numlist}
```

and are processed as:

```
:{residue numlist | namelist} & @{atom namelist | numlist}
```

e.g. ':1-10@CA' is equivalent to ":1-10 & @CA".

More examples:

:ALA,TRP All alanine and tryptophan residues.

:5,10@CA CA carbon in residues 5 and 10.

:*&!@H= All non-hydrogen atoms (equivalent to "!@H=").

@CA,C,O,N,H All backbone atoms.

!@CA,C,O,N,H All non-backbone atoms (=sidechains for proteins only).

:1-500@O&!(:WAT|:LYS,ARG) All backbone oxygens in residues 1-500 but not in water, lysine or arginine residues.

^1-2:ASP All residues named 'ASP' in the first two molecules.

::A,D@CA All atoms named 'CA' in chains A and D.

Distance-based Masks

<mask><distance operator><distance>

<mask> Atoms to consider.

<distance operator> Distance operator. `{<|>}{@|:|;|^}`

- **<** Distances less than <distance> will be selected.
- **>** Distances greater than or equal to <distance> will be selected.
- **@** Any atom.
- **:** Any atom within a residue.
- **;** Residue geometric center.
- **^** Any atom within a molecule.

<distance> The distance criteria in Angstroms.

There are two very important things to keep in mind when using distance based masks:

1. Distance-based masks that update each frame are currently only supported by the ***mask*** action.
2. Selection by distance for everything but the ***mask*** action requires defining a reference frame with ***reference***; distances are then calculated using the specified reference frame only. This reference frame can be changed using the ***activeref*** command.

The syntax for selection by distance is a **<mask>** expression followed by a **<distance operator>** followed by a **<distance>** (which is in Angstroms). The **<distance operator>** consists of 2 characters: '<' (within) or '>' (without) followed by either '^' (molecules), '**:**' (residues), ';' (residue centers), or '**@**' (atoms). For example, '<**:**3.0' means "residues within 3.0 Angstroms" etc. For ':' residue- and '^' molecule-based distance selection, if any atom in that residue/molecule meets the given distance criterion, the entire residue/molecule is selected. For ';' residue center, the geometric center of the residue must meet the given distance criterion in order to be selected.

In plain language, the entire distance mask can be read as "Select **<distance operator>** **<distance>** of **<mask>**". So for example, the mask expression:

```
:11-17<@2.4
```

Means "Select atoms within 2.4 Å distance of atoms selected by ':11-17' (residues numbered 11 through 17)".

To strip everything outside 3.0 Å (i.e. without 3.0 Å) from residue 4 using specified reference coordinates:

```
reference mol.rst7
trajin mol.rst7
strip !(:4<:3.0)
```

3.3 Ranges

For several commands some arguments are ranges (e.g. 'trajout onlyframes <range>', 'nastruct resrange <range>', 'rmsd perres range <range>'); **THESE ARE NOT ATOM MASKS**. They are simple number ranges using '-' to specify a range and ',' to separate different ranges. For example 1-2,4-6,9 specifies 1 to 2, 4 to 6, and 9, i.e. '1 2 4 5 6 9'.

3.4 Parameter/Reference Tagging

Parameter and reference files may be 'tagged' (i.e. given a nickname); these tags can then be used in place of the file name itself. A tag in *cpptraj* is recognized by being bounded by brackets ('[' and ']'). This can be particularly useful when reading in many parameter or reference files. For example, when reading in multiple reference structures:

```
trajin Test1.crd
reference 1LE1.NoWater.Xray.rst7 [xray]
reference Test1.crd lastframe [last]
reference Test2.crd 225 [open]
rms Xray ref [xray] :2-12@CA out rmsd.dat
rms Last ref [last] :2-12@CA out rmsd.dat
rms Open ref [open] :2-12@CA out rmsd.dat
```

This defines three reference structures and gives them tags [xray], [last], and [open]. These reference structures can then be referred to by their tags instead of their filenames by any action that uses reference structures (in this case the RMSD action).

Similarly, this can be useful when reading in multiple parameter files:

```
parm tz2.ff99sb.tip3p.truncoct.parm7 [tz2-water]
parm tz2.ff99sb.mbondi2.parm7 [tz2-nowater]
trajin tz2.run1.explicit.nc parm [tz2-water]
reference tz2.dry.rst7 parm [tz2-nowater] [tz2]
rms ref [tz2] !(:WAT) out rmsd.dat
```

This defines two parm files and gives them tags [tz2-water] and [tz2-nowater], then reads in a trajectory associated with one, and a reference structure associated with the other. Note that in the 'reference' command there are two tags; the first goes along with the 'parm' keyword and specifies what parameter file the reference should use, the second is the tag given to the reference itself (as in the previous example) and is referred to in the subsequent RMSD action.

4 Variables and Control Structures

As of version 18, CPPTRAJ has limited support for "script" variables and 'for' loops. Script variables are referred to by a dollar sign ('$') prefix and are

replaced when they are processed. These are stored in the master data set list like other data and are assigned the type "string variable". **Note that to use script variables in CPPTRAJ input that is inside another script (e.g. a BASH script), they must be escaped with the '\' character,** e.g.

```
#!/bin/bash
TOP=MyTop.parm7
cpptraj <<EOF
set topname=$TOP # TOP is a BASH script variable
parm \$topname   # topname is a CPPTRAJ script variable
EOF
```

Note that regular CPPTRAJ 1D Data Sets that contain a single value can be used as script variables (if the Data Set contains more than 1 value only the first value will be used).

Command	Description
for	Create a 'for' loop.
set	Set or update a script variable.
show	Show all current script variables and their values.

4.1 for

```
for { {atoms|residues|molecules|molfirstres|mollastres}
    <var> inmask <mask> [parm <name> | parmindex <#> | <#>] |
      <var> in <list> |
      <var> indata <data set name> |
      <var> oversets <list> |
      <var> datasetblocks <set> blocksize <#> [blockoffset <#>]
        [cumulative [firstblock <#>]] |
  <var>=<start>;[<var><end OP><end>;]<var><increment OP>[<value>] ... }
END KEYWORD: 'done'
  Available 'end OP'       : '<' '>' '<=' '>='
  Available 'increment OP' : '++', '--', '+=', '-='
```

atoms|residues|molecules|molfirstres|mollastres <var> inmask <mask>
Loop over atoms/residues/molecules/first residue in molecules/last residue in molecules selected by the given mask expression, set as script variable <var>.

parm <name> | parmindex <#> <#> Select topology that <mask> should be based on (default first topology).

<var> in <list> Loop over a comma-separated list of strings. File name wildcards can be used.

<var> in <data set name> Loop over elements of specified data set. Currently only 1D scalar sets and string sets can be specified.

<**var**> **oversets** <**list**> Loop over sets selected by comma-separated list of names. Data set wildcards can be used.

<**var**> **datasetblocks** <**set**> Loop over blocks in specified DataSet.

blocksize <#> Size of blocks to use.

[blockoffset <#>**]** Offset between blocks.

[cumulative] Instead of blocks of fixed size, use blocks of increasing size incremented by blocksize.

[firstblock <#>**]** When cumulative, the size of the first block (default is first data set element).

<**var**>=<**start**>;[<**var**><**end OP**><**end**>;]<**var**><**increment OP**>[<**value**>] Loop over integer script variable <var> starting from <start>, optionally ending at <end>, increment by <value>.

Data Sets Created (datasetblocks loops):

<**var**>**[block]:**<**start idx**> (Data set blocks only) Data set block of blocksize starting at <start idx>.

<**var**>**[cumul]:**<**end idx**> (Cumulative data set blocks only) Data set block starting at firstblock and ending at <end idx>.

Create a for loop using one or more mask expressions, integers, etc. Loops can be nested inside each other. Integer loops may be used without an end condition, but in that case at least one descriptor in the loop should have an end condition or refer to a mask. Loops are ended by the **done** keyword.

Note that non-integer variables (e.g. 'inmask' loops) are NOT incremented after the final loop iteration, i.e. these loop variables always retain their final value.

For example:

```
for atoms A0 inmask :1-3@CA i=1;i++
  distance d$i :TCS $A0 out $i.dat
done
```

This loops over all atoms in the mask expression ':1-3@CA' (all atoms named CA in residues 1 to 3) and creates a variable named 'i' that starts from 1 and is incremented by 1 each iteration. Inside the loop, the mask selection is referred to by **$A0** and the integer by **$i**. This is equivalent to doing 3 distance commands like so:

```
distance d1 :TCS :1@CA out 1.dat
distance d2 :TCS :2@CA out 2.dat
distance d3 :TCS :3@CA out 3.dat
```

To loop over files named trajA*.nc and trajB*.nc:

```
for TRAJ in trajA*.nc,trajB*.nc
  trajin $TRAJ 1 last 10
done
```

4.2 set

```
set { <variable> <OP> <value> |
      <variable> <OP> {atoms|residues|molecules|atomnums|
                  resnums|oresnums|molnums|
                      charge|mass} inmask <mask>
    [parm <name> | crdset <set> | parmindex <#> | <#>]
  <variable> <OP> trajinframes }
  Available <OP> : '=', '+='
```

<variable> <OP> <value> Set or append a script variable.

<variable> <OP> {atoms|residues|molecules|atomnums|resnums |oresnums|molnums} inmask <mask> Set/append a script variable to/by the total number of atoms/residues/molecules in, a range expression of selected atom #s/residue #s/original residue #s/molecule #s in, or the total charge/mass of atoms selected by the given mask expression.

parm <name> | parmindex <#> | <#> Topology to which mask should correspond (default first).

<variable> <OP> trajinframes Set/append a script variable to/by the total number of frames in trajectories currently loaded by *trajin* commands.

Set (<OP> = '=') or append (<OP> = '+=') a script variable. Script variables are character strings, and are referred to in CPPTRAJ input by using a dollar sign '$' prefix.

For example, the following input will load files my.parm7 and my.rst7:

```
set PREFIX = my
trajin $PREFIX.parm7
trajin $PREFIX.rst7
```

For example, the following input will print info for the last 10 atoms in a topology to 'last10.dat':

```
set Natom = atoms inmask *
last10 = $Natom - 10
show
atoms "@$last10 - $Natom" out last10.dat
```

The following input will put a range of residues selected by :LYS:

```
> set SELECTED1 = resnums inmask :1-183&:LYS
Using topology: FtuFabI.NAD.TCL.parm7
Variable 'SELECTED1' set to '7-8,18,26,44,49,71,79,128,135,151,163,183'
```

4.3 show

```
show [<var1> ...]
```

If no variable names specified, show all current script variables and their values. Otherwise, show the values of the specified script variables.

5 Data Sets and Data Files

In *cpptraj*, Actions and Analyses can generate one or more data sets which are available for further processing. For example, the ***distance*** command creates a data set containing distances vs time. The data set can be named by the user simply by specifying a non-keyword string as an additional argument. If no name is given, a default one will be generated based on the action name and data set number. For example:

```
distance d1-2 :1 :2 out d1-2.dat
```

will create a data set named "d1-2". If a name is not specified, e.g.:

```
distance :1 :2 out d1-2.dat
```

the data set will be named "Dis_00000".

Data files are created automatically by most commands, usually via the "**out**" keyword. Data files can also be explicitly created with the ***write***/***writedata*** and ***create*** commands. Data can also be read in from files via the ***readdata*** command. Cpptraj currently recognizes the formats listed in 1, although it cannot write in all formats. In addition, a data set must be valid for the data file format. For example, 3D data (such as a grid) can be written to an OpenDX format file but not a Grace format file.

The default file format is called 'Standard', which simply has data in columns, like *ptraj*, although multiple data sets can be directed to the same output file. The format of a file can be changed either by specifying a recognized keyword (either on the command line itself or later via a 'datafile' command) or by giving the file an extension corresponding to te format, so 'filename.agr' will output in Grace format, and 'filename.gnu' will output in Gnuplot contour, and so on. The xmgrace/gnuplot output is particularly nice for the secstruct sumout and rmsd perresout files. Additional options for data files can be found in 6 on page 27.

Any action using the "out" keyword will allow data sets from separate commands to be written into the same file. For example, the commands:

```
dihedral phi :1@C :2@N :2@CA :2@C out phipsi.dat
dihedral psi :2@N :2@CA :2@C :3@N out phipsi.dat
```

will assign the "phi" and "psi" data sets generated from each action to the standard data output file "phipsi.dat":

```
#Frame   phi   psi
```

Note that when reading the Amber Prep and Amber OFF Library formats, a COORDS data set will be created for each unit present in these files.

5.1 Data Set Selection Syntax

Many analysis commands can be used to analyze multiple data sets. The general format for selecting data sets is:

```
<name>[<aspect>]:<index>
```

The '*' character can be used as a wild-card for *entire* names (no partial matches).

- **<name>:** The data set name, usually specified in the action (e.g. in 'distance d0 @1 @2' the data set name is "d0").
- **<aspect>:** Optional; this is set for certain data sets internally in order to easily select subsets of data. **The brackets are required**. For example, when using 'hbond series', both solute-solute and solute-solvent hydrogen bond time series may be generated. To select all solute-solute hydrogen bonds one would use the aspect "[solutehb]"; to select solute-solvent hydrogen bonds the aspect "[solventhb]" would be used. Aspects are hard-coded and are listed in the commands that use them.
- **<index>:** Optional; for actions that generate many data sets (such as 'rmsd perres') an index is used. Depending on the action, the index may correspond to atom #s, residue #s, etc. A number range (comma and/or dash separated) may be used.

For example: to select all data sets with aspect "[shear]" named NA_00000:

```
NA_00000[shear]
```

To select all data sets with aspect "[stagger]" with any name, indices 1 and 3:

```
*[stagger]:1,3
```

In ensemble mode, data set selection has additional syntax:

```
<name>[<aspect>]:<index>%<member>
```

Where <member> is the ensemble member number starting from 0.

Format	Filename Extensions	Keyword	Valid Dimensions	Notes
Standard	.dat	dat	1D, 2D, 3D	
Grace	.agr, .xmgr	grace	1D	
Gnuplot	.gnu	gnu	1D, 2D	
Xplor	.xplor, .grid	xplor	3D	
OpenDX	.dx	opendx	3D	
Amber REM log	.log	remlog	-	Read Only
Amber MDOUT	.mdout	mdout	-	Energy information, Read Only
Amber Energy File	.ene	amberene	1D	Read Only
Amber Evecs	.evecs	evecs	Modes data set only	
Amber Constant pH output	.cpout	cpout	pH data only	
Amber GBNSR6 output	.gbnsr6	gbnsr6	-	Energy information, Read Only
Density Peaks	.peaks	peaks	3D density peaks (spam/volmap)	
Vector pseudo-traj	.vectraj	vectraj	Vector data set only.	Write Only
Gromacs XVG	.xvg	xvg	-	Read Only
CCP4	.ccp4	ccp4	3D	
Charmm REPD log	.exch	charmmrepd	-	Read Only
Charmm Output	.charmmout	charmmout	-	Energy information, Read Only
Pairwise Cache (binary)	.cmatrix	cmatrix	pairwise distances	Used for cluster analysis.
Pairwise Cache (NetCDF)	.nccmatrix	nccmatrix	pairwise distances	Used for cluster analysis.
NetCDF Data	.nc	netcdf	All data	Only state info saved for pH data.
Amber Prep File	.prepin	prepin	COORDS	Read Only
Amber OFF Library File	.off, .lib	off,lib	COORDS	Read Only
Amber Force Field	.parm	amberff	Parameters	Read Only
Amber Force Mod	.frcmod	frcmod	Parameters	Read Only
Amber leaprc File	.leaprc	leaprc	Parameters, COORDS	Read Only
Numpy array	.npy	numpy	COORDS	Read Only
Topology/Coordinates	Various	coords	COORDS	Read Only

Table 1: DataFile formats recognized by *cpptraj*. 'Valid Dimensions' shows what

5.2 Data Set Math

As of version 15, *cpptraj* can perform basic math operations, even on data sets (with some limitations). Currently recognized operations are:

Operation	Symbol
Minus	-
Plus	+
Divide	/
Multiply	*
Power	^
Negate	-
Assign	=

Several functions are also supported:

Function	Form
Square Root	sqrt()
Exponential	exp()
Natural Logarithm	ln()
Absolute Value	abs()
Sine	sin()
Cosine	cos()
Tangent	tan()
Summation	sum()
Average	avg()
Standard Deviation	stdev()
Minimum	min()
Maximum	max()

Numbers can be expressed in scientific notation using "E" notation, e.g. 1E-5 = 0.00001. The parser also recognizes PI as the number pi. Expressions can also be enclosed in parentheses. So for example, the following expression is valid:

```
> 1 - ln(sin(PI/4) * 2)^2
Result: 0.879887
```

Results of numerical calculations like the above can be assigned to a variable (essentially a data set of size 1) for use in subsequent calculations, e.g.

```
> R = 1 - ln(sin(PI/4) * 2)^2
Result stored in 'R'
> R + 1 Result: 1.879887
```

Data sets can be specified in expressions as well. Currently data sets in an expression must be of the same type and only 1D, 2D, and 3D data sets are supported. Functions are applied to each member of the data set. So for example, given two 1D data sets of the same size named D0 and D1, the following expression:

```
> D2 = sqrt( D0 ) + D1
```

would take the square root of each member of D0, add it to the corresponding member of D1, and assign the result to D2. The following table lists which operations are valid for data set types. If a type is not listed it is not supported:

Data Set Type	Supported Ops	Supported Funcs	Notes
1D (integer, double, float)	All	All	
1D (vector)	+, -, *, /, =	None	'*' is dot product
2D (matrices)	+, -, /, *, =	sum, avg, stdev, min, max	
3D (grids)	+, -, /, *, =	sum, avg, stdev, min, max	

6 Data File Options

Data file output can be handled multiple ways in cpptraj. Output data files can be created by Actions/Analyses/Commands, or can be explicitly created with ***writedata*** (9.32 on page 76) or ***create*** (9.4 on page 62) commands. Reading data from files is only done via the ***readdata*** command (9.22 on page 73).

In general, data files which have been declared with an **'out'** keyword will recognize data file write keywords on the same command line. For example, the **'time'** argument can be passed directly to the output from a ***distance*** command:

```
distance d0 :1 :2 out d0.agr time 0.001
```

The data file format can be changed from standard implicitly by using specific filename extensions or keywords. If the extension is not recognized or no keyword is give the default format is 'Standard'. Keywords and extensions for data file formats recognized by *cpptraj* are shown in 1. Note that the use of certain options may be restricted for certain data file formats. These options can also be passed to data files via the ***datafile*** command (9.6 on page 63).

```
[<format keyword>]
[{xlabel|ylabel|zlabel} <label>] [{xmin|ymin|zmin} <min>] [sort]
[{xstep|ystep|zstep} <step>] [time <dt>] [prec <width>[.<precision>]]
[xprec <width>[.<precision>]] [xfmt {double|scientific|general}]
[noensextension]
```

{xlabel | ylabel | zlabel} <**label**> Set the x-axis label for the specified datafile to <label>. For regular data files this is the header for the first column of data. If the data is at least 2-dimensional 'datafile ylabel <label>' will likewise set the y-axis label.

{xmin | ymin | zmin} <**min**> Set the starting X coordinate value to <min>. If the data is at least 2-dimensional 'datafile ymin <min>' will likewise set the starting Y coordinate value.

sort Sort data sets prior to write. Ordering is by name, aspect, then index (all descending).

{xstep | ystep | zstep} <**step**> Multiply each frame number by <step> (x coordinates). If the data is at least 2-dimensional 'datafile ystep <step>' will likewise multiply y coordinates by <step>.

time <**dt**> Equivalent to the *ptraj* argument 'time' that could be specified with many actions. Multiplies frame numbers (x-axis) by <dt>.

prec <**width**>**[.**<**precision**>**]** Change the output format width (and optionally precision) of all sets *subsequently* added to the data file (i.e. does not change the precision of any data sets currently in the file). For example,

```
prec 12.4
prec 10
```

xprec <**width**>**[.**<**precision**>**]** Change output ordinate width and precision.

xfmt {double|scientific|general} Change output ordinate format.

[noensextension] Omit ensemble extension in ensemble processing mode. NOTE: THIS OPTION HAS NOT BEEN FULLY TESTED IN PARALLEL.

6.1 Standard Data File Options

Write

```
[invert] [noxcol] [groupby <type>] [noheader] [square2d|nosquare2d]
[nosparse|sparse [cut <cutoff>]]
```

invert Normally, data is written out with X-values pertaining to frames (i.e. data over all trajectories is printed in columns). This command flips that behavior so that X-values pertain to data sets (i.e. data over all trajectories is printed in rows).

groupby <**type**> (1D) group data sets by <type>:

name Group by name.

aspect Group by aspect.

idx Group by index.

ens Group by ensemble number.

dim Group by dimension.

xcol Write indices for the specified datafile. This is usually the default behavior.

noxcol Prevent printing of indices (i.e. the #Frame column in most datafiles) for the specified datafile. Useful e.g. if one would like a 2D plot such as phi vs psi. For example, given the input:

```
dihedral phi :1@C :2@N :2@CA :2@C out phipsi.dat
dihedral psi :2@N :2@CA :2@C :3@N out phipsi.dat
datafile phipsi.dat noxcol
```

Cpptraj will write a 2 column datafile containing only phi and psi, no frame numbers will be written.

header Write header line at beginning of data file. This is usually the default behavior.

noheader Prevent printing of header line (e.g. '#Frame D1') at the beginning of data file.

square2d Write 2D data as a square matrix, e.g.:

```
<1,1> <2,1> <3,1>
<1,2> <2,2> <3,2>
```

nosquare2d Write 2D data in 3 columns as:

```
<X> <Y> <Value>
```

sparse Only write 3D grid voxels with value > cutoff (default 0).

cut <**cut**> Cutoff for 'sparse'; default 0.

nosparse Write all 3D voxels (default).

Read

```
[prec {flt|dbl}]
{[read1d [index <col>] [onlycols <range>] [floatcols <range>]
         [intcols <range>] [stringcols <range>]] |
 [read2d [{square2d|nosquare2d}]] |

 [read3d [dims <nx>,<ny>,<nz>] [origin <ox>,<oy>,<oz>] |
         [delta <dx>,<dy>,dz>] [prec {dbl|flt}] [bin {center|corner} ]
 [vector [magnitude]] |
 [mat3x3] |
 [namemap]
}
```

prec {flt|dbl} Read 2d/3d data as single (flt) or double (dbl, default) precision.

read1d Read data as 1D data sets (default).

index <col> Use column <col> (starting from 1) as index column (1D data only).

onlycols <range> Only read columns in range.

floatcols <range> Force specified columns to be read as single-precision floats.

intcols <range> Force specified columns to be read as integers.

stringcols <range> Force specified columns to be read as strings.

read2d Read data as 2D matrix.

square2d Read data as square matrix (default).

nosquare2d Read data as XYZ matrix (i.e. each line contains '<column> <row> <data>').

read3d Read data as 3D grid. If no dimension data in file must also speify 'dims'.

dims <dx>,<dy>,<dz> Grid dimensions.

origin <ox>,<oy>,<oz> Grid origins (default 0,0,0).

delta <dx>,<dy>,dz> Grid spacings (default 1,1,1).

prec {dbl|flt} Grid precision, double or float (default float).

bin {center|corner} Coords specify bin centers or corners (default corners).

vector Read data as vector. If indices are present they will be skipped. Assume first 3 columns after the index column are vector X, Y, and Z, and (if present) the next 3 columns contain vector origin X, Y, and Z.

magnitude If specified, assume vector file last column contains vector magnitudes; read these into a set with Aspect 'Mag'.

mat3x3 Read data as 3x3 matrix. If indices are present they will be skipped. Assume matrices are in row major order on each line, i.e. M(1,1) M(1,2) ... M(3,2) M(3,3).

namemap Read data as atom name map ('#TgtAt Tgt RefAt Ref' or '#Tgt Ref')

By default, standard data files are assumed to contain 1D data in columns. Data set legends will be read in if the file has a header line (denoted by '#'). Columns labeled '#Frame' are automatically considered the 'index' column and skipped. Data sets are stored as <name>:<idx> where <name> is the given data set name (the file name if not specified) and <idx> corresponds to the column the data was read from starting from 1. *Cpptraj* assumes the data increases monotonically and will automatically attempt to determine the dimensions of the data set(s); a warning will be printed if this is not successful.

If a file contains the header:

```
#F1 F2 <name>
```

CPPTRAJ will assume the file contains pairwise distances for clustering, where the F1 and F2 columns contain the frame numbers, and the <name> column contains the distance.

6.2 Grace Data File Options

For more information on Grace see http://plasma-gate.weizmann.ac.il/Grace/.

Write

`[{invert|noinvert}] [{xydy|noxydy}] [<label set>]`

invert `Normally, data is written out with X-values pertaining to frames (i.e. data over all trajectories is printed in columns). This command flips that behavior so that X-values pertain to data sets.`

noinvert `Do not flip X-Y axes (default).`

xydy `Combine consecutive pairs of sets into XYDY sets.`

noxydy `Do not combine consecutuve pairs of sets into XYDY sets (default).`

<label set> `If a string dataset is specified, assume it has data point labels.`

If a single string data set is specified when writing Grace format, it is assumed they are data point labels.

Read

Cpptraj will read set legends from grace files, and data sets are stored as <name>:<idx> where <name> is the given data set name (the file name if not specified) and <idx> corresponds to the set number the data was read from starting from 0.

6.3 Gnuplot Data File Options

For more information on these options it helps to look at the PM3D options in the Gnuplot manual (see http://www.gnuplot.info/).

Write

`[{nolabels|labels}] [{usemap|pm3d|nopm3d}] [title <title>] [jpeg] [noheader] [{xlabels|ylabels|zlabels} <labellist>]`

nolabels Do not print axis labels.

labels Print axis labels.

usemap pm3d output with 1 extra empty row/col (may improve look).

pm3d Normal pm3d map output.

nopm3d Turn off pm3d

jpeg Plot will write to a JPEG file when used with gnuplot.

title <**title**> Set plot title (default is file name).

binary Plot will be written in binary format.

header Format the plot so it can be directly processed by gnuplot. This is usually the default behavior.

noheader Do not format plot; data output only.

palette <**arg**> Change gnuplot pm3d palette to <arg>:

'rgb' Red, yellow, green, cyan, blue, magenta, red.

'kbvyw' Black, blue, violet, yellow, white.

'bgyr' Blue, green, yellow, red.

'gray' Grayscale.

xlabels|ylabels|zlabels <**labellist**> Set x, y, or z axis labels with comma-separated list, e.g. 'xlabels X1,X2,X3'.

6.4 Amber REM Log Options

Note that multiple REM logs can be specified in a single ***readdata*** command. See 13.30 on page 286 for more on replica log analysis.

Read

`[nosearch] [dimfile <file>] [crdidx <crd indices>]`

[nosearch] If specified do not automatically search for MREMD dimension logs.

[dimfile <file>] remd.dim file for processing MREMD logs.

[crdidx <crd indices>] Use comma-separated list of indices as the initial coordinate indices (H-REMD only). For example (4 replicas):

```
crdidx 4,2,3,1
```

6.5 Amber MDOUT Options

Note that multiple MDOUT files can be specified in a single ***readdata*** command.

6.6 Evecs File Options

Read

[ibeg <firstmode>] [iend <lastmode>]

ibeg <firstmode> Number of the first mode (or principal component) to read from evecs file. Default 1.

iend <lastmode> Number of the last mode (or principal component) to read from evecs file. Default is to read all for newer evecs files (generated by *cpptraj* version > 12), 50 for older evecs files.

6.7 Vector psuedo-traj Options

This can be used to write out a representation of a vector data set which can then be visualized. See 12.92 on page 232 for more on generating vector data sets.

Write

[trajfmt <format>] [parmout <file>] [noorigin]

trajfmt <format> Output pseudo-trajectory format. See 11 on page 98 for trajectory format keywords.

parmout <file> File to write pseudo-trajectory topology to.

[noorigin] Do not write vector origin coordinates.

6.8 OpenDX file options

Read

[type {float|double}]

type {float|double} Precision to read in 3D grid (default float).

Write

`[bincenter] [gridwrap] [gridext]`

bincenter `Center grid points on bin centers instead of corners.`

gridwrap `Like 'bincenter', but also wrap grid density. Useful when grid encompasses unit cell.`

gridext `Like 'bincenter', but also print extra layer of empty bins.`

6.9 CCP4 file options

Write

`[title <title>]`

[title <title>] `Set CCP4 output title.`

6.10 Charmm REPD log options

Read

`[nrep <#>] [crdidx <crd indices>]`

nrep <# > `Total number of replicas.`

crdidx <**crd indices**> `Comma-separated list of indices to use as initial coordinate indices.`

6.11 Amber Constant pH Out options

Read

`cpin <file>`

cpin <**file**> `Constant pH input (CPIN) file name.`

Note that when reading in constant pH data the data set aspect will be set to the residue name and the index will be set to the residue number. When reading in constant pH REMD data the data is unsorted, and sortensembledata should be used to create sorted constant pH data sets (see 9.30 on page 76).

6.12 Amber prep file options

Read

`[keepdummyatoms]`

keepdummyatoms `Keep dummy atoms instead of removing them.`

6.13 Amber Library (OFF) file options

Read

`[allowoverwrite]`

allowoverwrite `If specified, allow existing sets to be overwritten.`

6.14 Amber Parameter (main force field) file options

Read

`[nbset <nonbond set name>]`

nbset <nonbond set name> `Nonbonded set name to use when multiple nonbond parameters sets are present.`

6.15 Amber leaprc file options

For a list of supported LEaP commands in leaprc files, see 7.3 on page 43.

6.16 Coords file options

The ***readdata*** command can be used to read in a file format that contains Topology **and** Coordinate info (e.g. PDB, Mol2, CIF, etc.). For a list of topology formats recognized by CPPTRAJ see 10 on page 77, and for a list of coordinate formats recognized by CPPTRAJ see 11 on page 98. For example, to read in a PDB file as COORDS set named 'MyCrd':

```
readdata Mypdb.pdb as coords name MyCrd
```

7 System Build and Parameterization Commands

As of version 7.0, CPPTRAJ has the ability to create full coordinates and Amber Topology files for MD simulations.

The following build and parameterization commands are available:

Command	Description
build	Fully build and parameterize a COORDS set or input file using template libraries and force field parameter sets.
sequence	Create and parameterize a COORDS set using specified residues from template libraries and force field parameter sets.
source	Limited version of the LEaP 'source' command, intended to load Amber force field "leaprc" files.

7.1 build

```
build [name <output COORDS>] {crdset <COORDS set>|<file>} [{frame <#>|doassembly}]
[nowat [watermask <watermask>] [noh]
[keepaltloc {<alt loc ID>|highestocc}]
[stripmask <stripmask>]
[title <title>] [verbose <#>] [keepmissingatoms] [nofixorder]
[parmout <topology file>] [crdout <coord file>] [simplecheck]
    [reportfile <check file>] [flexiblewater]
[gb {bondi|amber6|mbondi|pbamber|mbondi2|parse|mbondi3}]
LJ 12-6-4 options:
[lj1264 [lj1264mask <mask>] [tunfactor <fac>] [c4file <c4file>] [polfile <polfile>]
    [lj1264solvent <solvent>]]
Atom Scan direction:
[atomscandir {f|b}]
Residue Templates and Parameters to use:
[{lib <template setname>} ...]
[{parmset <parameter setname>} ...]
Solvation/box:
[{{solvatebox|solvateoct} {buffer <buffer> | bufx <bufx> bufy <bufy> bufz <bufz> |
                                nsolvent <#>}
          solventbox <unit> [closeness <closeness>] [{iso|aniso}] [nocenter] [solvchain
```

```
  setbox [{buffer <buffer> | bufx <bufx> bufy <bufy> bufz <bufz>}]}]
Adding ions:
[addionsrand ion1 <name1> nion1 <num1> [ion2 <name2> nion2 <num2>]
  [minsep <dist>] [ionseed <seed>] [ionchain <id>]]
preparefor leap options:
[{nohisdetect |
  [nd1 <nd1>] [ne2 <ne2] [hisname <his>] [hiename <hie>]
  [hidname <hid>] [hipname <hip]} [defaulthis <default>]]
[{nodisulfides |
  existingdisulfides |
  [cysmask <cysmask>] [disulfidecut <cut>] [newcysname <name>]}]
[{nosugars |
  sugarmask <sugarmask> [noc1search] [nosplitres]
  [rescut <residue cutoff>] [bondoffset <offset>]
  [resmapfile <file>]
  [hasglycam] [determinesugarsby {geom|name}]
 }]
```

[name <OUTPUT COORDS>] Optional name of the output COORDS set to create. If not specified the input structure will be altered.

{crdset <COORDS set>|<file>} REQUIRED. Name of the input COORDS set to build, or name of the input file to build directly. The input <file> if specified must be a format that contains some topology information (like atom names and residue numbers).

[{frame <#>|doassembly}] If the input structure contains multiple frames/models, specify the one to use with frame, or if the frames/models are part of an assembly doassembly will put them all into a single output structure.

[nowat] Remove any input residues identified as solvent (by watermask).

[watermask <watermask>] Mask for identifying input residues as solvent; default ":HOH".

[noh] Remove any input atoms identified as hydrogen.

[keepaltloc {<alt loc ID>|highestocc}] When input atoms have alternate location specifiers, specify how to choose. If highestocc is specified and input coordinates includes occupancy, choose the atom with the highest occupancy. Otherwise use the specified alternate location identifier.

[stripmask <stripmask>] If specified, remove input atoms selected by <stripmask>.

[title <title>] Optional title to give the output topology.

[verbose <#>] Parameter assignment verbosity; higher values will provide more output.

[keepmissingatoms] By default, input atoms not found in residue templates will be removed. If this option is specified those atoms will be kept (like LEaP).

[nofixorder] By default, CPPTRAJ will rearrange atoms so that atoms in the same molecule are contiguous. If this option is specified no rearrangement will occur.

[parmout <topology file>] Name of the output topology file.

[crdout <coord file>] Name of the output coordinates file. Format can be chosen based on filename extension.

[simplecheck] (Not recommended) Do not check for overlaps or ring intersections; only check for abnormal bond lengths.

[reportfile <check file>] File to write details on problems with the final structure; if not specified write to STDOUT.

[flexiblewater] Option to turn on flexible water, i.e. water models with angle terms. Note that the loaded force field must have water angle (H-O-O) parameters.

[gb {bondi|amber6|mbondi|pbamber|mbondi2|parse|mbondi3}] Select with GB radii set to use. Default is mbondi.

bondi Bondi radii.

amber6 Amber6 modified Bondi radii.

mbondi Modified Bondi radii (default).

pbamber Huo and Kollman optimized radii.

mbondi2 H(N)-modified Bondi radii.

parse PARSE radii.

mbondi3 ArgH and AspGluO modified Bondi2 radii.

LJ 12-6-4 options:

[lj1264] Option to activate LJ 12-6-4 parameters.

[lj1264mask <mask>] Mask of atoms to assign LJ 12-6-4 parameters to (default ":ZN").

[tunfactor <fac>] Scaling factor to adjust interaction between two different ions (default 1.0).

[c4file <c4file>] File containing C4 parameters for each element. If not specified, use default parameters for whatever solvent model is in use.

[polfile <polfile>] File containing polarizabilities for each atom type. Default is '$AMBERHOME/dat/leap/parm/lj_1264_pol.dat'.

[lj1264solvent <solvent>]] Name of water box unit containing water model to set up for. If not specified, 'build' will try to guess based on the specified solvent box.

TIP3PBOX TIP3P water model.

TIP4PEWBOX TIP4P Ewald water model.

SPCBOX SPC Ewald water model.

OPC3BOX OPC 3 point water model.

OPCBOX OPC 4 point water model.

FB3BOX FB3 water model.

FB4BOX FB4 water model.

Atom Scan direction:

[atomscandir {f|b}] Mostly intended for debugging when compared to LEaP. LEaP generates bond/angle/dihedral lists within residues differently depending on where the residue was read from. For PDBs the scanning goes from back to front ('b'), while for Mol2s the scanning is from front to back ('f'). In CPPTRAJ the default scan direction is back to front since the assumption is that most systems built with LEaP have been read in from PDB files.

Residue templates and Parameters to use:

[{lib <template setname>} ...] Name of residue template set(s) to use. If not specified use all loaded templates. Can be specified multiple times.

[{parmset <parameter setname>} ...] Name of parameters set(s) to use. If not specified use all loaded parameters. Can be specified multiple times.

Solvation/box:

solvatebox|solvateoct Solvate the system in either an orthorhombic or truncated octahedral box.

buffer <buffer> | bufx <bufx> bufy <bufy> bufz <bufz> Buffer distance (in Angstroms) between solute and the edge of the box. Can either specify one uniform value or separate X Y and Z values. The separate X Y and Z values will not work for truncated octahedrons.

nsolvent <#> EXPERIMENTAL. Instead of a buffer, specify a target number of waters to solvate the system with.

solventbox <**unit**> Name of the solvent box to use (e.g. OPCBOX, TIP4PEWBOX, SPCBOX etc).

[closeness <**closeness**>**]** Specify how close solute and solvent are allowed to get (in Angstroms). Default is 1.0.

[{iso|aniso}] Specify if solute should be treated as isotropic (centered and aligned along principal axes) before solvating or not. Note that solvatebox is default aniso, while solvateoct is default iso.

[nocenter] If specified, do not center system in the center of the solvent box after solvating.

[solvchain <**id**>**]** If the original system has chain IDs, added waters will receive a chain ID of 'z'. Specify solvchain to change this chain ID.

setbox [{buffer <**buffer**> | **bufx** <**bufx**> **bufy** <**bufy**> **bufz** <**bufz**>**}]** If this is specified, do not solvate, just create an orthorhombic box with the given buffer.

Adding ions:

addionsrand Add specified number of ions to the system.

ion1 <**name1**> **nion1** <**num1**> Residue name of the first ion to use along with the number of ions to add. If a number of 0 is specified a number of ions required to neutralize the system will be added (if the system charge and ion charges are opposite).

[ion2 <**name2**> **nion2** <**num2**>**]** Optional residue name of second ion to use along with number of ions to add. If a number of 0 is specified a number of ions required to neutralize the system will be added, factoring in ions added by ion1 (and again if the system charge and ion charges are opposite).

[minsep <**dist**>**]** Minimum separation between any two ions in Angstroms.

[ionseed <**seed**>**]** Random number generator seed to use (default is system time).

[ionchain <**id**>**]** If the original system has chain IDs, added ions will receive a chain ID of 'z'. Specify ionchain to change this chain ID.

prepareforleap options: See 8.13 on page 54

Build the full coordinates and topology of a system for MD simulations using residue templates and force field parameters, including CMAP and LJ 12-6-4 parameters. Also includes the ability to add explicit solvent and ions, including the ability to solvate with a target number of water molecules. This command effectively includes '***prepareforleap***', '***checkstructure***', and '***fixatomorder***' functionality. If the **'doassembly'** keyword is specified it can create macromolecular assemblies from PDBs with multiple models. The build procedure is similar to that of LEaP, but CPPTRAJ's build tends to be faster and more robust, particularly for large systems and/or system containing CMAP terms.

Note that since LEaP uses an imprecise value of PI compared to CPPTRAJ/sander/pmemd, the topologies produced by CPPTRAJ will have slight differences in any terms involving PI (e.g. angles, dihedrals, etc). For 1:1 direct comparison to LEaP topologies, CPPTRAJ can be compiled using LEaP's value of PI by configuring with the '-leappi' configure flag, which activates the CPPTRAJ_USE_LEAP_PI compiler define; **this should only be used to compare directly to LEaP**. Note also that CPPTRAJ retains PDB information (chain ID, original residue number, Bfactor/Occupancy etc) which is printed to the output Topology. The parameter files used are also printed to the output Topology in the FORCE_FIELD_TYPE section.

The output from the ***build*** command tends to be more verbose than LEaP and is grouped into several phases:

1. Input coordinates details and general parameters. This is where the input coordinates will be cleaned up if needed (similar to ***prepareforleap***, see 8.13 on page 54).

2. Getting templates and parameters. If no templates/parameters were specified, all available templates and parameters will be used. If multiple parameter sets are available they will be combined, with later parameter sets having priority over earlier parameter sets.

3. Structure preparation. This is where histidine protonation states will be determined (if hydrogens are present), disulfide bonds will be searched for, and sugars will be prepared (see 8.13 on page 54).

4. Match residues to templates and build missing atoms. Note that unlike LEaP, if an atom name is not recognized within a residue that has a template, that atom will be ignored and built back in using the template unless **keepmissingatoms** is specified. After all atoms are built and linked, CPPTRAJ will ensure that atoms within molecules are contiguous (like ***fixatomorder***, see 12.36 on page 151) unless **nofixorder** is specified.

5. Solvate/add ions. If **solvatebox**/**solvateoct** and optionally **addionsrand** is specified, solvent/ions will be added to the system. Note that the neutralization argument (i.e. number of ions equal to zero) can be specified for either ion1, ion2, or both. Note that currently CPPTRAJ does

not support adding ions if no solvent has been added. Either a **buffer** size (in Angstroms) must be given, or a target number of waters given with **nsolvent**.

6. Parameter assignment. Here parameters will be assigned based on the atom types in templates. The gb keyword can be used to pick the GB radii set used. The lj1264 keyword and associated keywords can be used to add Lennard-Jones C coefficients if the loaded force field supports them.

7. Structure check. Here the final structure will be checked for long bonds, overlaps, and ring intersections (like the ***checkstructure*** Action, see 12.15 on page 128). CPPTRAJ will also check if there were missing residues and for problems with the overall system charge. Problems can be redirected to another file with the **reportfile** keyword, otherwise they will be printed to the standard output.

8. File output. If parmout/crdout were specified, prints details on the file writes.

9. Timing data. Will print detailed timing data for each phase.

Example - Solvate and add ions, system charge not known a priori

This example loads a PDB as a COORDS data set, then builds it and generates a topology and restart file. Solvent is added with a 10 Angstrom buffer, and enough Na+ or Cl- ions are added to neutralize the system depending on what the solute charge is.

```
source leaprc.protein.ff19SB
source leaprc.water.opc
readdata 6g37.pdb as coords name MyMol
build crdset MyMol name Out title 6g37 \
  parmout cpptraj.parm7 crdout cpptraj.rst7 \
  solvateoct solventbox TIP3PBOX buffer 10.0 \
  addionsrand ion1 Na+ nion1 0 ion2 Cl- nion2 0
```

7.2 sequence

```
sequence name <output set name> <unit0> <unit1> ... [verbose <#>]
[gb {bondi|amber6|mbondi|pbamber|mbondi2|parse|mbondi3}]
[atomscandir {f|b}]
[{lib <template setname>} ...]
[{parmset <parameter setname>} ...]
```

name <output set name> Name of output COORDS set.

<unit0> <unit1> ... Names of the residues/units to connect together in sequence.

[verbose <#>] Parameter assignment verbosity; higher values will provide more output.

[gb {bondi|amber6|mbondi|pbamber|mbondi2|parse|mbondi3}] Select with GB radii set to use. Default is mbondi. See 7.1 on page 36 for specific details on the GB radii set keywords.

[atomscandir {f|b}] Mostly intended for debugging when compared to LEaP. See 7.1 on page 36 for specific details on the atom scan direction.

[{lib <template setname>} ...] Name of residue template set(s) to use. If not specified use all loaded templates. Can be specified multiple times.

[{parmset <parameter setname>} ...] Name of parameters set(s) to use. If not specified use all loaded parameters. Can be specified multiple times.

Create a single molecule from a sequence of units. If parameter sets are loaded, parameters will be assigned to <output set name>. Internal coordinates are used to try to determine the correct geometry around connection sites. The COORDS sets must have connection information set, either from reading in an Amber OFF library file or set manually via ***dataset* connect** (see 9.8 on page 64).

For example, the following reads in two Mol2 files as COORDS sets, sets up connection atoms, then creates a molecule via ***sequence:***

```
parm MOC.mol2
loadcrd MOC.mol2 parm MOC.mol2 name MOC
dataset connect MOC tailmask @O5
parm CNALA.mol2
loadcrd CNALA.mol2 parm CNALA.mol2 name CNALA
dataset connect CNALA headmask @N
sequence MOC CNALA name Mol
crdout Mol Mol.mol2
```

7.3 source

```
source <filename>
```

Process <filename> as a leaprc file, mostly intended for loading force field parameters from Amber leaprc files. If AMBERHOME is set CPPTRAJ will look for leaprc files in $AMBERHOME/dat/leap/cmd, otherwise the full path must be specified.

Supported leap commands: addatomtypes, addpath, addpdbatommap, addpdbresmap, loadamberparams, loadamberprep, loadmol2, loadoff, loadpdb, quit, saveamberparm, set, source.

8 Coordinates (COORDS) Data Set Commands

Coordinate I/O tends to be the most time-consuming part of trajectory analysis. In addition, many types of analyses (for example two-dimensional RMSD and cluster analysis) require using coordinate frames multiple times. To simplify this, trajectory coordinates may be saved as a separate data set via the ***loadcrd*** command or ***createcrd*** action. Any action can then be performed on the COORDS data set with the ***crdaction*** command. The ***crdout*** command can be used to write coordinates to an output trajectory (similar to ***trajout***).

Although COORDS data sets store everything internally with single-precision, they can still use a large amount of memory. Because of this there is a specialized type of COORDS data set called a TRAJ data set (trajectory), which functions exactly like a COORDS data set except all data is stored on disk. TRAJ data sets can be created with the ***loadtraj*** command. *TRAJ data sets cannot be modified.*

There are several analyses that can be performed using COORDS data sets, either as part of the normal analysis list or via the ***runanalysis*** command. Note that while these analyses can be run on specified COORDS data sets, if one is not specified a default COORDS data set will be created, made up of frames from ***trajin*** commands.

As an example of where this might be useful is in the calculation of atomic positional fluctuations. Previously this required two steps: one to generate an average structure, then a second to rms-fit to that average structure prior to calculating the fluctuations. This can now be done in one pass with the following input:

```
parm topology.parm7
loadcrd mdcrd.nc
# Generate average structure PDB, @CA only
crdaction mdcrd.nc average avg.pdb @CA
# Load average structure PDB as reference
parm avg.pdb
reference avg.pdb parm avg.pdb
# RMS-fit to average structure PDB
crdaction mdcrd.nc rms reference @CA
# Calculate atomic fluctuations for @CA only
crdaction mdcrd.nc atomicfluct out fluct.dat bfactor @CA
```

The following COORDS data set commands are available:

Command	Description
catcrd	Concatenate two or more COORDS sets.
combinecrd	Combine two or more COORDS sets.
crdaction	Run a single Action on a COORDS set.
crdout	Write a COORDS set to a file.
crdtransform	Transform a COORDS set in one of several ways.
createcrd	(Action) Create a COORDS set during a Run.
emin	Run simple energy minimization on a frame of a COORDS set.
extendedcomp	Calculate extended comparison similarity values for each frame in COORDS set.
graft	Graft part of one COORDS set onto another COORDS set.
loadcrd	Create or append to a COORDS set from a file.
loadtraj	Create special COORDS set where frames remain on disk.
permutedihedrals	Rotate specified dihedral(s) in given COORDS set by specific interval or to random values.
prepareforleap	Prepare a structure (usually loaded from a PDB) for processing with LEaP from Amber.
reference	Load a single trajectory frame as a reference.
rotatedihedral	Rotate specified dihedral to specified value or by given increment.
splitcoords	Split molecules in a COORDS set into a trajectory.
zmatrix	Apply Z-matrix to a COORDS set or calculate Z-matrix for a molecule/frame in a COORDS set.

8.1 catcrd

`catcrd <crd1> <crd2> ... name <name>`

<crdX> `COORDS data sets to concatentate, specify 2 or more.`

name <name> `New COORDS set name`

Concatentate two or more COORDS data sets into a single COORDS data set. The topologies must have the same number of atoms for this to work. If the topologies differ in other ways, the topology of the first COORDS set takes priority.

8.2 combinecrd

`combinecrd <crd1> <crd2> ... [parmname <topname>] [crdname <crdname>] [nobox] [verbose <#>]`

<crdX> `COORDS data sets to combine, specify 2 or more.`

[parmname <topname>] `Name of combined Topology.`

[crdname <crdname>] `Name of combined COORDS data set.`

[nobox] `Remove any unit cell information from combined coordinates.`

[verbose <#>] `Verbosity during parameter assignment.`

Combined two or more COORDS data sets into a single COORDS data set. Note that the resulting topology will most likely **not** be usable for MD simulations. Box information will be retained - the largest box dimensions will be used.

For example, to load two MOL2 files as COORDS data sets, combine them, and write them out as a single MOL2:

```
loadcrd Tyr.mol2 CRD1
loadcrd Pry.mol2 CRD2
combinedcrd CRD1 CRD2 parmname Parm-1-2 crdname CRD-1-2
crdout CRD-1-2 Tyr.Pry.mol2
```

8.3 crdaction

```
crdaction <crd set> <actioncmd> [<action args>] [crdframes <start>,<stop>,<offset>]
```

Perform action <actioncmd> on COORDS data set <crd set>. A subset of frames in the COORDS data set can be specified with 'crdframes'.

For example, to calculate RMSD for a previously created COORDS data set named crd1 using frames 1 to the last, skipping every 10:

```
crdaction crd1 rmsd first @CA out rmsd-ca.agr crdframes 1,last,10
```

8.4 crdout

```
crdout <crd set> <filename> [<trajout args>] [crdframes <start>,<stop>,<offset>]
```

Write COORDS data set <crd set> to trajectory named <filename>. A subset of frames in the COORDS data set can be specified with 'crdframes'.

For example, to write frames 1 to 10 from a previously created COORDS data set named "crd1" to separate PDB files:

```
crdout crd1 crd1.pdb multi crdframes 1,10
```

8.5 crdtransform

```
crdtransform <input crd set> [name <output crd set>]
             { rmsrefine [mask <mask>] [mass] [rmstol <tolerance>] |
               normcoords |
```

```
                trim [metric <metric>] [{ntrimmed <#>|cutoff <val>}]
                     [criterion {comp|medoid}]]
            }
```

<input crd set> COORDS set to transform.

[name <output crd set>] COORDS set to create; if not specified <input crd set> will be modified.

rmsrefine Do iterative RMS refinement.

[mask <mask>] Mask of atoms to fit during refinement.

[mass] Mass-weight the refinement.

[rmstol <tolerance>] Tolerance (in Ang.) below which RMS-refinement will stop.

normcoords Normalize coordinates between 0.0 and 1.0 using the minimum and maximum coordinate values.

trim Remove trajectory frames using extended similarity metrics.

[metric <metric>] Metric to use; default MSD.

[{ntrimmed <#>|cutoff <val>} # of frames or fraction of trajectory to trim.

[criterion {comp|medoid}] Trim frames by comparitive similarity (i.e. trim most dissimilar frames) or comparison to medoid (i.e. trim most dissimilar to medoid frame).

Transform a COORDS set in one of several ways. Does not yet work with TRAJ data sets. The iterative RMS refinement is similar to the procedure outlined by Klem et al. (J. Chem. Theory Comput. 2022, 18, 3218−3230). The extended similarity metrics are those defined by Racz et al. (J. Comp.-Aid. Mol. Design, 2022, 36, 157-173).

8.6 createcrd

This command is actually an Action that can be used to create COORDS data sets during trajectory processing, see 12.21 on page 134.

8.7 emin

```
emin crdset <name> [trajoutname <name>] [rmstol <tol>] [nsteps <#>]
  [<mask>] [frame <#>] [dx0 <step0>] [out <file>] [name <setname>]
  [{nonbond|openmm}] [<potential options>]
```

crdset <name> COORDS set to use.

[trajoutname <name>] Optional output trajectory for minimization steps.

[rmstol <tol>] Minimum RMS tolerance (default 1E-4).

[nsteps <#>] Number of minimization steps (default 1).

[<mask>] Atoms to minimize (default all).

[frame <#>] Frame from COORDS set to minimize (default 1).

[dx0 <step0>] Size of initial minimization step (default 0.01).

[out <file>] File to write energies to.

[name <setname>] If specified, create an energy per step data set.

[nonbond] If specified, use simple nonbonded potential term in additon to bonded terms.

[openmm] If specified and if CPPTRAJ was compiled with OpenMM support, use OpenMM to calculate the forces.

<potential options>

cut <cutoff> Set nonbonded interaction cutoff in Ang. (electrostatics and vdW). Default 8.0.

cutee <cutoff> Set electrostatics interaction cutoff in Ang.

cutnb <cutoff> Set vdW interaction cutoff in Ang.

scaleee <factor> Scaling factor to multiply 1-4 electrostatics interactions by.

scalenb <factor> Scaling factor to multiply 1-4 vdW interactions by.

shake <type> Use SHAKE constraints of <type>:

'hydrogen' Constrain bonds to hydrogen.

'all' Constrain all bonds.

nexclude <#> Number of bonded atoms within which nonbonded interactions are excluded. Default 4.

qfac <factor> Factor to use in electrostatic calculation.

DataSets Created

<setname>[Energy] Total energy at each minimization step.

THIS COMMAND IS STILL IN DEVELOPMENT AS OF VERSION 5.0.2.

Perform steepest descent minimization on a frame in a COORDS set using a very basic force field (bonds, angles, dihedrals). A simple nonbonded term can be added as well if desired.

8.8 extendedcomp

```
extendedcomp <input crd set> [name <output data set>]
             [metric <metric>] [out <file>]
  <metric> = msd bub fai gle ja jt rt rr sm ss1 ss2
```

<input crd set> Input COORDS set.

[name <output data set>] Output data set name containing values.

[metric <metric>] Metric to use.

[out ,file>] File to write values to.

DataSets generated:

<output set name> Set containing similarity values for each COORDS frame.

Calculate extended comparison similarity values for each frame in a COORDS set. The extended similarity metrics are those defined by Racz et al. (J. Comp.-Aid. Mol. Design, 2022, 36, 157-173). The metrics are as follows:

Keyword	Metric
msd	Mean-squared deviation.
bub	Bhattacharyya's U coefficient
fai	Faiman's coefficient
gle	Gleason's coefficient
ja	Jaccard's coefficient
jt	Jaccard-Tanimoto coefficient
rt	Rogers-Tanimoto coefficient
rr	Russell-Rao coefficient
sm	Simpson's coefficient
ss1	Sokal-Sneath 1 coefficient
ss2	Sokal-Sneath 2 coefficient

8.9 graft

```
graft src <source COORDS> [srcframe <#>] [srcmask <srcmask> [srccharge <srccharge>]]
   tgt <target COORDS> [tgtframe <#>] [tgtmask <tgtmask> [tgtcharge <tgtcharge>]]
      {ic | [srcfitmask <srcmask>] [tgtfitmask <tgtmask>]} [verbose <#>]
   name <output COORDS> [bond <tgt>,<src> ...]
```

src <source COORDS> Source coordinates.

[srcframe <#>] Frame # from source coordinates to use (default 1).

[srcmask <mask>] Atoms to keep from source (default all).

[srccharge <charge>] If trimming atoms from source, ensure sum of charges on remaining atoms equals <charge> via scaling.

tgt <target COORDS> Target coordinates that will be grafted onto.

[tgtframe <#> Frame # from target coordinates to use (default 1).

[tgtmask <mask>] Atoms to keep from target (default all).

[tgtcharge <charge>] If trimming atoms from target, ensure sum of charges on remaining atoms equals <charge> via scaling.

[ic] Connect source and target using internal coordinates. If source and target contain CONNECT information (see 9.8 on page 64), that will be used to create a bond between source and target if a bond has not otherwise been specified.

[srcfitmask <mask>] Atoms from source to use if RMS-fitting source onto target.

[tgtfitmask <mask>] Atoms from target to use if RMS-fitting source onto target.

name <output COORDS> Name of output COORDS set containing source grafted onto target.

[verbose <#>] Verbosity during parameter assignment.

[bond <tgt>,<src>] Create a bond between target atom selected by <tgt> and source atoms selected by <src> in the final structure. Must be specified only once if connecting via internal coordinates, otherwise may be specified multiple times.

Graft one COORDS set onto another. If **srcfitmask** and/or **tgtfitmask** is specified, the source coordinates will be RMS best-fit onto target using the specified atoms. Only the atoms specified by **srcmask** and **tgtmask** will be kept. The **bond** keyword can be used to create bonds between target and source in the final structure.

If using internal coordinates to connect the units, a bond will be created between the source and target automatically if they contain CONNECT information (see 9.8 on page 64). Otherwise exactly one bond must be specified.

Graft using RMSD and removing atoms.

```
readdata Tyr.mol2 as coords name TYR
readdata PRY.mol2 as coords name PRY
graft \
```

```
  tgt TYR \
  src PRY \
  name Final \
  srcfitmask @O1,C5,C6,C4,H6,H5,C7,C3,H7,H4,C2 \
  tgtfitmask @OH,CZ,CE1,CE2,HE1,HE2,CD1,CD2,HD1,HD2,CG \
  srcmask !(@1-4) \
  tgtmask @C,O,CA,HA,N,H,CB,HB2,HB3 \
  bond :1@CB,:1@C2
crdout Final Final.graft.mol2
```

8.10 loadcrd

```
loadcrd <filename> [parm <parm> | parmindex<#>] [<trajin args>] [name <name>]
        [prec {single|double}
```

<filename> Trajectory file to load.

[parm <parmfile/tag>] Topology filename/tag to associate with trajectory (default first topology).

[parmindex <#>] Index of Topology to associate with trajectory (default 0, first topology).

[<trajin args>] Additional 'trajin' args; see 11.4 on page 102.

[name <name>] Name of the COORDS set.

[prec {single|double}] Load as either a single-precision COORDS set (the default) or a double-precision FRAMES set (which will use much more memory).

Immediately load trajectory <filename> as a COORDS data set named <name> (default base name of <filename>). If <name> is already present the coordinates will be appended to the existing data set.

For example, to load frames from trajectories named 'traj1.nc' and 'traj2.nc' into a COORDS data set named Crd1:

```
loadcrd traj1.nc name Crd1
loadcrd traj2.nc name Crd2
```

8.11 loadtraj

```
loadtraj name <setname> [<filename>]
```

name <setname> Name of the TRAJ set.

[<filename>] If specified, trajectory to add to the TRAJ set.

This command functions in two ways. If <filename> is not provided, all currently loaded input trajectories (from ***trajin*** commands) are added to TRAJ data set named <setname>. **Note that if the input trajectory list is cleared (via 'clear trajin') this will invalidate the TRAJ data set.** In addition, currently all trajectories must have the same number of atoms. Otherwise add trajectory <filename> to TRAJ data set <setname>.

TRAJ data sets cannot be modified.

8.12 permutedihedrals

```
permutedihedrals crdset <COORDS set> resrange <range> [{interval | random}]
              {[outtraj <filename> [<outfmt>]]} [crdout <output COORDS>]
                 [<dihedral types>] [dihtype <name>:<a0>:<a1>:<a2>:<a3>[:<offset>] ...]
  Options for 'random':
[rseed <rseed>] [out <# problems file> [<set name>]] [noimage]
[ check [cutoff <cutoff>] [rescutoff <rescutoff>] [maxfactor <max_factor>]
  [checkrings] [backtrack <backtrack> [checkallresidues]
                   [increment <increment>]] ]
  Options for 'interval':
<interval deg>
  <dihedral types> =  alpha beta gamma delta epsilon zeta nu1 nu2 h1p c2p chin
                      phi psi chip omega
```

crdset <COORDS set> COORDS data set to operate on.

resrange <range> Residue range to search for dihedrals.

interval Rotate found dihedrals by <interval>. This is done in an ordered fashion so that every combination of dihedral rotations is sampled at least once.

random Rotate each found dihedral randomly.

[outtraj <filename>] Trajectory file to write coordinates to.

[<outfmt>] Trajectory file format.

[crdout <output COORDS>] COORDS data set to write coordinates to.

<dihedral type> One or more dihedral types to search for.

[dihtype <name>:<a0>:<a1>:<a2>:<a3>[:<offset>] Search for a custom dihedral type called <name> using atom names <a0>, <a1>, <a2>, and <a3>.

Offset: -2=<a0><a1> in previous res, -1=<a0> in previous res, 0=All <aX> in single res, 1=<a3> in next res, 2=<a2><a3> in next res.

Options for 'interval':

<**interval deg**> Amount to rotate dihedral by each step.

Options for 'random':

[rseed <**rseed**>**]** Random number seed.

[out <**# problems file**>**]** File to write number of problems (clashes) each frame to.

[<**set name**>**]** Number of problems data set name.

[noimage] Disable imaging when checking rotated structure for clashes.

[check] Check randomly rotated structure for clashes.

[cutoff <**cutoff**>**]** Atom cutoff for checking for clashes (default 0.8 Å).

[rescutoff <**cutoff**>**]** Residue cutoff for checking for clashes (default 10.0 Å).

[maxfactor <**max_factor**>**]** The maximum number of total attempted rotations will be <max_factor> * <total # of dihedrals> (default 2).

[checkrings] If specified, look to see if any rings in the residue to which the dihedral being rotated belongs to have a bond running through them, which counts as a clash. May be slow.

[backtrack <**backtrack**>**]** (No longer recommended as of version 5.1.0). If a clash is encountered at dihedral N and cannot be resolved, go to dihedral N-<backtrack> to try and resolve the clash (default is no backtracking).

[checkallresidues] If specified all residues checked for clashes, otherwise only residues up to the currently rotated dihedral check.

[increment <**increment**>**]** If a clash is encountered, first attempt to rotate dihedral by increment to resolve it; if it cannot be resolved by a full rotation the calculation will backtrack (default 1).

Create a trajectory by rotating specified dihedrals in a structure by regular intervals (**interval**), or create 1 structure by randomly rotating specified dihedrals (**random**). The resulting structure can be written to a file with **outtraj** or saved to a new COORDS set with **crdout**; at least one output option must be specified. When randomly rotating dihedrals steric clashes will be checked if **check** is specified using the same algorithm used by the ***check*** action (see 12.15 on page 128); in such cases the algorithm will attempt to resolve the clash

as best it can. If clashes are not being resolved you can increase the number of rotation attempts *cpptraj* will make by increasing **maxfactor**.

For example, to rotate all backbone dihedrals in a protein with coordinates in a file named tz2.rst7 in -120 degree intervals and write the resulting trajectory in Amber format to rotations.mdcrd:

```
reference tz2.rst7 [TZ2]
permutedihedrals crdset [TZ2] interval -120 outtraj rotations.mdcrd phi psi
```

To randomly rotate backbone dihedrals for the same structure and write to file random.mol2 in MOL2 format:

```
reference tz2.rst7 [TZ2]
permutedihedrals crdset [TZ2] random rseed 1 check maxfactor 10 phi psi \
                 outtraj random.mol2 multi
```

8.13 prepareforleap

```
prepareforleap crdset <coords set> [frame <#>] name <out coords set>
                   [pdbout <pdbfile> [terbymol]] [problemout <file>]
                   [leapunitname <unit>] [out <leap input file> [runleap <ff file>]]
                   [skiperrors] [{dlparams|nodlparams}] [{bondunknown|nobondunknown}]
                   [nowat [watermask <watermask>] [noh]
                      [keepaltloc {<alt loc ID>|highestocc}]
                   [stripmask <stripmask>] [solventresname <solventresname>]
                   [molmask <molmask> ...] [determinemolmask <mask>]
                   [{nohisdetect |
                     [nd1 <nd1>] [ne2 <ne2] [hisname <his>] [hiename <hie>]
                     [hidname <hid>] [hipname <hip]}]
                   [{nodisulfides |
                     existingdisulfides |
                     [cysmask <cysmask>] [disulfidecut <cut>] [newcysname <name>]}]
                   [{nosugars |
                     sugarmask <sugarmask> [noc1search] [nosplitres]
                        [rescut <residue cutoff>] [bondoffset <offset>]
                        [resmapfile <file>]
                     [hasglycam] [determinesugarsby {geometry|name}]
                    }]
```

crdset <**coords set**> COORDS data set containing coordinates and topology to prepare.

[frame <#>**]** Frame to use from COORDS set (default first).

name <**out coords set**> Output COORDS set containing prepared topology/coordinates.

[pdbout <pdbfile>] Output PDB name.

[terbymol] If specified, base TER cards on molecules instead of PDB chains.

[problemout <file>] If specified redirect found problems to <file> instead of stdout.

[leapunitname <unit>] LEaP unit name to use when writing to <leap input file> (i.e. the LEaP input file will contain '<unit> = loadpdb <pdbfile>').

[out <leap input file>] File containing LEaP input needed to read in the prepared system (loadpdb, bond commands for disulfides, etc).

[runleap <ff file>] If specified, CPPTRAJ will attempt to run LEaP directly to generate a topology and coordinates; <ff file> should contain the appropriate 'source' commands for loading the desired force field parameters. Will attempt to produce topology <unit>.parm7 and coordinates <unit>.rst7.

[skiperrors] If specified, the command will try to ignore any errors encountered. Can be useful for debugging.

[{dlparams|nodlparams}] If 'dlparams' is specified, try to download parameters for unknown residues (default is to not do this, 'nodlparams').

[{bondunknown|nobondunknown}] If 'bondunknown' is specified, try to determine bonds to unknown residues (default is to not do this, 'nobondunknown').

[nowat] If specified, remove waters from the system.

[watermask <watermask>] Mask selecting waters to remove (default ':<solventresname>').

[noh] If specified, strip all hydrogen atoms from the system (recommended).

[keepaltloc {<alt loc ID>|highestocc}] LEaP cannot handle alternate atom locations, so the command will choose location 'A' by default. This can be changed to either <alt loc id> or the location with the highest occupancy if 'highestocc' is specified.

[stripmask <stripmask>] Mask of atoms to remove from the system.

[solventresname <solventresname>] Solvent residue name (default 'HOH').

[molmask <mask>] If specified, atoms in <mask> will be considered all part of one molecule. May be specified multiple times.

[determinemolmask <mask>] If specified, determine if atoms selected in <mask> are in the same molecule via bonds.

Histidine Detection:

[nohisdetect] Disable renaming of histidine residues based on existing hydrogens.

[nd1 <nd1>] Delta nitrogen atom name (default 'ND1').

[ne2 <ne2<] Epsilon nitrogen atom name (default 'NE2').

[hisname <his>] Histidine residue name (default 'HIS').

[hiename <hie>] Epsilon-protonated histidine name (default 'HIE').

[hidname <hid>] Delta-protonated histidine name (default 'HID').

[hipname <hip>] Doubly-protonated histidine name (default 'HIP').

Disulfide Handling:

[nodisulfides] Disable handling of disulfides.

[existingdisulfides] Only handle disulfides already present; do not search for additional disulfides.

[cysmask <cysmask>] Mask for selecting cysteine residues (default 'CYS').

[disulfidecut <cut>] Sulfur to sulfur atom distance cutoff for forming a disulfide (default 2.5 Ang).

[newcysname <name>] Name to change cysteine residues that participate in a disulfide bond to (default 'CYX').

Sugar Handling:

[nosugars] Disable handling of sugars.

[sugarmask <sugarmask>] Mask selecting sugars to be handled. If not specified the default is all residues defined in resmapfile.

[noc1search] If specified, disable search for missing linkages to sugar C1 atom bonds.

[nosplitres] If specified, do not attempt to split off functional groups from sugars into separate residues.

[rescut <residue cutoff>] Initial distance cutoff (default 8 Ang.) for residue center to residue center distance when looking for missing sugar linkages.

[bondoffset <offset>] Offset (default 0.2 Ang.) to add to "ideal" bond distances when looking for missing sugar linkages. Can be increased to accommodate distorted structures.

[resmapfile <file>] File containing sugar residue/atom name mapping. Default is '$CPPTRAJHOME/dat/Carbohydrate_PDB_Glycam_Names.txt'.

[hasglycam] If specified, assume sugars already have GLYCAM residue names; just check sugar anomer type/configuration/linkage.

[determinesugarsby {geometry|name}] Determine whether sugar anomer type/configuration should be chosen based on sugar geometry (default) or the residue name. CPPTRAJ will report when a mismatch is detected between the sugar anomer type/configuration based on geometry and anomer type/configuration based on the residue name.

This command will prepare a structure (usually from a PDB) for processing with the Amber program LEaP to generate topology and coordinates files for MD simulations.[3] It will handle things like choosing alternate atom locations, removing waters/hydrogen atoms from the structure, renaming residues and generating 'bond' commands for disulfide bonds, change histidine names based on any existing protonation, and renaming residues/atoms and generating 'bond' commands for carbohydrates. The command can also call LEaP directly to generate the parameters once the structure is prepared.

If hydrogen atoms are present in the structure, the command will attempt a simple and straightforward determination of the protonation state of any histidine residues based on where hydrogens are bonded, and assign the appropriate residue name. The command will also identify any existing disulfide bonds as well as potential disulfide bonds and generate the corresponding LEaP 'bond' commands which can be applied after the structure is loaded in LEaP. Potential disulfide bonding atoms can be identified via a user-specifiable mask expression.

By default, sugars will have their residue names changed to those compatible with the GLYCAM force field based on their anomer type (alpha/beta), configuration (D/L), and linkages (glycosidic and covalent sugar to non-sugar). Any recognized functional groups that are part of sugar residues (hydroxyl, acetyl, sulfate, etc) will be split into separate residues as required by GLYCAM. If this happens and 'runleap' has not been specified, CPPTRAJ will warn about any residues/atoms that require charge to be adjusted. If 'runleap' has not

been specified the command will warn about any atoms that need to have their charges adjusted after LEaP is run.

The command will try to report any potential problems that LEaP might encounter. These include residue names that may be unrecognized (and therefore may not have parameters), mismatches between detected sugar anomer type/configuration and anomer type/configuration based on the sugar residue name, unrecognized sugar linkages, and so on.

For example, the following input prepares PDB 4zzw for processing with PDB, putting the proper leap commands in leap.4zzw.in, writing the prepared PDB to 4zzw.cpptraj.pdb, removing waters and hydrogen atoms, and keeping alternate atom locations with the highest occupancy:

```
parm 4zzw.pdb
loadcrd 4zzw.pdb name MyCrd
prepareforleap crdset MyCrd name Final out leap.4zzw.in leapunitname m \
  pdbout 4zzw.cpptraj.pdb nowat noh keepaltloc highestocc
```

Sugar Residue/Atom Name Mapping File

This file controls how CPPTRAJ will name sugars based on sugar form/chirality linkage. It consists of three sections separated by a blank line. The first section defines sugar PDB residue names and how they are mapped to GLYCAM residue characters:

```
Format: <ResName> <GlycamCode> <Anomer> <Config> <RingType> "<Name>"
Anomer: A=alpha, B=beta
Config: D/L
RingType: P=pyranose, F=furanose
Example: 64K A A D P "alpha-D-arabinopyranose"
```

The second section contains PDB to GLYCAM atom name maps for residues:

```
Format: <GLYCAM residue codes> <PDB atom name>,<GLYCAM atom name>[,<anomer>] ...
If <anomer> (A=alpha, B=beta) is specified, the atom name map is only valid for that sp
Example: V,W,Y C7,C2N O7,O2N C8,CME
```

The third section contains PDB to GLYCAM linkage residue (i.e. non-sugar residues bonded to sugars) name maps:

```
Format: <PDB residue name> <GLYCAM residue name>
Example: SER OLS
```

8.14 reference

Reference coordinates can now be used and manipulated like COORDS data sets. See 11.3 on page 101 for command syntax.

8.15 rotatedihedral

```
rotatedihedral crdset <COORDS set> [frame <#>] [name <output set name>]
               {value <value> | increment <increment>}
               { <mask1> <mask2> <mask3> <mask4> |
                 res <#> type <dih type> }
<dih type> = alpha beta gamma delta epsilon zeta nu1 nu2 h1p c2p chin
             phi psi chip omega
```

crdset <COORDS set> Coordinates data set to work on. If a TRAJ data set is specified, name must also be specified.

[frame <#>] Frame of the COORDS set to work on.

[name <output set name>] Output COORDS set. If not specified the input COORDS set will be modified.

value <value> Set specified dihedral to given value in degrees.

increment <increment> Increment specified dihedral by increment in degrees.

<mask1> <mask2> <mask3> <mask4> Define dihedral by atom masks. Each mask should only select one atom.

res <#> Rotate dihedral specified by type in residue number <#>.

type <dih type> Dihedral type to rotate in specified residue.

Rotate the specified dihedral in given COORDS set to a target value or by given increment. For example, to set the protein chi dihedral in residue 8 to 35 degrees and write out to a mol2 file:

```
parm ../tz2.parm7
loadcrd ../tz2.nc 1 1 name TZ2
rotatedihedral crdset TZ2 value 35 res 8 type chip
crdout TZ2 tz2.rotate.1.mol2
```

8.16 sequence

Syntax for this command is now located here: 7.2

8.17 splitcoords

```
splitcoords <crd set> name <output set name>
```

<crd set> COORDS set to split.

name <output set name> Name of new set to create.

Split trajectory specified by <crd set> by molecule into a new COORDS set. All molecules in <crd set> must be the same size. For example, if there are 10 molecules and 10 frames in COORDS set "Set0", the following would create a new COORDS set with 100 frames (original molecules 1-10 frame 1, original molecules 1-10 frame 2, etc):

```
splitcoords Set0 name Set0Split
```

8.18 zmatrix

```
zmatrix <COORDS set name> [name <output set name>]
        { zset <input zmatrix set> [parm <top>|parmindex <#>]|
          [complete][molnum <mol#>] [frame <frame#>] [out <zmatrix file>] }
```

<COORDS set name> COORDS set to calculate Z-matrix from or use as topology for applied Z-matrix.

[name <output set name>] Name of output COORDS set (if 'zset') or output Z-matrix set.

zset <input zmatrix set> Name of Z-matrix set to use to generate coordinates.

parm <top> Use specified topology name as topology for generated coordinates.

parmindex <#> Use topology index as topology for generated coordinates.

complete If specified, generate all possible internal coordinates, otherwise generate a minimal set.

[molnum <mol#>] Calculate Z-matrix from specified molecule (default first molecule).

[frame <frame#>] Calculate Z-matrix from specified molecule in specified frame (default first frame).

[out <zmatrix file>] File to write calculated Z-matrix to.

Data sets created:

<output set name> If 'zset', COORDS set containing final coordinates. Otherwise contains Z-matrix data.

Command for working with Z-matrices. If 'zset' is specified, generate coordinates from the specified Z-matrix data set and topology. Otherwise, calculate a Z-matrix for a single molecule from the specified frame of given COORDS data set.

9 General Commands

The following general commands are available:

Command	Description
activeref	Select the reference for distance-based masks.
calc	Evaluate the given mathematical expression.
clear	Clear various objects from the cpptraj state.
create	Create (but do not yet write) a data file.
createset	Create a dataset from a simple mathematical expression.
datafile	Used to manipulate data files.
datafilter	Filter data sets based on given criteria.
dataset	Use to manipulate data sets.
debug | prnlev	Set debug level. Higher levels give more info.
ensextension	Enable/disable ensemble number extension for files in ensemble mode.
exit | quit	Quit cpptraj.
flatten	Distribute elements of 2d matrix across 1d array.
go | run	Start a trajectory processing Run.
help	Provide help for commands.
list	List various objects in the cpptraj state.
noexitonerror	Attempt to continue even if errors are encountered.
noprogress	Do not print a progress bar during a Run.
parallelanalysis	(MPI only) Divide current Analyses among MPI processes.
parsedata	Parse timing data from CPPTRAJ output.
precision	Change the output precision of data sets.
printdata	Print data set to screen.
random	Change default random number generator, create random sets.
readdata	Read data sets from files.
readensembledata	Read data files in ensemble mode.
readinput	Read cpptraj input from a file.
removedata	Remove specified data set(s).
rst	Generate Amber-style distance/angle/torsion restraints.
runanalysis	Run an analysis immediately or run all queued analyses.
select	Print the results of an atom mask expression.
selectds	Print the results of a data set selection expression.
silenceactions	Prevent Actions from writing information to STDOUT.
sortensembledata	Sort data sets using replica information (currently constant pH only).
usediskcache	Turn caching of data sets to disk on or off.
write | writedata	Immediately write data to a file or write to all current data files.

9.1 activeref

```
activeref <#>
```

Set which reference structure should be used when setting up distance-based masks for everything but the 'mask' action. Numbering starts from 0, so 'activeref 0' selects the first reference structure read in, 'activeref 1' selects the second, and so on.

9.2 calc

```
calc <expression>
[prec <width>.<precision>] [format {double|general|scientific}]
```

<expression> Mathematical expression to evaluate. See 5.2 on page 26 for details.

prec <width>.<precision> Set the width and precision of the result.

format {double|general|scientific} Set the format of the result.

Evaluate the given mathematical expression. This version gives more control over the format of the output.

9.3 clear

```
clear [{all | <type>}]
      (<type> = actions,trajin,trajout,ref,parm,analysis,datafile,dataset)
```

Clear list of indicated type, or all lists if 'all' specified. Note that when clearing actions or analyses, associated data sets and data files are not cleared and vice versa.

9.4 create

```
create <filename> <datasetname0> [<datasetname1> ...] [<DataFile Options>]
```

Add specified data sets to the data file named <filename>; if the file does not exist, it will be added to the DataFileList. Data files created in this way are only written at the end of coordinate processing, analyses, or via the ***'writedata'*** command. See 6 on page 27 for more data file format options.

9.5 createset

```
createset <expression> [xmin <min>] xstep <step> nx <nxvals>
```

expression Simple mathematical expression, must contain equals sign, can contain X (e.g. Y=2*X). If not enclosed in quotes must not contain whitespace.

xmin <**min**> Minimum X value.

xstep <**step**> X step.

nx <**nxvals**> Number of X values.

Generate a data set from a simple mathematical expression.

9.6 datafile

```
datafile <filename> <datafile arg>
```

Pass <datafile arg> to data file <filename>. See 6 on page 27 for more details.

9.7 datafilter

```
datafilter {<dataset arg> min <min> max <max> ...} [out <file>] [name <setname>]
           {[multi] | [filterset <set> [newset <newname>]] [countout <countfile>]}
```

<**dataset arg**> **min** <**min**> **max** <**max**> Data set name and min/max cutoffs to use; can specify more than one.

[out <**file**>**]** Write out to file named <file>.

[name <**setname**>**]** Name of filter data set containing 1 when cutoffs satisfied, 0 otherwise.

[multi] Filter each set separately instead of all together (creates filter set for each input set). Cannot be used with 'filterset'.

[filterset <**set**>**]** If specified, <set> will be filtered to only contain data that satisfies cutoffs. Cannot be used with 'multi'.

[newset <**newname**>**]** If specified a new set will be created from 'filterset' instead of replacing 'filterset'.

[countout <**count**>**]** If specified, write number of elements passed and filtered to <countfile>. Cannot be used with 'multi'.

Sets Created (not 'multi')

<**setname**> For each input element contains 1 for elements that "passed", 0 otherwise.

<**setname**>**[npassed]** Number of elements that passed.

<**setname**>**[nfiltered]** Number of elements filtered out.

Sets Created ('multi')

<**setname**>:<**idx**> For each input set (number with
<idx>, starting from 0) contains 1 for elements that
"passed", 0 otherwise.

Create a data set (optionally named <setname>) containing 1 for data within given <**min**> and <**max**> criteria for each specified data set. There must be at least one <**min**> and <**max**> argument, and can be as many as there are specified data sets. If **'multi'** is specified then only filter data sets will be created for each data set instead. If **'filterset'** is specified, the specified <**set**> will be modified to only contain '1' frames; cannot be used with **'multi'**. If **'newset'** is also specified, a new set will be created containing the '1' frames instead. The 'filterset' functionality only works for 1D scalar sets. If **'countout'** is specified, the final number of elements passed and filtered out will be written to <countfile>.

For example, to read in data from two separate files (d1.dat and a1.dat) and generate a filter data set named FILTER having 1 when d1 is between 0.0 and 3.0 and a1 is between 135.0 and 180.0:

```
readdata a1.dat name a1
readdata d1.dat name d1
datafilter d1 min 0.0 max 3.0 a1 min 135.0 max 180.0 out filter.dat name FILTER
```

Note that a similar command that can be used with data generated by Actions during trajectory processing is ***filter*** (see page 150).

9.8 dataset

```
dataset { legend <legend> <set> |
          makexy <Xset> <Yset> [name <name>] |
          vectorcoord {X|Y|Z} <set> [name <name>] |
       cat <set0> <set1> ... [name <name>] [nooffset] |
          make2d <1D set> cols <ncols> rows <nrows> [name <name>] |
          {drop|keep}points {range <range arg> | [start <#>] [stop <#>] [offset <#>]}
                   [name <output set>] <set arg1> ... |
          remove <criterion> <select> <value> [and <value2>] [<set selection>] |
          connect {[head <head atom>] [tail <tail atom>]|[headmask <headmask>] [tailmas
          dim {xdim|ydim|zdim|ndim <#>} [label <label>] [min <min>] [step <step>] |
          outformat {double|scientific|general} <set arg1> [<set arg 2> ...] |
          invert <set arg0> ... name <new name> [legendset <set>] |
          shift [above <value> by <offset>] [below <value> by <offset>] <set arg0> ...
       [mode <mode>] [type <type>] <set arg1> [<set arg 2> ...]
        }
  <mode>:  'distance' 'angle' 'torsion' 'pucker' 'rms' 'matrix' 'vector'
  <type>:  'alpha' 'beta' 'gamma' 'delta' 'epsilon' 'zeta' 'nu0' 'nu1' 'nu2' 'nu3'
           'nu4' 'h1p' 'c2p' 'chin' 'phi' 'psi' 'chip' 'omega' 'chi2' 'chi3' 'chi4'
           'chi5' 'pucker' 'noe' 'distance' 'covariance' 'mass-weighted covariance'
           'correlation' 'distance covariance' 'IDEA' 'IRED' 'dihedral covariance'
```

```
Options for 'type noe':
   [bound <lower> bound <upper>] [rexp <expected>] [noe_strong] [noe_medium]
      [noe_weak]
```

[name <name>] New data set name for makexy/vectorcoord/cat/make2d/droppoints/keeppoints.

legend <legend> <set> Set the legend for data set <set> to <legend>.

makexy <Xset> <Yset> Create a new data set (optionally named <name>) with X values from <Xset> and Y values from <Yset>.

vectorcoord {X|Y|Z} <set> Extract X/Y/Z coordinates from vector data set into a new 1D data set.

cat <set0> <set1> ... Concatenate two or more data sets into a new data set (optionally named <name>). Only works for scalar 1D and string sets.

make2d <1D set> cols <ncols> rows <nrows> Convert 1D data set into row-major 2D data set with specified number of rows and columns.

{drop|keep}points <set arg1> ... Drop or keep specified points from data set(s), optionally creating a new data set.

range <range arg> Range of points to drop/keep.

[start <#>] [stop <#>] [offset <#>]
Start/stop/offset values of points to drop/keep.

remove <criterion> <select> <value> [and <value2>] [<set selection>]
Remove data sets from <set selection> according to specified criterion and selection.

```
<criterion>:  'ifaverage' 'ifsize' 'ifmode' 'iftype'
<select>   :  'equal' '==' 'notequal' '!=' 'lessthan' '<'
              'greaterthan' '>' 'between' 'outside'
```

connect <set args> Add/change connect atom information (used by the sequence command, 7.2 on page 42) to COORDS set(s). Head atoms connect to previous residue, tail atoms connect to next residue. Can use either absolute atom numbers or atom mask expressions.

[head <head atom>] [tail <tail atom>] Specify the head/tail atoms by atom number.

[headmask <headmask>] [tailmask <tailmask>]
Specify the head/tail atoms by atom mask.

dim {xdim|ydim|zdim|ndim <#>} Change specified dimension in set(s).

label <label> Change dimension label to <label>

min <min> Change dimension minimum to <min>.

step <step> Change dimension step to <step>.

invert <set arg0> ... name <new name> [legendset <set>]

<set arg0> ... Specify sets to invert.

name <new name> Inverted output set name.

[legendset <set>] String data set containing legends

shift

[above <value> by <offset>] Values in set(s) above <value> will be shifted by <offset>.

[below <value> by <offset>] Values in set(s) below <value> will be shifted by <offset>.

<set arg0> ... Set(s) to shift.

[mode <mode>] Set data set(s) mode to <mode>.

[type <type>] Set data set(s) type to 'type', useful for e.g. analysis with *statistics*. Note this can also be done with 'type <type>' for certain commands (*distance*, *dihedral*, *pucker* etc). Note that not every <type> is compatible with a given <mode>.

Options for 'type noe' only:

[bound <lower> bound <upper>] Lower and upper bounds for NOE (in Angstroms); must specify both.

[rexp <expected>] Expected value for NOE (in Angstroms); if not given '(<lower> + <upper>)' / 2.0 is used.

[noe_strong] Set lower and upper bounds to 1.8 and 2.9 Å respectively.

[noe_medium] Set lower and upper bounds to 2.9 and 3.5 Å respectively.

[noe_weak] Set lower and upper bounds to 3.5 and 5.0 Å respectively.

Either set the legend for a single data set, create a new set with X values from one set and Y values from another, concatenate 2 or more sets, make a 2D set from 1D set, remove sets according to a certain criterion, or change the mode/type for one or more data sets.

Setting the mode/type can be useful for cases where the data set is being read in from a file; for example when reading in a dihedral data set the type can be set to 'dihedral' so that various Analysis routines like ***statistics*** know to treat it as periodic. A brief description of possible modes and types follows:

Mode	Type	Description
distance	noe	NOE distance.
angle		Angle.
torsion	alpha	Nucleic acid alpha.
	beta	Nucleic acid beta.
	gamma	Nucleic acid gamma.
	delta	Nucleic acid delta.
	epsilon	Nucleic acid epsilon.
	zeta	Nucleic acid zeta.
	nu1	Nucleic pucker (O4').
	nu2	Nucleic pucker (C4').
	h1p	Nucleic acid H1'.
	c2p	Nucleic acid C2'.
	chin	Nucleic acid chi.
	phi	Protein Phi.
	psi	Protein psi.
	chip	Protein chi.
	omega	Protein omega.
pucker	pucker	Sugar pucker.
rms		RMSD.
matrix	distance	Distance matrix.
	covariance	Cartesian covariance matrix.
	'mass-weighted covariance'	Mass weighted Cartesian covariance matrix.
	correlation	Dynamic cross correlation matrix.
	'distance covariance'	Distance covariance matrix.
	IDEA	IDEA matrix.
	IRED	IRED matrix.
	'dihedral covariance'	Dihedral covariance matrix.
vector	IRED	IRED vector.

The invert mode takes a group of M 1D data sets of size N and create N new "inverted" data sets of size M. This is similar to the invert keyword already available for standard and Grace data writes, but operates directly on data sets. For example, given the following two data sets:

```
D0 D1
 1  4
 2  5
 3  6
```

The new data sets will be laid out like so:

```
N0 N1 N2
 1  2  3
 4  5  6
```

The dataset invert command can be useful if you want to easily view output from multiple analysis commands in a single graph. For example, to view state counts from two different simulations side by side:

```
calcstate name Sim1 state bound1,dist1,0.0,2.0
calcstate name Sim2 state bound1,dist1,0.0,2.0
runanalysis dataset invert Sim*[Count] name Inverted legendset Sim1[Name]
dataset dim xdim label Simulation min 1 step 1 Inverted*
writedata statecount.agr Inverted*
```

The dataset shift command can be used for wrapping circular values, such as torsions. For example, to ensure a pucker has a range from 0 to 360 instead of -180 to 180:

```
pucker Furanoid @C2 @C3 @C4 @C5 @O2 cremer out CremerF.dat amplitude
run
dataset shift Furanoid below 0 by 360
```

9.9 debug | prnlev

```
debug [<type>] <#>
      (<type> = actions,trajin,trajout,ref,parm,analysis,datafile,dataset)
```

Set the level of debug information to print. In general the higher the <#> the more information that is printed. If <type> is specified only set the debug level for a specific area of *cpptraj*.

9.10 ensextension

```
ensextension {on|off}
```

Turn printing of ensemble member number filename extensions on or off. By default ensemble extensions are printed in parallel and not in serial.

NOTE: THE 'ensextension off' OPTION HAS NOT BEEN FULLY TESTED IN PARALLEL AND IS NOT CURRENTLY RECOMMENDED.

9.11 exit | quit

Exit normally.

9.12 flatten

```
flatten name <output set name> [mode {sum|avg}] <input set args>
```

name <output set name> Name of "flattened" 1D output set(s).

mode {sum|avg} If sum, matrix elements will be summed. If avg, matrix elements will be averaged.

<input set args> Specify matrices to "flatten".

DataSets Created

<output set name> Flattened 1D set if only one input matrix.

<output set name>:<idx> Flattened 1D sets when more than one input matrix; index starts from 1.

Flatten 1 or more matrices into 1D array(s) by summing or averaging elements. For example, given a matrix with values like this:

```
X Y Value
1 3 5.0
1 4 4.0
2 3 2.0
```

The "flattened" 1D array with mode SUM would be determined as follows:

```
Element 1 = (5.0/2) + (4.0/2) = 4.5
Element 2 = (2.0/2) = 1.0
Element 3 = (5.0/2) + (2.0/2) = 3.5
Element 4 = (4.0/2) = 2.0
```

And the final 1D array would look like so:

```
Index Value
1     4.5
2     1.0
3     3.5
4     2.0
```

9.13 go | run

Begin trajectory processing, followed by analysis and datafile write.

9.14 help

```
help [ { All |
     <cmd> |
      <command category> |
      Form[ats] [{read|write}] |
      Form[ats] [{trajin|trajout|readdata|writedata|parm|parmwrite} [<fmt key>]] |
      Mask     } ]
```

```
Command Categories: Gen[eral] Sys[tem] Coor[ds] Traj[ectory] Top[ology]
                    Act[ion] Ana[lysis] Con[trol]
  All                : Print all known commands.
  <cmd>              : Print help for command <cmd>.
  <command category> : Print all commands in specified category.
  Form[ats]          : Help for file formats.
  Mask               : Help for mask syntax.
```

If 'All' is specifed, list all commands known to *cpptraj*. If given with a command, print help for that command. Otherwise, list all commands of a certain category (General, System, Coords, Trajectory, Topology, Action, Analysis, or Control), help for various file formats, or help with atom mask syntax.

9.15 list

```
list <type>
     (<type> = actions,trajin,trajout,ref,parm,analysis,datafile,dataset)
```

List the currently loaded objects of <type>. If no type is given then list all loaded objects.

9.16 noexitonerror

```
noexitonerror
```

Normally *cpptraj* will exit if actions fail to initialize properly. If ***noexitonerror*** is specified, *cpptraj* will attempt to continue past such errors. This is the default if in interactive mode.

9.17 noprogress

```
noprogress
```

Do not display read progress during trajectory processing.

9.18 parallelanalysis

```
parallelanalysis [sync]
```

MPI only. Divide all currently set up analyses as evenly as possible among available MPI processes and execute. Each analysis will get a single MPI process. If **sync** is specified all data will be synced back to the master process (for e.g. subsequent analysis). For an example of how to use the parallelanalysis command, see 13.16 on page 269.

9.19 parsedata

```
parsetiming <filename args> ... [out <file>] [name <setname>]
         [sortby {time|cores|filename}] [includebad] [showdetails]
         [type {trajproc|trajread|actframe}] [reverse]
         [groupout <file> [grouptype {prefix|name|kind}]]
```

<filename args> Files containing CPPTRAJ output to get timing data from.

[out <file>] Write total sorted timing sets to <file>.

[name <setname>] Set name for timing data sets.

[sortby {time|cores|filename}] Sort timing data sets by either time, number of cores (MPI processes * OpenMP threads), or file name.

[includebad] If specified, include run output for which timing data cannot be extracted (e.g. an incomplete/failed run).

[showdetails] If specified, details about each run will be printed to STDOUT.

[type {trajproc|trajread|actframe} If specified, report time other than the total time (which is the default):

- **trajproc** Total trajectory processing time (trajectory I/O plus action frame time).
- **trajread** Trajectory read time (requires compiling with '-timer' configure option/-DTIMER compiler define).
- **actframe** Action frame time (requires compiling with '-timer' configure option/-DTIMER compiler define).

[reverse] Instead of longest time to shortest time, sort shortest time to longest time.

[groupout <file>] Group run output by a property and write to a file. Additional details will be written like speedup and efficiency (relative to the slowest run).

- **[grouptype {prefix|name|kind}]** Property to group runs by in group output file.
  - **prefix** Group by directory prefix.
  - **name** Group by run type name (see *<setname>[name]* below).
  - **kind** Group by run type name; OpenMP runs are separated by number of OpenMP threads.

```
DataSets Created:
```

<setname> Set containing sorted run times.

<setname>[name] Set containing shortedhand run names. Consists of a prefix (S for serial, O for OpenMP, M for MPI, H for hybrid MPI/OpenMP) followed by numbers indicating number of MPI processes 'x' OpenMP threads; e.g., H16x4 means a hybrid run consisting of 16 MPI processes and 4 OpenMP threads per process. If CUDA is active, the name will be wrapped in 'G()', e.g. G(H16x4).

<setname>[dir] Set containing output directory prefixes. If no directory prefix, just contains output file name.

The ***parsedata*** command can be used to extract timing data from CPPTRAJ output.

9.20 precision

```
precision {<filename> | <dataset arg>} [<width>] [<precision>]
```

Set the precision for all data sets in data file <filename> or data set(s) specified by <dataset arg> to *width.precision*, where width is the column width and precision is the number of digits after the decimal point. Note that the <precision> argument only applies to floating-point data sets.

For example, if one wanted to set the precision of the output of an Rmsd calculation to 8.3, the input could be:

```
trajin ../run0.nc
rms first :10-260 out prec.dat
precision prec.dat 8 3
```

and the output would look like:

```
#Frame RMSD_00000
1 0.000
2 0.630
```

9.21 random

```
random [setdefault {marsaglia|stdlib|mt|pcg32|xo128}]
    [createset <name> count <#> [seed <#>]
        settype {int|float01|gauss [mean <mean>] [sd <SD>]}]
```

setdefault If specified, change the default random number generator (RNG).

marsaglia Use the Marsaglia RNG that is used in the Amber MD programs sander/pmemd.

stdlib Use the C standard library RNG.

mt Use the C++11 implementation of the Mersenne twister (mt19937); only available with C++11 support.

pcg32 Use the 32 bit version of the Permuted Congruential Generator.[4]

xo128 Use the Xoshiro128++ RNG.[5]

createset If specified, create a 1D data set filled with random numbers of the specified type.

<**name**> Name of created set.

count <#> The number of elements to put into the set.

settype {int|float01|gauss} Type of numbers to use; integer, floating point between 0 and 1, Gaussian distribution.

mean <**mean**> Mean of distribution for 'gauss'.

sd <**SD**> Standard deviation of distribution for 'gauss'.

seed <#> Optional seed for the RNG.

This command can be used to set the default random number generator used in CPPTRAJ, and/or create a 1D data set filled with random values.

9.22 readdata

`readdata <filename> [name <dsname>] [as <fmt>] [separate] [<format options>]`

name <**dsname**> Name for read-in data set(s). Default is <filename>.

as <**fmt**> Force <filename> to be read as a specific format using given format keyword.

separate Read each file specified into separate data sets indexed from 0.

Read data from file <filename> and store as data sets. For more information on formats currently recognized by cpptraj see 1 on page 25. For format-specific options see 6. For example, given the file calc.dat:

```
#Frame  R0   D1
1      1.7 2.22
```

The command '`readdata calc.dat`' would read data into two data sets, calc.dat:2 (legend set to "R0") and calc.dat:3 (legend set to "D1").

9.23 readensembledata

```
readensembledata <filename> [filenames <additional files>] [<readdata args>]
```

<**filename**> Lowest replica file name.

filenames <**additional files**> Specified additional members of the ensemble. If not specified ensemble members will be search for using numerical extensions.

<**readdata args**> Additional data file arguments.

Read data sets as an ensemble, i.e. each file is a different member of an ensemble. This command is MPI-aware.

If one filename is given, it is assumed it is the "lowest" member of an ensemble with a numerical extension, e.g. 'file.001' and the remaining files are searched for automatically. Otherwise all other members of the ensemble can be specified with **'filenames'** and a comma-separated list e.g. 'file.001 filenames file.002,file.003,file.004. For additional 'readdata' arguments that can be passed in see 6 on page 27.

For example, to read in data files named cpout.001 to cpout.006 automatically:

```
readensembledata cpout.001 cpin cpin name PH
```

Or specified:

```
readensembledata cpout.001 \
                 filenames cpout.002,cpout.003,cpout.004,cpout.005,cpout.006 \
                 cpin cpin name PH
```

9.24 readinput

```
readinput <filename>
```

Read *cpptraj* commands from file <filename>.

9.25 removedata

```
removedata <arg>
```

Remove data set corresponding to <arg>.

9.26 rst

```
rst <mask1> <mask2> [<mask3>] [<mask4>]
    r1 <r1> r2 <r2> r3 <r3> r4 <r4> rk2 <rk2> rk3 <rk3>
    {[parm <parmfile / tag> | parmindex <#>]}
    [{ref <refname> | refindex <#> | reference} [offset <off>] [width <width>]]
    [out <outfile>]
```

<mask1> (Required) First atom mask.

<mask2> (Required) Second atom mask. If only two masks assume distance restraint.

[<mask3>] (Optional) Third atom mask. If 3 atom masks assume angle restraint.

[<mask4>] (Optional) Fourth atom mask. If 4 atom masks assume dihedral restraint.

rX <rX> Value of RX (X=1-4, default 0.0)

rk2 <rk2> Value of RK2 (force constant to be applied when R is R1 <= R < R2)

rk3 <rk3> Value of RK3 (force constant to be applied when R is R3 <= R < R4)

[parm <parmfile / tag> | parmindex <#>] Topology to be used for atom masks.

{ref <refname> | refindex <#> | reference} Use distance/angle/dihedral in reference structure to determine values for r1, r2, r3, and r4. The value of r2 is set to <r2> + <off>, r3 = r2, r1 = r2 - <width>, r4 = r3 + <width>.

[offset <off>] (Reference only) Value to offset distance/angle/torsion in reference by (default 0.0).

[width <width>] (Reference only) Width between r1 and r2, r3 and r4 (default 0.5).

[out <outfile>] Write restraints to outfile. If not specified, write to STDOUT.

Generate Amber-style distance restraints for use with nmropt=1. This is particularly useful for generating distance restraints based off of reference coordinates. For example to generate a distance restraint between two C5' atoms using the current distance between them in a reference structure, offsetting the distance by 1.0 Ang.:

```
parm 30bp-longbox-tip3p-na.parm7
reference 30bp-longbox.rst7
rst :1@C5' :31@C5' reference offset 1.0 rk2 10.0 rk3 10.0 out output
```

9.27 runanalysis

```
runanalysis [<analysiscmd> [<analysis args>]]
```

Run given analysis command immediately and write any data generated. If no command is given run any analysis currently set up. NOTE: When 'runanalysis' is specified alone, data is not automatically written; to write data generated with 'runanalysis' use the 'writedata' command (this allows multiple analysis runs between output if desired).

9.28 select

```
select <mask>
```

Prints the number of selected atoms corresponding to the given mask, as well as the atom numbers with format:

```
Selected= <#atom1> <#atom2> ...
```

This does not affect the state in any way, but is intended for use in scripts etc. for testing the results of a mask expression.

9.29 selectds

```
selectds <dataset arg>
```

Show the results of a data set selection. Data set selection has the format:

```
<name>[<aspect>]:<index>
```

Either the [<aspect>] or the <index> arguments may be omitted. A '*' can be used in place of <name> or [<aspect>] as a wildcard. The <index> argument can be a single number or a range separated by '-' and ','.

This command does not affect the state in any way, but is particularly useful in interactive mode for determining the results of a dataset argument.

9.30 sortensembledata

```
sortensembledata <dset arg0> [<dset arg1> ...]
```

<dset arg0> [<dset arg1> ...] `Data set(s) to sort.`

Sort unsorted data sets. Currently only works for constant pH REMD data.

9.31 usediskcache

```
usediskcache {on|off}
```

If on, CPPTRAJ will attempt to cache data sets to disk if possible. This currently only works for integer data sets (e.g. ***hbond* series** data sets, etc).

9.32 write | writedata

```
write [<filename> <datasetname0> [<datasetname1> ...]] [<DataFile Options>]
```

With no arguments, write all files currently in the data file list. Otherwise, write specified data set(s) to <filename>. This is like the 'create' command except a data file is not added to the data file list; it is written immediately. See 6 on page 27 for more data file format options.

9.33 System Commands

These commands call the equivalent external system commands.

gnuplot <args> Call `gnuplot` (if it is installed on your system) with the given arguments.

head <args> Call `head`, which lists the first few lines of a file.

less <args> Call `less`, which can be used to view the contents of a file.

ls <args> List the contents of a directory.

pwd <args> Print the current working directory.

xmgrace <args> Call `xmgrace` (if it is installed on your system) with the given arguments.

10 Topology File Commands

These commands control the reading and writing of topology files. Cpptraj supports the following topology file formats:

Format	Keyword	Extension	Notes
Amber Topology	amber	.parm7	Only fully-supported format for write.
PDB	pdb	.pdb	Read Only
Mol2	mol2	.mol2	Read Only
CIF	cif	.cif	Read Only
Charmm PSF	psf	.psf	Limited Write
Gromacs Topology	gromacs	.top	Read only
SDF	sdf	.sdf	Read Only
Tinker ARC	arc	.arc	Read Only

For most commands that require a topology one can be specified via two keywords:

parm [<name>] Select topology corresponding to given file name, tag, or name.

parmindex [<#>] Select topology by order in which it was loaded, starting from 0.

The following topology related commands are available:

Command	Description
angleinfo, angles, printangles	Print angle info for selected
atominfo, atoms, printatoms	Print details for selected at
bondinfo, bonds, printbonds	Print bond info for selected
bondparminfo	Print the bond parameter t
change	Change specified parts of a to
charge	Print total charge for selected
comparetop	Compare two topologies and repor
dihedralinfo, dihedrals, printdihedrals	Print dihedral info for selected
hmassrepartition	Perform hydrogen mass repart
improperinfo, impropers, printimpropers	Print improper info for selecte
mass	Print total mass for selected
molinfo	Print molecule info for selected
parm	Load a topology file.
parmbox	Modify box info for a loaded t
parminfo	Print details for selected top
parmstrip	Remove selected atoms from t
parmwrite	Write selected topology to
printub, ubinfo	Print Urey-Bradley info for selec
resinfo	Print residue info for selected
scaledihedralk	Scale selected dihedral force co
solvent	Change which molecules are consid
timap	Map a residue onto a user template and write a sorted Amber O
updateparameters	Update/add parameters in/to a

10.1 angleinfo | angles | printangles

```
angleinfo [parm <name> | parmindex <#> | <#>]
          [<mask1>] [<mask2> <mask3>] [noindices]
          [out <file>]
```

[parm <**name**> | **parmindex** <#> | <#>**]** Name/tag or index of topology. Default is first loaded topology.

[<**mask1**>**]** Mask to print angle info for.

[<**mask2**> <**mask3**>**]** If specified, angles must match all masks.

[noindices] Do not print angle indices.

[out <**file**>**]** File to print to (default STDOUT).

Print angle information of atoms in <mask> for selected topology (first loaded topology by default) with format:

```
# Angle Kthet degrees atom names (numbers)
```

Where `Angle` is the internal angle index, `Kthet` is the angle force constant, `degrees` is the angle equilibrium value, `atom names` shows the atoms involved in the angle with format `:<residue num>@<atom name>`, and `(numbers)` shows the atom indices involved in a comma-separated list. Atom types will be shown in the last column.

If 3 masks are given instead of 1, print info for angles with first atom in <mask1>, second atom in <mask2>, and third atom in <mask3>.

10.2 atominfo | atoms | printatoms

```
atominfo [parm <name> | parmindex <#> | <#>] <mask> [out <file>]
```

[parm <name> | parmindex <#> | <#>] Name/tag or index of topology. Default is first loaded topology.

<mask> Mask selecting atoms to print info for.

[out <file>] File to print to (default STDOUT).

Print information on atoms in <mask> for selected topology (first loaded topology by default) with format:

```
#Atom Name #Res Name #Mol Type Charge Mass GBradius El [rVDW] [eVDW]
```

where `#Atom` is the internal atom index, the first `Name` column is the atom name, `#Res` is the atom's residue number, the second `Name` column is residue name, `#Mol` is the atom's molecule number, `Type` is the atom's type (certain topologies only), `Charge` is the atom charge (in units of electron charge), `Mass` is the atom's mass (in amu), `GBradius` is the generalized Born radius of the atom (Amber topologies only), and `El` is the 2 character element string. The final two columns are only shown if the topology contains non-bonded parameters: `rVDW` is the atom's Lennard-Jones radius and `eVDW` is the atom's Lennard-Jones epsilon.

10.3 bondinfo | bonds | printbonds

```
bondinfo [parm <name> | parmindex <#> | <#>]
         [<mask1>] [<mask2>] [out <file>] [nointrares] [noindices]
```

[parm <name> | parmindex <#> | <#>] Name/tag or index of topology. Default is first loaded topology.

[<mask1>] Mask to print bond info for.

[<mask2>] If specified, bonds must match both masks.

[out <file>] File to print to (default STDOUT).

[nointrares] Do not print intra-residue bonds.

[noindices] Do not print bond indices.

Print bond information for atoms in <mask> for selected topology (first loaded topology by default) with format:

```
# Bond Kb Req atom names (numbers)
```

where `Bond` is the internal bond index, `Kb` is the bond force constant, `Req` is the bond equilibrium value (in Angstroms), `atom names` shows both atom names with format `:<residue num>@<atom name>`, and `(numbers)` shows both atom numbers in a comma-separated list. Atom types will be shown in the last column.

If 2 masks are given instead of 1, print info for bonds with first atom in <mask1> and second atom in <mask2>.

10.4 bondparminfo

```
bondparminfo [parm <name> | crdset <set> | parmindex <#> | <#>] [out <file>]
```

[parm <name> | parmindex <#> | <#>] Name/tag or index of topology. Default is first loaded topology.

[out <file>] File to print to (default STDOUT).

Print the bond parameter table with format:

```
#Idx Rk Req
```

Where Idx is the internal bond parameter index, Rk is the bond force constant (in kcal/mol*Ang^2), and Req is the bond equilibrium value (in Ang.).

10.5 change

```
change [parm <name> | parmindex <#> | <#> |
        crdset <COORDS set> ]
{ resname from <mask> to <value> |
      chainid of <mask> to <value> |
      oresnums of <mask> min <range min> max <range max> |
  icodes of <mask> min <char min> max <char max> resnum <#> |
  atomname from <mask> {to <value>|namemap <mapset>} | |
      addbond <mask1> <mask2> [req <length> <rk> <force constant>]
      removebonds <mask1> [<mask2>] [out <file>] |
      bondparm <mask1> [<mask2>] {setrk|scalerk|setreq|scalereq} <value> |
      {mass|charge} [of <mask>] {to <value> |by <offset> |
                                 byfac <factor> |fromset <data set>} |
```

```
      mergeres firstres <start res#> lastres <stop res#> |
      gb {bondi|amber6|mbondi|pbamber|mbondi2|parse|mbondi3} |
      lj1264 [lj1264mask <mask>] [tunfactor <fac>] [c4file <c4file>]
             [polfile <polfile>] [lj1264solvent <solvent>]
    }
```

parm <**name**> | **parmindex** <#> | <#> | **crdset** <**COORDS set**>
Topology to change.

resname from <**mask**> **to** <**value**> Change residue names for residues in <mask> to the given <value>.

chainid of <**mask**> **to** <**value**> Change the chain ID of residues in <mask> to given <value>.

oresnums of <**mask**> **min** <**range min**> **max** <**range max**> Change original residue numbers (to e.g. original PDB numbers) of residues in <mask> to a range starting from <min> and ending with <max>.

icode of <**mask**> **min** <**char min**> **max** <**char max**> <**resnum**> <#> Change residue insertion codes of residues in <mask> to a range of characters starting from <min> and ending with <max>; set the original residue number to <resnum>.

atomname from <**mask**> Change atoms names for atoms in <mask>.

to <**value**> Change atom names for atoms in <mask> to the given <value>.

namemap <**mapset**> Change atom names from reference name to target name according to the given name map set (#Tgt Ref). See 6.1 on page 30 for details on reading in atom name maps.

addbond <**mask1**> <**mask2**> Add bond between atom specified by <mask1> and atom specified by <mask2>.

[req <**length**>**]** The equilibrium bond length in Angstroms.

[rk <**force constant**>**]** The bond force constant in kcal/mol*Angstrom.

removebonds <**mask1**> **[**<**mask2**>**]** Remove bonds from atoms in <mask1>. If <mask2> also given, remove bonds between atoms in <mask1> and atoms in <mask2>.

[out <**file**>**]** If specified, write removed bonds to <file> with format '<residue name> <residue num> <atom name> <atom num>'.

bondparm <**mask1**> [<**mask2**>] {**setrk**|**scalerk**|**setreq**|**scalereq**} <**value**>
Modify bond parameters in bonds selected by <mask1> (and <mask2> if specified) by specified <value>.

setrk Set bond force constants to <value>.

scalerk Scale bond force constants by <value>.

setreq Set bond equilibrium lengths to <value>.

scalereq Scale bond equilibirum lengths by <value>.

mass|**charge** Change mass or charge in specified topology.

of <**mask**> Atoms to change mass/charge of.

to <**value**> Value to change mass/charge to.

by <**offset**> Value to offset masses/charges by.

byfac <**factor**> Value to multiply masses/charges by.

fromset <**data set**> Use values in <data set> for mass/charge; must have the same number of values as atoms selected by <mask>.

mergeres Merge consecutive residues.

firsres <**start res#**> Index (starting from 1) of first residue to merge.

lastres <**stop res#**> Index (starting from 1) of last residue to merge. Should be greater than firstres.

gb {**bondi**|**amber6**|**mbondi**|**pbamber**|**mbondi2**|**parse**|**mbondi3**}
Add/change the GB radii set. Default is mbondi.
See 7.1 on page 36 for details on the GB keywords.

[lj1264] Option to add LJ 12-6-4 parameters. See 7.1 on page 36 for details on LJ 12-6-4 keywords.

Change specified parts of the specified topology. For example, to change atoms named 'HN' to 'H' in topology 0:

```
change parmindex 0 atomname from @HN to H
```

10.6 charge

```
charge [parm <name> | parmindex <#> | <#>] <mask> [out <file>] [name <set>]
```

parm <**name**> | **parmindex** <#> Topology to calculate charge from.

<**mask**> Atom(s) to calculate total charge for (default all).

[out <**file**>**]** File to write total charge to.

[name <set>] If specified, a data set named <set> will be cretaed containing total charge.

Print the total charge of atoms in <mask> (in units of electron charge) for selected topology (first loaded topology by default).

10.7 comparetop

```
comparetop {parm <name> | parmindex <#>} {parm <name> | parmindex <#>} [out <file>]
           [atype] [lj] [bnd] [ang] [dih] [atoms]
```

parm <name> | parmindex <#> Topologies to compare.

out <file> Print results to file instead of screen.

[atype] Only report atom type differences.

[lj] Only report differences in Lennard-Jones parameters.

[bnd] Only report differences in bond parameters.

[ang] Only report differences in angle parameters.

[dih] Only report differences in dihedral parmeters.

[atoms] Only report differences in atom properties.

Compare and report differences in atoms/parameters between two topologies. Differences are reported in standard 'diff' format, with '<' prefix indicating the parameter is from the first topology and '>' prefix indicating the parameter is from the second topology.

10.8 dihedralinfo | dihedrals | printdihedrals

```
dihedralinfo [parm <name> | parmindex <#> | <#>] [<mask1>] [<mask2> <mask3> <mask4>]
             {[<mask1>] [<mask2> <mask3> <mask4>] | tgtidx <#>} [noindices]
             [out <file>] [extra]
```

[parm <name> | parmindex <#> | <#>] Name/tag or index of topology. Default is first loaded topology.

[<mask1>] Mask to print dihedral info for.

[<mask2> <mask3> <mask4>] If specified, dihedrals must match all masks.

tgtidx <#> If specified, print dihedrals only with specified parameter index (starting from 1).

[noindices] Do not print dihedral indices.

[out <file>] File to print to (default STDOUT).

[extra] Print SCEE/SCNB info as well.

Print dihedral information of atoms in <mask> for selected topology (first loaded topology by default) with format:

```
#Dihedral pk phase pn atoms
```

where `#Dihedral` is the internal dihedral index, `pk` is the dihedral force constant, `phase` is the dihedral phase, `pn` is the dihedral periodicity, and `atoms` shows the names of the atoms involved in the angle with format `:<residue num>@<atom name>`, followed by the atom indices involved in a comma-separated list. In addition if the dihedral is an end dihedral, improper dihedral, or both it will be prefaced with an `E`, `I`, or `B` respectively. Atom types will be shown in the last column.

If 4 masks are given instead of 1, print info for dihedrals with first atom in <mask1>, second atom in <mask2>, third atom in <mask3>, and fourth atom in <mask4>.

10.9 hmassrepartition

```
hmassrepartition [parm <name> | crdset <set> | parmindex <#> | <#>]
                 [<mask>] [hmass <hydrogen new mass>] [dowater]
```

parm <**name**> Modify topology selected by name.

crdset <**set**> Modify topology of COORDS set.

parmindex <#> | <#> Modify topology selected by index <#> (starting from 0).

<**mask**> Atoms to modify (all solute atoms by default).

hmass <**hydrogen new mass**> Mass to change hydrogens to (3.024 u by default).

dowater If specified, modify water hydrogen mass as well.

Perform hydrogen mass repartitioning on the specified topology. Hydrogen mass repartitioning means that for a given heavy atom, the mass of all bonded hydrogens are increased (to 3.024 u by default) and the mass of that heavy atom is decreased so as to maintain the same overall mass. The main use case is to allow longer time steps for molecular dynamics integration due to reduced frequency of vibration of bonds to hydrogen atoms.

10.10 improperinfo | impropers | printimpropers

```
improperinfo [parm <name> | parmindex <#> | <#>] [<mask1>] [<mask2> <mask3> <mask4>]
             [out <file>]
```

[parm <name> | parmindex <#> | <#>] Name/tag or index of topology. Default is first loaded topology.

[<mask1>] Mask to print improper info for.

[<mask2> <mask3> <mask4>] If specified, impropers must match all masks.

tgtidx <#> If specified, print impropers only with specified parameter index (starting from 1).

[noindices] Do not print improper indices.

[out <file>] File to print to (default STDOUT).

For specified topology (first by default) either print CHARMM improper info for all atoms in <mask1>, or print info for dihedrals with first atom in <mask1>, second atom in <mask2>, third atom in <mask3>, and fourth atom in <mask4>.

10.11 mass

```
[<parmindex>] [parm <name> | parmindex <#> | <#>] <mask> [out <file>] [name <set>]
```

parm <name> | parmindex <#> Topology to calculate mass from.

<mask> Atom(s) to calculate total mass for (default all).

[out <file>] File to write total mass to.

[name <set>] If specified, a data set named <set> will be cretaed containing total mass.

Print the total mass of atoms in <mask> (in amu) for selected topology (first loaded topology by default).

10.12 molinfo

```
molinfo [parm <name> | parmindex <#> | <#>] <mask> [out <file>]
```

[parm <name> | parmindex <#> | <#>] Name/tag or index of topology. Default is first loaded topology.

<mask> Mask selecting molecules to print info for.

[out <file>] File to print to (default STDOUT).

Print molecule information for atoms in <mask> for selected topology (first loaded topology by default) with format:

```
#Mol  Natom  #Res Name C [SOLVENT]
```

where `#Mol` is the molecule number, `Natom` is the number of atoms in the molecule, `#Res` and `Name` are the residue number and residue name of the first residue in the molecule respectively, and `C` is the chain ID of the first residue. If the molecule is composed on non-consecutive fragments, `#Res`, `Name`, and `C` will be printed for each fragment. `SOLVENT` will be printed if the molecule is currently considered a solvent molecule.

10.13 parm

```
parm <filename> [{[TAG] | name <setname>}]
     [{ nobondsearch |
        [bondsearch <offset>] [searchtype {grid|pairlist}]
      }] [nomolsearch] [renumresidues]
```

<filename> Parameter file to read in; format is auto-detected.

'[TAG]' Optional tag (bounded in brackets) which can be referred to in place of the topology file name in order to simplify references to it (see 3.4 on page 19 for examples of how to use tags).

[name <setname>] Optional name that can be used to refer to the topology in place of the file name.

[bondsearch <offset>] Optional; when searching for bonds via geometry search (default for Topologies without bond information) add <offset> to distances (default 0.2 Å). Increase this if your system includes unusually long bonds.

[searchtype {grid|pairlist}] Change search algorithm from the default search between residues algorithm:

- **grid** Uses a grid when searching for bonds between residues. This can find bonds between residues that are not sequential (e.g. disulfide bonds).
- **pairlist** Uses a pair list to search for bonds between atoms. This can potentially find bonds across periodic boundaries, but is the more experimental of the two.

Advanced Options - Not recommended for general use

[nobondsearch] If specified do not search for bonds via geometry if Topology does not include bond information. May cause some Actions to fail.

[nomolsearch] If specified do not search for molecule information. May cause some Actions to fail.

[renumresidues] If specified, ensure that any residue cannot be part of more than 1 molecule (can occur with e.g. alternate sites). Residues will be renumbered according to molecule information in that case.

Read in parameter file. The file format will be auto-detected. Current formats recognized by cpptraj are listed on page 77. If the file does not contain bond information, cpptraj will attempt to assign bonds based on a simple distance search of atoms within and between residues. The distance cutoff for determining bonds between atoms depends on the elements of the two atoms in question, augmented by <offset>. Molecule information is then determined from bond information.

10.13.1 *PDB format:*

```
[pqr] [readbox] [conect] [noconect] [link] [nolink] [keepaltloc <char>]
```

[pqr] Read charge and radius information from the occupancy and B-factor columns.

[readbox] Read unit cell information from CRYST1 record if present.

[conect] Read CONECT records if present (default).

[noconect] Do not read in CONECT records from PDB file.

[link] Read LINK records if present.

[nolink] Do not read LINK records if present (default).

[keepaltloc <char>] If specified, only keep alternate atom location IDs matching the specified character <char>.

IMPORTANT NOTES FOR PDB FILES Sometimes PDB files can contain alternate coordinates for the same atom in a residue, e.g.:

```
ATOM    806  CA ACYS A 105       6.460 -34.012 -21.801  0.49 32.23
ATOM    807  CB ACYS A 105       6.054 -33.502 -20.415  0.49 35.28
ATOM    808  CA BCYS A 105       6.468 -34.015 -21.815  0.51 32.42
ATOM    809  CB BCYS A 105       6.025 -33.499 -20.452  0.51 35.38
```

If this is the case *cpptraj* will print a warning about alternate location IDs being present but will take no other action. Both residues are considered 'CYS' and the mask ':CYS@CA' would select both atom 806 and 808. If desired, a specific location ID can be kept via the **keepaltloc** keyword. If **keepaltloc** is specified, it should also be specified for any **trajin** commands (see 11.4.3 on page 105). Residue insertion codes are read in but also not used by the mask parser.

10.13.2 Charmm PSF:

```
[param <file>]
```

[param <file>] Read CHARMM parameters from given file.
Can do multiple times.

10.13.3 Gromacs Top

By default cpptraj will look for Gromacs topology data (that is not in the same directory) in the directory defined by the GMXDATA environment variable; specifically, it expects things to be in the "$GMXDATA/top" directory.

10.14 parmbox

```
parmbox [parm <name> | parmindex <#> | <#>] [nobox] [truncoct]
     [x <xval>] [y <yval>] [z <zval>] [alpha <a>] [beta <b>] [gamma <g>]
```

[parm <name> | parmindex <#> | <#>] Name/tag or index of topology to modify. Default is first loaded topology.

[nobox] Remove box information.

[truncoct] Set truncated octahedon angles with lengths equal to <xval>.

[x <xval>] Box X length.

[y <yval>] Box Y length.

[z <zval>] Box Z length.

[alpha <a>] Box alpha angle.

[beta <b>] Box beta angle.

[gamma <g>] Box gamma angle.

Modify the box information for specified topology. Overwrites any box information if present with specified values; any that are not specified will remain unchanged. Note that unlike the ***box*** action this command affect box information immediately. This can be useful for e.g. removing box information from a parm when stripping solvent:

```
parm mol.water.parm7
parmstrip :WAT
parmbox nobox
parmwrite out strip.mol.nobox.parm7
```

10.15 parminfo

```
parminfo [parm <name> | parmindex <#> | <#>] [<mask>]
```

Print a summary of information contained in the specified topology (first loaded topology by default) .

10.16 parmstrip

```
parmstrip <mask> [parm <name> | parmindex <#> | <#>]
```

Strip atoms in <**mask**> from specified topology (by default the first topology loaded). Note that unlike the ***strip*** Action, this permanently modifies the topology for as long as *cpptraj* is running, so this should not be used if the topology is being used to read or write a trajectory via ***trajin***/***trajout***. This command can be used to quickly created stripped Amber topology files. For example, to strip all residues name WAT from a topology and write a new topology:

```
parm mol.water.parm7
parmstrip :WAT
parmwrite out strip.mol.parm7
```

10.17 parmwrite

```
parmwrite out <filename> [{parm <name> | parmindex <#> | <#> | crdset <setname>}]
          [<fmt>] [nochamber]
```

<**filename**> File to write to.

[parm <**name**> | **parmindex** <#> | <#>**]** Topology to write out.

[crdset <**setname**>**]** Write topology from specified COORDS data set.

[<**fmt**>**]** Format keyword. If not specified the file name extension will be used. Default is Amber Topology.

[nochamber] (Amber topology only) Remove any CHAMBER information from the topology.

Write out specified topology (first topology loaded by default) to <**filename**> with format <**fmt**> (Amber topology if not specified). Note that the Amber topology format is the only fully supported format for topology writes.

10.17.1 Amber Topology

```
[nochamber] [writeempty] [nopdbinfo]
```

[nochamber] Do not write CHAMBER information to topology (useful for e.g. using topology for visualization with older versions of VMD).

[writeempty] Write Amber tree, join, and rotate info even if not present.

[nopdbinfo] Do not write "PDB" info (e.g. chain IDs, original res #s, etc).

10.17.2 Charmm PSF

```
[oldpsf] [ext]
```

[oldpsf] Write atom type indices instead of type names (not recommended).

[ext] Use extended format.

10.18 printub | ubinfo

```
printub [parm <name> | parmindex <#> | <#>]
        [<mask1>] [<mask2>] [out <file>] [noindices]
```

[parm <name> | parmindex <#> | <#>] Name/tag or index of topology. Default is first loaded topology.

[<mask1>] Atoms to print UB info for.

[<mask2>] If specified, UB info must match both masks.

[out <file>] File to print to (default STDOUT).

[noindices] Do not print UB indices.

For specified topology (first by default) either print CHARMM Urey-Bradley info for all atoms in <mask1>, or print info for bonds with first atom in <mask1> and second atom in <mask2>.

10.19 resinfo

```
resinfo [parm <name> | parmindex <#> | <#>] <mask>
        [short {nucleic|[maxwidth <#res>] [groupsize <#res>]}]
        [out <file>]
```

[parm <name> | parmindex <#> | <#>] Name/tag or index of topology. Default is first loaded topology.

<mask> Mask selecting residues to print info for.

[short] Use a short 1 character residue name format

- **[maxwidth <#res>]** Max # of residues to print in one line (default 50).
- **[groupsize <#res>]** Max # of residues to put in a group (default 10).
- **[nucleic]** Do a printout suitable for nucleic acid residues (maxwidth 45, groupsize 3).

[out <file>] File to print to (default STDOUT).

Print residue information for atoms in <mask> for selected topology (first loaded topology by default) with format:

```
#Res  Name First  Last Natom #Orig #Mol C
```

where `#Res` is the residue number, `Name` is the residue name, `First` and `Last` are the first and last atom numbers of the residue, `Natom` is the total number of atoms in the residue, `#Orig` is the original residue number (in PDB files), #Mol is the molecule number, and C is the chain ID.

If **short** is specified then residues will be printed out in a condensed format. Each residue name will be shortened to 1 character, and residues are printed out in groups of 10, 5 groups to a line, with each line beginning with a residue number, e.g.

```
> resinfo short 4
1        MGFLAGKKIL ITGLLSNKSI AYGIAKAMHR EGAELAFTYV GQFKDRVEKL
51       CAEFNPAAVL PCDVISDQEI KDLFVELGKV WDGLDAIVHS IAFAPRDQLE
```

If the 1 character name for a residue is unknown it will be shown as the first letter of the residue name in lower-case.

10.20 scaledihedralk

```
scaledihedralk [parm <name> | parmindex <#>] <scale factor> [<mask> [useall]]
```

Scale dihedral force constants for dihderals selected by <mask> for specified topology. If **useall** is specified all atoms in <mask> must be present to select a dihedral, otherwise any atom in <mask> will selected a dihedral.

10.21 solvent

```
solvent [parm <name> | parmindex <#> | <#>] { <mask> | none }
```

Set solvent for selected topology (first loaded topology by default) based on <**mask**>, or set nothing as solvent if **none** is specified.

10.22 timap

```
timap <tgt> [template <name>] [out <file>] [tiout <prefix>]
        [mapout <file>] [name <newparm>]
        [maponly] [replace] [naorder] [aaorder]
        [seed {auto|names|na|aa|none}] [anchor <atomname>]
        [series <a> <b> ...] [outprefix <pfx>] [tioutprefix <pfx>]
        [mapoutprefix <pfx>] [parentout <file>]
Align atoms in topology <tgt> to a user-supplied
template so shared atoms occupy the same indices.  By
default this writes <tgt> as an Amber OFF .lib in
```

template atom order (no dummy atoms). Dual-topology TI files are written only if tiout is given. This is intended for preparing residue libraries for thermodynamic integration (TI) of nucleic acids, amino acids, and small molecules, where two (or more) end states must list common atoms in the same order. For a series of analogs with no predetermined parent, series auto-selects a minimum parent that shares the most with the rest, then maps every analog onto it. Unlike atommap, a one-to-one correspondence is not required: extra atoms on the target are insertions. Partial maps are expected and useful.
The template atom order is the shared-atom order used for mapping. Any topology can be a template (mol2, Amber OFF unit loaded with readdata, and so on). Example ModXNA fragments used by the tests live in test/Test_TIMap/ (see PARENTS.txt). The command does not load them.

<tgt> Topology (or COORDS set) whose atoms will be reordered.

template <name> Parent topology whose current atom order is the shared-atom order. If omitted, <tgt> is mapped to itself; combine with naorder to invent Amber's nucleic-acid walk with no parent file.

out <file> Write <tgt> as an Amber OFF library in template atom order. Default (when maponly is not given): <residue>.sorted.lib.

mapout <file> Write the atom map (output index, target atom, template atom, insertion flag).

name <newparm> Store the remapped topology as a new topology set.

maponly Write the map (and tiout files, if requested) but do not write the default aligned .lib and do not store a remapped topology.

replace Overwrite <tgt> with the remapped atom order.

naorder Walk the template as P → O5' → C5' → C4' → O4' → C1' → base → C3' → C2' → O3' . No parent is required: <tgt> is walked as itself. If template is also given, that parent is walked instead, then <tgt> is mapped onto it.

aaorder Walk <tgt> (or the template, if given) in ff19SB amino19.lib order: N → H → CA → HA → side chain from CB (each heavy atom, then its hydrogens;

smaller branch first) → C → O. Proline is N → CD → ... → CB → CA → C → O. No parent is required. Use this to put a noncanonical amino-acid .lib into the same shared-atom order as Amber ff19SB for TI. The walk is built into the command; it does not read amino19.lib. A smaller amino-acid library already in the test tree is test/Test_Build/amino12.lib.

seed How the correspondence is started. auto (default) uses nucleic-acid scaffold roles when they are detected, otherwise amino-acid N/CA/C/O/CB when a peptide motif is found, otherwise unique atom names. names uses unique names only. na forces nucleic-acid scaffold seeding. aa forces amino-acid N/CA/C/O/CB seeding. none performs no matching (not generally useful). The map is then grown by neighbor element/degree signatures. Partial maps are expected.

anchor <**atomname**> Name of the template atom before which completely unmatched leftovers are inserted (default O3'). Atoms that are bonded to a mapped parent are inserted immediately after that parent instead.

tiout <**prefix**> Optional. Write a dual-topology TI pair of equal size. Lambda 0 is the template with charge-0 dummy atoms for target insertions; lambda 1 is the target with charge-0 dummy atoms for unmatched template atoms. Shared atoms occupy the same indices in both files. Writes <prefix>.0.mol2 / <prefix>.0.lib, <prefix>.1.mol2 / <prefix>.1.lib, <prefix>.scmask (pmemd scmask1 / scmask2), and <prefix>.atoms. Dummy atoms copy the partner's name and coordinates, have charge 0, mass 0, and Amber type DUM. Does not suppress the default aligned .lib unless maponly is also given. A remapped target topology is stored only if name or replace is also given.

series <**a**> <b> ... List two or more analog topologies. Chooses one parent that shares the most with the rest, then maps every listed analog onto that parent (star topology for TI). Do not combine with template. Parent selection: maximize the sum of mapped atoms when every other member is matched onto the candidate; on ties prefer the fewest atoms, then a leadopt-style similarity sum

$\sum_j \exp(-0.1 \cdot (\text{insertions}_j + \text{unmapped}_j))$. That score is adapted from util/leadopt/similarity.py (exp_delta / by_heavy_atom_count; Summa Lab / Jonathan Redmann & Christopher Summa, University of New Orleans). The common substructure is approximated by TIMatch's partial map rather than an external MCS engine (util/leadopt/mcs.py, rule.py, graph.py). The star-parent use case is inspired by util/leadopt/GraphGenerator4.py (Redmann & Summa) without importing that TI-path planner. The leadopt/ tree is reference-only and is not linked into the cpptraj build.

outprefix <**pfx**> With series, write each aligned OFF library as <pfx><name>.sorted.lib (default: <name>.sorted.lib).

tioutprefix <**pfx**> With series, write dual-topology TI files for every non-parent member as <pfx><name>.{0,1}.{mol2,lib}, .scmask, and .atoms.

mapoutprefix <**pfx**> With series, write each atom map as <pfx><name>.map.

parentout <**file**> With series, write the selected parent name and per-candidate scores.

Generating your own templates. If template is given, that parent's current atom order is used. If it is omitted, naorder or aaorder invents Amber's canonical walk on <tgt> itself.

```
# 1. Parent given: analog is sorted to that residue's atom order.
# 2. No parent: naorder / aaorder invents Amber's canonical walk on the analog.
# 3. Optional tiout writes dual-topology TI files.
```

Canonical NA order, no parent (sort this residue the way Amber walks a nucleotide).

```
> readdata FLE.lib name FLE
> timap FLE[FLE] naorder out FLE.lib
> go
```

Nucleic acids onto a parent (example: FLE = unmodified rA onto ERN = unmodified dA). Shared atoms keep the dA indices; the 2'-OH is an insertion next to C2'; dA H2" is unmatched on the template. Default: write FLE in ERN atom order as an OFF library.

```
> readdata ERN.lib name ERN
> readdata FLE.lib name FLE
```

```
> timap FLE[FLE] template ERN[ERN] out FLE.lib
> go
```

Add tiout to also write dual-topology libraries (34 atoms each) and pmemd scmask lines.

```
> timap FLE[FLE] template ERN[ERN] tiout fle_ern
> go
```

Small molecules (example: phenol onto benzene). The ring maps by unique names; OH inserts after C1; benzene H1 is unmatched.

```
> parm benzene.mol2 name benzene
> parm phenol.mol2 name phenol
> timap phenol template benzene out phenol.lib
> go
```

Amino acids (example: selenocysteine onto cysteine). Use Amber OFF so selenium is elmnt 34. Mol2 atom name SE is read as sulfur. Backbone names map; SE is an insertion at CB; cysteine SG is unmatched.

```
> readdata cys.lib name CYS
> readdata sec.lib name SEC
> timap SEC[SEC] template CYS[CYS] out SEC.lib
> go
```

Canonical amino-acid order, no parent (sort a noncanonical .lib the way ff19SB walks Cys/Ala/...).

```
> readdata ncaa.lib name ncaa
> timap ncaa[ncaa] aaorder out ncaa.lib
> go
```

Series of analogs (auto-select parent, then map each onto it for TI). Example: phenol and benzene; benzene is chosen (same mapped total, fewer atoms).

```
> parm benzene.mol2 name benzene
> parm phenol.mol2 name phenol
> timap series phenol benzene outprefix series_ tioutprefix series_ti_ parentout se
> go
```

How the nucleic-acid walk was chosen

ModXNA (https://github.com/modna-ff) is the baseline chemistry for naorder. It parameterizes nucleic acids as fragments (nucleobase, sugar, backbone) rather than as whole residues. Combining those fragments into one

.lib does not put shared atoms in a stable order. That breaks thermodynamic integration (common atoms must occupy the same indices) and makes residues harder for nastruct to treat as nucleotides, because nastruct identifies sugars and bases from connectivity and Amber-like names (C1', N9/N1, and so on), not from file order.
The walk is therefore not copied from any one ModXNA file. The fragment library was grouped by chemical class (backbone with or without phosphate, purine vs pyrimidine base, 2' pattern of the sugar). One consensus parent was kept for each class; those 11 example fragments are in test/Test_TIMap/ (see PARENTS.txt). They are test data, not installed with cpptraj. Each parent's atom list is the recommended shared-atom order for mapping other members of that class. Combined nucleotides are a separate case: they are mapped to a user residue (for example unmodified rA onto dA), not to those fragments.
The naorder walk is a 5' $\rightarrow$ 3' sugar-phosphate traversal chosen so that (1) the shared scaffold is a fixed prefix independent of how the file was written, (2) chemical insertions sit next to their attachment atom (nucleobase analogs after the glycosidic nitrogen χ, 2'-OH / OMe / F after C2'), and (3) the 3' linker O3' remains last among scaffold atoms so unmatched leftovers can be placed just before it. Hydrogens follow their heavy atom, sorted by name, matching Amber convention.

```
P -> OP (name-sorted) -> O5' -> C5' -> C4' -> O4' -> C1' ->
  base (BFS from chi, never recrossing C1') -> C3' -> C2' + 2' substituents -> O3'
```

That is the order naorder applies when no template is given (the residue is walked as itself). When a ModXNA parent is given, timap uses that parent's current atom order instead; those files were already written in the class order above. The amino-acid walk (aaorder) plays the same role using ff19SB amino19.lib as the baseline.
Alias: timatch.

10.23 updateparameters

parm <name> | parmindex <#> setname <parm set> [verbose <#>]

parm <**name**> | **parmindex** <#> Topology to update.

setname <**parm set**> Topology or parameter data set containing parameters to use.

[verbose <#>**]** Verbosity during parameter update.

NOTE: This command is provided for convenience only. For editing topology files, ParmEd is a much better alternative.

Update parameters in specified topology with those from <parm set>. <parm set> can either be a parameter set or a topology. If a parameter from <parm set> does not exist in the topology it will be added.

For example, to modify parameters in a topology file named lys.parm7 with those from parameter file kcx.str:

```
# Read Topology to modify
parm lys.parm7
# Read CHARMM parameters
readdata kcx.str as charmmrtfprm name MyParm
# Update parameters in Topology with those from kcx.str
updateparameters parmindex 0 setname MyParm
# Write out the updated Topology
parmwrite out lys.kcx.parm7
```

11 Trajectory File Commands

These commands control the reading and writing of trajectory files. There are three trajectory types in *cpptraj*: input, output, and reference. In *cpptraj*, trajectories are always associated with a topology file. If a topology file is not specified, a trajectory file will be associated with the first topology file loaded by default (this is true for both input and output trajectories.

Cpptraj currently understands the following trajectory file formats:

Format	Keyword(s)	Extension	Notes
Amber Trajectory	crd	.crd	Default format if keywords/extensions not recognized.
Amber NetCDF	cdf, netcdf	.nc	No compression.
Amber Restart	restart	.rst7, .rst	
Amber NetCDF Restart	ncrestart, restartnc	.ncrst	
Charmm "DCD" Trajectory	dcd, charmm	.dcd	
Charmm COORdinates	cor	.cor	
Charmm Restart	charmmres	.res	Read Only
PDB	pdb	.pdb	
Mol2	mol2	.mol2	
Scripps Binpos	binpos	.binpos	
Gromacs TRR	trr	.trr	
Gromacs GRO	gro	.gro	Read Only
Gromacs XTC	xtc	.xtc	
Gromacs TNG	tng	.tng	Read Only
CIF	cif	.cif	Read Only
Tinker ARC	arc	.arc	Read Only
SQM Input	sqm	.sqm	Write Only
SDF	sdf	.sdf	Read Only
XYZ	xyz	.xyz	
Desmond DTR (Anton)	dtr	.dtr	Read Only
LMOD Conflib	conflib	.conflib	Read Only, Detection by extension
MDTraj H5	h5	.h5	Read Only
MDAnalysis H5MD	h5md	.h5md	Read Only

The following trajectory-related commands are available:

Command	Description
ensemble	Set up a trajectory ensemble for reading during a run.
ensemblesize	(MPI only) specify number of members expected in subsequent ***ensemble*** commands.
reference	Read in a reference structure.
trajin	Set up a trajectory for reading during a Run.
trajout	Set up an output trajectory or ensemble for writing during a Run.

11.1 ensemble

```
ensemble <file0> {[<start>] [<stop> | last] [offset]} | lastframe
         [parm <parmfile / tag> | parmindex <#>]
         [trajnames <file1>,<file2>,...,<fileN>
         [{nosort |
       bycrdidx |
           bytemp |
           remlog <remlogfile> [nstlim <nstlim> ntwx <ntwx>]}]
```

<file0> Lowest replica filename.

[<start>] Frame to begin reading ensemble at (default 1).

[<stop> | last] Frame to stop reading ensemble at; if not specified or 'last' specified, end of trajectories.

[<offset>] Offset for reading in trajectory frames (default 1).

[lastframe] Select only the final frame of the trajectories.

[parm <parmfile>] Topology filename/tag to associate with trajectories (default first topology).

[parmindex <#>] Index of Topology to associate with trajectories (default 0, first topology).

[trajnames <file1>,...,<fileN>] Do not automatically search for additional replica trajectories; use comma-separated list of trajectory names.

[nosort] Do not attempt to sort trajectories. Useful for H-REMD trajectories which are already sorted by replica/Hamiltonian, or collections of MD trajectories.

[bycrdidx] For H-REMD trajectories, sort by coordinate indices stored in trajectory files. This is preferred over sorting via 'remlog'.

[bytemp] If specified the ensemble will be sorted by temperature values instead of replica indices.

[remlog <remlogfile>] For H-REMD trajectories only, use specified REMD log file to sort trajectories by coordinate index (instead of by replica/Hamiltonian).

[nstlim <nstlim> ntwx <ntwx>] If trajectory and REMD log were not written at the same rate, these are the values for nstlim (steps between

```
each exchange) and ntwx (steps between
trajectory write) used in the REMD simulation.
```

Read in and process trajectories as an ensemble. Similar to '***trajin*** remdtraj', except instead of processing one frame at a target temperature, process all frames. This means that action and trajout commands apply to the entire ensemble; note however that not all actions currently function in ***'ensemble'*** mode. For example, to read in a replica ensemble, convert it to temperature trajectories, and calculate a distance at each temperature:

```
parm ala2.99sb.mbondi2.parm7
ensemble rem.crd.000 trajnames rem.crd.001,rem.crd.002,rem.crd.003
trajout temp.crd
distance d1 out d1.ensemble.dat @1 @21
```

This will output 4 temperature trajectories named 'temp.crd.X', where X ranges from 0 to 3 with 0 corresponding to the lowest temperature, and 'd1.ensemble.dat' containing 4 columns, each corresponding to a temperature. If run with MPI, data will be written to separate files named 'd1.ensemble.dat.X', similar to the output trajectories.

Note that in parallel (i.e. MPI) users should specify the ***ensemblesize*** command prior to ***ensemble*** in order to improve set up efficiency.

H-REMD trajectories which are typically already sorted by replica/Hamiltonian can be sorted by coordinate index instead with 'bycrdidx' (if the trajectory contains coordinate indices) or by REMD log data specified with the 'remlog' keyword. For example, to sort by coordinate index using a REMD log and write sorted trajectories:

```
parm ../tz2.nhe.parm7
ensemblesize 4
ensemble rem.crd.001 remlog rem.log nstlim 1000 ntwx 1000
trajout sorted.remlog.nc
```

To sort by coordinate index when trajectories contain coordinate indices:

```
parm ../tz2.nhe.parm7
ensemblesize 4
ensemble rem.crd.001 bycrdidx
trajout sorted.crdidx.nc
```

11.2 ensemblesize

```
ensemblesize <#>
```

This command is MPI only. It is used to set the expected number of members in any subsequent ***ensemble*** command, which dramatically improves set up efficiency.

11.3 reference

```
reference <name> [<frame#>] [<mask>] ([tag]) [lastframe] [crdset]
          [parm <parmfile / tag> | parmindex <#>]
```

<name> File name (or COORDS set name if 'crdset' specified) to read in as reference; any trajectory recognized by 'trajin' can be used.

[<frame#>] Frame number to use (default 1).

[<mask>] Only load atoms corresponding to <mask> from reference.

([tag]) Tag to give this reference file, e.g. "[MyRef]"; BRACKETS MUST BE INCLUDED.

[lastframe] Use last frame of reference.

[crdset] Use for COORDS data set named <name> instead of file.

[parm <parmfile/tag>] Topology filename/tag to associate with reference (default first topology).

[parmindex <#>] Index of Topology to associate with reference (default 0, first topology).

Use specified trajectory as reference coordinates. For trajectories with multiple frames, the first frame is used if a specific frame is not specified. An optional tag can be given (bounded in brackets) which can then be used in place of the name (see 3.4 on page 19 for examples of how to use tags). If desired, an atom mask can be used to read in only specified atoms from a reference.

Reference coordinates are now considered COORDS data sets and can be used anywhere a COORDS data set could, which allows reference structures to be manipulated once they are loaded. For example, a reference structure could be centered on the origin like so:

```
reference tz2.rst7 [MyRef]
crdaction [MyRef] center origin
```

Note that the 'average' keyword has been deprecated for reference. If desired, an averaged reference COORDS data set can be created from a trajectory using the 'average' command like so:

```
parm myparm.parm7
trajin mytraj.nc
rms first :1-12
average crdset RefAvg
run
rms ToAvg reference :1-12 out ToAvg.dat
```

11.4 trajin

```
trajin <filename> {[<start> [<stop> | last] [<offset>]]} | lastframe
       [parm <parmfile / tag> | parmindex <#>]
       [mdvel <velocities>] [mdfrc <forces>]
       [as <format keyword>] [ <Format Options> ]
       [ remdtraj {remdtrajtemp <Temperature> | remdtrajidx <idx1,idx2,...>
                   | remdtrajvalues <value1,value2,...>}
                  [trajnames <file1>,<file2>,...,<fileN>] ]
```

<filename> Trajectory file to read in.

[<start>] Frame to begin reading at (default 1). If a negative value is given it means "<start> frames before <stop>".

[<stop> | last] Frame to stop reading at; if not specified or 'last' specified, end of trajectory.

[<offset>] Offset for reading in trajectory frames (default 1).

[lastframe] Select only the final frame of the trajectory.

[parm <parmfile/tag>] Topology filename/tag to associate with trajectory (default first topology).

[parmindex <#>] Index of Topology to associate with trajectory (default 0, first topology).

[mdvel <velocities>] Use velocities from specified file.

[mdfrc <forces>] Use forces from specified file.

[as <format keyword>] Force file to be read as specified format; overrides file autodetection.

[<Format Options>] See below.

[remdtraj] Read <filename> as the first replica in a group of replica trajectories.

remdtrajtemp <Temperature> | remdtrajidx <idx1,idx2,...> Use frames at <Temperature> (for temperature replica trajectories) or index <idx1,idx2,...> (for Hamiltonian replica trajectories); For Multidimensional REMD simulations, multiple values are comma-separated.

remdtrajvalues <value1,value2,...> Use frames at <value1,value2,...> (for Multidimensional REMD trajectories). Each value may correspond to either temperature, pH, Redox Potential or Hamiltonian index. The values need to be

entered in the same order as the dimensions in the Multidimensional REMD simulation. For example, for T,pH-REMD value1 would correspond to a temperature and value2 to a pH. In the command, the values are comma-separated.

[trajnames <file1>,...,<fileN>] Do not automatically search for additional replica trajectories; use comma-separated list of trajectory names.

Read in trajectory specified by filename. See page 98 for currently recognized trajectory file formats. If just the <start> argument is given, all frames from <start> to the last frame of the trajectory will be read. To read in a trajectory with offsets where the last frame # is not known, specify the **last** keyword instead of a <stop> argument, e.g.

```
trajin Test1.crd 10 last 2
```

This will process Test1.crd from frame 10 to the last frame, skipping by 2 frames. To explicitly select only the last frame, specify the **lastframe** keyword:

```
trajin Test1.crd lastframe
```

Here is an example of loading in multiple trajectories which have difference topology files:

```
parm top0.parm7
parm top1.parm7
parm top2.parm7 [top2]
parm top3.parm7
trajin Test0.crd
trajin Test1.crd parm top1.parm7
trajin Test2.crd parm [top2]
trajin Test3.crd parmindex 3
```

Test0.crd is associated with top0.parm7; since no parm was specified it defaulted to the first parm read in. Test1.crd was associated with top1.parm7 by filename, Test2.crd was associated with top2.parm7 by its tag, and finally Test3.crd was associated with top3.parm7 by its index (based on the order it was read in).

Replica Trajectory Processing

If the **remdtraj** keyword is specified the trajectory is treated as belonging to the lowest # replica of a group of REMD trajectories. The remaining replicas can be either automatically detected by following a naming convention of <REMDFILENAME>.X, where X is the replica number, or explicitly specified in a comma-separated list following the **trajnames** keyword. All trajectories will be processed at the same time, but only frames with a temperature matching the one specified by **remdtrajtemp** or **remdtrajidx** will be processed.

For example, to process replica trajectories rem.001, rem.002, rem.003, and rem.004, grabbing only the frames at temperature 300.0 (assuming that this is a temperature in the ensemble):

```
trajin rem.001 remdtraj remdtrajtemp 300
```

or

```
trajin rem.001 remdtraj remdtrajtemp 300 trajnames rem.002,rem.003,rem.004
```

Note that the **remdout** keyword is deprecated. For this functionality see the **ensemble** keyword.

11.4.1 *Options for Amber NetCDF, Amber NC Restart, Amber Restart:*

`[usevelascoords] [usefrcascoords]`

usevelascoords `Read in velocities in place of coordinates if present.`

usefrcascoords `Read in forces in place of coordinates if present.`

11.4.2 *Options for CHARMM DCD:*

`[{shape | namdcell | charmmcell}]`

shape `Force reading of box info as CHARMM shape matrix (XX XY YY XZ YZ ZZ).`

namdcell `Force reading of box info as NAMD unit cell (X cos(g) Y cos(b) cos(a) Z).`

charmmcell `Force reading of box info as old CHARMM unit cell (X Y Z a b g).`

Note that CHARMM trajectories can have unit cell data stored in one of two ways. Older versions (<22) of charmm store the 3x lengths (X Y Z, in Angstroms) and 3x angles (alpha beta gamma, in degrees). Newer versions (>=22) store elements of the symmetric shape matrix (XX, XY, YY, XZ, YZ, ZZ). CPPTRAJ will attempt to automatically detect which type of parameters are present, but this can be overridden with the **shape** and **charmmcell** keywords. The **namdcell** keyword is provided for compatibility with DCD trajectories produced by VMD/NAMD, but note these trajectories only store a version of the shape matrix that is correct if the unit cell is also X-aligned.

11.4.3 Options for PDB files:

```
[keepaltloc <char>]
```

[keepaltloc <char>] If specified, only keep alternate atom location IDs matching the specified character <char>.

Note that if **keepaltloc** is specified, the associated topology should not have alternate location IDs, i.e. if the topology is from a PDB the **keepaltloc** keyword may need to be used with the **parm** command (see 10.13.1 on page 87).

11.5 trajout

```
trajout <filename> [<format>] [append] [nobox] [novelocity]
        [notemperature] [notime] [noforce] [noreplicadim]
        [parm <parmfile> | parmindex <#>] [onlyframes <range>] [title <title>]
        [onlymembers <memberlist>]
        [start <start>] [stop <stop>] [offset <offset>]
        [ <Format Options> ]
```

<filename> Trajectory file to write to.

[<format>] Keyword specifying output format (see Table on page 98). If not specified format will be determined from extension, otherwise default to Amber trajectory.

[append] If <filename> exists, frames will be appended to <filename>.

[nobox] Do not write box coordinates to trajectory.

[novelocity] Do not write velocities to trajectory.

[notemperature] Do not write temperature to trajectory.

[notime] Do not write time to trajectory.

[noreplicadim] Do not write replica dimensions to trajectory.

[parm <parmfile>] Topology filename/tag to associate with trajectory (default first topology).

[parmindex <#>] Index of Topology to associate with trajectory (default 0, first topology).

[onlyframes <range>] Write only the specified input frames to <filename>.

[title <title>] Output trajectory title.

[onlymembers <memberlist>] Ensemble processing only; only write from specified members (starting from 0).

[start <start>] `Begin output at frame <start> (1 by default).`

[stop <stop>] `End output at frame <stop> (last frame by default).`

[offset <offset>] `Skip <offset> frames between each output (1 by default).`

During a run, write frames to trajectory specified by filename in specified file format (Amber trajectory if none specified) after all Action processing has occurred. To write out trajectories within the Action queue see the outtraj Action (12.59 on page 201). See page 98 for currently recognized output trajectory formats and their associated keyword(s). Note that now the file type can be determined from the output extension if not specified by a keyword. Multiple output trajectories of any format can be specified.

Frames will be written to the output trajectory when the parameter file being processed matches the parameter file the output trajectory was set up with. So given the input:

```
parm top0.parm7
parm top1.parm7 [top1]
trajin input0.crd
trajin input1.crd parm [top1]
trajout output.crd parm [top1]
```

only frames read in from input1.crd (which is associated with top1.parm7) will be written to output.crd. The trajectory input0.crd is associated with top0.parm7; since no output trajectory is associated with top0.parm7 no frames will be written when processing top0.parm7/input0.crd.

If **onlyframes** is specified, only input frames matching the specified range will be written out. For example, given the input:

```
trajin input.crd 1 10
trajout output.crd onlyframes 2,5-7
```

only frames 2, 5, 6, and 7 from input.crd will be written to output.crd.

Cell not X-aligned Warning

Certain Actions (e.g. ***align***, ***rms***, ***principal***, etc.) can rotate the unit cell vectors (i.e. the box) if they are present. Some trajectory formats do not support writing out box coordinates if the unit cell is not "X-aligned"; in other words, if the unit cell "A" vector is not aligned with the coordinate X-axis and the "B" vector is not in the X-Y plane. If this is the case, the following warnings may appear:

```
Warning: Unit cell is not X-aligned. Box cannot be properly stored as <format>.
Warning: Set <#>; unit cell is not X-aligned. Box cannot be properly stored as <format>
```

This means that the frame will be written with the X-aligned unit cell instead of the actual unit cell. Imaging will not be possible with a trajectory written this way. Currently the only trajectory formats that support writing non-X-aligned cells are the Gromacs TRR and XTC formats.

If unit cell information is no longer needed, it can be removed (via e.g. the ***box*** action, the ***strip*** action with the **'nobox'** keyword, etc.) to prevent these warnings from triggering.

11.5.1 *Options for pdb format*

```
[dumpq | parse | vdw] [pdbres] [pdbatom]
[pdbv3] [pdbchain] [teradvance] [terbyres | pdbter | noter]
[model | multi] [chainid <ID>] [sg <group>]
[include_ep] [conect] [conectmode <m>] [keepext] [usecol21]
[bfacdefault <#>] [occdefault <#>]
[bfacdata <set>] [occdata <set>] [bfacbyres] [occbyres]
[bfacscale] [occscale] [bfacmax <max>] [occmax <max>]
[adpdata <set>] [{hybrid36|wrapnumbers}]
```

dumpq PQR format; write charges (in units of e-) and GB radii to occupancy and B-factor columns respectively.

parse PQR format; write charges and PARSE radii to occupancy/B-factor columns.

vdw PQR format; write charges and vdW radii to occupancy/B-factor columns.

pdbres Use PDB V3 residue names. Will write a default chain ID ('Z') for each residue if the corresponding topology does not have chain ID information.

pdbatom Use PDB V3 atom names.

pdbv3 Use PDB V3 residue/atom names. Same as specifying 'pdbres' and 'pdbatom'.

pdbchain Restrict PDB chain ID to a single character (PDB V3 standard), otherwise allow chain IDs up to 2 characters.

topresnum Use topology residue numbers; otherwise use original residue numbers.

teradvance Increment record (atom) number for TER records (not done by default).

terbyres Print TER cards based on residue sequence instead of molecules.

pdbter Print TER cards according to original PDB TER (if available).

noter Do not write TER cards.

model (Default) Frames will be written to a single PDB file separated by MODEL/ENDMDL keywords.

multi Each frame will be written to a separate file with the frame # appended to <filename>.

chainid <**ID**> Write PDB file with chain ID <ID>.

sg <**group**> Space group for CRYST1 record; only used if box coordinates written.

include_ep Include extra points.

conect Write CONECT records for all bonds.

conectmode <**m**> Write CONECT records for <m>='all' (all bonds), 'het' (HETATM only), 'none' (no CONECT).

keepext Keep filename extension; write '<name>.<num>.<ext>' instead (implies 'multi').

usecol21 Use column 21 for 4-letter residue names.

bfacdefault <#> Default value to use in B-factor column (default 0.0).

occdefault <#> Default value to use in occupancy column (default 1.0).

bfacdata <**set**> Use data in <set> for B-factor column.

occdata <**set**> Use data in <set> for occupancy column.

bfacbyres If specified assume X values in B-factor data set are residue numbers.

occbyres If specified assume X values in occupancy data set are residue numbers.

bfacscale If specified scale values in B-factor column between 0 and <bfacmax>.

occscale If specified scale values in occupancy column between 0 and <occmax>.

bfacmax <**max**> Max value for bfacscale.

occmax <**max**> Max value for occscale.

adpdata <**set**> Use data in <set> (e.g. from the *atomicfluct* command, on page 119) for anisotropic B-factors.

hybrid36 Use hybrid36 formatting for large atom/residue numbers (default).

wrapnumbers Wrap large atom/residue numbers to zero (previous behavior).

11.5.2 *Options for Amber ASCII format:*

```
[remdtraj] [highprecision] [mdvel|mdfrc]
```

remdtraj Write REMD header to trajectory that includes temperature: 'REMD <Replica> <Step> <Total_Steps> <Temperature>'. Since *cpptraj* has no concept of replica number, 0 is printed for <Replica>. <Step> and <Total_Steps> are set to the current frame #.

highprecision (EXPERT USE ONLY) Write with 8.6 precision instead of 8.3. Note that since the width does not change, the precision of large coords may be lower than 6.

mdvel Write velocities instead of coordinates.

mdfrc Write forces instead of coordinates.

11.5.3 *Options for Amber NetCDF format:*

```
[remdtraj] [mdvel] [mdfrc] [mdcrd]
```

remdtraj Write replica temperature to trajectory.

mdvel Write only velocity information in trajectory.

mdfrc Write only force information in trajectory.

mdcrd Write coordinates to trajectory (only required with mdvel/mdfrc).

hdf5 Create file as NetCDF4/HDF5 instead of NetCDF4 (classic).

compress Use compression in NetCDF4/HDF5 file.

icompress Use lossy compression in NetCDF4/HDF5 file via conversion to integers.[6]

11.5.4 *Options for Amber Restart/NetCDF Restart format:*

```
[remdtraj] [novelocity] [notime] [time0 <initial time>] [dt <timestep>] [keepext]
```

remdtraj Write replica temperature to restart. Note that this will automatically include time in the restart file (see the time0 keyword).

time0 <initial time> Time for first frame (default 1.0).

dt <timestep> Time step between frames (default 1.0). Time is calculated as t=(time0+frame)*dt.

keepext Keep filename extension; write '<name>.<num>.<ext>' instead.

11.5.5 *Options for CHARMM COORdinates:*

```
[keepext] [ext] [segid <segid>] [segmask <mask> <segid> ...]
```

keepext Keep filename extension; write '<name>.<num>.<ext>'

ext Use 'extended' format (default when > 99999 atoms).

segid <**segid**> Use <segid> as segment ID for all atoms.

segmask <**mask**> <**segid**> Use <segid> as segment ID for atoms selected by <mask>. Can be specified more than once.

11.5.6 *Options for CHARMM DCD:*

```
[x64] [ucell] [veltraj] [{shape | namdcell | charmmcell}]
```

x64 Use 8 byte block size (default 4 bytes).

veltraj Write velocity trajectory instead of coordinates.

dt Set trajectory time step in ps.

nstep # steps between frames.

step0 Initial step.

shape Force writing box info as CHARMM shape matrix (XX XY YY XZ YZ ZZ).

namdcell Force writing box info as NAMD unit cell (X cos(g) Y cos(b) cos(a) Z).

charmmcell Force writing box info as old CHARMM unit cell (X Y Z a b g).

Note that by default CPPTRAJ will try to write the symmetric shape matrix if box information is present. If this is not possible, CPPTRAJ will fall back to writing unit cell parameters (lengths and angles) as long as the cell is X-aligned. For more information see 11.4.2 on page 104.

11.5.7 *Options for GROMACS TRX/XTC format:*

```
[dt <time step>]
```

dt Time step tp multiply set numbers by (default 1.0). Ignored if time already present.

Note: these formats can write rotated (i.e. non-X-aligned) unit cells.

11.5.8 *Options for mol2 format:*

[single | multi] [sybyltype] [sybylatom <file>] [sybylbond <file>] [keepext]

single (Default) Frames will be written to a single Mol2 file separated by MOLECULE keywords.

multi Each frame will be written to a separate file with the frame # appended to <filename>.

sybyltype Convert Amber atom types (if present) to SYBYL types. Requires $AMBERHOME is set.

sybylatom File containing Amber to SYBYL atom type correspondance (optional).

sybylbond File containing Amber to SYBYL bond type correspondance (optional).

keepext Keep filename extension; write '<name>.<num>.<ext>' instead (implies 'multi').

atombondorder Sort bonds by first atom index (will produce Mol2 files similar to LEaP).

11.5.9 Options for SQM input format:

[charge <c>]

charge <c> Set total integer charge. If not specified it will be calculated from atomic charges.

11.5.10 Options for XYZ format:

[ftype {namexyz|atomxyz|xyz}] [titletype {none|single|perframe}] [width <#>] [prec <#>]

ftype {atomxyz|xyz} Choose either 'NAME X Y Z' (default), 'ATOM X Y Z', or 'X Y Z' output format. 'namexyz' format is the standard XYZ format, where each frame is preceded by the number of atoms and a comment. The comment written by CPPTRAJ will include the set number and box information (if present).

titletype {none|single|perframe} No title, one title (default), or title before every frame. Only applies if not 'namexyz'.

width <#> Output format width.

prec <#> Output format precision.

12 Action Commands

Actions in *cpptraj* operate on frames read in by the ***trajin*** or ***ensemble*** commands one at a time and extract derived data, modify the coordinates/topology in some way, or both. Most Actions in *cpptraj* function exactly the way they do in *ptraj* and are backwards-compatible. Some Action commands in *cpptraj* have extra functionality compared to *ptraj* (such as the per-residue RMSD function of the ***rmsd*** Action, or the ability to write out stripped topologies for visualization in the ***strip*** Action), while other Actions produce slightly different output (like the ***hbond***/***secstruct*** Actions).

Unlike some other command types, when an Action command is issued it is by default added to the Action queue and is not executed until trajectory processing is started (e.g. by a ***run*** or ***go*** command). However, Actions can be executed immediately on COORDS data sets via the ***crdaction*** command (8.3 on page 46).

When a frame is modified by an Action, it is modified for every Action that follows them during trajectory processing. For example, given a solvated system with water residues named WAT and the following Action commands:

```
rmsd R1 first :WAT out water-rmsd.dat
strip :WAT
rmsd R2 first :WAT out water-rmsd-2.dat
```

the first ***rms*** command will be valid, but the second ***rms*** command will not since all residues named WAT are removed from the state by the ***strip*** command.

Note that for commands which can use a reference mask as well as a target mask (e.g. ***rms***, ***drmsd***, ***symmrmsd***, etc.) there must be a 1 to 1 correspondence between the atoms in each mask, i.e. the *number of atoms and the ordering of selected atoms must be the same.*

The following Actions are available. If an Action may modify coordinate/topology information for subsequent Actions it is denoted with an X in the `Mod` column.

Command	Description	Mod
addatom	Temporarily add an atom to the system.	X
align	Align structure to a reference.	X
angle	Calculate the angle between three points.	
areapermol	Calculate area per molecule for molecules in a specified plane.	
atomiccorr	Calculate average correlation between motions of specified atoms.	
atomicfluct, rmsf	Calculate root mean square fluctuation of specified atoms/residues.	
atommap	Attempt to create a map between atoms in molecules with different atom ordering.	X

autoimage	Automatically re-image coordinates.	X
average	Calculate average structure.	
avgbox	Calculate average unit cell (box), primarily for unwrapping NPT trajectories.	
bounds	Calculate the min/max coordinates for specified atoms. Can be used to create grid data sets.	
box	Set or overwrite box information for frames.	
center	Center specified coordinates to box center or onto reference structure.	X
check, checkoverlap, checkstructure	Check for bad atomic overlaps or bond lengths. Can be used to skip corrupted frames.	
checkchirality	Report chirality around alpha carbons in amino acids (L, D).	
closest, closestwaters	Retain only the specified number of solvent molecules closest to specified solute.	X
clusterdihedral	Assign frames into clusters based on binning of backbone dihedral angles in amino acids.	
contacts	Older version of ***nativecontacts***, retained for backwards compatibility.	
createcrd	Create a COORDS data set from input frames.	
createreservoir	Create a structure reservoir for use with reservoir REMD simulations.	
density	Calculate density along a coordinate.	
diffusion	Calculate translational diffusion of molecules.	
dihedral	Calculate the dihedral angle using four points.	
dihrms, dihedralrms	Calculate the RMSD of dihedrals to dihedrals in a reference structure.	
dipole	Bin dipoles of solvent molecules in 3D grid. Not well tested, may be obsolete.	
distance	Calculate the distance between two points.	
drms, drmsd	Calculate the RMSD of distance pairs within selected atoms.	
dssp, secstruct	Calculate secondary structure content using the DSSP algorithm	
enedecomp	Perform per-atom energy decomposition.	
energy	Calculate simple bond, angle, dihedral, and non-bonded energy terms (no PME).	
esander	Calculate energies using via SANDER; requires compilation with the SANDER API.	
filter	Filter frames for subsequent Actions using data sets and user defined criteria.	
fixatomorder	Fix atom ordering so that all atoms in molecules are sequential.	X

fiximagedbonds	Fix bonds which have been split across periodic boundaries by imaging.	
gist	Perform grid inhomogenous solvation theory.	
grid	Bin selected atoms on a 3D grid.	
hbond	Calculate hydrogen bonds using geometric criteria.	
image	Re-image coordinates. The ***autoimage*** command typically provides better results.	X
jcoupling	Calculate J-coupling values from specified dihedral angles.	
keep	Keep specified atoms in system.	X
lessplit	Split/average frames from LES trajectories.	
lie	Calculate linear interaction energy between user-specified ligand and surroundings.	
lipidorder	Calculate order parameters for lipids in planar membranes.	
lipidscd	Calculate lipid order parameters SCD (|<P2>|) for lipid chains. Automatically identifies lipids.	
makestructure	Modify structure by applying dihedral values to specified residues.	X
mask	Print the results of selection by specified atom mask. Good for distnace-based masks.	
matrix	Calculate a matrix of the specified type from input coordinates.	
mindist/maxdist	Calculate the minimum or maximum distance between pairs of atoms/residues/molecules.	
minimage	Calculate minimum non-self imaged distance between atoms in specified masks.	
molsurf	Calculate Connolly surface area of specified atoms. Cannot do partial surface areas.	
multidihedral	Calculate multiple dihedral angles of specified/given types.	
multivector	Calculate multiple vectors between specified atoms.	
nastruct	Perform nucelic acid structure analysis.	
nativecontacts	Calculate native contacts within a region or between two regions using a given reference. Can also be used to get min/max distances between groups of atoms.	
outtraj	Write frames to a trajectory file within a list of Actions.	
pairdist	Calculate pair distribution function.	
pairwise	Calculate pair-wise non-bonded energies.	
principal	Calculate and optionally align system along principal axes.	X
projection	Project coordinates along given eigenvectors.	

pucker	Calculate ring pucker using five or six points.	
radgyr, rog	Calculate radius of gyration (and optionally tensor) for specified atoms.	
radial, rdf	Calculate radial distribution function.	
randomizeions	Swap specified ions with randomly selected solvent molecules.	X
remap	Re-map atoms according to a given data set.	X
replicatecell	Replicate unit cell in specified (or all) directions for specfied atoms and write to trajectory.	
rms, rmsd	Perform best fit of coordinates to reference and calculate coordinate RMSD. Fitting can be disabled.	X
rotate	Rotate the system around X/Y/Z axes, a specified axis, or via given rotation matrices.	X
runavg, runningaverage	Calculate the running average of coordinates over specified window size.	X
scale	Scale coordinates in X/Y/Z directions by specified factors.	X
setvelocity	Set velocities for specified atoms using Maxwellian distribution based on given temperature.	
spam	SPAM method for estimating relative free energies of waters in hydration shell around proteins.	X
stfcdiffusion	Alternative translational diffusion calculation which can calculate diffusion in specified regions.	
strip	Remove specified atoms from the system.	X
surf	Calculate the LCPO surface area of specified atoms. Can do partial surface areas.	
surftension	Calculate capillary-wave surface tension of a liquid slab.	
symmrmsd	Calculate symmetry-corrected RMSD.	X
temperature	Calculate system temperature using velocities of specified atoms.	
time	Add/remove/modify time information in frames.	X
tordiff	Calculate diffusion using the toroidal-view-preserving scheme.	
trans, translate	Translate specified atoms by specified amounts in X/Y/Z directions.	X
unstrip	Undo all previous ***strip*** Action commands.	
unwrap	Reverse of ***image***; unwrap selected atoms so they have continuous trajectories.	X
vector	Calculate various types of vector quantities.	
velocityautocorr	Calculate velocity autocorrelation function.	

volmap	Create volumetric map for specified coordinates; similar to ***grid*** but takes into account atomic radii. Similar to VMD ***volmap***.	
volume	Calculate unit cell volume.	
watershell	Calculate the number of waters in the first and second solvation shells based on distance critera.	

12.1 addatom

```
addatom aname <name> [elt <element>] [rname <res name>]
        [xyz <X> <Y> <Z>] [mass <mass>] [charge <charge>]
        [outprefix <prefix>] [nobox] [parmout <filename>]
        [parmopts <comma-separated-list>]
```

aname <name> New atom name. Required.

[elt <element>] One or two character element string (e.g. 'H' is hydrogen etc.). Default is 'H'.

[rname <res name>] New residue name for the new atom. Default is 'TMP'.

[xyz <X> <Y> <Z>] Cartesian XYZ coordinates of the new atom. Default is 0 0 0.

[mass <mass>] Mass of the new atom. Default is based off of the element type.

[charge <charge>] Charge of the new atom. Default is 0.

[outprefix <prefix>] Write out modified topology file with name '<prefix>.<Original Topology Name>'.

[nobox] Remove any box information from the modified topology.

[parmout <file>] Write modified topology to file with name <file>.

[parmopts <list>] Options for writing modified topology file.

Temporarily add an atom to the system. This is mostly useful for adding a placeholder "dummy" atom for subsequent actions to use. For example, this can be used in conjunction with the ***'mask'*** command in order to get a list of atoms within a certain distance of a specified point in space. For example, the following input gets a list of atoms within 3.0 Angstroms of coordinates 1, 1, 1:

```
parm tz2.pdb
trajin tz2.pdb 1 1
addatom aname TEMP rname TMP elt H xyz 1 1 1
mask :TMP<@3.0&!:TMP out tz2.mask.dat name TZ2
```

12.2 align

```
align <mask> [<refmask>] [move <mask>] [mass]
   [ first | reference | ref <name> | refindex <#> | previous |
        reftraj <name> [parm <name> | parmindex <#>] ]
```

<mask> Target atoms to fit.

[<refmask>] Reference atoms to fit (default is target mask).

[move <mask>] Atoms to move when aligning (default is target mask).

[mass] Mass-weight the fit.

Reference keywords:

first Use the first trajectory frame processed as reference.

reference Use the first previously read in reference structure (refindex 0).

ref <name> Use previously read in reference structure specified by filename/tag.

refindex <#> Use previously read in reference structure specified by <#> (based on order read in).

previous Use frame prior to current frame as reference.

reftraj <name> Use frames from COORDS set <name> or read in from trajectory file <name> as references. Each frame from <name> is used in turn, so that frame 1 is compared to frame 1 from <name>, frame 2 is compared to frame 2 from <name> and so on. If <trajname> runs out of frames before processing is complete, the last frame of <trajname> continues to be used as the reference.

parm <parmname> | parmindex <#> If reftraj specifies a trajectory file, associate it with specified topology; if not specified the first topology is used.

Align structure using specified <mask> onto reference. If 'move' is specified, only move atoms in the move mask.

12.3 angle

```
angle [<dataset name>] <mask1> <mask2> <mask3> [out <filename>] [mass]
```

[<dataset name>] Output data set name.

<maskX> Three atom masks selecting atom(s) to calculate angle for.

[out <filename>] Output file name.

[mass] Use center of mass of atoms in <maskX> instead of geometric center.

Calculate angle (in degrees) between atoms in <mask1>, <mask2>, and <mask3>. For example, to calculate the angle between the first three atoms in the system:

```
angle A123 @1 @2 @3 out A123.agr
```

12.4 areapermol

```
areapermol [<name>] {[<mask1>] [nlayers <#>] | nmols <#>} [out <filename>]
           [{xy | xz | yz}]
```

[<name>] Data set name.

[<mask1>] Atom mask for selecting molecules. If any atom in a molecule is selected the whole molecule is selected.

[nlayers <#>] Number of layers of molecules. Total number of molecules used will be # molecules divided by # layers.

[nmols <#>] If <mask1> is not specified, the number of molecules to use when calculating area per molecule.

[out <filename>] Output file name.

[{xy|xz|yz}] Cross-section of box to calculate area of. Default is X-Y.

Calculate area per molecule as Area / # molecules. The area is determined from the specified cross-section of the box (X-Y by default). Currently the calculation is only guaranteed to work properly with orthorhombic unit cells. For example, to get the area per molecule of residues named "OL" which are arranged in 2 layers:

```
areapermol OL_area :OL nlayers 2 out apm.dat
```

12.5 atomiccorr

```
atomiccorr [<mask>] out <filename> [cut <cutoff>] [min <min spacing>]
           [byatom | byres]
```

<mask> Atoms to calculate motion vectors for.

out <filename> File to write results to.

cut <cutoff> Only print correlations with absolute value greater than <cutoff>.

min <min spacing> Only calculate correlations for motion vectors spaced <min spacing> apart.

byatom Default; calculate atomic motion vectors.

byres Calculate motion vectors for entire residues (selected atoms in residues only).

Calculate average correlations between the motion of atoms in <mask>. For each frame, a motion vector is calculated for each selected atom from its previous position to its current position. For each pair of motion vectors *Va* and *Vb*, the average correlation between those vectors is calculated as the average of the dot product of those vectors over all N frames.

$$AvgCorr(a,b) = \frac{\sum V_a(i) \cdot V_b(i)}{N}$$

The value of AvgCorr can range from 1.0 (correlated) to 0.0 (no correlation) to -1.0 (anti-correlated). For example, to calculate the correlation of motion vectors between residues 1 to 13, writing to a Gnuplot-readable formatted file:

```
atomiccorr :1-13 out acorr.gnu byres
```

12.6 atomicfluct | rmsf

```
atomicfluct [<name>] [out <filename>] [<mask>] [bfactor] [calcadp [adpout <file>]]
         [{byres [pdbres] [resrange <range>] | byatom | bymask}]
         [start <start>] [stop <stop>] [offset <offset>]
```

<name> Output data set name.

out <filename> Write data to file named <filename>

[<mask>] Calculate fluctuations for atoms in <mask> (all if not specified).

[bfactor] Calculate atomic positional fluctuations squared and weight by $\frac{8}{3}\pi^2$; this is similar but not necessarily equivalent to the calculation of crystallographic B-factors.

[calcadp [adpout <file>]] Calculate anisotropic displacement parameters and optionally output them to <file>.

byres [pdbres] Output the average (mass-weighted) fluctuation by residue.

pdbres If specified, the original residue numbering will be used.

resrange <range> Calculate fluctuations for residues in the given range argument. The residues selected by <mask> must be a subset of residues specified with <range>. Unselected residues will get a fluctuation of 0.0.

bymask Output the average (mass-weighted) fluctuation for all atoms in <mask>.

byatom (default) Output the fluctuation by atom.

[<start>] Frame to begin calculation at (default 1).

[<stop>] Frame to end calculation at (default last).

[<offset>] Frames to skip between calculations (default 1).

DataSets created

<name> Hold atomic fluctuations.

<name>[ADP] Hold anisotropic displacement parameters if 'calcadp' specified.

Compute the atomic positional fluctuations (also referred to as root-mean-square fluctuations, RMSF) for atoms specified in the **<mask>**. The RMSF of a given atom i is calculated as:

$$RMSF_i = \sqrt{\left\langle (x_i - \langle x_i \rangle)^2 \right\rangle}$$

where x denotes atomic positions and the averages are over all input frames.

Note that RMS fitting is not done implicitly. If you want fluctuations without rotations or translations (for example to the average structure), perform an RMS fit to the average structure (best) or the first structure (see ***rmsd***) prior to this calculation. The units are (Å) for RMSF or $Å^2 \times \frac{8}{3}\pi^2$ if **bfactor** is specified.

If **byres** or **bymask** are specified, the mass-weighted average of atomic fluctuations of each atom for either each residue or the entire mask will be calculated respectively:

$$\langle Fluct \rangle = \frac{\sum AtomFluct_i * Mass_i}{\sum Mass_i}$$

If **calcadp** is specified, anisotropic displacement factors for atoms will be calculated and written to the file specified by **adpout** (or STDOUT if not specified) using PDB ANISOU record format. The displacement factors will be saved to a data set. Note that **calcadp** automatically implies **bfactor**.

With *cpptraj* it is possible to perform coordinate averaging, the fit to average coordinates, and the atomic fluctuation calculation in a single execution like so:

```
parm myparm.parm7
trajin mytrajectory.crd
rms first
average crdset MyAvg
run
rms ref MyAvg
atomicfluct out fluct.agr
```

To write the mass-weighted B-factors for the protein backbone atoms C, CA, and N, averaged by residue use the command:

```
atomicfluct out back.agr @C,CA,N byres bfactor
```

To write the RMSF or atomic positional fluctuations of the same atoms, use the command:

```
atomicfluct out backbone-atoms.agr @C,CA,N
```

To write a PDB of averaged coordinates (after fitting to the first frame) with both B-factors and anisotropic temperature factors:

```
parm myparm.parm7
trajin mytraj.nc
rms first
average crdset MyAvg
atomicfluct MyFluct calcadp
run
crdout MyAvg mypdb.pdb adpdata MyFluct[ADP] bfacdata MyFluct
```

12.7 atommap

```
atommap <target> <reference> [mapout <filename>] [maponly]
        [rmsfit [ rmsout <rmsout> ]]
        [changenames] [chiralimpcut <cut>]
```

<**target**> Reference structure whose atoms will be remapped.

<**reference**> Reference structure that <target> should be mapped to.

mapout <**filename**> Write atom map to <filename> with format:
TargetAtomNumber TargetAtomName ReferenceAtomNumber ReferenceAtomName
Target atoms that cannot be mapped to a reference atom are denoted "--".

maponly Write atom map but do not reorder atoms.

rmsfit Any input frames using the same topology as <target> will be RMS fit to <reference> using whatever atoms could be mapped.

rmsout <**rmsout**> If rmsfit specified, write resulting RMSDs to <rmsout>.

changenames If specified, change names of mapped atoms in <target> to match those in <reference>.

chiralimpcut <**cut**> sets the improper dihedral angle cutoff for determining mapping via chirality (default 10 deg.).

Attempt to map the atoms of <target> to those of <reference> based on structural similarity. This is useful e.g. when there are two files containing the same structure but with different atom names or atom ordering. Both <target> and <reference> need to have been read in with a previous ***reference*** command. The state will then be modified so that any trajectory read in with the same parameter file as <target> will have its atoms mapped (i.e. reordered) to match those of <reference>. If the number of atoms that can be mapped in <target> are less than those in <reference>, the reference structure specified by <reference> will be modified to include only mapped atoms; this is useful if for example the reference structure is protonated with respect to the target. The **rmsfit** keyword is useful in cases where the atom mapping will not be complete (e.g. two ligands with the same scaffold but different substituents). If **changenames** is specified, in addition to remapping, the target atom names will be changed to match the reference atom names.

Part of the mapping process involves mapping atoms bonded to chiral centers, which in turn involves calculating so-called "improper" dihedral angles to determine the orientation of the bonded atoms. By default the code assumes the orientation of the atoms around the chiral centers are fairly close, hence there is a small improper dihedral angle cutoff of 10 degrees. However, this can be increased via the **chiralimpcut** keyword to handle cases where one structure is distorted with respect to the other.

For example, say you have the same ligand structure in two files, Ref.mol2 and Lig.mol2, but the atom ordering in each file is different. To map the atoms in Lig.mol2 onto those of Ref.mol2 so that Lig.mol2 has the same ordering as Ref.mol2:

```
parm Lig.mol2
```

```
reference Lig.mol2
parm Ref.mol2
reference Ref.mol2 parmindex 1
atommap Lig.mol2 Ref.mol2 mapout atommap.dat
trajin Lig.mol2
trajout Lig.reordered.mol2 mol2
```

12.8 autoimage

```
autoimage [{<mask> | anchor <mask> [fixed <mask>] [mobile <mask>]}]
          [origin] [firstatom] [{familiar|triclinic}] [moveanchor]
          [mode {bydist|byvec}]
```

[<mask> | anchor <mask>] Atoms to image around; this is the region that will be centered. Default is the entire first molecule.

[fixed <mask>] Molecules that should remain 'fixed' to the anchor region; default is all non-ion/non-solvent molecules.

[mobile <mask>] Molecules that can be freely imaged; default is all ion/solvent molecules.

[origin] Center anchor region at the origin; if not specified, center at box center.

[firstatom] Image based on molecule first atom; default is to image by molecule center of mass.

[familiar] Image to familiar truncated-octahedral shape; this is on by default if the original cell is truncated octahedron.

[triclinic] Force general triclinic imaging.

[moveanchor] When treating "fixed" molecules, the anchor point will be set to the previous "fixed" molecule; this is only expected to work well when "fixed" molecules that are sequential are also geometrically close. Most useful in more condensed systems like those containing membranes.

[mode {bydist|byvec}] How to treat 'fixed' molecules.

bydist The default. 'Fixed' molecules will use the image closest to the "anchor" molecule.

byvec Fixed molecules will use the image closest to their orientation with respect to the anchor in the first frame. May work better than 'bydist' for systems containing membranes.

Automatically center and image (by molecule) a trajectory with periodic boundaries. For most cases just specifying ***'autoimage'*** alone is sufficient. The atoms of the **'anchor'** region (default the entire first molecule) will be centered; all **'fixed'** molecules will be imaged only if imaging brings them closer to the **'anchor'** molecule (default for **'fixed'** molecules is all non-solvent non-ion molecules). All other molecules (referred to as **'mobile'**) will be imaged freely.

The autoimage command works for the majority of systems; however, for very densely packed systems the default anchor (entire first molecule) may not be appropriate. In these cases, it is recommended to choose as the anchor a small region which should lie near the center of your system. For example, in a protein dimer system one could choose a single residue that is near the center of the interface between the two monomers. The **'moveanchor'** and **'mode byvec'** options may also help in cases where the system is more condensed, such as those containing membranes.

12.9 average

```
average {crdset <set name> | <filename>} [<mask>]
        [start <start>] [stop <stop>] [offset <offset>]
        [Trajout Args]
```

<filename> `If specified, write averaged coordinates to <filename> (not compatible with crdset).`

crdset <set name> `If specified, save averaged coordinates to COORDS set <set name> (not compatible with <filename>).`

[<mask>] `Average coordinates in <mask> (all atoms if not specified).`

[<start>] `Frame to begin calculation at (default 1).`

[<stop>] `Frame to end calculation at (default last).`

[<offset>] `Frames to skip between calculations (default 1).`

[Trajout args] `Output trajectory format argument(s) (default Amber Trajectory).`

Calculate the average of input coordinates and write out to file named <**filename**> or save to COORDS set named <**set name**> in any trajectory format *cpptraj* recognizes (Amber Trajectory if not specified). If the number of atoms in <**mask**> are less than the total number of atoms, the topology will be stripped to match <**mask**>.

Note that since coordinates are being averaged over many frames, resulting structures may appear distorted. For example, if one averages the coordinates of a freely rotating methyl group the average position of the hydrogen atoms will be close to the center of rotation. Also note that typically one will want to

remove global rotational and translation movement prior to this command by using e.g. the ***rms*** (12.70 on page 211) command.

Any arguments that are valid for the ***trajout*** command (11.5 on page 105) can be passed to this command in order to control the format of the output coordinates. For example, to write out a PDB file containing the averaged coordinates over all frames:

```
average test.pdb pdb
```

To write out a mol2 file containing only the averaged coordinates of residues 1 to 10 for frames 1 to 100:

```
average test.mol2 mol2 start 1 stop 100 :1-10
```

To create an average structure of atoms named CA and then use it as a reference for an rms command in a subsequent run:

```
trajin Input.nc
average crdset MyAvg @CA
run
rms ref MyAvg @CA out RmsToAvg.dat
run
```

12.10 avgbox

`avgbox [name <setname>] [out <file>]`

[name <**setname**>**]** `Average unit cell data set name.`

[out <**file**>**]** `File to write average unit cell data to.`

`DataSets created:`

<**setname**>**[avg]** `Hold average unit cell as 3x3 matrix data.`

Calculate the average unit cell vectors for incoming frames and store them in a 3x3 matrix data set, The average unit cell is particularly useful when unwrapping trajectories from NPT simulations where the box size fluctuates (see the ***unwrap*** command, 12.91 on page 231).

If writing to a .dat file, the output will look something like:

```
#Frame
       1 42.433046075  0.000000000  0.000000000 -14.144347550 40.006259905  0.000000000
```

Where the first 3 floating point numbers are the average X unit cell vector, the next 3 floating point numbers are the average Y unit cell vector, and the last 3 floating point numbers are the average Z unit cell vector.

12.11 avgcoord

This command is deprecated. Use 'vector center' (optionally with keyword 'magnitude') instead.

12.12 bounds

```
bounds [<mask>] [out <filename>]
       [dx <dx> [dy <dy>] [dz <dz>] name <gridname> [offset <bin offset>]]
```

[<mask>] Mask of atoms to determine bounds of.

[out <filename>] File to write bounds to (default STDOUT if not specified).

[dx <dx> [dy <dy>] [dz <dz>]] Triggers creation of a grid data set from bounds. Spacings of generated grid in the X, Y and Z directions. If only dx is specified <dx> will be used for <dy> and <dz> as well.

[name <gridname>] Name of generated data sets.

[offset <bin offset>] Number of bins to add/subtract in each direction to generated grid.

DataSets Generated

<gridname> The 3D grid (only if 'dx' etc specified).

<gridname>[xmin] The minimum x coordinate encountered.

<gridname>[xmax] The maximum x coordinate encountered.

<gridname>[ymin] The minimum y coordinate encountered.

<gridname>[ymax] The maximum y coordinate encountered.

<gridname>[zmin] The minimum z coordinate encountered.

<gridname>[zmax] The maximum z coordinate encountered.

Calculate the boundaries (i.e. the max/min X/Y/Z coordinates) of atoms in **<mask>** and write to **<filename>** (STDOUT if not specified). Useful for determining dimensions for the ***grid*** command, and can be used to generate a grid data set that can be used by ***grid*** (see 12.39 on page 165).

12.13 box

```
box {[x <xval>] [y <yval>] [z <zval>] {[alpha <a>] [beta <b>] [gamma <g>] |
 [truncoct] [x <length>] |
     nobox |
     auto [offset <offset>] [radii {vdw|gb|parse|none}] |
     getbox {ucell|frac|shape} [name <setname>] [out <file>]
    }
```

[x <xval>] [y <yval>] [z <zval>] Change box length(s) to specified value(s).

[alpha <a>] [beta <b>] [gamma <g>] Change box angle(s) to specified value(s).

[truncoct [x <length>] Set box angles (and optionally a length) to truncated octahedron.

[nobox] Remove any existing box information.

auto Set an orthogonal bounding box enclosing all atoms by the specified radii and an optional offset.

- **offset <offset>** Offset in Angstroms to add to each box length (both + and -).
- **radii {vdw|gb|parse|none}** Radii to use for each atom: van der Waals, generalized Born, PARSE, or no radii.

getbox Save existing box information to a 3x3 matrix data set.

- **{ucell|frac|shape}** Specify the kind of box information to save: ucell saves the unit cell vectors, frac saves the fractional unit cell vectors, and shape saves the symmetric shape matrix unit cell vectors.
- **name <setname>** The name of the 3x3 matrix data set.
- **out <file>** File to write the 3x3 matrix data to.

Modify box information during trajectory processing. Note that this will permanently modify the box information for topology files during trajectory processing as well. It is possible to modify any number of the box parameters (e.g. only the Z length can be modified if desired while leaving all other parameters intact). If no box is present, an orthogonal bounding box enclosing all atoms can be created with the **auto** keyword. If 'getbox' is specified, the existing box information will be saved to a data set.

12.14 center

```
center [<mask>] [origin] [mass]
       [ reference | ref <name> | refindex <#> [<refmask>]]
```

[<mask>] Center based on atoms in mask; default is all atoms.

[origin] Center to origin (0, 0, 0); default is center to box center (X/2, Y/2, Z/2).

[mass] Use center of mass instead of geometric center.

[reference | ref <name> | refindex <#> [<refmask]] Center using coordinates in specified reference structure selected by <refmask> (<mask> if not specified.

Move all atoms so that the center of the atoms in <**mask**> is centered at the specified location: box center (default), coordinate origin, or reference coordinates.

For example, to move all coordinates so that the center of mass of residue 1 is at the center of the box:

```
center :1 mass
```

12.15 check | checkoverlap | checkstructure

```
check [<mask>] [around <mask2>] [reportfile <report>] [noimage]
      [skipbadframes] [offset <offset>] [minoffset <minoffset>]
      [cut <cut>] [nobondcheck] [silent] [plcut <cut>]
      [{noringcheck | [ringshortdist <rsdist>] [ringdcut <ringdcut>]
                      [ringacut <ringacut>]}]
      [{checkxp | xpmask <xpmask>}]
```

[<mask>] Check structure of atoms in <mask> (all if not specified).

[around <mask2>] If specified, only check for problems between atoms in <mask> and atoms in <mask2>.

[reportfile <report>] Write any problems found to <report> (STDOUT if not specified).

[noimage] Do not image distances.

[skipbadframes] If errors are encountered for a frame, subsequent actions/trajectory output will be skipped.

[offset <offset>] Report bond lengths greater than the equilibrium value plus <offset> (default 1.15 Å).

[minoffset <minoffset>] Report bond lengths less than the equilibrium value minus <minoffset> (default 0.5 Å).

[cut <cut>] Report atoms closer than <cut> (default 0.8 Å).

[nobondcheck] Check overlaps only.

[silent] Do not print information for bad frames - useful in conjunction with the skipbadframes option.

[plcut <cut>] Pair list cutoff (default 4.0 Å); only matters if box is present.

[noringcheck] If specified, do not check for ring-bond intersections.

[ringshortdist <rsdist>] Report ring-bond intersection when ring to bond center distance is less than <rsdist> (default 0.5 Ang).

[ringdcut <ringdcut>] [ringacut <ringacut>] Report ring-bond intersection when ring to bond center distance is less than <ringdcut> (default 1.25 Ang.) and the angle between the bond vector and perpendicular ring vector is less than <ringacut> (default 65 degrees).

[checkxp] If specified, check extra points as well.

xpmask <xpmask> Specify mask to select extra points; default is '&@/XP' (atom element XP).

Check the structure and report problems related to atomic overlap/unusual bond length/ring-bond intersections. By default extra points are skipped because by design they are quite close to some atoms. The **checkxp** keyword can be specified to check extra points as well. Problems are reported when any two atoms in <**mask**> (or between <**mask**> and <**mask2**> if using **'around'**) are closer than <**cut**>; atoms that are bonded to each other are ignored (except if using the **'around'** mask). If bonds are being checked then bond lengths greater than their equilibrium value plus <**offset**> and less than their equilibrium value minus <**minoffset**> are reported as well. If ring-bond intersections are being checked for they will be reported when the ring center to bond center is less than <**rsdist**>, or less than <**ringdcut**> and the angle between the bond vector and ring perpendicular vector is less than <**ringacut**>. If box information is present and not using the **'around'** mask, a pairlist will be used to speed up the calculation.

This command can also be used to skip corrupted frames in a trajectory during processing. For example, if this message is encountered:

```
Warning: Frame 10 coords 1 & 2 overlap at origin; may be corrupt.
```

One could use ***check*** so that e.g. a subsequent ***distance*** command is not processed for bad frames:

```
check @1,2 skipbadframes silent
distance d1 :1 :10
```

Usually frame corruption can be detected using only a few atoms, but this may not catch all types of corruption. The more atoms that are used the better the corruption detection will be, but the slower it will be to process the command. Typically a good procedure to follow when corruption is suspected is to run ***check*** using all important atoms (e.g. all solute heavy atoms) with the **skipbadframes** keyword followed by a ***trajout*** command to write all non-corrupt frames, for example:

```
trajin corrupted.crd
check :1-13 skipbadframes silent
trajout fixed.corrupted.nc
```

12.16 checkchirality

`checkchirality [<name>] [<mask>] [out <filename>] [byatom]`

[<name>] Data set name.

[<mask>] Atoms to check.

[out <filename>] File to write results to.

[byatom] Check the chirality of any atoms in <mask1> that are chiral centers.

DataSet Aspects:

<name>[L] Number of frames 'L' for each residue.

<name>[D] Number of frames 'D' for each residue.

If 'byatom':

<name>:<atom#> For each frame, will contain 'S' or 'R' (corresponding to 'L' or 'D'), or "Unknown" if chirality could not be determined.

Check the chirality around the alpha carbon in amino acid residues selected by <mask>. Note that CPPTRAJ expects atom names to correspond to the PDB V3 standard: N, CA, C, CB. For each residue, the number of frames in which the amino acid is 'L' or 'D' will be recorded. If **byatom** is specified, the chirality ('S' or 'R') for each atom selected by the atom mask will be determined if possible; otherwise 'Unknown' will be printed.

For example, to check the chirality of all amino acids in a system and write to a file named chiral.dat with data set name DPDP:

```
checkchirality DPDP out chiral.dat
```

Output will have format similar to:

```
#Res      DPDP[L]  DPDP[D]
   2.000      100        0
```

So in this example residue 2 was 'L' for 100 frames and 'D' for 0 frames.
To check the chirality of CA atoms in residues 1 to 8 in a system:

```
parm ../DPDP.parm7
trajin ../DPDP.nc
checkchirality DPDP out dpdp.byatom.dat byatom :1-8@CA
```

Output will look like:

```
#Frame   :2@CA :3@CA :4@CA :5@CA :6@CA :7@CA   :8@CA
       1     S     S     S     S     S     R Unknown
       2     S     S     S     S     S     R Unknown
```

12.17 closest | closestwaters

```
closest <# to keep> <mask> [solventmask <solvent mask>] [noimage]
     [first | oxygen] [center] [closestout <filename> [name <setname>]]
     [outprefix <prefix>] [nobox] [parmout <filename>]
     [parmopts <comma-separated-list>]
```

<# to keep> Number of solvent molecules to keep around <mask>

<mask> Mask of atoms to search for closest waters around.

[solventmask <solvent mask>] Optional mask for selecting solvent atoms. If not specified, atoms in all molecules marked as "solvent" will be used.

[noimage] Do not perform imaging; only recommended if trajectory has previously been imaged.

[first | oxygen] Calculate distances between all atoms in <mask> and the first atom of solvent only (recommended for standard water models as it will increase speed of calculation).

[center] Search for waters closest to geometric center of <mask> instead of each atom in <mask>.

[closestout <filename>] Write information on the closest solvent molecules to <filename>.

[outprefix <prefix>] Write corresponding topology to file with name prefix <prefix>.

[nobox] Remove any box information from the topology.

[parmout <file>] Write corresponding topology to file with name <file>.

[parmopts <list>] Comma-separated list of options for writing the topology file.

DataSet Aspects:

[Frame] Frame number.

[Mol] Original solvent molecule number.

[Dist] Solvent molecule distance in Å.

[FirstAtm] First atom number of original solvent molecule.

Similar to the ***strip*** command, but modify coordinate frame and topology by keeping only the specified number of closest solvent molecules to the region specified by the given mask. Solvent molecules can be determined automatically by *cpptraj* (by default residues named WAT, HOH, or TIP3), can be specified prior via the ***solvent*** command (10.21 on page 91), or can be selected by **solventmask**.

The format of the **closestout** file is:

```
Frame    Molecule    Distance    FirstAtom#
```

For example, to obtain the 10 closest waters to residues 1-268 by distance to the first atom of the waters, write out which waters were closest for each frame to a file called "closestmols.dat", and write out the stripped topology with prefix "closest" containing only the solute and 10 waters:

```
closest 10 :1-268 first closestout closestmols.dat outprefix closest
```

As of version 17 this command is CUDA-enabled in CUDA versions of CPPTRAJ.

12.18 cluster

Although the **'cluster'** command can still be specified as an action, it is now considered an analysis. See 13.5 on page 248.

12.19 clusterdihedral

```
clusterdihedral [phibins <N>] [psibins <M>] [out <outfile>]
                [dihedralfile <dfile> | <mask>]
                [framefile <framefile>] [clusterinfo <infofile>]
                [clustervtime <cvtfile>] [cut <CUT>]
```

Cluster frames in a trajectory using dihedral angles. To define which dihedral angles will be used for clustering either an atom mask or an input file specified by the **dihedralfile** keyword should be used. If dihedral file is used, each line in the file should contain a dihedral to be binned with format:

```
ATOM#1 ATOM#2 ATOM#3 ATOM#4 #BINS
```

where the ATOM arguments are the atom numbers (starting from 1) defining the dihedral and #BINS is the number of bins to be used (so if #BINS=10 the width of each bin will be 36^{o}). If an atom mask is specified, only protein backbone dihedrals (Phi and Psi defined using atom names C-N-CA-C and N-CA-C-N) within the mask will be used, with the bin sizes specified by the phibins and psibins keywords (default for each is 10 bins).

Output will either be written to STDOUT or the file specified by the **out** keyword. First, information about which dihedrals were clustered will be printed. Then the number of clusters will be printed, followed by detailed information of each cluster. The clusters are sorted from most populated to least populated. Each cluster line has format

```
Cluster CLUSTERNUM CLUSTERPOP [ dihedral1bin, dihedral2bin ... dihedralNbin ]
```

followed by a list of frame numbers that belong to that cluster. If a cutoff is specified by **cut**, only clusters with population greater than CUT will be printed.

If specified by the **clustervtime** keyword, the number of clusters for each frame will be printed to <cvtfile>. If specified by the **framefile** keyword, a file containing cluster information for each frame will be written with format

```
Frame CLUSTERNUM CLUSTERSIZE DIHEDRALBINID
```

where DIHEDRALBINID is a number that identifies the unique combination of dihedral bins this cluster belongs to (specifically it is a 3*number-of-dihedral-characters long number composed of the individual dihedral bins).

If specified by the **clusterinfo** keyword, a file containing information on each dihedral and each cluster will be printed. This file can be read by SANDER for use with REMD with a structure reservoir (-rremd=3). The file, which is essentially a simplified version of the main output file, has the following format:

```
#DIHEDRALS
dihedral1_atom1 dihedral1_atom2 dihedral1_atom3 dihedral1_atom4
...
#CLUSTERS
CLUSTERNUM1 CLUSTERSIZE1 DIHEDRALBINID1
...
```

12.20 contacts

```
contacts [ first | reference | ref <ref> | refindex <#> ] [byresidue]
         [out <filename>] [time <interval>] [distance <cutoff>] [<mask>]
```

NOTE: Users are encouraged to try the ***nativecontacts*** command (on page 197), an update version of this command.

For each atom given in *mask*, calculate the number of other atoms (contacts) within the distance *cutoff*. The default cutoff is 7.0 A. Only atoms in *mask* are potential interaction partners (e.g., a mask @CA will evaluate only contacts between CA atoms). The results are dumped to *filename* if the keyword "`out`" is specified. Thereby, the time between snapshots is taken to be *interval*. In addition to the number of overall contacts, the number of native contacts is also determined. Native contacts are those that have been found either in the first snapshot of the trajectory (if the keyword "`first`" is specified) or in a reference structure (if the keyword "`reference`" is specified). Finally, if the keyword "`byresidue`" is provided, results are output on a per-residue basis for each snapshot, whereby the number of native contacts is written to *filename*.native.

12.21 createcrd

```
createcrd [<name>] [ parm <name> | parmindex <#> ]
```

This command creates a COORDS data set named <name> using trajectory frames that are associated with the specified topology.

For example, to save frames that have been previously RMS-fit to a reference structure into a COORDS set named MyCrd you would use the input:

```
rms reference :1-12@CA
createcrd MyCrd
strip :6-8
```

Note that here the ***strip*** command will have no effect on the coordinates saved in MyCrd since it occurs after the ***createcrd*** command.

12.22 createreservoir

```
createreservoir <filename> ene <energy data set> [bin <cluster bin data set>]
                temp0 <temp0> iseed <iseed> [velocity]
                [parm <parmfile> | parmindex <#>] [title <title>]
```

<filename> File name of the reservoir to create.

ene <energy data set> Data set with energies corresponding to frames.

[bin <cluster bin data set>] Data set with bin numbers (for RREMD=3).

temp0 <temp0> Reservoir temperature.

iseed <iseed> Reservoir random number seed.

[velocity] Include velocities in the reservoir.

[parm <parmfile> | parmindex <#>] Associated topology.

[title <title>] Reservoir title.

Create structure reservoir for use with reservoir REMD simulations using energies in <energy data set>, temperature <temp0> and random seed <iseed> Include velocities if [velocity] is specified. If <cluster bin data set> is specified from e.g. a previous 'clusterdihedral' command, the reservoir can be used for non-Boltzmann reservoir REMD (rremd==3).

12.23 density

```
density [out <filename>] [name <set name>]
        [ <mask1> ... <maskN> [delta <resolution>] [{x|y|z}]
          [{number|mass|charge|electron}] [{bincenter|binedge}]
          [restrict {cylinder|square} cutoff <cut>] ]
```

[out <filename>] Output file for histogram(s) (relative distances vs. densities for each mask) or total density.

[name <set name>] Output data set name.

<mask1> ... <maskN> Arbitrary number of masks for atom selection; a dataset is created and the output will contain entries for each mask.

[delta <resolution>] Resolution, i.e. determines number of slices (i.e. histogram bins). (default 0.25 Å)

[{x|y|z}] Coordinate (axis) for density calculation. (default z)

[{number|mass|charge|electron}] Number, mass, partial charge (q) or electron (Ne - q) density. Electron density will be converted to e-/Å3 by dividing the average area spanned by the other two dimensions. (default number)

[{bincenter|binedge}] Determine whether histogram bin coordinates will be based on bin center (default) or bin edges.

[restrict {cylinder|square}] If 'restrict' is specified, only calculate the density that is within a cylinder or square shape from the specified axis as defined by a distance cutoff.

cutoff <**cut**> The distance cutoff for 'restrict'.

DataSets Created if masks specified:

<**set name**>**[avg]:**<**idx**> Average density over coordinate for mask number <idx>.

<**set name**>**[sd]:**<**idx**> Standard deviation of density over coordinate for mask number <idx>.

DataSets Created if no masks specified:

<**set name**> Total system density each frame.

If no atom masks are specified, calculate the total system density. Otherwise, calculate specified density along the given axis for atoms in specified mask(s). Defaults are shown in parentheses above. The format of the file is as follows. Comments are lines starting with '#' or empty lines. All other lines must contain the atom type followed by an integer number for the electron number. Entries must be separated by spaces or '='. Example input:

```
density out number_density.dat number delta 0.25 ":POPC@P1" ":POPC@N" \
        ":POPC@C2" ":POPC"
density out mass_density.dat mass delta 0.25 ":POPC@P1" ":POPC@N" \
        ":POPC@C2" ":POPC"
density out charge_density.dat charge delta 0.25 ":POPC@P1" ":POPC@N" \
        ":POPC@C2" ":POPC"
density out electron_density.dat electron delta 0.25 efile Nelec.in \
        ":POPC@P1" ":POPC@N" ":POPC@C2" ":POPC" ":TIP3" \
        ":POPC | :TIP3" "*"
density out ion_density.dat number delta 0.25 ":SOD" ":CLA"
```

See also $AMBERHOME/AmberTools/test/cpptraj/Test_Density.

It can be useful to write out the average and standard deviation as an XYDY set to a Grace data file, e.g.

```
density :WAT@O out wato.agr xydy
```

12.24 diffusion

Note that although the syntax for ***diffusion*** *has changed as of version 16, the old syntax is still supported.*

```
diffusion [{out <filename>|separateout <suffix>}] [time <time per frame>] [noimage]
          [<mask>] [<set name>] [individual] [diffout <filename>] [nocalc]
          [avgucell <avg ucell set>]
          [allowmultipleorigins]
```

[out <filename>] Write mean-square displacement (MSD) data set output to file specified by <filename>.

[separateout <suffix>] Write each MSD data set type to files with suffix <suffix>; see description below.

[time <time_per_frame>] Time in-between each coordinate frame in ps; default is 1.0.

[noimage] If specified do not perform imaging. If this is specified coordinates should be unwrapped prior to this command.

[<mask>] Mask of atoms to calculate diffusion for; default all atoms.

[<set name>] MSD data set name.

[individual] Write diffusion for each individual atom as well as average diffusion for atoms in mask.

[diffout <filename>] Write diffusion contants calculated from fits of MSD data sets to <filename>.

[nocalc] Do not calculate diffusion constants.

[avgucell] Remove periodic box fluctuations from imaged NPT trajectories using average unit cell vectors.

[allowmultipleorigins] (MPI only). For imaged trajectories in parallel, calculate diffusion by averaging over multiple time origins. Should be used with caution.

DataSet Aspects:

[X] MSD(s) in the X direction.

[Y] MSD(s) in the Y direction.

[Z] MSD(s) in the Z direction.

[R] Overall MSD(s).

[A] Overall displacement(s).

[D] Diffusion constants ($1x10^{-5}$ cm^2/s).

[Label] Diffusion constant lablels.

[Slope] Linear regression slopes.

[Intercept] Linear refression Y-intercepts.

[Corr] Linear regression correlation coefficients.

[aX]:<atomN> (individual only) Atom <N> MSD in the X direction.

[aY]:<atomN> (individual only) Atom <N> MSD in the Y direction.

[aZ]:<**atomN**> `(individual only) Atom <N> MSD in the Z direction.`

[aR]:<**atomN**> `(individual only) Atom <N> overall MSD.`

[aA]:<**atomN**> `(individual only) Atom <N> overall displacement.`

Compute mean-squared displacement (MSD, in Angstroms squared) plots (using distance traveled from initial position) for the atoms in <**mask**>. By default only the diffusion averaged over all atoms in <**mask**> is calculated; if **individual** is specified diffusion for individual atoms is calculated as well.

In order to correctly calculate diffusion molecules should take continuous paths, so imaging of atoms is autoimatically performed. If the trajectory is already unwrapped (or the unwrap command is used prior to this command) the **noimage** keyword can be used. To remove the "noise" caused by box fluctuations in NPT trajectories, the average unit cell vectors describing the average box can be provided with the **avgucell** keyword; see the ***avgbox*** command (12.10 on page 125). Alternatively, the trajectory can be unwrapped prior using the ***unwrap*** command, 12.91 on page 231. If the trajectory is unwrapped, the **noimage** keyword should be specified.

Note that in parallel, imaging becomes difficult because there is no way to correct for any wrapping that has been done on preceding MPI ranks. Therefore this command will not work on imaged trajectories in parallel by default. There are two workarounds. 1) Unwrap the trajectory prior to ***diffusion*** with the ***unwrap*** command, then run the diffusion calculation with the **noimage** keyword (this is the recommended way), or 2) specify the **allowmultipleorigins** keyword to calculate MSD separately on each MPI rank, then averaging over all MSD plots. This means the maximum length of any given MSD plot will be <# frames> / <# MPI ranks>, and the calculated diffusion constants will not be as accurate.

The following types of displacements are calculated. If **separateout** is specfied the following files will be created:

x_<suffix> Mean square displacement(s) in the X direction (in Å^2/ps).

y_<suffix> Mean square displacement(s) in the Y direction (in Å^2/ps).

z_<suffix> Mean square displacement(s) in the Z direction (in Å^2/ps).

r_<suffix> Overall mean square displacement(s) (in Å^2/ps).

a_<suffix> Total distance traveled (in Å/ps).

The diffusion coefficient ***D*** can be calculated using the Einstein relation:

$$2nD = \lim_{t \to \infty} \frac{MSD}{t}$$

Where ***n*** is the number of dimensions; for overall MSD n = 3, for single dimension MSD (e.g. X) n = 1, etc. Unless **nocalc** is specified, the diffusion

constant is calculated automatically from MSD data sets (and written to the file specified by **diffout**) in the following manner. The slope the plot of MSD versus time is obtained via linear regression. To convert from units of $Å^2$/ps to 1x10^{-5} cm^2/s, the slope is multiplied by 10.0/(2n). Both the calculated diffusion constants as well as the results of the fit are reported.

Due to the fact that diffusion is currently calculated from initial positions only, diffusion calculated for small numbers of atoms will be inherently stochastic, so the results are most sensible when averaged over many atoms; for example, the diffusion of water should be calculated using all waters in the system. If more averaging is needed, the ***calcdiffusion*** Analysis command (13.3 on page 244) can be used to calculate diffusion from multiple time origins.

For example, to calculate the diffusion of water in a system:

```
diffusion :WAT@O out WAT_O.agr WAT_O diffout DC.dat
```

12.25 dihedral

```
dihedral [<name>] <mask1> <mask2> <mask3> <mask4> [out <filename>] [mass]
         [type {alpha|beta|gamma|delta|epsilon|zeta|chi|c2p|h1p|phi|psi|omega|pchi}]
         [range360]
```

[<name>] Output data set name.

<maskX> Four atom masks selecting atom(s) to calculate dihedral for.

[out <filename>] Output file name.

[mass] Use center of mass of atoms in <maskX>; default is geometric center.

[range360] Output dihedral angle values from 0 to 360 degrees instead of -180 to 180 degrees.

[type <type>] Label dihedral as <type> for use with *statistics* analysis; note 'chi' is nucleic acid chi and 'pchi' is protein chi.

Calculate dihedral angle (in degrees) between the planes defined by atoms in <mask1>, <mask2>, <mask3> and <mask2>, <mask3>, <mask4>. To calculate multiple dihedral angles see the ***multidihedral*** command on page 188.

12.26 dihedralrms | dihrms

```
dihedralrms [<name>] <dihedral types> [out <file>]
             [ first | reference | ref <name> | refindex <#> | previous |
               reftraj <name> [parm <name> | parmindex <#>] ]
             [dihtype <name>:<a0>:<a1>:<a2>:<a3>[:<offset>] ...]
                [tgtrange <range> [refrange <range>]]
```

[<name>] Output data set name.

<dihedral types> Dihedral types to look for. Note that chip is 'protein chi', chin is 'nucleic chi'.

[out <filename>] Output file name.

[dihtype <name>:<a0>:<a1>:<a2>:<a3>[:<offset>] Search for a custom dihedral type called <name> using atom names <a0>, <a1>, <a2>, and <a3>.

Offset: -2=<a0><a1> in previous res, -1=<a0> in previous res, 0=All <aX> in single res, 1=<a3> in next res, 2=<a2><a3> in next res.

[tgtrange <range>] Residue range to look for target dihedrals in. Default is all solute residues.

[refrange <range>] Residues range to look for reference dihedrals in. If not specified, use target range.

Calculate RMSD of selected dihedrals to dihedrals in a reference structure. See the ***multidihedral*** command syntax on page 188 for a list of all available dihedral types.

12.27 dihedralscan

This command has been replaced by ***permutedihedrals***; see 8.12 on page 52.

12.28 dipole

```
dipole [out <filename>]
    { data <dsname> | boxref <ref name/tag> <nx> <ny> <nz> |
      <nx> <dx> <ny> <dy> <nz> <dz>
         [ { gridcenter <cx> <cy> <cz> |
          boxcenter |
          maskcenter <mask> |
          rmsfit <mask> [noxalign]} ]
    [box|origin|center <mask>] [negative] [name <gridname>]
       <mask1> [max <max_percent>]
```

[out <filename>] File to write out grid to. Use ".grid" or ".xplor" extension for XPLOR format, ".dx" for OpenDX format.

Options for setting up grid:

data <dsname> Use previously calculated/loaded grid data set named <dsname>. When using this option there is no need to specify grid bins/spacing/center.

boxref <**ref name/tag**> <**nx**> <**ny**> <**nz**> Set up grid using box information from a previously loaded reference structure. Currently the only way to set up non-orthogonal grids.

<**nx**> <**dx**> <**ny**> <**dy**> <**nz**> <**dz**> Number of grid bins and spacing in the X/Y/Z directions.

[gridcenter <**cx**> <**cy**> <**cz**>**]** Location of grid center, default is origin (0.0, 0.0, 0.0).

[boxcenter] Center grid on box center.

[maskcenter <**mask**>**]** Center the grid on the atoms selected by <mask>.

[rmsfit <**mask**>**]** Perform a best-fit rotation of the grid using the coordinates selected by <mask>.

[noxalign] If specified, grid will not be re-oriented to align with Cartesian axes once binning is finished. Will affect file formats that do not store full unit cell vectors (like Xplor).

Options for offset during grid binning (must center grid at origin):

[box] Offset each point by location of box center prior to gridding. Cannot be used with 'gridcenter'.

[origin] No offset (default)

[center <**mask**>**]** Offset each point by center of atoms in <mask> prior to gridding. Cannot be used with 'gridcenter'.

Other options:

[negative] Grid negative density instead of positive density.

[name <**gridname**>**]** Grid data set name.

<**mask1**> Mask selecting solvent atoms to bin.

[max <**max percent**>**]** Only keep density >= to <max_percent> of the maximum density.

NOTE: This command is not well-tested and may be obsolete.

Similar to **grid** (see 12.39 on page 165 below) except that dipoles of the solvent molecules are binned. The output file format is for Chris Bayly's discern delegate program that comes with Midas/Plus. Consult the code in Action_Dipole.cpp for more information.

12.29 distance

```
distance [<name>] <mask1> [<mask2>] [point <X> <Y> <Z>]
         [ reference | ref <name> | refindex <#> ]
      [out <filename>] [geom] [noimage] [type noe]
Options for 'type noe':
  [bound <lower> bound <upper>] [rexp <expected>] [noe_strong] [noe_medium] [noe_weak]
```

[<name>] Output data set name

<mask1> Atom mask selecting atom(s) to calculate distance between.

<mask2> If specified, second atom mask selection atom(s) to calculate distance from <mask1>.

point <X> <Y> <Z> If specified instead of second mask, calculate distance between <mask1> and specified XYZ coordinates.

reference | ref <name> | refindex <#> If specified, calculate distance between <mask1> in each input frame and <mask2> in the specified reference.

[out <filename>] Output filename.

[geom] Use geometric center of atoms in <mask1>/<mask2>; default is to use center of mass.

[noimage] Do not image distances across periodic boundaries.

[type noe] Mark distance as 'noe' for use with *statistics* analysis.

- **[bound <lower> bound <upper>]** Lower and upper bounds for NOE (in Angstroms); must specify both.
- **[rexp <expected>]** Expected value for NOE (in Angstroms); if not given '(<lower> + <upper>)' / 2.0 is used.
- **[noe_strong]** Set lower and upper bounds to 1.8 and 2.9 Å respectively.
- **[noe_medium]** Set lower and upper bounds to 2.9 and 3.5 Å respectively.
- **[noe_weak]** Set lower and upper bounds to 3.5 and 5.0 Å respectively.

Calculate distance between the center of mass of atoms in <mask1> to atoms in <mask2>, between atoms in <mask1> from each input frame and atoms in <mask2> in specified reference, or atoms in <mask1> and the specified point. If **geom** is specified use the geometric center instead. For periodic systems imaging is turned on by default; the **noimage** keyword disables imaging.

A distance can be labeled using 'type noe' for further analysis as an NOE using the ***'statistics'*** analysis command (13.37 on page 295).

12.30 drms | drmsd (distance RMSD)

```
drmsd [<dataset name>] [<mask> [<refmask>]] [out <filename>]
      [ first | ref <refname> | refindex <#> |
        reftraj <trajname> [parm <trajparm> | parmindex <parm#>] ]
```

[<dataset name>] Output data set name.

[<mask>] Atoms to calculate DRMSD for.

[<refmask>] Mask corresponding to atoms in reference; if not specified, <mask> is used.

[out <filename>] Output file name.

[first] Use the first trajectory frame processed as reference.

[reference] Use the first previously read in reference structure.

[ref <refname>] Use previously read in reference structure specified by <refname>.

[refindex <#>] Use previously read in reference structure specified by <#> (based on order read in).

previous Use frame prior to current frame as reference.

reftraj <name> Use frames from COORDS set <name> or read in from trajectory file <name> as references. Each frame from <name> is used in turn, so that frame 1 is compared to frame 1 from <name>, frame 2 is compared to frame 2 from <name> and so on. If <trajname> runs out of frames before processing is complete, the last frame of <trajname> continues to be used as the reference.

parm <parmname> | parmindex <#> If reftraj specifies a file associate trajectory <name> with specified topology; if not specified the first topology is used.

Calculate the distance RMSD (i.e. the RMSD of all pairs of internal distances) between atoms in the frame defined by <**mask**> (all if no <**mask**> specified) to atoms in a reference defined by <**refmask**> (<**mask**> if <**refmask**> not specified). Both <**mask**> and <**refmask**> must specify the same number of atoms, otherwise an error will occur.

Because this method compares pairs of internal distances and not absolute coordinates, it is not sensitive to translations and rotations the way that a no-fit RMSD calculation is. It can be more time consuming however, as (N^2-N)/2 distances must be calculated and compared for both the target and reference structures.

For example, to get the DRMSD of a residue named LIG to its structure in the first frame read in:

```
drmsd :LIG first out drmsd.dat
```

12.31 dssp

See 12.78 on page 216.

12.32 enedecomp

```
enedecomp [<name>] [<mask>] [out <filename>] [savecomponents]
          [ pme [cut <cutoff>] [dsumtol <dtol>] [ewcoeff <coeff>]
                [erfcdx <dx>] [skinnb <skinnb>] [ljswidth <width>]
                [order <order>] [nfft <nfft1>,<nfft2>,<nfft3>]
```

[<name>] Data set name.

[<mask>] Mask of atoms to calculate energy for.

[out <filename>] File to write results to.

[savecomponents] If specified, also save the individual components of the total energy (bond, angle, dihedral, etc.).

[pme] Use particle mesh Ewald for electrostatics; van der Waals energy will be calculated using a long-range correction for periodicity.

cut <cutoff> Direct space cutoff in Angstroms (default 8.0).

dsumtol <dtol> Direct sum tolerance (default 0.00001). Used to determine Ewald coefficient.

ewcoeff <coeff> Ewald coefficient in 1/Ang.

erfcdx <dx> Spacing to use for the ERFC splines (default 0.0002 Ang.).

skinnb Used to determine pairlist atoms (added to cut, so pairlist cutoff is cut + skinnb); included in order to maintain consistency with results from sander.

ljswidth <width> If specified, use a force-switching form for the Lennard-Jones calculation from <cutoff>-<width> to <cutoff>.

order <**order**> Spline order for charges.

nfft <**nfft1**>,<**nfft2**>,<**nfft3**> Explicitly set the number of FFT grid points in each dimension. Will be determined automatically from unit cell dimensions if not specified.

DataSets created:

<**name**> Set containing atom index and the corresponding average total energy over frames.

If 'savecomponents' is specified:

<**name**>**[bond]** Set containing atom index and average bond energy over frames.

<**name**>**[angle]** Set containing atom index and average angle energy over frames.

<**name**>**[dih]** Set containing atom index and average dihedral energy over frames.

<**name**>**[vdw14]** Set containing atom index and average 1-4 van der Waals energy over frames.

<**name**>**[elec14]** Set containing atom index and average 1-4 electrostatic energy over frames.

<**name**>**[elec]** Set containing atom index and average electrostatic energy over frames.

<**name**>**[vdw]** Set containing atom index and average van der Waals energy over frames.

Perform per-atom energy decomposition for selected atoms. The energy is calculated for the entire system but only the energies for selected atoms will be reported. The energy is composed of the regular bond, angle, torsion, 1-4 nonbonded, and nonbonded terms. If **'savecomponents'** is specified, each of the energy components will be saved in addition to the total energy for each atom. If **'pme'** is specified the non-bonded terms will us PME for electrostatics and a long-range periodic correction for van der Waals, otherwise a simple model with no cutoff will be used.

12.33 energy

```
energy [<name>] [<mask1>] [out <filename>] [nobondstoh] [openmm [<mdopts>]]
    [bond] [angle] [dihedral] {[nb14]|[e14]|[v14]} {[nonbond]|[elec] [vdw]}
       [cmap]
    [{nokinetic|kinetic [ketype {vel|vv}] [dt <dt>]}] [lj1264]
    [ etype { simple |
              directsum [npoints <N>] |
              ewald [cut <cutoff>] [dsumtol <dtol>] [ewcoeff <coeff>]
```

```
                  [erfcdx <dx>] [skinnb <skinnb>] [ljswidth <width>]
                  [rsumtol <rtol>] [maxexp <max>] [mlimits <X>,<Y>,<Z>] |
          pme [cut <cutoff>] [dsumtol <dtol>] [ewcoeff <coeff>]
              [erfcdx <dx>] [skinnb <skinnb>] [ljswidth <width>]
              [order <order>] [nfft <nfft1>,<nfft2>,<nfft3>]
              [ljpme [ewcoefflj <ljcoeff>]]
      } ]
```

[<name>] Data set name.

[<mask1>] Mask of atoms to calculate energy for.

[out <filename>] File to write results to.

[nobondstoh] Skip calculating the energy of bonds to hydrogen.

[openmm] If specified and CPPTRAJ is compiled with OpenMM support, use OpenMM to calculate energy. Note this will only calculate total energy; any keywords pertaining to individual energy components are not available. For a list of potential options that can be used with 'openmm', see 8.7 on page 47.

[bond] Calculate bond energy.

[angle] Calculate angle energy.

[dihedral] Calculate dihedral energy.

[nb14] Calculate nonbonded 1-4 energy.

[e14] Calculate 1-4 electrostatics.

[v14] Calculate 1-4 van der Waals.

[nonbond] Calculate nonbonded energy (electrostatics and van der Waals).

[elec] Calculate electrostatic energy (Coulomb potential).

[vdw] Calculate van der Waals energy (Lennard-Jones 6-12 potential).

[cmap] Calculate CMAP energy.

[nokinetic] Do not calculate kinetic energy even if velocity/force information present.

[kinetic] Attempt to calculate kinetic energy. Requires force and/or velocity information.

ketype {vel|vv} Specify kinetic energy type. If not specified, if velocity and force information use a velocity verlet-type calculation (vv), i.e. assume velocities are a half-step ahead of the forces. If only velocity information is present, calculate from on-step velocities (vel).

dt <dt> Time step for vv calculation in ps.

[lj1264] Turn on LJ 12-6-4 contribution if topology contains LJ C coefficients.

[etype <type>] Calculate electrostatics via specified type.

[simple] Use simple Coulomb term for electrostatics, no cutoff.

[directsum] Use direct summation method for electrostatics.

[npoints <N>] Number of cells in each direction to calculate the direct sum.

[ewald] Use Ewald summation for electrostatics. If van der Waals energy will be calculated a long-range correction for periodicity will be applied.

cut <cutoff> Direct space cutoff in Angstroms (default 8.0).

dsumtol <dtol> Direct sum tolerance (default 0.00001). Used to determine Ewald coefficient.

ewcoeff <coeff> Ewald coefficient in 1/Ang.

erfcdx <dx> Spacing to use for the ERFC splines (default 0.0002 Ang.).

skinnb Used to determine pairlist atoms (added to cut, so pairlist cutoff is cut + skinnb); included in order to maintain consistency with results from sander.

ljswidth <width> If specified, use a force-switching form for the Lennard-Jones calculation from <cutoff>-<width> to <cutoff>.

rsumtol <rtol> Reciprocal sum tolerance (default 0.00005). Used to determine number of reciprocal space vectors.

mlimits <X>,<Y>,<Z> Explicitly set the number of reciprocal space vectors in each dimension. Will be determined automatically if not specified.

[pme] Use particle mesh Ewald for electrostatics. If van der Waals energy will be calculated a long-range correction for periodicity will be applied.

cut <cutoff> Direct space cutoff in Angstroms (default 8.0).

dsumtol <dtol> Direct sum tolerance (default 0.00001). Used to determine Ewald coefficient.

ewcoeff <**coeff**> Ewald coefficient in 1/Ang.

erfcdx <**dx**> Spacing to use for the ERFC splines (default 0.0002 Ang.).

skinnb Used to determine pairlist atoms (added to cut, so pairlist cutoff is cut + skinnb); included in order to maintain consistency with results from sander.

ljswidth <**width**> If specified, use a force-switching form for the Lennard-Jones calculation from <cutoff>-<width> to <cutoff>.

order <**order**> Spline order for charges.

nfft <**nfft1**>,<**nfft2**>,<**nfft3**> Explicitly set the number of FFT grid points in each dimension. Will be determined automatically from unit cell dimensions if not specified.

ljpme If specified use particle mesh Ewald for calculating Lennard-Jones interactions.

ewcoefflj Ewald coefficient for Lennard-Jones PME (implies ljpme).

DataSet Aspects:

[bond] Bond energy.

[angle] Angle energy.

[dih] Dihedral energy.

[cmap] CMAP energy.

[vdw14] 1-4 van der Waals energy.

[elec14] 1-4 electrostatic energy.

[vdw] van der Waals energy.

[elec] Electrostatic energy.

[kinetic] Kinetic energy.

[total] Total energy.

Calculate the energy for atoms in <mask>. If no terms are specified, all terms are calculated. Note that the non-bonded energy terms for **'simple'** do not take into account periodicity and there is no distance cut-off. Electrostatics can also be determined via the direct sum, Ewald, or particle-mesh Ewald summation procedures. The particle mesh Ewald functionality requires that CPPTRAJ be compiled with FFTW and a C++11 compliant compiler.

Calculation of energy terms requires that the associated topology file have parameters for any of the calculated terms, so for example angle calculations are not possible when using a PDB file as a topology, etc. All nonbonded calculations methods other than **simple** require unit cell parameters. By default, to

match SANDER/PMEMD behavior the LJ 12-6-4 contribution is not included in the van der Waals energy term unless the **lj1264** keyword is specified.

For example, to calculate all energy terms and write to a Grace-format file:

```
parm DPDP.parm7
trajin DPDP.nc
energy DPDP out ene.agr
```

12.34 esander

```
esander [<name>] [out <filename>] [saveforces] [parmname <file>] [keepfiles]
        [<namelist vars> ...]
```

[<name>] Data set name.

[out <filename>] File to write results to.

[saveforces] If specified, save forces to frames.
Requires writing frames in NetCDF format.

[parmname <file>] Name of temporary topology file
(default: 'CpptrajEsander.parm7').

[keepfiles] Keep temporary topology file after program
execution.

[<namelist vars>] Namelist variables supported by the
sander API in format 'var <value>'; see below.

Calculate energies for input frames using the sander API. It requires compilation with the SANDER API (sanderlib). This can be considered as a faster alternative to energy post-processing with sander (imin = 5). Currently the following sander namelist variables are supported: **extidel**, **intdiel**, **rgbmax**, **saltcon**, **cut**, **dielc**, **igb**, **alpb**, **gbsa**, **lj1264**, **ipb**, **inp**, **vdwmeth**, **ew_type**, **ntb**, **ntf**, **ntc**. See **??** on page ?? for details.

If ntb/cut/igb are not specified cpptraj will attempt to pick reasonable values based on the input system. The defaults for a non-periodic system are ntb=0, cut=9999.0, igb=1. The defaults for a periodic system are ntb=1, cut=8.0, igb=0. This currently requires writing a temporary Amber topology, the name of which can be set by **parmname**. If **keepfiles** is specified this temporary topology will not be deleted after execution.

For example, to calculate energies for a non-periodic system using igb=1 (the default) with GB surface area turned on (gbsa=1):

```
parm DPDP.parm7
trajin DPDP.nc
esander DPDP out Edpdp.dat gbsa 1
```

12.35 filter

filter {<dataset arg> min <min> max <max> ...} [out <file>] [name <setname>]
{[multi] | [filterset <set> [newset <newname>]] [countout <countfile>]}

<**dataset arg**> Data set name(s) to use for filtering

min <**min**> Allow values greater than <min> in dataset(s).

max <**max**> Allow values greater than <max> in dataset(s).

[out <**file**>**]** File containing 1 for frames that were allowed, 0 for frames that were filtered.

[name <**setname**>**]** Filtered data set name containing 1 for allowed frames, 0 for filtered frames.

[multi] Filter each set separately instead of all together (creates filter set for each input set). Cannot be used with 'filterset'.

[filterset <**set**>**]** If specified, <set> will be filtered to only contain data that satisfies cutoffs. Cannot be used with 'multi'.

[newset <**newname**>**]** If specified a new set will be created from 'filterset' instead of replacing 'filterset'.

[countout <**count**>**]** If specified, write number of elements passed and filtered to <countfile>. Cannot be used with 'multi'.

Sets Created (not 'multi')

<**setname**> For each input element contains 1 for elements that "passed", 0 otherwise.

<**setname**>**[npassed]** Number of elements that passed.

<**setname**>**[nfiltered]** Number of elements filtered out.

Sets Created ('multi')

<**setname**>:<**idx**> For each input set (number with <idx>, starting from 0) contains 1 for elements that "passed", 0 otherwise.

For all following actions, only include frames that are between <**min**> and <**max**> of data sets in <**dataset arg**>. There must be at least one <**min**> and <**max**> argument, and there must be as many <**min**>/<**max**> arguments as there are specified data sets. If **'multi'** is specified then only filter data sets will be created for each data set instead. If **'filterset'** is specified, the

specified <set> will be modified to only contain '1' frames; cannot be used with **'multi'**. If **'newset'** is also specified, a new set will be created containing the '1' frames instead. The **'filterset'** functionality only works for 1D scalar sets. If **'countout'** is specified, the final number of elements passed and filtered out will be written to <countfile>.

For example, to write only frames in-between an RMSD of 0.7-0.8 Angstroms for a given input trajectory:

```
trajin ../tz2.truncoct.nc
rms R1 first :2-11
filter R1 min 0.7 max 0.8 out filter.dat
outtraj maxmin.crd
```

The output trajectory will only contain frames that meet the RMSD requirement, and the *filter.dat* file can be used to see which frames those were that were output.

A similar command that can be used with data that already exists (e.g. it has been read in with ***readdata***) is ***datafilter*** (see page 63).

12.36 fixatomorder

```
fixatomorder [outprefix <prefix>] [nobox] [parmout <filename>]
             [parmopts <comma-separated-list>]
             [pdborder [hetatm <mask>]] (EXPERIMENTAL)
```

outprefix <**prefix**> Write re-ordered topology to <prefix>.<originalname>

[nobox] Remove any box information from the re-ordered topology.

parmout <**filename**> Write re-ordered topology to <filename>

parmopts <**list**> Options for writing topology file

pdborder (EXPERIMENTAL) Try to reorder atoms according to PDB information.

hetatm <**mask**> Mark atoms in mask as HETATM, order them after other atoms.

Cpptraj (and most of Amber) expects that atom indices in molecules to increase monotonically. However, occasionally atom indices in molecules can become disordered or non-sequential, in which case cpptraj will print an error message such as the following:

```
Error: Atom 45 was assigned a lower molecule # (1) than previous atom (2).
```

and:

```
Error: Could not determine molecule information for <topology file>.
```

. This command fixes atom ordering so that all atoms in molecules are sequential. The **outprefix** keyword will write out the re-ordered topology with name <**name**>.<**original name**>.

For example, given an out of order topology named 'outoforder.parm7' and a corresponding trajectory 'min1.crd', the following will produce a reordered topology named 'reorder.outoforder.parm7' and a reordered trajectory named 'reorder.mdcrd':

```
parm outoforder.parm7
trajin min1.crd 1 10
fixatomorder outprefix reorder
trajout reorder.mdcrd
```

If **'pdborder'** is specified, attempt to organize atoms by PDB information (i.e. Chain ID, original residue numbering, and insertion codes). Atoms optionally specified by **'hetatm** <**mask**>' will be placed after all other atoms. *Note that the 'pdborder' keyword is still experimental, and requires that the Topology have PDB-type information present.*

12.37 fiximagedbonds

```
fiximagedbonds [<mask>]
```

<**mask**> Mask expression of atoms to check.

Fix bonds that have been split across periodic boundary conditions by imaging. It may be desirable to reimage the coordinates after this with ***autoimage***.

12.38 gist (Grid Inhomogeneous Solvation Theory)

```
gist [name <dataset name>] [doorder [nopl] [plcut <plcut>]]
     [doeij] [skipE] [skipS] [refdens <rdval>] [temp <tval>]
     [noimage] [gridcntr <xval> <yval> <zval>]
     [rmsfit <fitmask>]
     [griddim <nx> <ny> <nz>] [gridspacn <spaceval>] [neighborcut <ncut>]
     [prefix <filename prefix>] [ext <grid extension>] [out <output suffix>]
     [floatfmt {double|scientific|general}] [floatwidth <fw>] [floatprec <fp>]
  [intwidth <iw>]
     [info <info suffix>]
     [nopme|pme [cut <cutoff>] [dsumtol <dtol>] [ewcoeff <coeff>]
   [erfcdx <dx>] [skinnb <skinnb>] [ljswidth <width>]
   [order <order>] [nfft <nfft1>,<nfft2>,<nfft3>]]
```

[name <dataset name>] Name for output data sets.

[doorder] Calculate the water order parameter [7] for each voxel.

[nopl] If specified, do not use the pair list for the order calculation (may be much slower).

[plcut <plcut>] Pair list cutoff for order calculation (default 10.0 Ang.).

[doeij] Calculate the triangular matrix representing the water-water interactions between pairs of voxels (see below).

[skipE] Skip all energy calculations (cannot be specified with 'doeij').

[skipS] Skip all entropy calculations.

[refdens rdval>] Reference density of bulk water, used in computing g_O, g_H, and the translational entropy. Default is 0.0334 molecules/Å^3.

[temp <tval>] Temperature of the input trajectory.

[noimage] Disable distance imaging in energy calculation.

[gridcntr <xval> <yval> <zval>] Coordinates (Å) of the center of the grid (default 0.0, 0.0, 0.0).

[rmsfit <fitmask>] If specified, grid will be centered and rotated to follow atoms selected by <fitmask>.

[griddim <nx> <ny> <nz>] Grid dimensions (number of bins/voxels) along each coordinate axis (default 40, 40, 40).

[gridspacn <spaceval>] Grid spacing (linear dimension of each voxel) in Angstroms. Values greater than 0.75 Å are not recommended (default 0.5 Å).

[neighborcut <ncut>] Cutoff in Å for determining solvent O-O neighbors (default 3.5 Å).

[prefix <filename prefix>] Output file name prefix (default "gist").

[ext <grid extension>] Output grid file name extension (default ".dx").

[out <output suffix>] Suffix for main GIST output file name. If not specified, output file will be set to '<prefix>-output.dat'.

[floatfmt {double|scientific|general}] Format for floating point values in GIST output file: double (regular

fixed decimal point), scientific, or general (default, chooses fixed or scientific, whichever fits better).

[floatwidth <fw>] Changes width of floating point values in GIST output file. Default is no width restriction.

[floatprec <fp>] Changes precision of floating point values in GIST output file. Default is to use whatever the system default is.

[intwidth <iw>] Changes width of integer values in GIST output file. Default is no width restriction.

[info <info suffix>] Suffix for main GIST info file name. If not specified, info will be written to standard output.

[oldnnvolume] Use the old reference volume for the nearest neighbor entropy, instead of the more precice new implementation.

[nnsearchlayers <nlayers>] Number of layers of neighboring voxels that should be used when searching for nearest neighbors. This has to be at least 1 to obtain the correct entropy. Higher values can help to obtain better convergence of the translational and 6D entropy with little sampling or fine grid spacings, but increase the calculation time (default 1).

[solute <mask>] Selection mask for the solute. All other molecules will be solvent. If this is omitted, the standard solute/solvent assignment will be used.

[solventmols <MOLS>] Comma-separated list of names of solvent molecules. Energies will be computed per solvent molecule. For the entropy, only the main solvent (the first one) will be used. Use, e.g., solventmols WAT,NA,CL for a GIST calculation including ions. This needs to be specified if there is more than one solvent species.

[nocom] Do not use the center of mass to define the molecular position. Instead, use the first atom in rigidatoms. Use this flag to restore the behavior of old GIST runs.

[rigidatoms <CENTRAL> <SUBST1> <SUBST2>] Specifies how to define the molecular orientation for the entropy. By default, a simple heuristic

will be used. This works for water, but not for all solvents. The atoms should be representative of the molecular orientation and should not be collinear. Note that the central atom goes first. For water, the default is equivalent to rigidatoms O H1 H2, corresponding to H1-O-H2 as the rigid substructure.

[nopme] Do not use particle mesh Ewald for the non-bonded calculation (default).

[pme] Use particle mesh Ewald for the non-bonded electrostatics calculation. The van der Waals energy will be calculated using a long-range correction for periodicity. Does not support doeij.

cut <**cutoff**> Direct space cutoff in Angstroms (default 8.0).

dsumtol <**dtol**> Direct sum tolerance (default 0.00001). Used to determine Ewald coefficient.

ewcoeff <**coeff**> Ewald coefficient in 1/Ang.

erfcdx <**dx**> Spacing to use for the ERFC splines (default 0.0002 Ang.).

skinnb Used to determine pairlist atoms (added to cut, so pairlist cutoff is cut + skinnb); included in order to maintain consistency with results from sander.

ljswidth <**width**> If specified, use a force-switching form for the Lennard-Jones calculation from <cutoff>-<width> to <cutoff>.

order <**order**> Spline order for charges.

nfft <**nfft1**>,<**nfft2**>,<**nfft3**> Explicitly set the number of FFT grid points in each dimension. Will be determined automatically if not specified.

DataSet Aspects:

[gO] Number density of oxygen centers found in the voxel, in units of the bulk density.

[gH] Number density of hydrogen centers found in the voxel in units of the reference bulk density.

[Esw] Mean solute-water interaction energy density.

[Eww] Mean water-water interaction energy density.

[dTStrans] First order translational entropy density.

[dTSorient] First order orientational entropy density.

[dTSsix] First order six-dimensional entropy density.

[neighbor] Mean number of waters neighboring the water molecules found in this voxel multiplied by the voxel number density.

[dipole] Magnitude of mean dipole moment (polarization).

[order] Average Tetrahedral Order Parameter.

[dipolex] x-component of the mean water dipole moment density

[dipoley] y-component of the mean water dipole moment density

[dipolez] z-component of the mean water dipole moment density

[Eij] Water-water interaction matrix.

[PME] (pme only) Mean water energy on the GIST grid.

[U_PME] (pme only) Mean solute energy on the GIST grid.

DataSets if the main solvent is not water:

[gELEM] For every element ELEM in the main solvent, the atomic density relative to rho0 (e.g., gC and gH for benzene).

DataSets if there are multiple solvents:

[g_mol_NAME] for every solvent species NAME (e.g., g_mol_WAT and g_mol_NA if solventmols WAT,NA was specified).

[Esw_mol_NAME] for every solvent species NAME (e.g., Esw_mol_WAT and Esw_mol_NA if solventmols WAT,NA was specified).

[Eww_mol_NAME] for every solvent species NAME (e.g., Eww_mol_WAT and Eww_mol_NA if solventmols WAT,NA was specified).

Grid Inhomogeneous Solvation Theory [8, 9] (GIST) is a method for analyzing the structure and thermodynamics of solvent in the vicinity of a solute molecule. The current implementation works for only water, but the method can be generalized to other solvents whose molecules are rigid like water, such as chloroform or dimethylsulfoxide (DMSO). GIST post-processes explicit solvent simulation data to create a three-dimensional mapping of water density and thermodynamic properties within a region of interest, which is defined by a user-specified 3D rectangular grid. The small grid boxes are referred to as voxels, and each voxel is associated with solvent properties. (See Fig. 1.) The GIST implementation incorporated into AmberTools *cpptraj* also calculates a number of other local water properties, as listed below. GIST works for the nonpolarizable water models currently supported by AMBER.

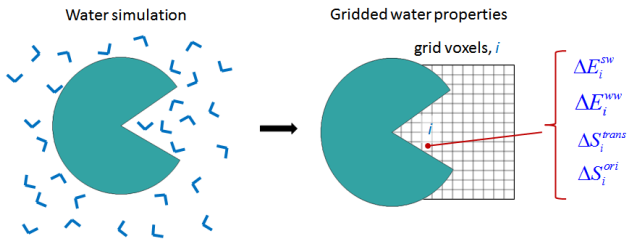


Figure 1: Diagram, in 2D, of GIST's gridded water properties in a binding site.

In order to carry out a GIST calculation, you must have a trajectory file generated with explicit water, as well as the corresponding topology file. To generate the most readily interpretable results, it is recommended that the solute (e.g., a protein) be restrained into essentially one conformation. GIST will then provide information about the structure and thermodynamics of the solvent for that conformation. For a room-temperature simulation of a solvent-exposed binding site, and a grid-spacing of 0.5 Å, it is recommended that the simulation be at least 10-20 ns in duration, and it is also a good idea to check for convergence of the GIST properties you are interested in by loading and then processing successively more frames of your trajectory file. Because GIST assumes that the solute of interest comprises all molecules in the simulation that are not waters, it is a good idea to remove all counterions and cosolutes with cpptraj's strip command before running GIST. A sample series of cpptraj commands for running GIST is provided below.

Although it is not mandatory to supply values of **gridcntr**, **griddim** and **gridspcn**, these parameters should be carefully chosen, because they determine the region to be analyzed (**gridcntr** and **griddim**) and the spatial resolution and convergence properties of the results (**gridspcn**). In particular, although smaller grid spacings will give finer spatial resolution, longer simulation times will be needed to converge the properties in the smaller voxels that result. A larger grid spacing will allow earlier convergence, but will smooth the spatial distributions. When computing the sum over voxel values in a larger region, the result is independent of the grid spacing as long as **nlayers** is high enough for the given sampling.

The reference density of water (**rdval**) is taken by default to be the experimental number density of pure water at 300 K and 1 atm. However, different water models may yield slightly different bulk densities under these conditions, and the density also depends on T and P. If you know that the bulk density of the water model you are using, at the T and P of your simulation, deviates significantly from 0.0334 water molecules/Å^3, it would be advisable to supply the actual value with the **refdens** keyword, instead of allowing GIST to supply the default value.

For GIST, a GPU accelerated version is available, in which the interaction energy is calculated using CUDA. When using the GPU accelerated version of

GIST, the **doeij** keyword is not available. It is recommended to use a grid covering the entire box, when using the GPU implementation. You may also choose a smaller grid, but all interaction energies, i.e., each atom with each atom, will always be calculated independent of the chosen grid. This ensures optimum performance when calculating the interaction energies. Thus, the additional time required to calculate the order parameters (**doorder**) is negligible.

The nonbonded energy calculation can also be accelerated using particle mesh Ewald via the pme keyword (CPU only).[10]

GIST Output

GIST generates a main output file and a collection of grid data files that by default are in Data Explorer format (.dx); this can be changed via the **ext** keyword. These grid files enable visualization of the various gridded quantities, such as with the program VMD [11]. If the **doeij** keyword is provided, GIST also writes out a matrix of water-water interactions between pairs of voxels. In addition, run details are written to stdout, which can be redirected into a log file.

Note that a number of quantities are written out as both densities and normalized quantities. For example, the output file includes both the solute-water energy density and the normalized (per water) solute-water energy. In all cases, the normalized quantity at voxel i, $X_{i,norm}$ is related to the corresponding density, $X_{i,dens}$, by the relationship $X_{i,norm} = \rho_i X_{i,dens}$, where ρ_i is the number density of water in the voxel. The normalized quantity provides information regarding the nature of the water found in the voxel. The density has the property that, if the grid extended over the entire simulation volume, the total system quantity would be given by $X_{tot} = V_{voxel} \sum_i X_{i,dens}$, where V_{voxel} is the volume of one grid voxel.

The main output file takes the form of a space-delimited-variable file, where each row corresponds to one voxel of the grid. This file can easily be opened with and manipulated with spreadsheet programs like Excel and LibreOffice Calc. The columns are as follows.

- **index** - A unique, sequential integer assigned to each voxel
- **xcoord** - x coordinate of the center of the voxel (Å)
- **ycoord** - y coordinate of the center of the voxel (Å)
- **zcoord** - z coordinate of the center of the voxel (Å)
- **population** - Number of water molecule, n_i, found in the voxel over the entire simulation. A water molecule is deemed to populate a voxel if its oxygen coordinates are inside the voxel. The expectation value of this quantity increases in proportion to the length of the simulation.

- **g_O** - Number density of oxygen centers found in the voxel, in units of the bulk density (rdval). Thus, the expectation value of **g_O** for a neat water system is unity.

- **g_H** - Number density of hydrogen centers found in the voxel in units of the reference bulk density (2×rdval). Thus, the expectation value of **g_H** for a neat water system would be unity.

- **g_ELEM** - (if the main solvent is not water) Density of every further element **ELEM** in the main solvent. Scaled such that the expectation value in pure solvent is unity.

- **g_mol_NAME** - (if there is more than one solvent) Density of every solvent species **NAME** specified in solventmols. Scaled by **rho0**.

- **dTStrans-dens** - First order translational entropy density (kcal/mole/Å^3), referenced to the translational entropy of bulk water, based on the value rdval.

- **dTStrans-norm** - First order translational entropy per water molecule (kcal/mole/molecule), referenced to the translational entropy of bulk water, based on the value rdval. The quantity **dTStrans-norm** equals **dTStrans-dens** divided by the number density of the voxel in units of number/Å^3.

- **dTSorient-dens** - First order orientational entropy density (kcal/mole/Å^3), referenced to bulk solvent (see below).

- **dTSorient-norm** - First order orientational entropy per water molecule (kcal/mole/water), referenced to bulk solvent (see below). This quantity equals **dTSorient-dens** divided by the number density of the voxel.

- **Esw-dens** - Mean solute-water interaction energy density (kcal/mole/Å^3). This is the interaction of the solvent in a given voxel with the entire solute. Both Lennard-Jones and electrostatic interactions are computed without any cutoff, within the minimum image convention but without Ewald summation. This quantity is referenced to bulk, in the trivial sense that the solute-solvent interaction energy is zero in bulk.

- **Esw-norm** - Mean solute-water interaction energy per water molecule (kcal/mole/molecule). This equals **Esw-dens** divided by the number density of the voxel.

- **Eww-dens** - Mean water-water interaction energy density, scaled by $\frac{1}{2}$ to prevent double-counting, and not referenced to the corresponding bulk value of this quantity (see below). This quantity is one half of the mean interaction energy of the water in a given voxel with all other waters in the system, both on and off the GIST grid, divided by the volume of the voxel (kcal/mole/Å^3). Unless PME is used, both Lennard-Jones

and electrostatic interactions are computed without any cutoff, within the minimum image convention.

- **Esw_mol_NAME-dens** and **Esw_mol_NAME-norm** - (if there are multiple solvent species) Mean solute-solvent energy per molecule of species **NAME**, for each solvent specified in **solventmols**. Follows the same conventions as **Esw**.
- **Eww_mol_NAME-dens** and **Eww_mol_NAME-norm** - (if there are multiple solvent species) Mean solvent-solvent energy per molecule of species **NAME**, for each solvent specified in **solventmols**. Follows the same conventions as **Eww**.
- **PME-norm** - (Only if PME was used) Mean PME solvent energy per water molecule (kcal/mole/molecule). This equals **PME-dens** divided by the number density of the voxel.
- **PME-dens** - (Only if PME was used) Mean PME solvent energy density (kcal/mole/Å^3). This corresponds roughly to **Eww-norm** plus one half of **Esw-norm** in a non-PME GIST calculation.
- **Eww-norm** - Mean water-water interaction energy, normalized to the mean number of water molecules in the voxel (kcal/mole/water). See prior column definition for details.
- **Dipole_x-dens** - x-component of the mean water dipole moment density (Debye/Å^3).
- **Dipole_y-dens** - y-component of the mean water dipole moment density (Debye/Å^3).
- **Dipole_z-dens** - z-component of the mean water dipole moment density (Debye/Å^3).
- **Dipole-dens** - Magnitude of mean dipole moment (polarization) (Debye/Å^3).
- **Neighbor-dens** - Mean number of waters neighboring the water molecules found in this voxel multiplied by the voxel number density. Two waters are considered neighbors if their oxygens are within 3.5 angstroms of each other. For any given frame, the contribution to the average is set to zero if no water is found in the voxel (units of number/Å^3).
- **Neighbor-norm** - Mean number of neighboring water molecules, per water molecule found in the voxel (units of number per water).
- **Order-norm** - Average Tetrahedral Order Parameter [7], q_{tet}, for water molecules found in the voxel, normalized by the number of waters in the voxel. The order parameter for water i in a given frame is given by: $q_{tet}(i) = 1 - \frac{3}{8}\sum_{j=1}^{3}\sum_{k=j+1}^{4}(cos\phi_{ijk} + \frac{1}{3})^2$ where j and k index the 4 closest water neighbors to water i, and ϕ_{ijk} is the angle formed by water

i, j, and k. If the doorder keyword is not provided or is set to FALSE, then this calculation will not be done, and the entries in this column will be set to zero.

Grid files are provided for all computed quantities listed above, except that the normalized quantities are not included. The filenames are as follows: gist-gO.dx, gist-gH.dx, gist-dTStrans-dens.dx, gist-dTSorient-dens.dx, gist-Esw-dens.dx, gist-Eww-dens.dx, gist-dipolex-dens.dx, gist-dipoley-dens.dx, gist-dipolez-dens.dx, gist-dipole-dens.dx, gist-neighbor-dens.dx, gist-neighbor-norm.dx, gist-order-norm.dx. If the **doorder** keyword is not provided, then the data in gist-order-norm.dx will all be zeroes. Note that the file of voxel water densities, gist-gO.dx, can be used as input to the program Placevent [12], in order to define spherical hydration sites based on the density distribution. More detailed descriptions of the files follows:

- **gist-dipole-dens.dx** - Magnitude of mean dipole moment (polarization) (Debye/Å3).
- **gist-dipolex-dens.dx** - X-component of the mean water dipole moment density (Debye/Å3).
- **gist-dipoley-dens.dx-** Y-component of the mean water dipole moment density (Debye/Å3).
- **gist-dipolez-dens.dx** - Z-component of the mean water dipole moment density (Debye/Å3).
- **gist-dTSorient-dens.dx** - Density weighted first order orientational entropy (kcal/mole/Å3). The more negative the isovalue, the more restricted or unfavorable the orientation of the water is. The value at bulk density is expected to be zero, most values will fall between 0 and -1.
- **gist-dTStrans-dens.dx** - Density weighted first order tranlational entropy (kcal/mole/Å3). The more negative isovalue, the more restricted the water is positionally. The value at bulk density is expected to be zero, most values will fall between 0 and -1.
- **gist-Esw-dens.dx** - Density weighted Solute-Water interaction energy (kcal/mole/Å3). This is the interaction of the water with the entire solute. Both Lennard-Jones and electrostatic interactions are computed without any cutoff, within the minimum image convention. The more negative the number, the more favorable the interaction between the water and solute is. Isovalues will be negative numbers.
- **gist-Eww-dens.dx** - Density weighted Water-Water interaction energy (kcal/mole/Å3). This is the interaction of the water with the entire solvent. Both Lennard-Jones and electrostatic interactions are computed without any cutoff, within the minimum image convention. The more negative the number, the more favorable the interaction between water

within this voxel and all other water molucules is. Isovalues will be negative numbers.

- **gist-gH.dx** - Number density of hydrogen centers found in the voxel, in units of the bulk density. The expectation value of g_H for a neat water system is unity. The units of this dx file are the density/bulk density. Therefore an isovalue of 1 represents every voxel at or greater than bulk density.

- **gist-gO.dx** - Number density of oxygen centers found in the voxel, in units of the bulk density. The expectation value of g_O for a neat water system is unity. The units of this dx file are the density/bulk density. Therefore an isovalue of 1 represents every voxel at or greater than bulk density.

- **gist-neighbor-norm.dx** - Mean number of neighboring water molecules, per water molecule found in the voxel (units of number per water). Two waters are considered neighbors if their oxygens are within 3.5 Angstroms of each other.

- **gist-order-norm.dx** - Average Tetrahedral Order Parameter for water molecules found in the voxel, normalized by the number of waters in the voxel. **doorder** must be declared in the command line for this file to be produced.

Similar grid files with other computed quantities can be generated by reading the gist.out file into a spreadsheet program, processing the numbers to generate a new column of voxel data of interest, and writing this column to an ascii text file. Then the Perl script write_dx_file.pl, which should be available on the GIST tutorial web-site, may be used to read in the column of data and create the corresponding dx file. The input format, and an example, are as follows:

```
./write_dx_file.pl [filename] [x-dimension y-dimension z-dimension]
[x-origin y-origin z-origin] [grid spacing]
./write_dx_file.pl file.dat 40 40 40 13.0 13.0 13.0 0.75
```

If the doeij keyword is provided, GIST also writes a large file, Eww_ij.dat, containing the mean water-water interaction energies between pairs of voxels, scaled by $\frac{1}{2}$. (See below.) This file has three columns. The first two columns are voxel indexes, i, j, where $j > i$, so that no pair appears more than once, and the third column is the mean interaction energy (kcal/mole) of water in voxels i and$j$, scaled by $\frac{1}{2}$. If the occupancy of either voxel is 0, such as for voxels covered by solute atoms, then the interaction energy is zero. In order to save space, such interactions are omitted from the file.

Sample cpptraj input file to run GIST

The following input file, gist.in, causes cpptraj to read a parameter file named topology.top; read in the first 5000 frames of the trajectory file named trajectoryfile.mdcrd; strip out all Na and Cl ions; and carry out a GIST run which computes order parameters, uses a 41x41x45 grid centered at (25.0, 31.0, 30.0) with a spacing of 0.5 Å, uses the default bulk water density of 0.0334 molecules/Å^3, and generates the main output file gist.out.

```
parm topology.top
trajin trajectoryfile.mdcrd 1 5000
strip @Na
strip @Cl
gist doorder doeij gridcntr 25.0 31.0 30.0 griddim 41 41 45
    gridspacn 0.50 out gist.out
go
```

To execute this run in the background, use

```
cpptraj<gist.in>gist.log& or cpptraj -i gist.in>gist.log&
```

Referencing GIST results to unperturbed (bulk) water

Inhomogeneous fluid solvation theory, which is the basis of GIST, is designed to provide information on how water structure and thermodynamics around a solute molecule, such as a protein, are changed relative to the structure and thermodynamics of unperturbed (bulk) water. Accordingly, the quantities reported by GIST are most informative when the results are referenced to the corresponding bulk water properties. For the orientational entropy, the reference value is the same regardless of water model or conditions, because the first order orientational distribution of water in the bulk is always uniform. Therefore, the GIST results for orientational entropies are already referenced to bulk. However, cpptraj reports unreferenced values for those GIST quantities whose reference values depend upon the water model and the simulation conditions; i.e., the energies. The translational entropy as well as the number densities will be referenced to bulk using the input referenced density or the default density value of 0.0334. The table below provides useful reference values for these quantities, computed for various water models at P=1atm, T=300K, using GIST in order to ensure a consistent minimum image treatment of periodic boundary conditions.

Users running calculations under significantly different conditions, or with different water models, should consider generating their own reference quantities by applying GIST to a simulation of pure water under their conditions of interest. The quantities of interest can then be obtained in their most precise available form by averaging over voxels, for the pure water simulation. If the

Water Model	Mean Energy (Eww-norm) (kcal/mol/water)	Number Density ($Å^{-3}$)
TIP3P	-9.533	0.0329
TIP4PEW	-11.036	0.0332
TIP4P	-9.856	0.0332
TIP5P	-9.596	0.0329
Tip3PFW	-11.369	0.0334
SPCE	-11.123	0.0333
SPCFW	-11.873	0.0329

Table 3: Water model energy and density.

quantity of interest is Q, then its average reference value is $Q_{reference} = \frac{\sum n_i Q_i}{\sum n_i}$, where Q_i and n_i are, respectively, GIST's reported values of the quantity and the population in voxel i. The densities, ρ_i, are referenced to the corresponding bulk densities, ρ^o, as $g_i = \rho_i/\rho^o$, while the energy and entropy terms are referenced by subtracting their bulk values.

Note that the Eww reference needs to be subtracted from the normalized water-water energy **Eww-norm**. A referenced **Eww-dens** can be obtained by multiplying the referenced **Eww-norm** by the solvent number density $\rho = g_O \rho^o = \frac{N_w}{N_f V_{vox}}$, where N_w is the number of water molecules in a voxel (**population**), N_f is the number of frames, and V_{vox} is the voxel volume.

Interpreting GIST results

GIST provides access to the first order entropies and the first- and second-order energies of inhomogeneous fluid solvation theory. Non-zero higher-order entropies exist but are not yet computationally accessible. However, for a pairwise additive force-field, such as those listed in the Table above, the energy is fully described at the second order provided by GIST.

GIST is a research tool, and its applications (to, for example, protein-ligand binding and protein function) are still being explored. The following general comments may be helpful to users studying GIST results.

1. The water in voxels near a solute (e.g., a protein) almost always has unfavorable water-water interaction energies, relative to bulk, simply because the solute displaces water, resulting in fewer proximal water-water interactions.

2. The unfavorable water-water energies mentioned in [8] may be balanced by favorable water-solute interactions. If they are not, as may occur especially for voxels in small, hydrophobic pockets, then the net energy of the water in the voxel may be unfavorable relative to bulk, in which case a ligand which displaces water from the voxel into bulk may get a boost in affinity.

3. Because the first order orientational distribution of bulk water is uniform, and a nonuniform distribution always has lower entropy than a uniform one, the

solute can only lower the orientational entropy of water, relative to bulk. Thus, this term always opposes solvation, and displacing oriented water into the bulk is always favorable from the standpoint of orientational entropy.

4. Localized water, which corresponds to voxels with high water density, has a low first order translational entropy, and the translational entropy around a solute is lower than that in bulk, as a nonuniform translational distribution takes the place of the uniform translational distribution of bulk water.

5. The displacement of highly oriented (low orientational entropy) and localized (low translational entropy) water into bulk leads to a favorable increase in these entropy terms.

6. However, highly oriented and localized water is often the consequence of strongly favorable polar interactions, such as hydrogen-bonding, between water and the solute. As a consequence, the net favorability of displacing such water is frequently a balance between favorable entropic consequences and unfavorable energetic consequences.

7. The water-water energy associated with a given voxel accounts for the interactions of the waters in this voxel with all other waters in the system, including waters in other voxels. This quantity is multiplied by $\frac{1}{2}$, so that, in a pure-water system where the GIST grid covers the entire simulation box, the sum over all voxels equals the correct mean water-water interaction energy. Note that Reference [9] does not include this factor of $\frac{1}{2}$.

8. For a typical GIST application, in which the grid occupies only part of the simulation box, the energy bookkeeping can become complicated, as discussed in Section II.B.3 (page 044101-6) of Reference [9]. That section also explains how one can compute the water-water energy associated with a region R defined by a set of voxels, E^R_{WW}. The regional water-water energy, on a normalized (per water) basis, is given by $E^R_{WW} = 2(\sum_{i \in R} E_{i,WW} - \sum_{i \in R} \sum_{j \in R, j>i} E_{i,j,WW})$ where $i \in R$ means that voxel i is in region R, $E_{i,WW}$ is the value of Eww-norm for voxel i, and $E_{i,j,WW}$ is the value of the water-water interaction energy between voxels i and j, taken from the file Eww_ij.dat. The extra factor of 2 in the present formula, relative to that in the paper, results from application of an extra factor of $\frac{1}{2}$ to the reported water-water interaction energies here.

9. If the GIST grid contains the entire solute and the calculation is sufficently converged, the energy and first-order entropy of hydration can be calculated by numerical integration. E.g., the energy of hydration is $\Delta E_{hyd} = \sum^{voxels}(E^{dens}_{sw} + E^{dens}_{ww}) \times V_{vox}$. For this, Eww has to be referenced carefully, since numerical inaccuracies can add up quickly. It can be advisable to omit all voxels above a certain distance to the solute to obtain more stable results.

12.39 grid

```
grid [out <filename>]
  { data <dsname> | boxref <ref name/tag> <nx> <ny> <nz> |
    <nx> <dx> <ny> <dy> <nz> <dz>
       [ { gridcenter <cx> <cy> <cz> |
        boxcenter |
```

```
        maskcenter <mask> |
        rmsfit <mask> [noxalign]} ]
  [box|origin|center <mask>] [negative] [name <gridname>]
  <mask> [normframe | normdensity [density <density>]]
 [pdb <pdbout> [max <fraction>]] [{byres|mymol}]
  [[smoothdensity <value>] [invert]] [madura <madura>]
```

[out <filename>] File to write out grid to. Use "`.grid`" or "`.xplor`" extension for XPLOR format, "`.dx`" for OpenDX format.

Options for setting up grid:

data <dsname> Use previously calculated/loaded grid data set named <dsname>. When using this option there is no need to specify grid bins/spacing/center.

boxref <ref name/tag> <nx> <ny> <nz> Set up grid using box information from a previously loaded reference structure. Currently the only way to set up non-orthogonal grids.

<nx> <dx> <ny> <dy> <nz> <dz> Number of grid bins and spacing in the X/Y/Z directions.

[gridcenter <cx> <cy> <cz>] Location of grid center, default is origin (0.0, 0.0, 0.0).

[boxcenter] Center grid on box center.

[maskcenter <mask>] Center the grid on the atoms selected by <mask>.

[rmsfit <mask>] Perform a best-fit rotation of the grid using the coordinates selected by <mask>.

[noxalign] If specified, grid will not be re-oriented to align with Cartesian axes once binning is finished. Will affect file formats that do not store full unit cell vectors (like Xplor).

Options for offset during grid binning (must center grid at origin):

[box] Offset each point by location of box center prior to gridding. Cannot be used with 'gridcenter'.

[origin] No offset (default)

[center <mask>] Offset each point by center of atoms in <mask> prior to gridding. Cannot be used with 'gridcenter'.

Other options:

[negative] Grid negative density instead of positive density.

[name <gridname>] Grid data set name.

<mask> Mask of atoms to grid.

[normframe] Normalize grid bins by the number of frames.

[normdensity [density <density>]] Normalize grid bins by density: GridBin = GridBin / (Nframes * BinVolume * density). Default particle density (molecules/Ang^3) for water based on 1.0 g/mL.

[pdb <pdbout> [max <fraction>]] Write a pseudo-PDB of grid points that have density greater than <fraction> (default 0.80) of the grid max value.

[{byres|bymol}] Grid the centers of mass of residues or molecules selected by <mask>.

Less common options:

[smoothdensity <smooth>] Used to smooth density. The smoothing takes the form of GridBin = 0 if GridBin < smooth, otherwise GridBin = GridBin - (GridBin * exp[-(GridBin - smooth)^2 / (0.2 * smooth^2)]).

[invert] (Only used if smoothdensity also used) Do inverse smoothing (i.e. if GridBin > smooth).

[madura <madura>] Grid values lower than <madura> become flipped in sign, exposes low density.

Data Sets Created:

<dsname> Grid data set.

Create a grid representing the histogram of atoms in *mask1* on the 3D grid that is "*nx* * *x_spacing* by *ny* * *y_spacing* by *nz* * *z_spacing* angstroms (cubed). By default the grid is centered at the origin unless **gridcenter** is specified. Grid points can be offset by either the box center (using **box**) or the center of specified atoms (using **center <mask>**); if either of these options are used the grid must be centered at the origin. Note that the ***bounds*** command (on page 126) can be very useful for determining grid dimensions.

Note that when calculating grid densities for things like solvent/ions, the solute of interest (about which the atomic densities are binned) should be rms fit, centered and imaged prior to the ***grid*** call in order to provide any meaningful representation of the density. If the optional keyword `negative` is also specified, then these density will be stored as negative numbers. Output can be in the XPLOR or OpenDX data formats.

Examples

Example 1: Grid water density around a solute. The solute is imaged to the origin and rms fit to the first frame. The grid will be centered on the origin as well.

```
trajin tz2.truncoct.nc
autoimage origin
rms first :1-13
# Create average of solute to view with grid.
average avg.mol2 :1-13
grid out.dx 20 0.5 20 0.5 20 0.5 :WAT@O
```

Example 2: Grid water density around a solute. The grid is centered on the solute.

```
trajin tz2.truncoct.nc
autoimage
grid out.dx 20 0.5 20 0.5 20 0.5 :WAT@O maskcenter :1-13
```

Example 3: Grid water density around a solute. The grid is centered on the solute and rms-fit. The density obtained should be equivalent to the first example.

```
trajin tz2.truncoct.nc
image :WAT
grid out.dx 20 0.5 20 0.5 20 0.5 :WAT@O rmsfit :1-13
```

Example 4: Generate grid from bounds command.

```
trajin tz2.ortho.nc
autoimage
rms first :1-13&!@H= mass
bounds :1-13 dx .5 name MyGrid out bounds.dat
average bounds.mol2 :1-13
# Save coordinates for second pass.
createcrd MyCoords
run
# Grid using grid data set from bounds command.
crdaction MyCoords grid bounds.xplor data MyGrid :WAT@O
```

Example 5: Create non-orthogonal grid based on the box.

```
trajin tz2.truncoct.nc
reference ../tz2.truncoct.nc [REF]
autoimage triclinic
grid nonortho.dx boxref [REF] 50 50 50 :WAT@O pdb nonortho.pdb
```

12.40 hbond

```
hbond [<dsname>] [out <filename>] [<mask>] [angle <acut>] [dist <dcut>]
      [donormask <dmask> [donorhmask <dhmask>]] [acceptormask <amask>]
      [avgout <filename>] [printatomnum] [nointramol] [image]
      [solventdonor <sdmask>] [solventacceptor <samask>]
      [solvout <filename>] [bridgeout <filename>] [bridgebyatom]
      [series [uuseries <filename>] [uvseries <filename>]]
      [bseries [bseriesfile <filename>]]
      [uuresmatrix [uuresmatrixnorm {none|frames}] [uuresmatrixout <file>]]
      [splitframe <comma-separated-list>]
```

[<dsname>] Data set name.

[out <filename>] Write # of solute-solute hydrogen bonds (aspect [UU]) vs time to this file. If searching for solute-solvent hydrogen bonds, write # of solute-solvent hydrogen bonds (aspect [UV]) and # of bridging solvent molecules (aspect [Bridge]), as well as the residue # of the bridging solvent and the solute residues being bridged with format '<solvent resnum>(<solute res1>+<solute res2>+...+),...' (aspect [ID]).

[<mask>] Atoms to search for solute hydrogen bond donors/acceptors.

[angle <acut>] Angle cutoff for hydrogen bonds (default 135°). Can be disabled by specifying -1.

[dist <dcut>] Distance cutoff for hydrogen bonds (acceptor to donor heavy atom, default 3.0 Å).

[donormask <dmask>] Use atoms in <dmask> as solute donor heavy atoms. If 'donorhmask' not specified only atoms bonded to hydrogen will be considered donors.

[donorhmask <dhmask>] Use atoms in <dmask> as solute donor hydrogen atoms. Should only be specified if 'donormask' is. Should be a 1 to 1 correspondence between donormask and donorhmask.

[acceptormask <amask>] Use atoms in <amask> as solute acceptor atoms.

[avgout <filename>] Write solute-solute hydrogen bond averages to <filename>.

[printatomnum] Add atom numbers to the output, in addtion to residue name, residue number and atom name.

[nointramol] Ignore intramolecular hydrogen bonds.

[image] Turn on imaging of distances/angles.

[solventdonor <sdmask>] Use atoms in <sdmask> as solvent donors. Can specify ions as well.

[solventacceptor <samask>] Use atoms in <samask> as solvent acceptors. Can specify ions as well.

[solvout <filename>] Write solute-solvent hydrogen bond averages to <filename>. If not specified and 'avgout' is, solute-solvent hydrogen bonds averages will be written to that file.

[bridgeout <filename>] Write information on detected solvent bridges to <filename>. If not specified, will be written to same place as 'solvout'.

[bridgebyatom] Report bridging results by atom instead of by residue.

[series] Save hydrogen bond formed (1.0) or not formed (0.0) per frame for any detected hydrogen bond. Solute-solute hydrogen bonds are saved with aspect [solutehb], solute-solvent hydrogen bonds are saved with aspect [solventhb].

[uuseries <filename>] File to write solute-solute hbond time series data to.

[uvseries <filename>] File to write solute-solvent hbond time series data to.

[bseries] Save bridge formed (1.0) or not formed (0.0) per frame for any detected bridge. Bridges are saved with aspect [bridge_<indexlist>], where <indexlist> is an underscore ('_') delimited list of bridged atom/residue numbers (depending on bridgebyatom).

[bseriesfile <filename>] File to write bridge time series data to.

[uuresmatrix] If specified, create a matrix with aspect [UUresmat] containing # of hydrogen bonds between each possible solute residue pair.

[uuresmatrixnorm {none|frames}] Control how matrix is normalized: none=no normalization, frames=normalize by total # frames.

[uuresmatrixout <file>] If specified, write matrix data to specified file.

[splitframe <comma-separated-list>] If specified, aplit the average hydrogen bond (avgout, solvout, bridgeout) analysis into sections delimited by the frame numbers. For example, 'splitframe 250,500,1000' will divide analysis into frames 1-249, 250-499, 500-999, and 1000 to end.

Data Sets Created:

<dsname>[UU] Number of solute-solute hydrogen bonds.

<dsname>[UV] (only for solventdonor/solventacceptor) Number of solute-solvent hydrogen bonds.

<dsname>[Bridge] (only for solventdonor/solventacceptor) Number of bridging solvent molecules.

<dsname>[ID] (only for solventdonor/solventacceptor) String identifying bridging solvent residues and the solute residues they bridge.

<dsname>[solutehb] (series only) Time series for solute-solute hydrogen bonds; 1 for present, 0 for not present.

<dsname>[solventhb] (series only) Time series for solute-solvent hydrogen bonds; 1 for present, 0 for not present.

<dsname>[bridge_<indexlist>] (bseries only) Time series for bridge; 1 for present, 0 for not present. The <indexlist> is an underscore ('_') delimited list of bridged atom/residue numbers (depending on bridgebyatom).

<dsname>[UUresmatr] (uuresmatrix only) Solute residue hydrogen bond matrix.

*Note that **series** data sets are not generated until hydrogen bonds are actually determined (i.e. **run** is called).*

Determine hydrogen bonds in each coordinate frame using simple geometric criteria. A hydrogen bond is defined as being between an acceptor heavy atom A, a donor hydrogen atom H, and a donor heavy atom D. If the A to D distance is less than or equal to the distance cutoff and the A-H-D angle is greater than or equal to the angle cutoff a hydrogen bond is considered formed. Imaging of distances/angles is not performed by default, but can be turned on using the **image** keyword.

Potential hydrogen bond donor/acceptor atoms are searched for as follows:

1. If just <**mask**> is specified donors and acceptors will be automatically determined from <**mask**>.

2. If **donormask** is specified donors will be determined from <**dmask**> (only atoms bonded to hydrogen will be considered valid). Optionally, **donorhmask** can be used in conjunction with **donormask** to explicitly specify the hydrogen atoms bonded to donor atoms. Acceptors will be automatically determined from <**mask**>.

3. If **acceptormask** is specified acceptors will be determined from <**amask**>. Donors will be automatically determined from <**mask**>.

4. If both **acceptormask** and **donormask** are specified only <**amask**> and <**dmask**> will be used; no searching will occur in <**mask**>.

Automatic determination of hydrogen bond donors/acceptors uses the simplistic criterion that "hydrogen bonds are FON", i.e., hydrogens bonded to F, O, and N atoms are considered donors, and F, O, and N atoms are considered acceptors. Intra-molecular hydrogen bonds can be ignored using the **nointramol** keyword.

The number of hydrogen bonds present at each frame will be determined and written to the file specified by **out**. If desired, the bridge [ID] data can be used in conjunction with the ***keep*** command to generate structures that only contain bridging solvent (12.43 on page 176). If the **series** keyword is specified the time series for each hydrogen bond (1 for present, 0 for not present) will also be saved for subsequent analysis (e.g. with ***lifetime***, see on page 276); solute-solute hydrogen bonds will be saved to '<dataset name>[solutehb]' and solute-solvent hydrogen bonds will be saved to '<dataset name>[solventhb]'. The data set legends are set with the residues and atoms involved in the hydrogen bonds. In the case of solute to non-specific solvent hydrogen bonds, a V is used in place of solvent.

If **avgout** is specified the average of each solute-solute hydrogen bond (sorted by population) formed over the course of the trajectory is printed with the format:

```
Acceptor   DonorH   Donor   Frames   Frac   AvgDist   AvgAng
```

where *Acceptor*, *DonorH*, and *Donor* are the residue and atom name of the atoms involved in the hydrogen bond, *Frames* is the number of frames the bond is present, *Frac* is the fraction of frames the bond is present, *AvgDist* is the average distance of the bond when present, and *AvgAng* is the average angle of the bond when present. The **printatomnum** keyword can be used to print atom numbers as well.

Solute to non-specific solvent hydrogen bonds can be tracked by using the **solventdonor** and/or **solventacceptor** keywords. The number of solute-solvent hydrogen bonds and number of "bridging" solvent molecules (i.e. solvent that is hydrogen bonded to two or more different solute residues at the same time) will also be written to the file specified by **out**. These keywords can also be used to track non-specific interactions with ions. If **avgout** or **solvavg** is specified the average of each solute solvent hydrogen bond will be printed with the format:

```
Acceptor   DonorH   Donor   Count   Frac   AvgDist   AvgAng
```

where *Acceptor*, *DonorH*, and *Donor* are either the residue and atom name of the solute atoms or "SolventAcc"/"SolventH"/"SolventDnr" representing solvent, *Count* is the total number of interactions between solute and solvent (note this can be greater than the total number of frames since for any given frame more than one solvent molecule can hydrogen bond to the same place on solute and vice versa), *AvgDist* is the average distance of the bond when present, and *AvgAng* is the average angle of the bond when present. If **avgout** or **bridgeout** is specified information on residues that were bridged by a solvent molecule over the course of the trajectory will be written to <bfilename> with format:

```
Bridge Res <N0:RES0> <N1:RES1> ... , <X> frames.
```

where '<N0:RES0> ...' is a list of residues that were bridged (residue # followed by residue name) and <X> is the number of frames the residues were bridged.

hbond Examples

To search for all hydrogen bonds within residues 1-22, writing the number of hydrogen bonds per frame to "nhb.dat" and information on each hydrogen bond found to "avghb.dat":

```
hbond :1-22 out nhb.dat avgout avghb.dat
```

To search for all hydrogen bonds formed between donors in residue 1 and acceptors in residue 2:

```
hbond donormask :1 acceptormask :2 out nhb.dat avgout avghb.dat
```

To search for all intermolecular hydrogen bonds only and solute-solvent hydrogen bonds, saving time series data to HB:

```
hbond HB out nhb.dat avgout solute_avg.dat \
  solventacceptor :WAT@O solventdonor :WAT \
  solvout solvent_avg.dat bridgeout bridge.dat \
  series uuseries uuhbonds.agr uvseries uvhbonds.agr
```

To search for non-specific hydrogen bonds between solute and ions named Na+:

```
hbond HB-Ion out nhb.agr avgout ion_avg.dat \
  solventacceptor :Na+ solventdonor :Na+
```

12.41 image

```
image [origin] [center] [triclinic | familiar [com <commask>]] [<mask>]
      [ bymol | byres | byatom ] [xoffset <x>] [yoffset <y>] [zoffset <z>]
```

[origin] Image to coordinate origin (0.0, 0.0, 0.0);
default is to image to box center.

[center] For bymol/byres, image by center of mass;
default is to image by first atom position.

[triclinic] Force imaging with triclinic code. This is
the default for non-orthorhombic cells.

[familiar [com <commask>]] Image to truncated
octahedron shape. If 'com <commask>' is given,
image with respect to the center of mass of atoms in
<commask>.

[<mask>] Image atoms/residues/molecules in mask.

[bymol] Image by molecule (default).

[byres] Image by residue.

[byatom] Image by atom.

[xoffset <x>] Shift atoms by a factor of <x> in the
X-direction.

[yoffset <y>] Shift atoms by a factor of <y> in the
Y-direction.

[zoffset <z>] Shift atoms by a factor of <z> in the
Z-direction.

Note this command is intended for advanced use; for most cases the ***autoimage*** command should be sufficient.

For periodic systems only, image molecules/residues/atoms that are outside of the box back into the box. Currently both orthorhombic and non-orthorhombic boxes are supported. A typical use of ***image*** is to move molecules back into the box after performing ***center***. For example, the following commands move all atoms so that the center of residue 1 is at the center of the box, then image so that all molecules that are outside the box after centering are wrapped back inside:

```
center :1
image
```

The xoffset etc. keywords can be used to shift the entire unit cell in a certain direction by the given factor, which can be useful for visualizing trajectories with periodic boundary conditions. For example, to generate a trajectory that is offset by 1.0 box length in the X direction, one could use:

```
image xoffset 1.0
trajout traj.offsetx1.nc
```

12.42 jcoupling

```
jcoupling <mask> [outfile <filename>] [kfile <param file>] [out <filename>]
          [name <dsname>]
```

<mask> Atom mask in which to search for dihedrals within.

[outfile <filename>] File to write j-coupling values to with fixed format.

[kfile <param file>] File containing Karplus parameters. If not specified will check CPPTRAJHOME, AMBERHOME, and KARPLUS environment variables (see below).

[out <filename>] File to write data set output to.

[name <dsname>] Data set name.

*Note data sets are not generated until **run** is called.*

Calculate J-coupling values for all dihedrals found within **<mask>** (all atoms if no mask given). In order to use this function, Karplus parameters for all dihedrals which will be calculated must be loaded. By default *cpptraj* will use the data found in either $CPPTRAJHOME/dat/Karplus.txt or $AMBERHOME/dat/Karplus.txt; if this is not found *cpptraj* will look for the file specified by the $KARPLUS environment variable.

In the Karplus parameter file each parameter set consists of two lines for each dihedral with the format:

```
[<Type>]<Name1><Name2><Name3><Name4><A><B><C>[<D>]
<Resname1>[<Resname2>...]
```

The first line defines the parameter set for a dihedral. <Type> is optional; if not given the form for calculating the J-coupling will be as described by Chou et al.[13]; if 'C' the form will be as described by Perez et al.[14]. The <NameX> parameters define the four atoms involved in the dihedral. Each <NameX> parameter is 5 characters wide, starting with a plus '+', minus '-' or space ' ' character indicating the atom belongs to the next, previous, or current residue. The remaining 4 characters are the atom name. The parameters <A>, <B>, <C>, and <D> are floating point values 6 characters wide describing the Karplus parameters. For the 'C' form A, B, and C correspond to C0, C1, and C2; D is unused and should not be specified. The second line is a list of residue names (4 characters each) to which the dihedral applies. For example:

```
C HA   CA   CB   HB    5.40 -1.37  3.61
ILE VAL
```

Describes a dihedral between atoms HA-CA-CB-HB using the Perez et al. form with constants C0=5.40, C1=-1.37, C2=3.61 applied to ILE and VAL residues.

Output can be in both a fixed format (**outfile** <**filename**>) and using cpptraj data set/data file formatting (**out** <**filename**>). The fixed format has each dihedral that is defined from <**mask1**> printed along with its calculated J-coupling value for each frame, e.g.:

```
#Frame 1
1 SER HA CA CB HB2 45.334742 4.024759
1 SER HA CA CB HB3 -69.437134 1.829510
...
```

First the frame number is printed, then for each dihedral: Residue number, residue name, atom names 1-4 in the dihedral, the value of the dihedral, the J-coupling value.

In *cpptraj* format, only the J-coupling value is written.

12.43 keep

```
keep [ bridgedata <bridge data set> [nbridge <#>] [nobridgewarn]
       [bridgeresname <res name>] bridgeresonly <resrange>] ]
     [keepmask <atoms to keep>] [charge <new charge>]
     [outprefix <prefix>] [nobox] [parmout <filename>]
     [parmopts <comma-separated-list>]
```

bridgedata <**bridge data set**> Data set containing bridge ID strings from the *hbond* command (12.40 on page 169).

nbridge <#> Number of bridging residues to keep (default 1).

nobridgewarn If specified, suppress warnings for when active # bridges does not equal requested number.

bridgeresname <**res name**> Name of bridging residues (default 'WAT').

bridgeresonly <**range**> If specified, only keep bridges that bridge residues in the <resrange> list.

keepmask <**atoms to keep**> Mask of atoms to keep.

charge <**new charge**> Scale charges so total charge of remaining atoms matches the specified <new charge>.

outprefix <**prefix**> Write modified topology to <prefix>.<originalname>

[nobox] Remove any box information from the modified topology.

parmout <**filename**> Write modified topology to <filename>.

parmopts <**list**> Options for writing topology file.

Keep only specified atoms (opposite of ***strip***). This can also be used in conjunction with output from the ***hbond*** command to retain solute and only bridging residues (e.g. bridging waters). For example, the following run generates bridging data with the ***'hbond'*** command in a first pass, then uses the bridge ID data to retain only 1 single bridging water between residues 10 and 11:

```
parm tz2.ortho.parm7
trajin tz2.ortho.nc
# First pass, generate bridge time series
hbond hb solventacceptor :WAT@O solventdonor :WAT out hb.dat
run
# Second pass, retain only frames where the bridge is present
# for residues 10 and 11.
keep bridgedata hb[ID] nbridge 1 bridgeresonly 10,11 parmout keep.parm7
# Write trajectory
trajout keep.nc
run
```

This run reads in bridge ID data from a previous hbond run and uses it to keep only residues 10, 11, and a bridging water:

```
parm tz2.ortho.parm7
trajin tz2.ortho.nc
readdata hb.dat
keep keepmask :10,11 bridgedata hb.dat:5 nbridge 1 bridgesonly 10,11 \
  parmout keep.10.11.parm7
trajout keep.10.11.nc
run
```

12.44 lessplit

```
lessplit [out <filename prefix>] [average <avg filename>] <trajout args>
```

[out <**filename prefix**>**]** Write split LES trajectories to <filename prefix>.X, where X is an integer.

[average <**avg filename**>**]** Write trajectory of averaged LES regions to <avg filename>.

<**trajout args**> Arguments for output trajectories.

Split and/or average LES trajectory. At least one of **'out'** or **'average'** must be specified. If both are specified they share <trajout args>.

12.45 lie

```
lie [<name>] <Ligand mask> [<Surroundings mask>] [out <filename>] [nopbc]
    [noelec] [novdw] [cutvdw <cutoff>] [cutelec <cutoff>] [diel <dielc>]
DataSet Aspects:
```

[EELEC] `Electrostatic energy (kcal/mol).`

[EVDW] `van der Waals energy (kcal/mol).`

For each frame, calculate the non-bonded interactions between all atoms in <Ligand mask> with all atoms in <Surroundings mask>. Electrostatic and van der Waals interactions will be calculated for all atom pairs. A separate electrostatic and van der Waals cutoff can be applied, the default is 12.0 Angstroms for both. <dielc> is an optional dielectric constant. Either the electrostatic or van der Waals calculations can be suppressed via the keywords noelec and novdw, respectively. Periodic boundary conditions (and the minimum image convention) can be abandoned with the "nopbc" keyword. Note, however, that no prior imaging is performed if the frames contain periodic boundaries. This may be useful for instances when you are simulating a microscopic droplets.

The electrostatic interactions are calculated according to a simple shifting function shown below. The data file will contain two data sets—one for electrostatic interactions and one for van der Waals interactions. Periodic topologies and trajectories are required (i.e., explicit solvent is necessary). The minimum image convention is followed.

$$E_{elec} = k\frac{q_i q_j}{r_{ij}}\left(1 - \frac{r_{ij}^2}{r_{cut}^2}\right)^2$$

12.46 lipidorder

```
order out <filename> [x|y|z] [scd] [unsat <mask>]
      [taildist <filename> [delta <resolution>] tailstart <mask>
       tailend <mask>] <mask0> ... <maskN>
```

out `Output file for order parameters: Sx, Sy, Sz (each succeeded by the standard deviation), and two estimates for the deuterium-order parameter |SCD| = 0.5Sz and |SCD| = -(2Sx + Sy)/3. If scd is set then the order parameter directly computed from the C-H vectors is output.`

x|y|z `Reference axis. (z)`

unsat `Mask for unsaturated bonds. Sz is calculated for vector Cn-Cn+1. This is only relevant if scd (below) is not set, i.e. order parameters are calculated from carbon position only.`

scd Calculate the deuterium-order parameter |SCD| directly from the C-H vectors (masks must contain C-H-H triplets, see below). Otherwise the order parameter is estimated from carbon positions only (masks must contain only relevant carbons). (false)

taildist Optional output file for end-to-end distances.

delta Optional resolution for taildist. (0.1)

tailstart Mask for the start of the tail. Must be given if taildist.

tailend Mask for the end of the tail. Must be given if taildist.

mask0 ... maskN Masks for each group in the lipid chain.

The order parameters S_x, S_y, S_z and |SCD| are calculated. Carbons must be given in bonding order. If **scd** the masks must be made up of C-H-H triples, hence hydrogens to double bonds must be enumerated twice while methyl groups require an additional mask which will also create two entries in the output.

$S_z$is the vector joining carbons C_{n-1} and C_{n+1}, S_x the vector normal to the $C_{n-1} - C_n$ and $C_n - C_{n+1}$ plane and S_y is the third axis in the molecular coordinate system. The order parameter is then calculated from $Sc = 0.5 < 3\cos(2\theta) > -1$, where θ is the angle to the chosen reference axis. See example input file.

Example input (all atom names according to CHARMM27 force field for POPC).

sn1 chain: order parameters S_x, S_y, S_z and $|SCD| = 0.5 \times S_z$ and $|SCD| = -(2S_x + S_y)/3$

```
lipidorder out sn1.dat z taildist e2e_sn1.dat delta 0.1 \
           tailstart ":POPC@C32" tailend ":POPC@C316" \
           ":POPC@C32" ":POPC@C33" ":POPC@C34" ":POPC@C35" \
           ":POPC@C36" ":POPC@C37" ":POPC@C38" ":POPC@C39" \
           ":POPC@C310" ":POPC@C311" ":POPC@C312" ":POPC@C313" \
           ":POPC@C314" ":POPC@C315" ":POPC@C316"
```

See also `$AMBERHOME/AmberTools/test/cpptraj/Test_LipidOrder`.

12.47 lipidscd

`lipidscd [<name>] [<mask>] [{x|y|z}] [out <file>] [p2]`

<**name**> Output data set name.

<**mask**> Atom mask specifying where to search for lipids.

x|y|z Axis to calculate order parameters with respect to (default z).

out <**file**> File to write order parameters to.

p2 If specified, report raw <P2> values.

DataSets Generated:

<**name**>**[H1]:**<**idx**> Hold lipid order parameters for each C-H1. Each lipid type will have a different <idx> starting from 0.

<**name**>**[H2]:**<**idx**> Hold lipid order parameters for each C-H2. If no H2, the C-H1 value will be used.

<**name**>**[H3]:**<**idx**> Hold lipid order parameters for each C-H3. If no H3, the C-H2/C-H1 value will be used.

<**name**>**[SDHX]:**<**idx**> Hold standard deviation of lipid order parameters for each C-HX.

Calculate lipid order parameters SCD (|<P2>|) for lipid chains in mask <mask>. Lipid chains are identified by carboxyl groups, i.e. O-(C=O)-C1-...-CN, where C1 is the first carbon in the acyl chain and CN is the last. Order parameters will be determined for each hydrogen bonded to each carbon. If 'p2' is specified the raw <P2> values will be reported.

12.48 makestructure

```
makestructure <List of Args>
```

Apply dihedrals to specified residues using arguments found in <List of Args>, where an argument is 1 or more of the following arg types:

<sstype keyword>:<res range>

Apply secondary structure type (via phi/psi backbone angles) to residues in given range. If the secondary structure type is a turn, the residue range must correspond to a multiple of 2 residues.

Keyword	phi, psi (deg.)	# residues
alpha	-57.8, -47.0	1
left	-57.8, 47.0	1
pp2	-75.0, 145.0	1
hairpin	-100.0, 130.0	1
extended	-150.0, 155.0	1
typeI	-60.0, -30.0 | -90.0, 0.0	2
typeII	-60.0, 120.0 | 80.0, 0.0	2
typeVIII	-60.0, -30.0 | -120.0, 120.0	2
typeI'	60.0, 30.0 | 90.0, 0.0	2
typeII	60.0, -120.0 | -80.0, 0.0	2
typeVIa1	-60.0, 120.0 | -90.0, 0.0	2
typeVIa2	-120.0, 120.0 | -60.0, 0.0	2
typeVIb	-135.0, 135.0 | -75.0, 160.0	2

<custom ss name>:<res range>[:<phi>:<psi>]

If <phi> and <psi> are given, define a custom secondary structure conformation named <custom_ss> and apply to residues in range. If <custom_ss> has been previously defined then apply it to residues in range.

<custom turn name>:<res range>[:<phi1>:<psi1>:<phi2>:<psi2>]

If <phi1>, <psi1>, <phi2>, and <psi2> are given, defined a custom turn conformation named <custom_turn> and apply to residues in range (range must correspond to a multiple of 2 residues). If <custom_turn> has been previously defined then apply it to residues in range.

<custom dih name>:<res range>[:<dih type>:<angle>]

```
<dih type> = alpha beta gamma delta epsilon zeta nu0 nu1 nu2 nu3 nu4
             h1p c2p chin phi psi chip omega chi2 chi3 chi4 chi5
```

If <dih type> and <angle> are given, apply <angle> to selected dihedrals of type in range. If <custom dih> has been previously defined then apply it to residues in range.

<custom dih name>:<res range>[:<at0>:<at1>:<at2>:<at3>:<angle>[:<offset>]]

Apply <angle> to dihedral defined by atoms <at1>, <at2>, <at3>, and <at4>, or use previously defined <custom_dih>.

<offset>	Description
-2	<at0> and <at1> in previous residue.
-1	<at0> in previous residue.
0	All atoms in single residue.
1	<at3> in next residue.
2	<at2> and <at3> in next residue.

ref:<range>:<refname>[:<ref range>[:<dih types>]] [refvalsout <file>] [founddihout <file>]

Apply dihedrals from residues <ref_range> in previously loaded reference structure <refname> to dihedrals in <range>. If <ref range> is specified, use those residues from reference. The dihedral types to be used (see **<dih_type>** above) can be specified in a comma-separated list; default is phi/psi. Note that in order to specify <dih types>, <ref range> must be specified. The 'refvalsout' and 'founddihout' keywords can be used to print dihedrals found in the reference and target structures respectively to files.

Examples

Assign polyproline II structure to residues 1 through 13:

```
makestructure pp2:1-13
```

Make residues 1 and 12 'extended', residues 6 and 7 a type I' turn, and two custom assignments, one (custom1) for residues 2-5, the other (custom2) for residues 8-11:

```
makestructure extended:1,12 \
              custom1:2-5:-80.0:130.0:-130.0:140.0 \
              typeI':6-7 \
              custom2:8-11:-140.0:170.0:-100.0:140.0
```

Assign residue 5 phi 90 degrees, residues 6 and 7 phi=-70 and psi=60 degrees:

```
makestructure customdih:5:phi:90 custom:6,7:-70:60
```

Create a new dihedral named chi1 and assign it a value of 35 degrees in residue 8:

```
makestructure chi1:8:N:CA:CB:CG:35
```

Assign 'extended' structure to residues 1 and 12, a custom turn to residues 2-5 and 8-11, and a typeI' turn to residues 6-7:

```
makestructure extended:1,12 \
              custom1:2-5:-80.0:130.0:-130.0:140.0 \
              typeI':6-7 \
              custom1:8-11
```

Assign secondary structure from reference structure:

```
parm ../tz2.parm7
reference ../tz2.rst7
trajin pp2.rst7.save
makestructure "ref:1-13:tz2.rst7" rmsd reference
trajout fromref.pdb multi
```

12.49 mask

```
mask <mask> [maskout <filename>] [out <filename>] [nselectedout <filename>]
     [name <setname>] [ {maskpdb <filename> | maskmol2 <filename>}
                        [trajargs <comma-separated args>] ]
```

<**mask**> Atom mask to process.

maskout <**filename**> Write information on atoms in <mask> to <filename>.

out <**filename**> Write the frame, atom number, atom name, residue number, residue name, and molecule number for each selected atom to file.

nselectedout <**filename**> Write the total number of selected atoms to file.

name <**setname**> Name for output data sets.

maskpdb <**filename**> Write PDB of atoms in <mask> to <name>.X.

maskmol2 <**filename**> Write Mol2 of atoms in <mask> to <name>.X.

trajargs <**comma-separated args**> When writing output PDB/Mol2, additional trajectory arguments to pass to the output trajectory.

DataSets Created

<**name**> Number of atoms selected each frame.

<**name**>**[Frm]** Frame number for each selected atom.

<**name**>**[AtNum]** Atom number for each selected atom.

<**name**>**[Aname]** Atom name for each selected atom.

<**name**>**[Rnum]** Residue number for each selected atom.

<**name**>**[Rname]** Residue name for each selected atom.

<**name**>**[Mnum]** Molecule number for each selected atom.

For each frame determine all atoms that correspond to <**mask**>. This is most useful when using distance-based masks, since the atoms in the mask are updated for every frame read in. If **maskout** is specified information on all atoms in <mask> will be written to <filename> with format:

```
#Frame AtomNum Atom ResNum Res MolNum
```

where `#Frame` is the frame number, `AtomNum` is the number of the selected atom, `Atom` is the name of the selected atom, `ResNum` is the residue number of the selected atom, `Res` is the residue name, and `MolNum` is the molecule number of the selected atom.

If **maskpdb** or **maskmol2** are specified a PDB/Mol2 file corresponding to <mask> will be written out every frame with name "*<name>.frame#*".

For example, to write out all residues within 3.0 Angstroms of residue 195 that are named WAT to "Res195WAT.dat", as well as write out corresponding PDB files:

```
mask "(:195<:3.0)&:WAT" maskout Res195WAT.dat maskpdb Res195WAT.pdb
```

To write all out atoms outside of 5.0 Angstroms of residues named ARG to PDB files with a chain ID of 'B':

```
mask :ARG>@5.0 maskpdb Outside5Arg.pdb trajargs "chainid 'B'"
```

12.50 matrix

```
matrix [out <filename>] [start <#>] [stop|end <#>] [offset <#>]
       [name <name>] [ byatom | byres [mass] | bymask [mass] ]
       [ ired [order <#>] ]
       [ {distcovar | idea} <mask1> ]
       [ {dist | correl | covar | mwcovar} <mask1> [<mask2>] ]
       [ dihcovar dihedrals <dataset arg> ]
```

[out <filename>] `If specified, write matrix to <filename>.`

[start <#>] [stop|end <#>] [offset <#>] `Start, stop, and offset frames to use (as a subset of all frames read in).`

[name <name>] `Name of the matrix dataset (for referral in subsequent analysis).`

byatom `Write results by atom (default). This is the sole option for covar, mwcovar, and ired.`

byres `Write results by calculating an average for each residue (mass weighted if mass is specified).`

bymask `Write average over <mask1>, and if <mask2> is specified <mask1> x <mask2> and <mask2> as well (mass weighted if mass is specified).`

Calculate matrix of the specified type from input coordinate frames:

dist <**mask1**> [<**mask2**>] Distance matrix (default).

correl <**mask1**> [<**mask2**>] Correlation matrix (aka dynamic cross correlation[15]).

covar <**mask1**> [<**mask2**>] Coordinate covariance matrix.

mwcovar <**mask1**> [<**mask2**>] Mass-weighted coordinate covariance matrix.

distcovar <**mask1**> Distance covariance matrix.

idea <**mask1**> Isotropically Distributed Ensemble Analysis matrix.[16]

ired [**order** <#>] Isotropic Reorientational Eigenmode Dynamics matrix[17] with Legendre polynomials of specified order (default 1). IRED vectors must have been specified previously with '***vector* ired**' (see 12.92 on page 232).

dihcovar dihedrals <**dataset arg**> Dihedral covariance matrix. Dihedral data sets must have been previously defined with e.g. ***dihedral*** or ***multidihedral*** commands or read in externally with ***readdata*** and marked as dihedrals.

Matrix dimensions will be of the order of N x M for **dist**, **correl**, **idea**, and **ired**, 2N x 2N for **dihcovar**, 3N x 3M for **covar** and **mwcovar**, and N(N-1) x N(N-1) / 4 for **distcovar** (with N being the number of data sets in the case of **ired** and **dihcovar** and the number of atoms in <**mask1**> otherwise, and M being the number of atoms in <**mask2**> if specified or <**mask1**> otherwise). No mask is required for **ired**; the matrix will be made up of previously defined IRED vectors (see the ***vector*** command on page 232). Similarly no mask is required for dihcovar; dihedral data sets must have been previously defined. Only one mask can be used with **distcovar** and **idea** matrices (i.e. they can be symmetric only), otherwise one or two masks can be used (for symmetric and full matrices respectively). If two masks are specified the number of atoms covered by *mask1* must be greater than or equal to the number of atoms covered by *mask2,* and on output <**mask1**> corresponds to columns while <**mask2**> corresponds to rows.

Note that for backwards compatibility, output files written with '**out** <**filename**>' will have the options '**noheader noxcol square2d**' applied to them (see 6 on page 27 for more details). To prevent any of these from taking effect, simply specify '**header**', '**xcol**', and/or '**nosquare2d**' after '**out** <**filename**>'.

As a simple example, a distance matrix of all CA atoms is generated and output to 'distmat.dat'.

```
matrix dist @CA out distmat.dat
```

12.51 mindist/maxdist

```
{min|max}dist mask1 <mask1> [mask2 <mask2>] [{byatom|byres|bymol}]
              [noimage] [name <setname>] [out <file>] [resoffset <#>]
```

mask1 <**mask1**> First mask for selecting atoms.

[mask2 <**mask2**>**]** Optional second mask for selecting atoms.

[{byatom|byres|bymol}]

byatom Report the minimum or maximum distance between atoms in <mask1> or between atoms in <mask1> and atoms in <mask2>.

byres Report the minimum or maximum distance between all residue pairs selected by <mask1>, or pairs of residues selected by <mask1> and residues selected by <mask2> (excluding certain pairs, see resoffset).

bymol Report the minimum or maximum distance between all molecule pairs selected by <mask1>, or pairs of molecules selected by <mask1> and molecules selected by <mask2>.

[noimage] Do not use the minimum image convention for distances.

[name <**setname**>**]** Output data set name.

[out <**file**>**]** Write data to <file>.

[resoffset <#>**]** For byres, ignore residue pairs if the difference in residue numbers is greater than the cutoff (default 1).

Data Sets Created:

<**name**> For byatom, a set containing the minimum or maximum distance for each frame.

<**name**>**[**<#>_<#>**]** For byres/bymol, a set containing the minimum or maximum distance between the residue/molecule pair specified by the numbers in the aspect, e.g. '<name>[1_3]' for byres would be between residues 1 and 3.

Calculate the minimum or maximum distance in Angstroms between atoms or residue/molecule pairs.

12.52 minimage

```
minimage [<name>] <mask1> <mask2> [out <filename>] [geom] [maskcenter]
```

<name> Data set name.

<mask1> First atom mask.

<mask2> Second atom mask.

out <filename> File to write to.

geom (maskcenter only) If specified, use geometric center instead of center of mass.

maskcenter Calculate distance from center of masks instead of between each atom.

Data Sets Created:

<name> Minimum distance to an image in Ang.

<name>**[A1]** Atom number in mask 1 involved in minimum distance.

<name>**[A2]** Atom number in mask 2 involved in minimum distance.

Calculate the shortest distance to an image, i.e. the distance to a neighboring unit cell, as well as the numbers of the atoms involved in the distance. By default the distance between each atom in <mask1> and <mask2> is considered; if **maskcenter** is specified the center of the masks is used. By convention, the lower atom number is saved as A1 and the higher is saved as A2.

12.53 molsurf

```
molsurf [<name>] [<mask>] [out filename] [probe <probe_rad>]
     [radii {gb | parse | vdw}] [offset <rad_offset>]
```

[<name>**]** Name of surface area data set.

[<mask>**]** Atoms to calculate surface area of.

[out <filename>**]** File to write values to.

[probe <probe_rad>**]** Probe radius (default 1.4 Angstrom).

[offset <rad_offset>**]** Add <rad_offset> to each atom radius (default 0.0).

[radii {gb|parse|vdw}] Specify radii to use:

gb GB radii (default).

parse PARSE radii.

vdw van der Waals radii.

Calculate the Connolly surface area[18] of atoms in <mask> (default all atoms if no mask specified) using routines from molsurf (originally developed by Paul Beroza) using the probe radius specified by **probe** (1.4 Å if not specified). Note

that if GB/VDW radii are not present in the topology file (e.g. for PDB files), then PARSE[19] radii can be used. Also note that this routine only calculate absolute surface areas, i.e. it cannot be used to get the contribution of a subset of atoms to overall surface area; if such functionality is needed try the ***surf*** command (12.83 on page 224).

12.54 multidihedral

```
multidihedral [<name>] <dihedral types> [resrange <range/mask>] [out <filename>] [range
              [dihtype <name>:<a0>:<a1>:<a2>:<a3>[:<offset>] ...]
                  Offset -2=<at0><at1> in previous res, -1=<at0> in previous res,
                         0=All <atX> in single res,
                         1=<at3> in next res, 2=<at2><at3> in next res.
              <dihedral types> =  alpha beta gamma delta epsilon zeta
                                  nu0 nu1 nu2 nu3 nu4 h1p c2p chin
                                  phi psi chip omega chi2 chi3 chi4 chi5
```

[<name>] Output data set name.

<dihedral types> Dihedral types to look for. Note that chip is 'protein chi', chin is 'nucleic chi'.

[resrange <range/mask>] Residue range to look for dihedrals in. Default is all solute residues. If a mask expression is given, use residues selected by the mask expression; if any part of a residue is selcted it will be used.

[out <filename>] Output file name.

[range360] Wrap torsion values from 0.0 to 360.0 (default is -180.0 to 180.0).

[dihtype <name>:<a0>:<a1>:<a2>:<a3>[:<offset>] Search for a custom dihedral type called <name> using atom names <a0>, <a1>, <a2>, and <a3>.

Offset: -2=<a0><a1> in previous res, -1=<a0> in previous res, 0=All <aX> in single res, 1=<a3> in next res, 2=<a2><a3> in next res.

DataSets Generated:

<name>[<dihedral type>]:<#> Aspect corresponds to the dihedral type name (e.g. [phi], [psi], etc). The index is the residue number.

Note data sets are not generated until ***run*** *is called.*

Calculate specified dihedral angle types for residues in given range/mask. By default, dihedral angles are identified based on standard Amber atom names. The resulting data sets will have aspect equal to [<dihedral type>] and index

equal to residue #. To differentiate the chi angle, chip is used for proteins and chin for nucleic acids. For example, to calculate all phi/psi dihedrals for residues 6 to 9:

```
multidihedral MyTorsions phi psi resrange 6-9 out PhiPsi_6-9.dat
```

This will generate data sets named MyTorsions[phi]:6, MyTorsions[psi]:6, MyTorsions[phi]:7, etc. Dihedrals other than those defined in <**dihedral types**> can be searched for using **dihtype**. For example to create a custom dihedral type called chi1 using atoms N, CA, CB, and CG (all in the same residue), then search for and calculate the dihedral in all residues:

```
multidihedral dihtype chi1:N:CA:CB:CG out custom.dat
```

12.55 multipucker

```
multipucker [<name>] [<pucker types>] [out <filename>] [resrange <range>]
            [altona|cremer] [puckertype <name>:<a0>:<a1>:<a2>:<a3>:<a4>[:<a5>] ...]
         [amplitude [ampout <ampfile>]] [theta [thetaout <thetafile>]]
         [range360] [offset <offset>]
         <pucker types> =  nucleic furanose pyranose
```

[<name>] Output data set name.

<pucker types> Pucker types to look for.

[out <filename>] Output file name to write pucker data to.

[resrange <range>] Residue range to look for puckers in. Default is all solute residues.

[puckertype <name>:<a0>:<a1>:<a2>:<a3>:<a4>[:<a5>] Search for a custom pucker type called <name> using atom names <a0>, <a1>, <a2>, <a3>, and <a4> (also <a5> for 6 atom puckers).

[altona] Use method of Altona & Sundaralingam (5 atoms only). This is the default when pucker has 5 atoms.

[cremer] Use method of Cremer and Pople (5 or 6 atoms). This is the default when pucker has 6 atoms.

[amplitude] Also calculate amplitude (in degrees).

ampout <ampfile> File to write amplitude sets to.

[theta] (Valid for 6 atoms only) Also calculate theta (in degrees).

thetaout <thetafile> File to write theta sets to.

[range360] Wrap pucker values from 0.0 to 360.0 (default is -180.0 to 180.0).

[offset <offset>] Add <offset> to pucker values.

DataSets Generated:

<**name**>[<**pucker type**>]:<#> Aspect corresponds to the pucker type name (e.g. [nucleic], [furanose], etc). The index is the residue number.

<**name**>[<**pucker type**>**Amp**]:<#> amplitude only. Data set for pucker amplitude.

<**name**>[<**pucker type**>**Theta**]:<#> theta only. Data set for pucker theta.

Note data sets are not generated until ***run*** *is called.*

Calculate specified pucker types for residues in given range. By default, puckers are identified based on standard Amber atom names. The resulting data sets will have aspect equal to [<pucker type>] and index equal to residue #. In order to be identified as a pucker, all consecutive atoms in the pucker must be bonded, and the last atom of the pucker must be bonded to the first.

For example, to calculate all nucleic acid ribose puckers for residues 6 to 9:

```
multipucker MyPuckers nucleic resrange 6-9 out Pucker_6-9.dat
```

This will generate data sets named MyPuckers[nucleic]:6, MyPuckers[nucleic]:7, etc. Puckers other than those defined in <**pucker types**> can be searched for using **puckertype**. For example to create a custom pucker type called furanoid using atoms C2, C3, C4, C5, and O2, then search for and calculate that pucker (with amplitudes) using the method of Cremer and Pople in all residues:

```
multipucker Furanoid puckertype furanoid:C2:C3:C4:C5:O2 cremer \
  out furanoid.dat amplitude ampout furanoid.dat
```

12.56 multivector

```
multivector [<name>] [resrange <range>] name1 <name1> name2 <name2> [out <filename>]
            [ired]
```

[<name>] Data set name.

[resrange <range>] Range of residues to look for vectors in.

name1 <name1> Name of first atom in each residue.

name2 <name2> Name of second atom in each residue.

[out <filename>] File to write results to.

Search for and calculate atomic vectors between atoms named <name1> and <name2> in residues specified by the given <range>; each one is equivalent to the command '`vector <name1> <name2>`'. For example, to calculate all vectors between atoms named 'N' and atoms named 'H' in residues 5-20, storing the results in data sets named NH and writing to NH.dat:

```
multivector NH name1 N name2 H ired out NH.dat resrange 5-20
```

12.57 nastruct

```
nastruct [<dataset name>] [resrange <range>] [sscalc] [naout <suffix>]
      [noheader] [resmap <ResName>:{A,C,G,T,U} ...] [calcnohb]
         [noframespaces] [baseref <file>] ...
         [bpmode {3dna|babcock}] [allhb]
      [hbcut <hbcut>] [origincut <origincut>] [altona | cremer]
      [zcut <zcut>] [zanglecut <zanglecut>] [groovecalc {simple | 3dna}]
         [axesout <file> [axesoutarg <arg> ...] [axesparmout <file>]]
      [bpaxesout <file> [bpaxesoutarg <arg> ...] [bpaxesparmout <file>]]
      [stepaxesout <file> [stepaxesoutarg <arg> ...] [stepaxesparmout <file>]]
         [axisnameo <name>] [axisnamex <name>] [axisnamey <name>] [axisnamez <name>]
      [{ first | reference | ref <name> | refindex <#> |
            allframes |
            specifiedbp pairs <b1>-<b2>,... }]
```

[<dataset name>] Output data set name.

[resrange <range>] Residue range to search for nucleic acids in (default all).

[sscalc] Calculate parameters between consectuive bases in strands.

[naout <suffix>] File name suffix for output files; BP.<suffix> for base pair parameters, BPstep.<suffix> for base pair step parameters, and Helix.<suffix> for base pair step helical parameters. If sscalc is specified, also SS.<suffix> for parameters of consecutive bases in strands.

[noheader] Do not print header to naout file.

[resmap <ResName>:{A,C,G,T,U}] Attempt to treat residues named <ResName> as if it were A, C, G, T, or U; useful for residues with modifications or non-standard residue names. This will only work if enough reference atoms are present in <ResName>.

[calcnohb] Calculate parameters between bases in base pairs even if no hydrogen bonds present between them.

[noframespaces] If specified there will be no spaces between frames in the naout files.

[baseref <file>] Specify a custom nucleic acid base reference. One file per custom residue; multiple 'baseref' keywords may be present. See below for details.

[bpmode {3dna|babcock}] Specify axis conventions for calculating base pair parameters. If '3dna' (default), use conventions of 3DNA[20]; flip Y and Z of complimentary base for antiparallel. If 'babcock', use conventions of Babcock et al.[21] ; flip Y and Z of complimentary base for antiparallel, flip X and Y for parallel.

[allhb] Report the total number of hydrogen bonds detected instead of just the number of Watson-Crick-Franklin hydrogen bonds.

[hbcut <hbcut>] Distance cutoff (in Angstroms) for determining hydrogen bonds between bases (default 3.5).

[origincut <origincut>] Distance cutoff (in Angstroms) between base pair axis origins for determining which bases are eligible for base-pairing (default 2.5).

[altona] Use method of Altona & Sundaralingam to calculate sugar pucker (default, see *pucker* command).

[cremer] Use method of Cremer and Pople to calculate sugar pucker (see *pucker* command).

[zcut] Distance cutoff (in Angstroms) between base reference axes along the Z axis (i.e. stagger) for determining base pairing (default 2).

[zanglecut] Angle cutoff (in degrees) between base reference Z axes for determining base pairing (default 65).

[groovecalc] Groove width calculation method:

simple Use P-P distance for major groove, O4-O4 distance for minor groove. Output to 'BP.<suffix>'.

3dna Use groove width calculation of El Hassan and Calladine[22]. Output to 'BPstep.<suffix>'.

[axesout <file>] Trajectory file to write base axes to.

[axesoutarg <arg>] Trajectory argument to pass to base axes trajectory file (can specify more than once).

[axesparmout <file>] Topology file to write base axes pseudo topology to.

[bpaxesout <file>] Trajectory file to write base pair axes to.

[bpaxesoutarg <arg>] Trajectory argument to pass to base pair axes trajectory file (can specify more than once).

[bpaxesparmout <file>] Topology file to write base pair axes pseudo topology to.

[stepaxesout <file>] Trajectory file to write base pair step axes to.

[stepaxesoutarg <arg>] Trajectory argument to pass to base pair step axes trajectory file (can specify more than once).

[stepaxesparmout <file>] Topology file to write base pair step axes pseudo topology to.

[axisnameo <name>] Change name of axis origin pseudo atom (default 'Orig').

[axisnamex <name>] Change name of axis origin pseudo atom (default 'X').

[axisnamey <name>] Change name of axis origin pseudo atom (default 'Y').

[axisnamez <name>] Change name of axis origin pseudo atom (default 'Z').

How to determine base pairing:

[first] Use first frame to determine base pairing (default).

[reference | refindex <#> | ref <name>] Reference structure to use to determine base pairing.

[allframes] If specified determine base pairing each frame.

[specifiedbp pairs <b1>-<b2>,...] User specified base pairing. Base pairs are specified in a comma-separated list after the 'pairs' keyword as <b1>-<b2>, where <b1> and <b2> are the residue numbers of bases in the base pair, e.g. 'pairs 1-16,2-15,3-14,4-13'. Can specify 'pairs' multiple times.

DataSets Created:

<**name**>**[pucker]:X** Base X (residue number) sugar pucker.

Base pairs:

<**name**>**[shear]:X** Base pair X (starting from 1) shear.

<**name**>**[stretch]:X** Base pair stretch.

<**name**>**[stagger]:X** Base pair stagger.

<**name**>**[buckle]:X** Base pair buckle.

<**name**>**[prop]:X** Base pair propeller.

<**name**>**[open]:X** Base pair opening.

<**name**>**[hb]:X** Number of WC hydrogen bonds between bases in base pair.

<**name**>**[bp]:X** Contain 1 if bases are base paired, 0 otherwise.

<**name**>**[major]:X** (If groovecalc simple) Major groove width calculated between P atoms of each base.

<**name**>**[minor]:X** (If groovecalc simple) Minor groove width calculated between O4 atoms of each base.

Base pair steps:

<**name**>**[shift]:X** Base pair step X (starting from 1) shift.

<**name**>**[slide]:X** Base pair step slide.

<**name**>**[rise]:X** Base pair step rise.

<**name**>**[title]:X** Base pair step tilt.

<**name**>**[roll]:X** Base pair step roll.

<**name**>**[twist]:X** Base pair step twist.

<**name**>**[zp]:X** Base pair step Zp value.

<**name**>**[major]:X** (If groovecalc 3dna) Major groove width, El Hassan and Calladine.

<**name**>**[minor]:X** (If groovecalc 3dna) Minor groove width, El Hassan and Calladine.

Helical steps:

<**name**>**[xdisp]:X** Helical step X (starting from 1) X displacement.

<**name**>**[ydisp]:X** Helical Y displacement.

<**name**>**[hrise]:X** Helical rise.

<**name**>**[incl]:X** Helical inclination.

<name>[tip]:X Helical tip.

<name>[htwist]:X Helical twist.

Strands (sscalc only):

<name>[dx]:X Strand pair X (starting from 1) X displacement.

<name>[dy]:X Y displacement.

<name>[dz]:X Z displacement.

<name>[rx]:X Relative rotation around X axis.

<name>[ry]:X Relative rotation around Y axis.

<name>[rz]:X Relateive rotation around Z axis.

Note that base pair data sets are not created until base pairing is determined.

Calculate basic nucleic acid (NA) structure parameters for all residues in the range specified by **resrange** (or all NA residues if no range specified). Residue names are recognized with the following priority: standard Amber residue names DA, DG, DC, DT, RA, RG, RC, and RU; 3 letter residue names ADE, GUA, CYT, THY, and URA; and finally 1 letter residue names A, G, C, T, and U. Non-standard/modified NA bases can be recognized by using the **resmap** keyword. For example, to make *cpptraj* recognize all 8-oxoguanine residues named '8OG' as a guanine-based residue:

```
nastruct naout nastruct.dat resrange 274-305 resmap 8OG:G
```

The **resmap** keyword can be specified multiple times, but only one mapping per unique residue name is allowed. Note that **resmap** may fail if the residue is missing heavy atoms normally present in the specified base type.

Base pairs are determined either once from the first frame or from a reference structure, or can be determined each frame if **allframes** is specified. Base pairing can also be specified via the **specifiedbp** and **pairs** keywords. Base pairing is determined first by base reference axis origin distance, then by stagger, then by angle between base Z axes, then finally by hydrogen bonding (at least one hydrogen bond must be present). Base pair parameters will only be written for determined base pairs. Both Watson-Crick and other types of base pairing can be detected. Note that although all possible hydrogen bonds are searched for, only WC hydrogen bonds are reported in the BP.<suffix> file.

The procedure used to calculate NA structural parameters is the same as 3DNA[20], with algorithms adapted from Babcok et al.[21] and reference frame coordinates from Olson et al.[23]. Given the same base pairs are determined, *cpptraj* ***nastruct*** should give the exact same numbers as 3DNA. One notable exception are parameters for G-quadruplex structures.

Calculated NA structure parameters are written to three separate files, the suffix of which is specified by **naout**. Base pair parameters (shear, stretch, stagger, buckle, propeller twist, opening, # WC hydrogen bonds, base pairing,

and simple groove widths) are written to BP.<suffix>, along with the number of WC hydrogen bonds detected. Base pair step parameters (shift, slide, rise, tilt, roll, twist, Zp, and El Hassan and Calladine groove widths) are written to BPstep.<suffix>, and helical parameters (X-displacement, Y-displacement, rise, inclination, tip, and twist) are written to Helix.<suffix>. If **noheader** is specified a header will not be written to the output files. Note that although base puckering is calculated, it is not written to an output file by default. You can output pucker to a file via the create or write/writedata commands after the data has been generated, e.g.:

```
nastruct NA naout nastruct.dat resrange 1-3,28-30
run
writedata NApucker.dat NA[pucker]
```

Note that while the underlying procedure is geared towards calculating parameters for base pairs, the code can be made to calculate parameters between consecutive bases in single strands by specifying **sscalc**.

Base axes, base pair axes, and base pair step axes can be written to trajectory files using the **axesout**, **bpaxesout**, and **stepaxesout** and related keywords. The axes are written using 4 points: an origin, and X Y and Z which are bonded to the origin. The names of these pseudo atoms can be changed using the **axisnameo**, **axisnamex**, **axisnamey**, and **axisnamez** keywords.

Custom Nucleic Acid Base References

Users can now specify **baseref** <**file**> to load a custom nucleic acid base reference. The base reference files are white-space delimited, begin with the line NASTRUCT REFERENCE, and have the following format:

```
NASTRUCT REFERENCE
<base character> <res name 0> [<res name 1> ...]
<atom name> <X> <Y> <Z> <HB type> <RMS fit>
...
```

There is a line for each reference atom. Lines beginning with '#' are ignored as comments.

<**base character**> Used to identify the underlying base type: A G C T or U. If none of these, it will be considered an unknown residue (which just means WC hydrogen bonding will not be identified).

<**res name X**> Specifies what residue names this reference corresponds to. There must be at least one residue name. There can be any number of these specified.

<**atom name**> A reference atom name.

<**X**> <**Y**> <**Z**> The X Y and Z coordinates of the reference atom.

<**HB type**> Denotes if and how the atom participates in hydrogen bonding. Can be 'd'onor, 'a'cceptor, or 'n'one (or the numbers 1, 2, 0 respectively). Only the first character of the word actually matters.

<**RMS fit**> Denotes whether the atom is involved in RMS-fitting.

Here is an example for GUA:

```
NASTRUCT REFERENCE
G G G5 G3
# Modified into format readable by cpptraj nastruct
C1' -2.477   5.399   0.000 0      0
N9  -1.289   4.551   0.000 0      1
C8   0.023   4.962   0.000 0      1
N7   0.870   3.969   0.000 accept 1
C5   0.071   2.833   0.000 0      1
C6   0.424   1.460   0.000 0      1
O6   1.554   0.955   0.000 accept 0
N1  -0.700   0.641   0.000 donor  1
C2  -1.999   1.087   0.000 0      1
N2  -2.949   0.139  -0.001 donor  0
N3  -2.342   2.364   0.001 accept 1
C4  -1.265   3.177   0.000 0      1
```

12.58 nativecontacts

```
nativecontacts [<mask1> [<mask2>]] [writecontacts <outfile>] [resout <resfile>]
               [noimage] [distance <cut>] [out <filename>] [includesolvent]
               [ first | reference | ref <name> | refindex <#> ]
               [resoffset <n>] [contactpdb <file>] [pdbcut <cut>] [mindist] [maxdist]
               [name <dsname>] [byresidue] [map [mapout <mapfile>]]
               [series [seriesout <file>]]
               [savenonnative [seriesnnout <file>] [nncontactpdb <file>]]
               [resseries { present | sum } [resseriesout <file>]] [skipnative]
```

<**mask1**> First mask to calculate contacts for.

[<**mask2**>] (Optional) Second mask to calculate contacts for.

[**writecontacts** <**outfile**>] Write information on native contacts to <outfile> (STDOUT if not specified).

[**resout** <**resfile**>] File to write contact residue pairs to.

[**noimage**] Do not image distances.

[**distance** <**cut**>] Distance cutoff for determining native contacts in Angstroms (default 7.0 Ang).

[out <filename>] File to write number of native contacts and non-native contacts.

[includesolvent] By default solvent molecules are ignored; this will explicitly include solvent molecules.

[first | reference | ref <name> | refindex <#>] Reference structure to use for determining native contacts.

[resoffset <n>] (byresidue only) Ignore contacts between residues spaced less than <n> residues apart in sequence.

[contactpdb <file>] Write PDB with B-factor column containing relative contact strength for native contacts (strongest is 100.0).

[pdbcut <cut>] If writing contactpdb, only write contacts with relative contact strength greater than <cut>.

[mindist] If specified, determine the minimum distance between any atoms in the mask(s).

[maxdist] If specified, determine the maximum distance between any atoms in the mask(s).

[name <dsname>] Data set name.

[byresidue] Write out the contact map by residue instead of by atom.

[map] Calculate matrices of native contacts ([nativemap]) and non-native contacts ([nonnatmap]). These matrices are normalized by the total number of frames, so that a value of 1.0 means "contact always present". If byresidue specified, the values for each individual atom pair are summed over the residues they belong to (this means for byresidue values greater than 1.0 are possible).

[mapout <mapfile>] Write native/non-native matrices to 'native.<mapfile>' and 'nonnative.<mapfile>' respectively.

[series] Calculate native contact time series data, 1 for contact present and 0 otherwise.

[seriesout <file>] Write native contact time series data to file.

[savenonnative] Save non-native contacts; series must also be specified. This is enabled by default if skipnative specified.

[seriesnnout <file>] Write non-native contact time series data to file.

[nncontactpdb <file>] Write PDB with B-factor column containing relative contact strength for non-native contacts (strongest is 100.0).

[resseries {present | sum} Create contacts time series by residue; series must also be specified.

present Record a 1 if *any* contact is present and 0 if no contact is present for the residue pair.

sum The sum of all individual contacts is recorded for the residue pair.

[resseriesout <file>] Write residue time series data to <file>.

[skipnative] If specified, skip native contacts determination, i.e. treat all sonctacts as non-native contacts. Implies savenonnative.

Data Sets Created:

<**dsname**>**[native]** Number of native contacts.

<**dsname**>**[nonnative]** Number of non-native contacts.

<**dsname**>**[mindist]** (mindist only) Minimum observed distance each frame.

<**dsname**>**[maxdist]** (maxdist only) Maximum observed distance each frame.

<**dsname**>**[nativemap]** (map only) Native contacts matrix (2D).

<**dsname**>**[nonnatmap]** Non-native contacts matrix (2D).

<**dsname**>**[NC]** Native contacts time series.

<**dsname**>**[NN]** Non-native contacts time series.

<**dsname**>**[NCRES]** Residue native contacts time series.

<**dsname**>**[NNRES]** Residue non-native contacts time series.

Define and track "native" contacts as determined by a simple distance cut-off, i.e. any atoms which are closer than <**cut**> in the specified reference frame (the first frame if no reference specified) are considered a native contact. If one mask is provided, contacts are looked for within <**mask1**>; if two masks are provided, only contacts between atoms in <**mask1**> and atoms in <**mask2**> are looked for (useful for determining intermolecular contacts). By default only native contacts are tracked. This can be changed by specifying the **savenonnative** keyword or by specifying **skipnative**. The time series for contacts

can be saved using the **series** keyword; these can be further consolidated by residue using the **resseries** keyword. When using <resseries> the data set index is calculated as (r2 * nres) + r1 so that indices can be matched between native/non-native contact pairs. Non-native residue contact legends have an nn_ prefix.

Native contacts that are found are written to the file specified by writecontacts (or STDOUT) with format:

```
# Contact Nframes Frac. Avg Stdev
```

Where `Contact` takes the form ':<residue1 num>@<atom name>_:<residue2 num>@<atom name>, `Nframes` is the number of frames the contact is present, `Frac.` is the total fraction of frames the contact is present, `Avg` is the average distance of the contact when present, and `Stdev` is the standard deviation of the contact distance when present. If **resout** is specified the total fraction of contacts is printed for all residue pairs having native contacts with format:

```
#Res1 #Res2 TotalFrac Contacts
```

Where `#Res1` is the first residue number, `#Res2` is the second residue number, `TotalFrac` is the total fraction of contacts for the residue pair, and `Contacts` is the total number of native contacts involved with the residue pair. Since `TotalFrac` is calculated for each pair as the sum of each contact involving that pair divided by the total number of frames, it is possible to have `TotalFrac` values greater than 1 if the residue pair includes more than 1 native contact.

During trajectory processing, non-native contacts (i.e. any pair satisfying the distance cut-off which is not already a native contact) are also searched for. The time series for native contacts can be saved as well, with 1 for contact present and 0 otherwise (similar to the ***hbond*** command). This data can be subsequently analyzed using e.g.13.21 on page 276.

Contact maps (matrices) are generated for native and non-native contacts. If **byresidue** is specified, contact maps are summed over residues, and contacts between residues spaced <**resoffset**> residues apart in sequence are ignored.

If **contactpdb** is specified a PDB is generated containing relative contact strengths in the B-factor column. The relative contact strength is normalized so that a value of 100 means that atom participated in the most contacts with other atoms.

Example command looking for contacts between residues 210 to 260 and residue named NDP, using reference structure 'FtuFabI.WT.pdb' to define native contacts:

```
parm FtuFabI.parm7
trajin FtuFabI.nc
reference FtuFabI.WT.pdb
nativecontacts name NC1 :210-260&!@H= :NDP&!@H= \
    byresidue out nc.all.res.dat mindist maxdist \
    distance 3.0 reference map mapout resmap.gnu \
```

```
contactpdb Loop-NDP.pdb \
series seriesout native.dat
```

12.59 outtraj

```
outtraj <filename> [ trajout args ]
        [maxmin <dataset> min <min> max <max>] ...
```

<filename> Output trajectory file name.

[trajout args] Output trajectory arguments (see 11.5 on page 105).

[maxmin <dataset> min <min> max <max>] Only write frames to <filename> if values in <dataset> for those frames are between <min> and <max>. Can be specified for one or more data sets.

The outtraj command is similar in function to ***trajout***, and takes all of the same arguments. However, instead of writing a trajectory frame after all actions are complete outtraj writes the trajectory frame at its position in the Action queue. For example, given the input:

```
trajin mdcrd.crd
trajout output.crd
outtraj BeforeRmsd.crd
rms R1 first :1-20@CA out rmsd.dat
outtraj AfterRmsd.crd
```

three trajectories will be written: output.crd, BeforeRmsd.crd, and AfterRmsd.crd. The output.crd and AfterRmsd.crd trajectories will be identical, but the BeforeRmsd.crd trajectory will contain the coordinates of mdcrd.crd before they are RMS-fit.

The maxmin keyword can be used to restrict output using one more more data sets. For example, to only write frames for which the RMSD value is between 0.7 and 0.8:

```
trajin tz2.truncoct.nc
rms R1 first :2-11
outtraj maxmin.crd maxmin R1 min 0.7 max 0.8
```

12.60 pairdist

```
pairdist out <filename> mask <mask> [delta <resolution>]
```

Calculate pair distribution function. In the following, defaults are given in parentheses. The **out** keyword specifies output file for histogram: distance, P(r), s(P(r)). The **mask** option specifies atoms for which distances should be computed. The **delta** option specifies resolution. (0.1 Å)

12.61 pairwise

```
pairwise [<name>] [<mask>] [out <filename>] [cuteelec <ecut>] [cutevdw <vcut>]
         [ reference | ref <name> | refindex <#> ] [cutout <cut mol2 prefix>]
      [vmapout <vdw map>] [emapout <elec map>] [avgout <avg file>]
      [eout <eout file>] [pdbout <pdb file>] [scalepdbe] [printmode {only|or|and|}]
```

[<name>] Data set name; van der Waals energy will get aspect [EVDW] and electrostatic energy will get aspect [EELEC].

[<mask>] Atoms to calculate energy for.

[out <filename>] File to write total EELEC and EVDW to.

[eout <eout file>] File to write individual EELEC and EVDW interactions to.

[reference | ref <name> | refindex <#>] Specify a reference to compare frames to (i.e. calculate Eref - Eframe).

[cuteelec <cut>] Only report interaction EELEC (or delta EELEC) if absolute value is greater than <ecut> (default 1.0 kcal/mol).

[cutevdw <cutv>] Only report interaction EVDW (or delta EVDW) if absolute value is greater than <vcut> (default 1.0 kcal/mol).

[cutout <cut mol2 prefix>] Write out mol2 containing only atom pairs which satisfy <ecut> and <vcut>.

[vmapout <vdw map>] Write out interaction EVDW (or delta EVDW) matrix to file <vdw map>.

[emapout <elec map>] Write out interaction EELEC (or delta EELEC) matrix to file <elec map>.

[avgout <avg file>] Print average interaction EVDW|EELEC (or average delta EVDW|EELC) to <avg file>.

[pdbout <pdb file>] Write PDB with EVDW|EELEC in occupancy|B-factor columns to <pdb file>.

[scalepdbe] Scale energies written to PDB from 0 to 100.

[printmode {only|or|and}] Control when/how average energies are written

Data Sets Created:

<name>[EELEC] Electrostatic energy in (kcal/mol).

<name>[EVDW] van der Waals energy in (kcal/mol).

<name>[VMAP] van der Waals energy matrix.

<name>[EMAP] Electrostatic energy matrix.

This action has two related functions: 1) Calculate pairwise (i.e. non-bonded) energy (in kcal/mol) for atoms in <**mask**>, or 2) Compare pairwise energy of frames to a reference frame. This calculation does use an exclusion list but is not periodic.

When comparing to a reference frame, the **eout** file will contain the differences for each individual interaction (i.e. Eref - Eframe), otherwise the **eout** file will contain the absolute value of each individual interaction. The **cuteelc** and **cutevdw** keywords can be used to restrict printing of individual interactions to those for which the absolute value is above a cutoff. The VMAP and EMAP matrix elements will contain these values as well (differences for reference, absolute value otherwise) averaged over all frames. The **avgout** file will contain only these values averaged over all frames that satisfy the cutoffs. The **printmode** keyword controls when the average energies are written: **only** means only average energy components that satisfy cutoffs will be printed, **or** means that both energy components will be printed if either satistfy a cutoff, and **and** means that both energy components will be written only if both satisfy the cutoffs.

The **cutout** keyword can be used to write out MOL2 files each frame named '<cut mol2 prefix>.evdw.mol2.X' and '<cut mol2 prefix>.eelec.mol2.X' (where X is the frame number) containing only atoms with energies that satisfy the cutoffs. Similarly, the **pdbout** keyword can be used to write out a PDB file (with 1 MODEL per frame). The occupancy and B-factor columns will contain the total van der Waals and electrostatic energy for each atom if cutoffs are satisfied, or 0.0 otherwise.

12.62 principal

```
principal [<mask>] [dorotation] [out <filename>] [name <dsname>]
```

[<mask>] Mask of atoms used to determine principal axes (default all).

[dorotation] Align coordinates along principal axes.

[out <filename>] Write resulting eigenvalues/eigenvectors to <filename>.

[name <dsname>] Data set name (3x3 matrices).

Data Sets Created (name keyword only):

<**dsname**>**[evec]** Eigenvectors (3x3 matrix, row-major).

<**dsname**>**[eval]** Eigenvalues (vector).

Determine principal axes of each frame determined by diagonalization of the inertial matrix from the coordinates of the specified atoms. At least one of **dorotation**, **out**, or **name** must be specified. The resulting eigenvectors are sorted from largest eigenvalue to smallest, and the corresponding axes labelled

using the *cpptraj* convention of X > Y > Z (similar to '***vector* principal**'). If out is specified the eigenvectors and eigenvalues will be written for each frame N with format:

```
<N> EIGENVALUES: <EX> <EY> <EZ>
<N> EIGENVECTOR 0: <Xx> <Xy> <Xz>
<N> EIGENVECTOR 1: <Yx> <Yy> <Yz>
<N> EIGENVECTOR 2: <Zx> <Zy> <Zz>
```

NOTE: The eigenvector 3x3 matrix data set could subsequently be used e.g. with the ***rotate*** action.

Example: Align system (residues 1-76) along principle axes:

```
parm myparm.parm7
trajin protein.nc
principal :1-76 dorotation out principal.dat
```

12.63 projection

```
projection [<name>] evecs <dataset name> [out <outfile>] [beg <beg>] [end <end>]
           {[<mask>] | [dihedrals <dataset arg>] | [data <dataset arg> ...]}
           [start <start>] [stop <stop>] [offset <offset>]
```

[<name>] Output data set name.

evecs <dataset name> Data set containing eigenvectors (modes).

[out <outfile>] Write projections to <outfile>.

[beg <beg>] First eigenvector/mode to use (default 1).

[end <end>] Final eigenvector/mode to use (default 2).

[<mask>] (Not dihedral covariance) Mask of atoms to use in projection; MUST CORRESPOND TO HOW EIGENVECTORS WERE GENERATED.

[dihedrals <dataset arg>] (Dihedral covariance only) Dihedral data sets to use in projection; MUST CORRESPOND TO HOW EIGENVECTORS WERE GENERATED.

[data <dataset arg>] (Data covariance only, e.g. from TICA). 1D data sets to use in projection; MUST CORRESPOND TO HOW EIGENVECTORS WERE GENERATED.

[start <start>] Frame to start calculating projection.

[stop <stop>] Frame to stop calculating projection.

[offset <offset>] Frames to skip between projection calculations.

Data Sets Created:
DataSet indices correspond to mode #.

<**name**> (All execpt IDEA) Projection data set.

<**name**>**[X]** X component of mode (IDEA modes only).

<**name**>**[Y]** Y component of mode (IDEA modes only).

<**name**>**[Z]** Z component of mode (IDEA modes only).

<**name**>**[R]** Magnitude of mode (IDEA modes only).

Projects snapshots onto eigenvectors obtained by diagonalizing covariance or mass-weighted covariance matrices. Eigenvectors are taken from previously generated (e.g. with ***diagmatrix***/***tica***) or previously read-in (e.g. with ***readdata***) eigenvectors with name <dataset name>. The user has to make sure that the atoms selected by <**mask**> agree with the ones used to calculate the modes (i.e., if mask = '@CA' was used in the "***matrix***" command, mask = '@CA' needs to be set here as well). See 14 on page 305 for examples using the ***projection*** command. If only 1D data sets need to be projected, see the ***projectdata*** analysis command, 13.28 on page 285.

12.64 pucker

```
pucker [<name>] <mask1> <mask2> <mask3> <mask4> <mask5> [<mask6>] [geom]
   [out <filename>] [altona | cremer] [amplitude] [theta]
    [range360] [offset <offset>]
```

<**name**> Output data set name.

<**maskX**> Five (optionally six) atom masks selecting atom(s) to calculate pucker for.

[geom] Use geometric center of atoms in <maskX> (default is center of mass).

[out <**filename**>**]** Output file name.

[altona] Use method of Altona & Sundaralingam (5 masks only).

[cremer] Use method of Cremer and Pople (5 or 6 masks). This is the default when 6 masks are specified.

[amplitude] Also calculate amplitude.

[theta] (6 masks only) Also calculate theta.

[range360] Wrap pucker values from 0.0 to 360.0 (default is -180.0 to 180.0).

[offset <**offset**>**]** Add <offset> to pucker values.

Data Sets Created:

<name> Pucker in degrees.

<name>[Amp] Amplitude (if amplitude was specified).

<name>[Theta] Theta (if theta and 6 masks were specified).

Calculate the pucker (in degrees) for atoms in <mask1>, <mask2>, <mask3>, <mask4>, <mask5> using the method of Altona & Sundarlingam[24, 25] (default for 5 masks, or if **altona** specified), or the method of Cremer & Pople[26] (default for 6 masks, or if **cremer** is specified). If the **amplitude** or **theta** keywords are given, amplitudes/thetas (also in degrees) will be calculated in addition to pucker. The results from ***pucker*** can be further analyzed with the ***statistics*** analysis.

By default, pucker values are wrapped to range from -180 to 180 degrees. If the **range360** keyword is specified values will be wrapped to range from 0 to 360 degrees. Note that the Cremer & Pople convention is offset from Altona & Sundarlingam convention (with nucleic acids) by +90.0 degrees; the **offset** keyword will add an offset to the final value and so can be used to convert between the two. For example, to convert from Cremer to Altona specify "**offset** 90".

To calculate nucleic acid pucker specify C1' first, followed by C2', C3', C4' and O4'. For example, to calculate the sugar pucker for nucleic acid residues 1 and 2 using the method of Altona & Sundarlingam, with final pseudorotation values ranging from 0 to 360:

```
pucker p1 :1@C1' :1@C2' :1@C3' :1@C4' :1@O4' range360 out pucker.dat
pucker p2 :2@C1' :2@C2' :2@C3' :2@C4' :2@O4' range360 out pucker.dat
```

12.65 radgyr | rog

```
radgyr [name>] [<mask>] [out <filename>] [mass] [nomax] [tensor]
```

[<name>] Data set name.

[<mask>] Atoms to calculate radius of gyration for; default all atoms.

[out <filename>] Write data to <filename>.

[mass] Mass-weight radius of gyration.

[nomax] Do not calculate maximum radius of gyration.

[tensor] Calculate radius of gyration tensor, output format 'XX YY ZZ XY XZ YZ'.

Data Sets Created:

<name> Radius of gyration in Ang.

<name>[Max] Max radius of gyration in Ang.

<name>[Tensor] Radius of gyration tensor; format 'XX YY ZZ XY XZ YZ'.

Calculate the radius of gyration of specified atoms. For example, to calculate only the mass-weighted radius of gyration (not the maximum) of the non-hydrogen atoms of residues 4 to 10 and print the results to "RoG.dat":

```
radgyr :4-10&!(@H=) out RoG.dat mass nomax
```

12.66 radial | rdf

```
radial [out <outfilename>] <spacing> <maximum> <solvent mask1> [<solute mask2>]
       [noimage] [mass]
    [density <density> | volume] [<dataset name>] [intrdf <file>] [rawrdf <file>]
    [{{center1|center2|nointramol|toxyz <x>,<y>,<z>} |
         [byres1] [byres2] [bymol1] [bymol2]}]
```

[out <outfilename>] File to write RDF to.

<spacing> Bin spacing, required.

<maximum> Max bin value, required.

<solvent mask1> Atoms to calculate RDF for, required.

[<solute mask2>] (Optional) If specified calculate RDF of all atoms in <solvent mask1> to each atom in <solute mask2>.

[noimage] Do not image distances.

[mass] Use center of mass for centerX/byresX/bymolX keywords, otherwise use geometric center.

[density <density>] Use density value of <density> for normalization (default 0.033456 molecules $Å^{-3}$).

[volume] Determine density for normalization from average volume of input frames.

[<dataset name>] Name of output data sets.

[intrdf <file>] Calculate integral of RDF bin values (averaged over # of frames but otherwise not normalized) and write to <file> (can be same as <output_filename>).

[rawrdf <file>] Write raw (non-normalized) RDF values to <file>.

[center1] Calculate RDF from center of atoms in <solvent mask1> to all atoms in <solute mask2>.

[center2] Calculate RDF from center of atoms in <solute mask2> to all atoms in <solvent mask1>.

[nointramol] Ignore intra-molecular distances.

[toxyz <x>,<y>,<z>] Calculate RDF from atoms selected by <solvent mask1> to point specified by <x> <y> and <z> (in Ang.).

[byres1] Calculate using the centers of each residue in the first mask.

[bymol1] Calculate using the centers of each molecule in the first mask.

[byres2] Calculate using the centers of each residue in the second mask.

[bymol2] Calculate using the centers of each molecule in the second mask.

DataSet Aspects:

<setname> The radial distribution function.

<setname>[int] (intrdf only) Integral of RDF bin values.

<setname>[raw] (rawrdf only) Raw (non-normalized) RDF values.

Calculate the radial distribution function (RDF, aka pair correlation function) of atoms in **<solvent mask1>** (note that this mask does not need to be solvent, but this nomenclature is used for clarity). If an optional second mask (**<solute mask2>**) is given, calculate the RDF of ALL atoms in **<solvent mask1>** to EACH atom in **<solute mask2>**. If desired, the geometric center of atoms in **<solvent mask1>** or **<solute mask2>** can be used by specifying the **center1** or **center2** keywords respectively, or alternatively intra-molecular distances can be ignored by specifying the **nointramol** keyword. If **byresX** or **bymolX** are specified, distances will be between the centers of residues/molecules selected by **<solvent mask1>** or **<solute mask2>**. If **mass** is specified use the centers of mass for **centerX**/**byresX**/**bymolX**, otherwise use geometric center.

The RDF is calculated from the histogram of the number of particles found as a function of distance R, normalized by the expected number of particles at that distance. The normalization is calculated from:

$$Density * \frac{4\pi}{3} \left((R + dR)^3 - R^3 \right)$$

where dR is equal to the bin spacing. Some care is required by the user in order to normalize the RDF correctly. The default density value is 0.033456 molecules $Å^{-3}$, which corresponds to a density of water approximately equal to 1.0 g mL^{-1}. To convert a standard density in g mL^{-1}, multiply the density by $\frac{0.6022}{M_r}$, where M_r is the mass of the molecule in atomic mass units. Alternatively, if the **volume** keyword is specified the density is determined from the average volume of the system over all Frames.

Note that correct normalization of the RDF depends on the number of atoms in each mask; if multiple topology files are being processed that result in changes in the number of atoms in each mask, the normalization will be off.

The basic (i.e. no center1/center2/byres1/byres2/bymol1/bymol2) RDF calculations are now CUDA parallelized. However, the calculation is done in single-precision on GPUs so the resulting histograms may differ slightly from the CPU (on the order of 0.0002 - 0.0004).

12.67 randomizeions

```
randomizeions <mask> [around <ardoundmask> by <distance>] [{allowoverlap|overlap <value
              [noimage] [seed <value>] [originalalgorithm]
```

<mask> `Mask of ions to randomize.`

around <mask> by <distance> `Ensure ions come no closer than <distance> Ang. to atoms in <aroundmask>.`

allowoverlap `No restrictions on how close ions can be to each other.`

overlap <value> `Ions in <mask> can be no closer than <value> Ang. to each other.`

[noimage] `Do not image distances.`

[seed <value>] `Seed for the random number generator.`

[originalalgorithm] `Use the original, slower algorithm (from versions before 5.1.0).`

This can be used to randomly swap the positions of solvent and single atom ions. The "`overlap`" specifies the minimum distance between ions, and the "`around`" keyword can be used to specify a solute (or set of atoms) around which the ions can get no closer than the distance specified. The optional keywords "`noimage`" disable imaging and "`seed`" update the random number seed. An example usage is

```
randomizeions @NA around :1-20 by 5.0 overlap 3.0
```

The above will swap Na^+ ions with water getting no closer than 5.0 Å from residues $1-20$ and no closer than 3.0 Å from any other Na^+ ion.

12.68 remap

```
remap data <setname>
      [outprefix <prefix>] [nobox] [parmout <filename>]
      [parmopts <comma-separated-list>]
```

data <**setname**> Data set to use for remapping; should be a 1D integer data set with X= reference (old) atom index, Y = target (new) atom index.

outprefix <**prefix**> Write remapped topology to <prefix>.<originalname>

[nobox] Remove any box information from the remapped topology.

parmout <**filename**> Write remapped topology to <filename>

parmopts <**list**> Options for writing topology file

Re-map atoms according to the given reference data set which is of the format:

```
Reference[Target]
```

with atom numbering starting from 1. E.g. Reference[1] = 10 would mean remap atom 10 in target to position 1.

12.69 replicatecell

```
replicatecell [out <traj filename>] [name <dsname>] [verbose <#>]
           { all | dir <XYZ> [dir <XYZ> ...] } [<mask>]
           [outprefix <prefix>] [nobox] [parmout <filename>]
           [parmopts <comma-separated-list>]
```

out <**traj filename**> Write replicated cell to output trajectory file.

name <**dsname**> If specified save replicated cell to COORDS data set.

[verbose <#>**]** Verbosity during parameter assignment.

all Replicate cell once in all possible directions.

dir <**XYZ**> Repicate cell once in specified directions. <XYZ> should consist of 3 numbers with no spaces in between them and are restricted to values of -1, 1, and 0. May be specified more than once.

<**mask**> Mask of atoms to replicate.

outprefix <**prefix**> Write replicated topology to <prefix>.<originalname>

[nobox] Remove any box information from the replicated topology.

parmout <**filename**> Write replicated topology to <filename>

parmopts <**list**> Options for writing topology file

Create a trajectory where the unit cell is replicated in 1 or more directions (up to 27). The resulting coordinates and topology can be written to a trajectory/topology file. They can also be saved as a COORDS data set for subsequent processing. Currently replication is only allowed 1 axis length in either direction. The **all** keyword will replicate the cell once in all directions. The **dir** keyword can be used to restrict replication to specific directions, e.g. 'dir 10-1' would replicate the cell once in the +X, -Z directions.

For example, to replicate a cell in all directions, writing out to NetCDF trajectory cell.nc:

```
parm ../tz2.truncoct.parm7
trajin ../tz2.truncoct.nc
replicatecell out cell.nc parmout cell.parm7 all
```

12.70 rms | rmsd

```
rmsd [<name>] <mask> [<refmask>] [out <filename>] [mass]
  [nofit | norotate | nomod]
  [savematrices [matricesout <file>]]
  [savevectors {combined|separate} [vecsout <file>]]
  [ first | reference | ref <name> | refindex <#> | previous |
    reftraj <name> [parm <name> | parmindex <#>] ]
  [perres perresout <filename> [perresavg <avgfile>]
   [range <resRange>] [refrange <refRange>]
   [perresmask <additional mask>] [perrescenter] [perresinvert]
```

[<**name**>**]** Output data set name.

[<**mask**>**]** Mask of atoms to calculate RMSD for; if not specified, calculate for all atoms.

[<**refmask**>**]** Reference mask; if not specified, use <mask>.

[out <**filename**>**]** Output data file name.

[mass] Mass-weight the RMSD calculation.

[nofit] Do not perform best-fit RMSD.

[norotate] If calculating best-fit RMSD, translate but do not rotate coordinates.

[nomod] If calculating best-fit RMSD, do not modify coordinates.

[savematrices] If specified save rotation matrices to data set with aspect [RM].

matricesout <**file**> Write rotation matrices to specified file.

[savevectors {combined|separate}] If specified save translation vectors: combined means save target-to-origin plus the origin-to-reference translation vectors, separate means save target-to-origin as Vx, Vy, Vz and save origin-to-reference as Ox Oy Oz in the output vector data set.

vecsout <file> Output translation vector data set to <file>.

Reference keywords:

first Use the first trajectory frame processed as reference.

reference Use the first previously read in reference structure (refindex 0).

ref <name> Use previously read in reference structure specified by filename/tag.

refindex <#> Use previously read in reference structure specified by <#> (based on order read in).

previous Use frame prior to current frame as reference.

reftraj <name> Use frames from COORDS set <name> or read in from trajectory file <name> as references. Each frame from <name> is used in turn, so that frame 1 is compared to frame 1 from <name>, frame 2 is compared to frame 2 from <name> and so on. If <trajname> runs out of frames before processing is complete, the last frame of <trajname> continues to be used as the reference.

parm <parmname> | parmindex <#> If reftraj specifies a trajectory file, associate it with specified topology; if not specified the first topology is used.

Per-residue RMSD keywords:

perres Activate per-residue no-fit RMSD calculation.

perresout <perresfile> Write per-residue RMSD to <perresfile>.

perresavg <avgfile> Write average per-residue RMSDs to <avgfile>.

range <res range> Calculate per-residue RMSDs for residues in <res range> (default all solute residues).

refrange <**ref range**> Calculate per-residue RMSDs to reference residues in <ref range> (use <res range> if not specified).

perresmask <**additional mask**> By default residues are selected using the mask ':X' where X is residue number; this appends <additional mask> to the mask expression.

perrescenter Translate residues to a common center of mass prior to calculating RMSD.

perresinvert Make X-axis residue number instead of frame number.

Data Sets Created:

<**name**> RMSD of atoms in mask to reference.

<**name**>**[RM]** (savematrices only) Rotation matrices of target to reference.

<**name**>**[TV]** (savevectors only) Translation vector.

<**name**>**[res]** (perres only) Per-residue RMSDs; index is residue number.

<**name**>**[Avg]** (perres only) Average per-residue RMSD for each residue.

<**name**>**[Stdev]** (perres only) Standard deviation of RMSD for each residue.

*Note that **perres** data sets are not generated until **run** is called.*

Calculate the coordinate RMSD of input frames to a reference frame (or reference trajectory). Both <mask> and <refmask> must specify the same number of atoms, otherwise an error will occur.

For example, say you have a trajectory and you want to calculate RMSD to two separate reference structures. To calculate the best-fit RMSD of the C, CA, and N atoms of residues 1 to 20 in each frame to the C, CA, and N atoms of residues 3 to 23 in StructX.crd, and then calculate the no-fit RMSD of residue 7 to residue 7 in another structure named Struct-begin.rst7, writing both results to Grace-format file "rmsd1.agr":

```
reference StructX.crd [structX]
reference md_begin.rst7 [struct0]
rmsd BB :1-20@C,CA,N ref [structX] :3-23@C,CA,N out rmsd1.agr
rmsd Res7 :7 ref [struct0] out rmsd1.agr nofit
```

Per-residue RMSD calculation

If the **perres** keyword is specified, after the initial RMSD calculation the no-fit RMSD of specified residues is also calculated. So for example:

```
rmsd :10-260 reference perres perresout PRMS.dat range 190-211 perresmask &!(@H=)
```

will first perform a best-fit RMSD calculation to the first specified reference structure using residues 10 to 260, then calculate the no-fit RMSD of residues 190 to 211 (excluding any hydrogen atoms), writing the results to PRMS.dat. Two additional recommendations for the 'perres' option: 1) try not including backbone atoms by using the 'perresmask' keyword, e.g. "perresmask &!@H,N,CA,HA,C,O", and 2) try using the 'perrescenter' keyword, which centers each residue prior to the 'nofit' calculation; this is useful for isolating changes in residue conformation.

12.71 rms2d | 2drms

Although the ***'rms2d'*** command can still be specified as an action, it is now considered an analysis. See 13.31 on page 287.

12.72 rmsavgcorr

Although the ***'rmsavgcorr'*** command can still be specified as an action, it is now considered an analysis. See 13.32 on page 288.

12.73 rmsf | atomicfluct

See 12.6 on page 119.

12.74 rotate

```
rotate [<mask>] { [x <xdeg>] [y <ydeg>] [z <zdeg>]  |
               axis0 <mask0> axis1 <mask1> <deg> |
               usedata <set name> [inverse] |
                  calcfrom <set name> [name <output set name>] [out <file>]
             }
```

[<mask>] Rotate atoms in <mask> (default all).

[x <xdeg] Degrees to rotate around the X axis.

[y <xdeg] Degrees to rotate around the Y axis.

[z <xdeg] Degrees to rotate around the Z axis.

axis0 <mask0> Mask defining the beginning of a user-defined axis.

axis1 <mask1> Mask defining the end of a user-defined axis.

<deg> Value in degrees to rotate around user defined axis.

usedata <set name> If specified, use 3x3 rotation matrices in specified data set to rotate coordinates.

[inverse] Perform inverse rotation from input rotation matrices.

calcfrom <**set name**> Instead of rotating coordinates, calculate rotations around the X Y and Z axes (as well as total rotation) in degrees from existing rotation matrices specified by <set name>.

[name <**output set name**>**]** Output set name.

[out <**file**>**}** File to write output sets to.

DataSets Created:

<**output set name**>**[TX]** (caclfrom only) Rotation around the X axis in degrees.

<**output set name**>**[TY]** (caclfrom only) Rotation around the Y axis in degrees.

<**output set name**>**[TZ]** (caclfrom only) Rotation around the Z axis in degrees.

<**output set name**>**[T]** (caclfrom only) Total rotation in degrees.

Rotate specified atoms around the X, Y, and/or Z axes by the specified amounts, around a user-defined axis (specified by <mask0> and <mask1>), or use a previously read in or generated data set of 3x3 matrices to perform rotations.

For example, to rotate the entire system 90 degrees around the X axis:

```
rotate x 90
```

To rotate residue 270 90 degrees around the axis defined between atoms C1, C2, C3, C4, C5, and C6 in residue 270 and atoms C7, C8, C9, C10, C11, and C12 in residue 270:

```
rotate :270 axis0 :270@C1,C2,C3,C4,C5,C6 axis1 :270@C7,C8,C9,C10,C11,C12 90.0
```

To rotate the system with rotation matrices read in from rmatrices.dat:

```
trajin tz2.norotate.crd
readdata rmatrices.dat name RM mat3x3
rotate usedata RM
```

To calculate rotations from rotation matrices generated by a previous RMSD calculation:

```
parm ../tz2.parm7
reference tz2.separate.rotate.rst7.save name REF
trajin ../tz2.nc
rms R0 reference savematrices matricesout matrices.dat
rotate calcfrom R0[RM] name Rot out rotations.dat
```

12.75 rotdif

The ***'rotdif'*** command is now an analysis (see 13.33 on page 290), and requires that rotation matrices be generated via an ***rmsd*** action. For example:

```
reference avgstruct.pdb
trajin tz2.nc
rms RO reference @CA,C,N,O savematrices
rotdif rmatrix RO[RM] rseed 1 nvecs 10 dt 0.002 tf 0.190 \
       itmax 500 tol 0.000001 d0 0.03 order 2 rvecout rvecs.dat \
       rmout matrices.dat deffout deffs.dat outfile rotdif.out
```

12.76 runavg | runningaverage

```
runavg [window <window_size>]
```

Note that for backwards compatibility with ptraj "runningaverage" is also accepted.

Replaces the current frame with a running average over a number of frames specified by **window** <window_size> (5 if not specified). This means that in order to build up the correct number of frames to calculate the average, the first <window_size> minus one frames will not be processed by subsequent actions. So for example given the input:

```
runavg window 3
rms first out rmsd.dat
```

the rms command will not take effect until frame 3 since that is the first time 3 frames are available for averaging (1, 2, and 3). The next frame processed would be an average of frames 2, 3, and 4, etc.

12.77 scale

```
scale x <sx> y <sy> z <sz> <mask>
```

Scale the X|Y|Z coordinates of atoms in <mask> by <sx>|<sy>|<sz>.

12.78 secstruct

```
secstruct [<name>] [out <filename>] [<mask>] [sumout <filename>]
          [assignout <filename>] [totalout <filename> [ptrajformat]
          [betadetail]
          [namen <N name>] [nameh <H name>] [nameca <CA name>]
          [namec <C name>] [nameo <O name>] [namesg <sulfur name>]
```

[<name>] Output data set name.

[out <filename>] Output file name for secondary structure vs time.

[<mask>] Atom mask in which residues should be looked for.

[sumout <sumfilename>] Write average secondary structure values for each residue to <sumfilename>; if not specified <filename>.sum is used.

[assignout <filename>] Write overall secondary structure assignment (based on dominant secondary structure type for each residue) to file.

[ptrajformat] Write secondary structure as a string of characters for each frame, similar to ptraj output.

[betadetail] Record anti-parallel beta and parallel beta in place of extended and bridge secondary structure. If a residue could be both only anti-parallel is reported.

[namen <N name>] Backbone amide nitrogen atom name (default 'N').

[nameh <H name>] Backbone amide hydrogen atom name (default 'H').

[nameca <CA name>] Backbone alpha carbon atom name (default 'CA').

[namec <C name>] Backbone carbonyl carbon atom name (default 'C').

[nameo <O name>] Backbone carbonyl oxygen atom name (default 'O').

[namesg <SG name>] Cysteine sulfur atom name, used to ignore disulfide connectivity (default 'SG').

Data Sets Created:

<name>[res] Residue secondary structure per frame; index corresponds to residue number. If ptrajformat specified these will be characters, otherwise integers (see table below).

<name>[avgss] Average of each type of secondary structure; index corresponds to secondary structure type (see table below; no index for "None").

<name>[None] Total fraction of residues with no structure vs time.

<name>[Para] Total fraction of residues with parallel beta structure vs time.

<name>[Anti] Total fraction of residues with anti-parallel beta structure vs time.

<name>[3-10] Total fraction of 3-10 helical structure vs time.

<name>[Alpha] Total fraction of alpha helical structure vs time.

<name>[Pi] Total fraction of Pi helical structure vs time.

<name>[Turn] Total fraction of turn structure vs time.

<name>[Bend] Total fraction of bend structure vs time.

As of version 4.18.0, this command now produces output that better conforms with the original definitions in Kabsch and Sander 1983; namely that Extended beta (i.e. 2 or more consecutive beta bridges of the same type) and beta Bridge (i.e. an isolated beta bridge) are now reported instead of anti-parallel and parallel beta. To restore the original behavior the 'betadetail' keyword must be specified.

Note that the residue and [avgss] data sets are not generated until ***run*** *is called.*

Calculate secondary structural propensities for residues in <**mask**> (or all solute residues if no mask given) using the DSSP method of Kabsch and Sander[27], which assigns secondary structure types for residues based on backbone amide (N-H) and carbonyl (C=O) atom positions. By default *cpptraj* assumes these atoms are named "N", "H", "C", and "O" respectively. If a different naming scheme is used (e.g. amide hydrogens are named "HN") the backbone atom names can be customized with the **nameX** keywords (e.g. 'nameH HN'). Note that it is expected that some residues will not have all of these atoms (such as proline); in this case *cpptraj* will print an informational message but the calculation will proceed normally. If a residue has no atoms selected it will be skipped. When determining residue connecivity, disulfide bonds will be ignored; *cpptraj* identifies such bonds based on the **namesg** atom name (default "SG").

Results will be written to filename specified by **out** with format:

```
<#Frame>    <ResX SS> <ResX+1 SS> ... <ResN SS>
```

where <#Frame> is the frame number and <ResX SS> is an integer representing the calculated secondary structure type for residue X. If the keyword **ptrajformat** is specified, the output format will instead be:

```
<#Frame>    STRING
```

where STRING is a string of characters (one for each residue) where each character represents a different structural type (this format is similar to what *ptraj* had

outputed and is retained for backwards compatibility). The various secondary structure types and their corresponding integer/character are listed below. If 'betadetail' is specified what is reported and the characters used change slightly.

STRING (betadetail)	Integer	DSSP	SS type (betadetail)
0	0	' '	None
E (b)	1	'E'	Extended beta (parallel beta)
B	2	'B'	Isolated beta (anti-parallel beta)
G	3	'G'	3-10 helix
H	4	'H'	Alpha helix
I	5	'I'	Pi (3-14) helix
T	6	'T'	Turn
S	7	'S'	Bend

Average structural propensities over all frames for each residue will be written to the file specified by **sumout** (or "*<filename>.sum*" if **sumout** is not specified). The total structural propensity over all residues for each secondary structure type will be written to the file specified by **totalout**. If assignout is specified, the overall secondary structure assignment for each residue will be printed in two line chunks of 50 residues, with the first line containing the residue number the line starts with and one character residue names, and the second line containing secondary structure assignment using DSSP-style characters, like so:

```
1 KCNTATCATQ RLANFLVHSS NNFGAILSST NVGSNTRn
    SSS    TH HHHTTSEEEE TTTEEEE SS     S
```

The output of secstruct command is amenable to visualization with gnuplot. To generate a 2D map-style plot of secondary structure vs time, with each residue on the Y axis simply give the output file a ".gnu" extension. For example, to generate a 2D map of secondary structure vs time, with different colors representing different secondary structure types for residues 1-22:

```
secstruct :1-22 out dssp.gnu
```

The resulting file can be visualized with gnuplot:

```
gnuplot dssp.gnu
```

Similarly, the **sumout** file can be nicely visualized using xmgrace (use ".agr" extension).

```
secstruct :1-22 out dssp.gnu sumout dssp.agr
xmgrace dssp.agr
C <X> <Y> <Z> <Density>
```

Values of **dgbulk** and **dhbulk** for different water models can be calculated from pure water simulations with the **purewater** keyword.

12.79 setvelocity

```
setvelocity [<mask>]
            [{ tempi <temperature> |
               scale [factor <fac>] [sx <xfac>] [sy <yfac>] [sz <zfac>] |
               add [value <val>] [vx <xval>] [vy <yval>] [vz <zval>] |
               none |
               modify}]
            [[ntc <#>]] [[dt <time>] [epsilon <eps>]]
          [zeromomentum] [ig <random seed>]
```

<mask> Mask of atoms to assign velocities to.

tempi <temperature> Assign velocities at specified temperature (default 300.0 K).

scale Scale existing velocities

[factor <fac>] Factor to scale velocities by.

[sx <xfac>] Factor to scale X component of velocities by.

[sy <yfac>] Factor to scale Y component of velocities by.

[sz <zfac>] Factor to scale Z component of velocities by.

add Add to existing velocities

[value <val>] Value to add to velocities.

[vx <xval>] Value to add to X component of velocities.

[vy <yval>] Value to add to Y component of velocities.

[vz <zval>] Value to add to Z component of velocities.

none Remove any velocities.

modify If specified, do not set, just modify any existing velocities (via 'ntc' or 'zeromomentum').

ig <random seed> Random seed to use to generate velocity distribution.

ntc <#> Correct set velocities for SHAKE constraints. Numbers match sander/pmemd: 1 = no SHAKE, 2 = SHAKE on hydrogens, 3 = SHAKE on all atoms.

dt <time> Time step for SHAKE correction.

epsilon <eps> Epsilon for SHAKE correction

zeromomentum If specified adjust velocities so the total momentum of atoms in <mask> is zero.

Set velocities in frame for atoms in <mask> using Maxwellian distribution based on given temperature, optionally adjusted for SHAKE constraints. Can also be used to modify existing velocity information or remove it entirely. The total momentum of the system can be set to zero as well, which can be useful for NVE simulations.

12.80 spam

```
spam [name <name>] [out <datafile>] [cut <cut>] [solv <solvname>]
  { purewater |
    <peaksname> [reorder] [info <infofile>] [summary <summary>]
    [site_size <size>] [sphere] [temperature <T>]
    [dgbulk <dgbulk>] [dhbulk <dhbulk>] }
```

name <**name**> Output data sets name.

out <**datafile**> Data file with all SPAM energies for each snapshot.

cut <**cut**> Non-bonded cutoff for energy evaluation

solv <**solvname**> Name of the solvent residues.

[purewater] The system is pure water. Used to parametrize the bulk values. If this is specified, none of the below options are relevant.

<**peaksname**> Data set or file (XYZ- format: see below) with the peak locations present .

[reorder] The solvent should be re-ordered so the same solvent molecule is always in the same site.

info <**infofile**> File with stats about which sites are occupied when.

summary <**summary**> File with the summary of all SPAM results. If not specified, no SPAM energies will be calculated.

site_size <size> Size of the water site around each density peak (sphere diameter/box edge length) in Ang.

[sphere] Treat each site like a sphere.

temperature <**T**> Temperature at which SPAM calculation was run.

dgbulk <**dgbulk**> SPAM free energy of the bulk solvent in kcal/mol; default is -30.3 kcal/mol (SPC/E water).

dhbulk <**dhbulk**> SPAM enthalpy of the bulk solvent in kcal/mol; default is -22.2 kcal/mol (SPC/E water).

Data Sets Created for 'purewater':

<**name**> Energies for each water at each frame.

Data Sets Created otherwise:

<**name**>:<#> SPAM energies for peak <#> starting from 1.

<**name**>**[DG]** SPAM delta G values for valid peaks.

<**name**>**[DH]** SPAM delta H values for valid peaks.

<**name**>**[-TDS]** SPAM -T * delta S values for valid peaks.

Perform profiling of bound water molecules via SPAM analysis[28]. Briefly, this method identifies and estimates the free energy profiles of bound waters via calculation of the distribution of interaction energies between the water and it's environment from explicit solvent MD trajectories. The interaction energies are calculated using a force- and energy-shifted electrostatic term with a hard cutoff. For a given peak, SPAM energies will only be calculated for peaks where the peak is singly-occupied (i.e. a multiple-occupied peak is not considered valid).

Prior to this command, the ***volmap*** command should be run with the **peakfile** keyword (see 12.94 on page 235) to generate the peaks file. If not using peaks from the ***volmap*** command, the peaks file should have one line per peak with format:

```
<# of peaks>
C     <X>      <Y>      <Z>       <Peak Density>
...
```

With a 'C' line for each peak.

12.81 stfcdiffusion

```
stfcdiffusion mask <mask> [out <file>] [time <time per frame>]
              [mask2 <mask> [lower <distance>] [upper <distance>]]
              [nwout <file>]) [avout <file>] [distances] [com]
              [x|y|z|xy|xz|yz|xyz]
```

mask Atoms for which MSDs will be computed.

out Output file: time vs. MSD.

time Time step in the trajectory. (1.0 ps)

mask2 Compute MSDs only within the lower and upper limit of mask2. IMPORTANT: may be very slow!!!

lower Smaller distance from reference point(s). (0.01 Å)

upper Larger distance from reference point(s). (3.5 Å)

nwout Output file containing number of water molecules in the chosen region, see mask2. (off)

avout Output file containing average distances. (off)

x|y|z|xy|xz|yz|xyz Computation of the mean square displacement in the chosen dimension. (xyz)

distances Dump un-imaged distances. By default only averages are output. (off)

com Calculate MSD for centre of mass. (off)

Calculate diffusion for selected atoms using code based on the 'diffusion' routine developed by Hannes Loeffler at STFC (http://www.stfc.ac.uk/CSE).

12.82 strip

```
strip <mask> [charge <new charge>]
   [outprefix <prefix>] [nobox] [parmout <filename>]
   [parmopts <comma-separated-list>]
```

<mask> Remove atoms specified by mask from the system.

charge <new charge> Scale charges so total charge of remaining atoms matches the specified <new charge>.

[outprefix <prefix>] Write out stripped topology file with name '<prefix>.<Original Topology Name>'.

[nobox] Remove any box information from the stripped topology.

[parmout <file>] Write stripped topology to file with name <file>.

[parmopts <list>] Options for writing topology file.

Strip all atoms specified by **<mask>** from the frame and modify the topology to match for any subsequent Actions. The **outprefix** keyword can be used to write stripped topologies; stripped Amber topologies are fully-functional. Available options for **<parmopts>** can be determined by running the ***help Formats parmwrite*** command.

Note that stripping a system renumbers all atoms and residues, so for example after this command:

```
strip :1
```

residue 1 will be gone, and the former second residue will now be the first, and so on.

For example, to strip all residues named WAT from each topology/coordinate frame:

```
strip :WAT
```

The next example uses a distance-based mask to strip atoms in a single frame. Note that with the exception of the ***mask*** command, distance-based masks do not update on a per-frame basis. To strip all residues outside of 6.0 from any atom in residues 1 to 14 and write out the stripped topology and coordinates, both with no box information:

```
parm parm7
trajin frame_1000.rst.1
reference frame_1000.rst.1
strip !(:1-14<:6.0) outprefix f1.1 nobox
trajout f1.1.x restart nobox
```

12.83 surf

```
surf [<name>] [<mask1>] [out <filename>] [solutemask <mask>]
[offset <offset>] [nbrcut <cut>]
```

<name> Output data set name.

<mask1> Atoms to calculate surface area for.

out <filename> File to write surface area to.

solutemask <mask> If specified, calculate the contribution of <mask1> to <mask>.

offset <offset> Increment van der Waals radii by <offset>; 1.4 Ang. is the default (as used by Amber).

nbrcut <cut> Only atoms with van der Waals radii greater than <cut> are considered to have neighbors (2.5 Ang Amber default).

Calculate the surface area in $Å^2$ of atoms in <mask> (if no mask specified, all atoms not marked as 'solvent' that are part of a molecule > 1 atom in size) using the LCPO algorithm of Weiser et al.[29]. In order for this to work, the topology needs to have bond information and atom type information.

Note that even if <mask> does not include all solute atoms, the neighbor list is still calculated for all solute atoms so the surface area calculated reflects the contribution of atoms in <mask> to the overall surface area, not the surface area of <mask> as an isolated system. As a result, it may be possible to obtain a negative surface area if only a small fraction of the solute is selected.

For example, to calculate the overall surface area of all solute atoms, as well as the contribution of residue 1 to the overall surface area, writing both results to "surf.dat":

```
surf out surf.dat
surf :1 out surf.dat
```

12.84 surftension

```
surftension [<name>] <mask> [mask2 <mask2>] temp <T>
[normal {x|y|z}] [nsurf {1|2}] [side {upper|lower}]
[interface {willard|itim}]
[gridspacing <d>] [dz <d> | dnormal <d>]
[sigmaxy <d>] [sigmaz <d> | sigmanormal <d>]
[bulkhalfwidth <d>] [threshold <frac>]
[qmin <q>] [qmax <q>] [lx <Lx>] [ly <Ly>] [lz <Lz>]
[nblock <frames>] [dt <ps>] [blocktime <ps>] [fprefix <prefix>]
[out <file> | spectrumout <file>] [roughout <file>] [blockout <file>]
[summaryout <file>]
[spectrumagr <file>] [roughagr <file>] [blockagr <file>]
[spectrumgnu <file>] [roughgnu <file>] [blockgnu <file>]
```

<name> Output data set name.

<mask> Atoms used to build the instantaneous interface (typically heavy atoms of the liquid, e.g. :WAT@O).

mask2 <mask2> Optional atoms for the lower surface (leaflet or second liquid). The upper surface then comes from <mask> with no mid-box split. Both masks share one circular recenter.

temp <T> Temperature in K (required).

normal {x|y|z} Cartesian slab normal (default z). The other two axes span the interface plane.

nsurf {1|2} Number of interfaces (default 2). Use 2 for a film with vacuum or a second phase on both sides.

side {upper|lower} Which interface when nsurf is 1 (default upper).

interface {willard|itim} Instantaneous interface: Willard-Chandler density isosurface (default) or ITIM per-column min/max.

gridspacing <d> Lateral histogram spacing in Ang. (default 2.5).

dz / dnormal <d> Bin spacing along the normal for Willard-Chandler (default 1.0).

sigmaxy / sigmaz / sigmanormal Gaussian widths in Ang. for the Willard-Chandler density (defaults 2.5 and 1.5).

qmin / qmax Fit window in Ang.^-1. If qmin is omitted it is 2*pi/max(L1,L2) from the first good frame.

lx / ly / lz Override Cartesian box lengths (NVT slabs with noisy box records).

nblock / dt / blocktime Block averaging. blocktime (ps) with dt (analyzed-frame spacing, ps) sets nblock.

fprefix <**prefix**> Prepended to each output file basename (directory unchanged) so multiple runs can share a directory.

out / spectrumout / roughout / blockout / summaryout Optional output files. out is an alias for spectrumout. Parent directories must already exist.

***agr** / *gnu Force Grace or gnuplot format for spectrum, roughness, or block files.

Calculate the capillary-wave surface tension of a liquid slab from height fluctuations of instantaneous interfaces[30, 31, 32, 33, 34]. Frames are recentered so the film sits at mid-box along the chosen normal. The default interface is a Willard–Chandler isosurface of a Gaussian-smoothed number-density field; interface itim uses per-column min/max of <mask> (probe radius to 0). The height field is Fourier transformed (numpy fft2 convention), shell-averaged to S(q), and gamma (mN/m) is taken from the small-q plateau of q^2 S(q). A Helfrich fit of $1/(q^2\,S)$ vs q^2 on the same window gives kappa in kT. The trajectory is assumed NVT (fixed lateral box lengths). The 3-D Gaussian filter is OpenMP-parallel.

For example, to analyze a water slab with vacuum along z:

```
surftension :WAT@O temp 300 qmax 0.30 summaryout st.summary.dat
spectrumout st.spectrum.dat roughout st.rough.dat
```

12.85 symmrmsd

```
symmrmsd  [<name>] [<mask>] [<refmask>] [out <filename>] [nofit] [mass] [remap]
          [ first | reference | ref <name> | refindex <#> | previous |
            reftraj <name> [parm <parmname> | parmindex <#>] ]
```

[<name>] Output data set name.

[<mask>] Mask of atoms to calculate RMSD for; if not specified, calculate for all atoms.

[<refmask>] Reference mask; if not specified, use <mask>.

[out <filename>] Output data file name.

[nofit] Do not perform best-fit RMSD (not recommended).

[mass] Mass-weight the RMSD calculation.

[remap] Re-arrange atoms according to symmetry. See below for more details.

Reference keywords:

first Use the first trajectory frame processed as reference.

reference Use the first previously read in reference structure (refindex 0).

ref <**name**> Use previously read in reference structure specified by filename/tag.

refindex <#> Use previously read in reference structure specified by <#> (based on order read in).

previous Use frame prior to current frame as reference.

reftraj <**name**> Use frames from COORDS set <name> or read in from trajectory file <name> as references. Each frame from <name> is used in turn, so that frame 1 is compared to frame 1 from <name>, frame 2 is compared to frame 2 from <name> and so on. If <trajname> runs out of frames before processing is complete, the last frame of <trajname> continues to be used as the reference.

parm <**parmname**> | **parmindex** <#> If reftraj specifies a file associate trajectory <name> with specified topology; if not specified the first topology is used.

Perform symmetry-corrected RMSD calculation. This is done by identifying potential symmetric atoms in each residue, performing an initial best-fit, then determining which configuration of symmetric atoms will give the lowest RMSD using atomic distance to reference atoms.

Note that when re-mapping, all atoms in the residues of interest should be selected to prevent cases where selected symmetric atoms are swapped but the atoms they are bonded to are not. Also, occasionally larger symmetric structures (e.g. 6 membered rings) may become distorted due to only part of the residue being corrected for symmetry. This appears to happen about 4% of the time but does not overly inflate the RMSD. The ***'check'*** command can be used after ***symmrmsd*** to look for such distortions.

Warning: the symmetry correction is generally robust enough to account for symmetries in the standard amino and nucleic acid residues, but has not been extensively tested on residues with more extended types of symmetry.

12.86 temperature

```
temperature [<name>] [out <filename>]
            { frame |
              [<mask>] [ntc <#>] [update] [remove {trans|rot|both}]
            }
```

[<name>] Data set name.

[out <filename>] File to write values to.

frame Do not calculate temperature; use existing frame temperature.

[<mask>] Atoms to calculate temperature for.

[ntc <#>] Value of SHAKE bond constraint: 1 - none, 2 - bonds to H, 3- all bonds (equivalent to SANDER/PMEMD).

[update] Update temperature in Frames with calculated temperatures.

[remove {trans|rot|both}] Correct for removed translational, rotational, or both kinds of degrees of freedom.

Calculate temperature in frame based on velocity information. If '**update**' is specified, update frame temperature too. If '**frame**' is specified just use frame temperature (e.g. read in from a REMD trajectory).

The 'ntc' keyword can be used to correct for lost degrees of freedom due to SHAKE constraints (2 = bonds to hydrogen, 3 = all bonds). The 'remove' keyword can be used to account for removed translational and/or rotational degrees of freedom.

For example, if using a trajectory that has been generated with SHAKE on hydrogens, no periodic boundary conditions (i.e. no box), and has had the center of mass periodically removed:

```
temperature T1 ntc 2 remove both out T1.dat
```

If using a trajectory that has been generated with SHAKE on hydrogens, periodic boundary conditions (i.e. with a box), and has had the center of mass periodically removed:

```
temperature T1 ntc 2 remove trans out T1.dat
```

If using a trajectory that has been generated with SHAKE on all bonds, periodic boundary conditions, and no center of mass motion removal:

```
temperature T1 ntc 3 out T1.dat
```

12.87 time

`time {time0 <initial time> dt <step> [update] | remove}`

time0 <initial time> Time of the first frame (ps).

dt <step> Time step between frames (ps).

[update] If specified, modify any existing time info.

remove Remove any time info from frame.

Either add time information to frames, modify existing time information in frames, or remove existing time information from frames. Note that currently COORDS data sets do not store time information, so using this command with the ***crdaction*** command will have no effect.

12.88 tordiff

tordiff [<set name>] [<mask>] [mass] [out <file>] [diffout <file>] [time <dt>]

[<set name>] Output mean-squared-displacement data sets name.

[<mask>] Mask of molecules to calculate diffusion for.

[mass] Use center of mass of molecules instead of geometric center.

[out <file>] File to write mean-squared-displacement sets to.

[diffout <file>] Write diffusion contants calculated from fits of mean-squared-displacent data sets to <filename>.

[time <dt>] Time between frames in ps.

DataSet Aspects:

[X] MSD(s) in the X direction.

[Y] MSD(s) in the Y direction.

[Z] MSD(s) in the Z direction.

[R] Overall MSD(s).

[A] Overall displacement(s) in Å.

[D] Diffusion constants ($1x10^{-5}$ cm^2/s).

[Label] Diffusion constant lablels.

[Slope] Linear regression slopes.

[Intercept] Linear refression Y-intercepts.

[Corr] Linear regression correlation coefficients.

Calculate the diffusion via mean-squared displacement (in $Å^2$/ps) of specified molecules using the toroidal-view-preserving (TOR) scheme of Hummer et al. **Note that currently this only works for orthogonal boxes**. (https://arxiv.org/abs/2303.09418). Unlike the ***diffusion*** (12.24 on page 136) and ***unwrap*** (12.91 on page 231) commands which correct for box fluctuations via fractional coordinates, the TOR scheme corrects for box fluctuations by

tracking the displacement of each molecule with respect to its position in the previous frame in Cartesian space.

Diffusion constants are calculated in the same manner as the ***diffusion*** command; for more details see 12.24 on page 136.

For example, to calculate the diffusion (with data set name TOR) of waters (name WAT) in an orthogonal box using the toroidal scheme:

```
parm tz2.ortho.parm7
trajin tz2.ortho.nc
tordiff TOR :WAT@O out tor.msd.dat diffout tor.diff.dat
```

12.89 trans | translate

```
translate [<mask>] {[x <dx>] [y <dy>] [z <dz>] | topoint <x>,<y>,<z> [mass]}
```

<mask> Mask of atoms to translate (all atoms if not specified).

x <dx> Translation (delta) in the X direction (Å).

y <dx> Translation (delta) in the Y direction (Å).

z <dx> Translation (delta) in the Z direction (Å).

topoint <x>,<y>,<z> If specified, translate center of specified atoms to a specific point defined by <x>, <y>, and <z> in the given comma-separated list instead of by deltas.

mass If specified, translate center of mass of specified atoms (topoint only).

Translate atoms in <**mask**> (all atoms if no mask specified) <**dx**> Å in the X direction, <**dy**> Å in the Y direction, and <**dz**> Å in the Z direction. If '**topoint**' is specified, translate atoms in <mask> to the specified coordinates (also in Å).

12.90 unstrip

```
unstrip
```

Requests that the original topology and frame be used for all following actions. This has the effect of undoing any command that modifies the state (such as strip). For example, the following code takes a solvated complex and uses a combination of strip, unstrip, and outtraj commands to write out separate dry complex, receptor, and ligand files:

```
parm Complex.WAT.pdb
trajin Complex.WAT.pdb
# Remove water, write complex
```

```
strip :WAT
outtraj Complex.pdb pdb
# Reset to solvated Complex
unstrip
# Remove water and ligand, write receptor
strip :WAT,LIG
outtraj Receptor.pdb pdb
# Reset to solvated Complex
unstrip
# Remove water and receptor, write ligand
strip :WAT
strip !(:LIG)
outtraj Ligand.pdb pdb
```

12.91 unwrap

```
unwrap [center] [{byatom | byres | bymol}] [avgucell <avg ucell set>]
       [ reference | ref <name> | refindex <#> ] [<mask>]
       [scheme {frac|tor}]
```

[center] Unwrap by center of mass; otherwise unwrap by first atom position (byres and bymol).

byatom Unwrap by atom (default).

byres Unwrap by residue.

bymol Unwrap by molecule.

[avgucell <avg ucell set>] Average unit cell data set; useful when unwrapping NPT trajectories.

[reference | ref <name> | refindex <#>] Reference structure to use in unwrapping.

[<mask>] Selection to unwrap.

[scheme frac|tor}] Unwrap using either fractional coordinates (default) or toroidal-view-preserving scheme (orthogonal boxes only).

Under periodic boundary conditions, MD trajectories are not continuous if molecules are wrapped(imaged) into the central unit cell. Especially, in sander, with *iwrap*=1, molecular trajectories become discontinuous when a molecule crosses the boundary of the unit cell. This command, ***unwrap*** processes the trajectories to force the *mask*ed molecules continuous by translating the molecules into the neighboring unit cells. It is the opposite function of ***image***, but this command can also be used to place molecules side by side, for example, two strands of a DNA duplex. However, this command may fail if the *mask*ed entities travel more than half of the box size within a single frame. Note that uwrapping by atom (the default behavior) is slower than unwrapping by residue

or molecule, but is usually the safer method, especially if it is unknown if the original imaging was done by atom, by residue, or by molecule. If the optional reference arguments are specified, then the first frame is unwrapped according to the reference structure. Otherwise, the first frame is not modified.

To remove the "noise" caused by box fluctuations in NPT trajectories, the average unit cell vectors describing the average box can be provided with the **avgucell** keyword; see the ***avgbox*** command (12.10 on page 125).

By default coordinates are unwrapped using fractional coordinates. To unwrap via the toroidal-view-preserving scheme (`https://arxiv.org/abs/2303.09418`) specify **scheme tor.** However, note that this currently **only works for orthogonal boxes** and may result in unrealistic trajectories (particularly at long times when molecules have had the chance to traverse multiple box lengths) and is only currently recommended for calculating diffusion.

As an example, assume that :1-10 is the first strand of a DNA duplex and :11-20 is the other strand of the duplex. Then the following commands could be used to create system where the two strands are not separated artificially:

```
unwrap :1-20
center :1-20 mass origin
image origin center familiar
```

To unwrap an NPT trajectory by using the average unit cell (box), the calculate diffusion from the unwrapped trajectory:

```
parm tz2.ortho.parm7
trajin tz2.ortho.nc
# Create average box data
avgbox MyBox
run
# Unwrap using average box data
unwrap bymol avgucell MyBox[avg]
# Calculate diffusion
diffusion Water :WAT@O out tz2.ortho.wato.dat
run
```

12.92 vector

```
vector [<name>] <Type> [out <filename> [ptrajoutput]] [<mask1>] [<mask2>]
    [magnitude] [geom] [ired] [gridset <grid>] [debye]
       <Type> = { mask      | minimage  | dipole | center   | corrplane |
                  box       | boxcenter | ucellx | ucelly   | ucellz
                momentum | principal [x|y|z]  | velocity | force }
```

[<name>] `Vector data set name.`

<Type> `Vector type; see below.`

[out <filename>] Write vector data to <filename> with format 'Vx Vy Vz Ox Oy Oz' where V denotes vector coordinates and 'O' denotes origin coordinates.

[ptrajoutput] Write vector data in *ptraj* style (Vx Vy Vz Ox Oy Oz Vx+Ox Vy+Oy Vz+Oz). This prevents additional formatting of <filename> and is not compatible with 'magnitude'.

[<mask1>] Atom mask, required for all types except 'box'.

[<mask2>] Second atom mask, only required for type 'mask'.

[magnitude] Store the magnitude of the vector with aspect [Mag].

[geom] If specified, use geometric centers instead of centers of mass.

[ired] Mark this vector for subsequent IRED analysis with commands 'matrix ired' and 'ired'.

[gridset <grid>] Name of grid data set to get box info from instead of frame for box, boxcenter, and ucell[x|y|z].

[debye] ('dipole' vector only) Report dipole vector in units of Debye instead of e-*Ang.

Data Sets Created:

<name> Vector data set.

<name>[Mag] (magnitude only) Vector magnitude.

This command will keep track of a vector value (and its origin) over the trajectory; the data can be referenced for later use based on the *name* (which must be unique). The types of vectors that can be calculated are:

mask (Default) Store vector from center of mass of atoms in **<mask1>** to atoms in **<mask2>**.

minimage Store minimum-imaged vector from center of mass of atoms in **<mask1>** to atoms in **<mask2>**.

dipole Store the dipole and center of mass of the atoms specified in **<mask1>**. The dipole vector has units of e-*Ang unless **'debye'** is specified for units of Debye. The center is always stored as simply Ang (since it is just coordinates). Note that the value may not be well-defined if the atoms in the mask are not overall charge neutral.

center Store the center of mass of atoms in **<mask1>**. The reference point is the origin (0.0, 0.0, 0.0).

corrplane This defines a vector perpendicular to the (least-squares best) plane through the atoms in <**mask1**>. The reference point is the center of mass of atoms in <**mask1**>.

box (No mask needed) Store the box lengths of the trajectory. The reference point is the origin (0.0, 0.0, 0.0).

boxcenter (No mask needed) Store the center of the box as a vector.

ucell{x|y|z}: (No mask needed) Store specified unit cell (i.e. box) vector.

momentum Store momentum of atoms selected by <mask1> (requires velocities).

principal [x|y|z] Store one of the principal axis vectors determined by diagonalization of the inertial matrix from the coordinates of the atoms specified by <**mask1**>. The eigenvector with the largest eigenvalue is considered "x" (i.e., the hardest axis to rotate around) and the eigenvector with the smallest eigenvalue is considered "z". If none of `x` or `y` or `z` are specified, then the "x" principal axis is stored. The reference point is the center of mass of atoms in <**mask1**>.

velocity Store velocity of atoms in <mask1> (requires velocities).

force Store force of atoms in <mask1> (requires forces).

Cpptraj supports writing out vector data in a pseudo-trajectory format for easy visualization. Once a vector data set has been generated the writedata command can be used with the vectraj keyword (see 6 on page 27 for more details) to write a pseudo trajectory consisting of two atoms, one for the vector origin and one for the vector from the origin (i.e. V+O). For example, to create a MOL2 containing a pseudo-trajectory of the minimum-imaged vector from residue 4 to residue 11:

```
trajin tz2.nc
vector v8 minimage out v8.dat :4 :11
run
writedata v8.mol2 vectraj v8 trajfmt mol2
```

Auto-correlation or cross-correlation functions can be calculated subsequently for vectors using either the ***corr*** analysis command or the ***timecorr*** analysis command (to calculate via spherical harmonic theory).

12.93 velocityautocorr

```
velocityautocorr [<set name>] [<mask>] [usevelocity] [out <filename>] [diffout <file>]
                 [maxlag <frames>] [tstep <timestep>] [direct] [norm]
```

[<set name>] `Data set name.`

[<mask>] Atoms(s) to calculate velocity autocorrelation (VAC) function for.

[usevelocity] Use velocity information in frame if present. This will only give sensible results if the velocities are recorded close to the order of the simulation time step.

[out <filename>] Write VAC function to <filename>.

[diffout <file>] File to write diffusion constants to.

[maxlag <frames>] Maximum lag in frames to calculate VAC function for. Default is half the total number of frames.

[tstep <timestep>] Time between frames in ps (default 1.0).

[direct] Calculate VAC function directly instead of via FFT (will be much slower).

[norm] Normalize resulting VAC function to 1.0.

DataSet Aspects:

[D] Diffusion constant calculated from integral over VAC function in $1x10^{-5}$ cm^2/s.

Calculate the velocity autocorrelation (VAC) function averaged over the atoms in <mask>. Pseudo-velocities are calculated using coordinates and the specified time step. As with all time correlation functions the statistical noise will increase if the maximum lag is greater than half the total number of frames. In addition to calculating the velocity autocorrelation function, the self-diffusion coefficient will be reported in the output, calculated from the integral over the VAC function.

12.94 volmap

```
volmap [out <filename>] <mask> [radscale <factor>] [stepfac <fac>]
    [sphere] [radii {vdw | element}] [splinedx <spacing>]
    [calcpeaks] [peakcut <cutoff>] [peakfile <xyzfile>]
    { data <existing set> |
      name <setname> <dx> [<dy> <dz>]
        { size <x,y,z> [center <x,y,z>] |
          centermask <mask> [buffer <buffer>] |
          boxref <reference> }  }
```

out <filename> The name of the output file with the grid density.

<mask> The atom selection from which to calculate the number density.

radscale <**factor**> Factor by which to scale radii (by division). To match the atomic radius of Oxygen used by the VMD volmap tool, a scaling factor of 1.36 should be used. Default 1.0.

stepfac <**factor**> Factor for determining how many voxels to smear Gaussian (default 4.1, 1.0 for sphere).

sphere When smearing Gaussian, skip voxels farther than radii/2.

radii {**vdw**|**element**} Specify either van der Waals radii (default) or elemental radii.

splinedx <**spacing**> Spacing to use for cubic spline interpolation (default 0.01 Ang.).

calcpeaks If specified, peaks in the grid density will be calculated and saved to set <setname> with aspect "peaks".

peakcut <**cutoff**> The minimum density required to consider a local maximum a 'density peak' in the outputted peak file (default 0.05).

peakfile <**xyzfile**> A file in XYZ-format that contains a carbon atom centered at the grid point of every local density maximum. This file is necessary input to the spam action command.

data <**setname**> Name of existing grid data set to use.

name <**setname**> Name of grid set that will be created (size/center or centermask/buffer keywords).

dx, **dy**, **dz** The grid spacing (Angstroms) in the X-, Y-, and Z-dimensions, respectively.

size <**x,y,z**> Specify the size of the grid in the X-, Y-, and Z-dimensions. Must be used alongside the center argument.

center <**x,y,z**> Specify the grid center explicitly. Note, the size argument must be present in this case. Default is the origin.

centermask <**mask**> The mask around which the grid should be centered (via geometric center). If this is omitted and the center and size are not specified, the default <mask> entered (see above) is used in its place.

buffer <**buffer**> A buffer distance, in Angstroms, by which the edges of the grid should clear every atom of the centermask (or default mask if

centermask is omitted) in every direction. The default value is 3. The buffer is ignored if the center and size are specified (see below).

boxref <**reference**> Set up the grid using the unit cell info in the specified reference.

Data Sets Created:

<**setname**> The 3D grid.

<**setname**>**[peaks]** The density peaks if calcpeaks specified.

Grid data as a volumetric map, similar to the 'volmap' command in VMD. The density is calculated by treating each atom as a 3-dimensional Gaussian function whose standard deviation is equal to the van der Waals radius. The density calculated is the number density averaged over the entire simulation. The grid can be specified in one of three ways:

1. An existing grid data set (from e.g. bounds), specified with the **data** keyword.
2. Via the sizes and center specified by the **size** and **center** keywords (comma-separated strings, e.g. '20,20,20').
3. Centered on the atoms in the mask given by **centermask** with an additional buffer in each direction specified by **buffer**.

The calculation is sped up by using cubic splines to interpolate the exponential function when calculating the Gaussians.[35]

12.95 volume

volume [<name>] [out <filename>]

<**name**> Data set name.

out <**filename**> Output file name.

Calculate unit cell volume.

12.96 watershell

watershell <solutemask> [out <filename>] [lower <lower cut>] [upper <upper cut>] [noimage] [<solventmask>]

<**solutemask**> Atom mask corresponding to solute of interest (required).

[out <**filename**>**]** Output file name.

[lower <lower cut>] Cutoff for the first water shell (default 3.4 Angstroms).

[upper <upper cut>] Cutoff for the second water shell (default 5.0 Angstroms).

[noimage] Do not image distances.

[<solventmask>] Optional atom mask corresponding to solvent.

DataSet Aspects:

[lower] Number of solvent molecules in first solvent shell.

[upper] Number of solvent molecules in second solvent shell.

This option will count the number of waters within a certain distance of the atoms in the <solutemask> in order to represent the first and second solvation shells. The optional <solventmask> can be used to consider other atoms as the solvent; the default is ":WAT".

This action is often used prior to the ***closest*** command in order to determine how many waters around a solute should be retained to maintain the first and/or second water shells.

As of version 17 this command is CUDA-enabled in CUDA versions of CPPTRAJ.

12.97 xtalsymm

```
xtalsymm <mask> group <space group> [collect [centroid]]
      [ first | reference | ref <name> | refindex <#> ]
      [na <na>] [nb <nb>] [nc <nc>]
```

<mask> Atom mask defining the asymmetric unit within the larger system (required).

group <space group> The space group to which the system belongs. Omit spaces in the name. Example: "P22(1)2(1)".

[collect] Optional flag to have all solvent particles, not just the asymmetric units, re-imaged. This will trigger cpptraj to compute the unit cell volume that constitutes the aymmetric unit and thereby classify all particles for re-imaging.

[centroid] If specified along with collect, re-image solvent molecules by centroids, not individual atom coordinates. This is useful for keeping water molecules intact.

[first | **reference** | **ref** <**name**> | **refindex** <#>**]** Reference structure to use for determining crystal symmetry.

[na <**na**>**] [nb** <**nb**>**] [nc** <**nc**>**]** The number of times the crystal unit cell is replicated along the "a," "b," or "c" axes (for orthorhombic unti cells, these are the x, y, and z axes) of the simulation; default is 1. Many crystal unit cells are too small in one or more dimensions for our simulation cutoffs, and replicating the unit cell is an effective way to counter imaging artifacts even for larger unit cells.

Calculate the optimal approach for superimposing symmetry-related subunits of the simulation back onto one another. The calculation assumes that the system is a simulation of an X-ray structure in its native crystal lattice, finds all copies of the asymmetric unit among the entire system, and devises plans for re-imagining their coordinates to superimpose them back on the original asymmetric unit. The space group information can be found in a PDB X-ray structure used as the initial coordinates for a simulation. All 230 space groups are supported, and a scan of the PDB was made to ensure that common variants of the names are included (P2(1)22(1) is the same as P22(1)2(1), but with different axis conventions). If your space group is not understood, contact the Amber mailing list. This command is compute intensive, especially for simulations that are "supercells" containing many crystallographic unit cells.

This command will cause cpptraj to locate all asymmetric units from within the topology, then determine what wrapping, if any, has occurred in order to bring about an optimal re-alignment based on the space group symmetry operations. The user need not worry about wrapping or drift of the simulation over time–the asymmetric units will be re-imaged frame by frame. Coordinate modifications due to this action are permanent and will affect the results of subsequent actions and analyses.

13 Analysis Commands

Analyses in *cpptraj* operate on data sets which have been generated by Actions in a prior Run or read in with a ***readdata*** command (9.22 on page 73). Unlike *ptraj*, Analysis commands in *cpptraj* do not need to be prefaced with `'analysis'`. The exception to this is '***analyze matrix***' in order to differentiate it from the ***matrix*** Action command; users are encouraged to use the new command ***diagmatrix*** instead.

Like Actions, when an Analysis command is issued it is by default added to the Analysis queue and is not executed until after trajectory processing is completed; a complete list of data sets available for analysis is shown after trajectory processing (prefaced by 'DATASETS') or can be shown with the

'***list dataset***' command. Analyses can also be executed immediately via the ***runanalysis*** command (9.27 on page 75).

Note that for Analysis commands that use COORDS data sets, if no COORDS data set is specified then a default one will be automatically created from frames read in by ***trajin*** commands.

Command	Description	Set Type(s)
autocorr	Calculate autocorrelation function for multiple data sets.	N 1D sclar
avg	Calculate average, standard deviation, min, and max for (or over) data sets.	N 1D scalar
calcdiffusion	Calculate diffusion using multiple time origins.	COORDS
calcstate	Calculate states based on given data sets and criteria.	N 1D scalar
cluster	Perform cluster analysis.	COORDS, N 1D scalar
corr, correlationcoe	Calculate auto or cross correlation for 1 or 2 data sets.	1D scalar, vector
cphstats	Calculate statistics for constant pH data sets.	pH data sets
crank, crankshaft	Calculate crankshaft motion between two data sets.	2 1D scalar
crdfluct	Calculate atomic fluctuations (RMSF) for atoms over time blocks.	COORDS
crosscorr	Calculate a matrix of Pearson product-moment coefficients between given data sets.	N 1D scalar
curvefit	Perform non-linear curve fitting on given data set.	1D scalar
diagmatrix	Calculate eigenvectors and eigenvalues from given symmetric matrix.	symmetric matrix
divergence	Calculate Kullback-Leibler divergence between two data sets.	2 1D scalar
evalplateau	Evaluate whether the data in a 1D set has reached a single exponential plateau.	
FFT	Perform a fast Fourier transform on data sets.	N 1D scalar
hausdorff	Calculate the Hausdorff distance for given matrix data set(s).	N 2D matrices

hist, histogram	Calculate N-dimensional histogram for N given data sets.	N 1D scalar
integrate	Perform integration on each of the given data sets.	N 1D scalar
ired	Perform isotropic reorientational eigenmode dynamics analysis using given IRED vectors.	N IRED vectors
kde	Calculate 1D histogram from given data set using a kernel density estimator. Also time-dependent Kullback-Leibler divergence analysis with another set.	1 or 2 1D scalar
lifetime	Perform lifetime analysis on given data sets.	N 1D scalar
lowestcurve	For each given data set, calculate a curve that traces the lowest N points over specified bins.	N 1D scalar
meltcurve	Calculate a melting curve from given data sets assuming simple 2 state kinetics.	N 1D scalar
modes	Perform various analyses on eigenmodes (from e.g. ***diagmatrix***).	eigenmodes
multicurve	Perform non-linear curve fitting for multiple input data sets.	N 1D scalar
multihist	Calculate 1D histograms (optionally with a kernel density estimator) from multiple input data sets.	N 1D scalar
phipsi	Calculate and plot the average phi and psi values from input dihedral data sets.	N phi/psi dihedrals
projectdata	Project data along eigenmodes.	eigenmodes, N 1D scalar
regress	Perform linear regression on multiple input data sets.	N 1D scalar
remlog	Calculate various statistics from a replica log data set.	replica log
rms2d, 2drms	Calculate 2D RMSD between frames in 1 or 2 COORDS data sets.	1 or 2 COORDS
rmsavgcorr	Calculate RMS average correlation curve for a COORDS data set.	COORDS
rotdif	Calculate rotational diffusion using given rotation matrices (from e.g. ***rms***).	rotation matrices

runningavg	Calculate running average for given data sets using given window size.	N 1D scalar
spline	Calculate cubic splines for given data sets.	N 1D scalar
stat, statistics	Calculate various statistics for given data sets.	N 1D scalar
ti	Peform Gaussian quadrature integration for given DV/DL data sets.	N 1D scalar
tica	Perform time-independent correlation analysis.	COORDS, N 1D scalar
timecorr	Calculate auto/cross-correlation functions for given vector(s) using spherical harmonics.	1 or 2 vector
vectormath	Perform math on given vector data sets.	2 vector
wavelet	Perform wavelet analysis on coordinates from given COORDS set.	COORDS

13.1 autocorr

```
autocorr [name <dsetname>] <dsetarg0> [<dsetarg1> ...] [out <filename>]
         [lagmax <lag>] [nocovar] [direct]
```

<dsetarg0> [dsetarg1> ...] `Argument(s) specifying datasets to be used.`

[name <dsetname>] `Store results in dataset(s) named <dsetname>:X.`

[out <filename>] `Write results to file named <filename>.`

[lagmax] `Maximum lag to calculate for. If not specified all frames are used.`

[nocovar] `Do not calculate covariance.`

[direct] `Do not use FFTs to calculate correlation; this will be much slower.`

This is for integer/double/float datasets only; for vectors see the ***'timecorr'*** *command.*

Calculate auto-correlation (actually auto-covariance by default) function for datasets specified by one or more dataset arguments. The datasets must have the same # of data points.

13.2 avg

```
avg <dset0> [<dset1> ...] [torsion] [out <file>] [oversets]
    [name <name>] [nostdout]
    [ffmt {GEN|DBL|SCI}] [fwidth <width>] [fprec <precision>]
```

<dsetX> Data set(s) to calculate the average for.

[torsion] If the data sets are not already marked periodic (e.g. if read in via 'readdata'), treat them as periodic torsion.

[out <file>] File to write results to.

[oversets] If specified, calculate the average over all inpout sets instead of each input set.

[name <name>] Output data set name.

[nostdout] If 'nostdout' specified do not write averages to STDOUT when 'out' not specified.

[ffmt {GEN|DBL|SCI}] Change the default floating point output format to GEN=general, DBL=double, or SCI=scientific.

[fwidth <width>] Change the default floating point output width to <width>.

[fprec <precision>] Change the default floating point output precision to <precision>.

DataSets Created (not oversets):

<name>[avg] Average of each set.

<name>[sd] Standard deviation of each set.

<name>[ymin] Y minimum of each set.

<name>[ymax] Y maximum of each set.

<name>[yminidx] Index of minimum Y value.

<name>[ymaxidx] Index of maximum Y value.

<name>[names] Name of each set.

DataSets Created (oversets)

<name> Average over all input sets for each frame.

<name>[SD] Standard deviation over all input sets for each frame.

Calculate the average, standard deviation, min, and max of given 1D data sets. Alternatively, if **oversets** is specified the average over each set for each point is calculated; this requires all input sets be the same size.

For example, to read in data from a file named perres.peptide.dat and calculate the averages etc for all the input sets:

```
readdata perres.peptide.dat
avg perres.peptide.dat out output.dat name V
```

13.3 calcdiffusion

```
calcdiffusion [crdset <coords set>] [maxlag <maxlag>] [<mask>] [time <dt>]
              [<name>] [out <file>] [diffout <file>]
```

[crdset <coords set>] Input COORDS set to calculate diffusion for.

[maxlag <maxlag>] Maximum lag to calculate diffusion for in frames. Defaults to half the number of input frames if not specified.

[<mask>] Mask of atoms to calculate diffusion for.

[time <dt>] Time between frames in ps.

[<name>] Output MSD data sets name.

[out <file>] File to write MSD data sets to.

[diffout <file>] Write diffusion contants calculated from fits of MSD data sets to <filename>.

DataSet Aspects:

[X] MSD(s) in the X direction.

[Y] MSD(s) in the Y direction.

[Z] MSD(s) in the Z direction.

[R] Overall MSD(s).

[A] Overall displacement(s) in Å.

[D] Diffusion constants ($1x10^{-5}$ cm^2/s).

[Label] Diffusion constant lablels.

[Slope] Linear regression slopes.

[Intercept] Linear refression Y-intercepts.

[Corr] Linear regression correlation coefficients.

Calculate diffusion via mean-squared-displacements (MSD) of specified atoms. Unlike the ***diffusion*** Action (12.24 on page 136), which calculates MSD from a single time origin, the ***calcdiffusion*** command calculates diffusion from multiple time origins up to a user-specified lag (in frames). Note that no imaging is performed for this command, so any unwrapping should be performed prior to this command (see 12.91 on page 231). Diffusion constants are calculated in the same manner as the ***diffusion*** command; for more details see 12.24 on page 136.

This command is both OpenMP- and MPI-parallelized; either or both can be active. In order to keep per-process memory requirements low, it is recommended that TRAJ (i.e. on-disk) data sets be used with MPI instead of CRD (in-memory) sets (see 8.11 on page 51).

For example, to calculate diffusion from multiple time origins (with a maximum lag of half the number of trajectrory frames) from an input trajectory in memory (unwrapping first):

```
parm tz2.ortho.parm7
loadcrd tz2.ortho.nc name TZ2
crdaction TZ2 unwrap bymol
runanalysis calcdiffusion crdset TZ2 out tz2.diff.dat :WAT@O
```

To do the same calculation using MPI parallelism, it will first be necessary to unwrap the trajectory (non-MPI parallel, but OpenMP parallelism can be used):

```
parm tz2.ortho.parm7
trajin tz2.ortho.nc
unwrap bymol
trajout unwrap.dcd
```

Then diffusion can be calculated using MPI (and/or OpenMP):

```
parm tz2.ortho.parm7
loadtraj unwrap.dcd name TZ2
runanalysis calcdiffusion crdset TZ2 out tz2.traj.diff.dat :WAT@O
```

13.4 calcstate

```
calcstate {state <ID>,<dataset>,<min>,<max>[,<dataset1>,<min1>,<max1>]} ...
       [out <state v time file>] [name <setname>]
       [curveout <curve file>] [stateout <states file>]
       [transout <transitions file>] [countout <count file>]
```

state <ID>,<dataset>,<min>,<max> Define a state according to given data set and criteria. Multiple states can be given, and each state can have multiple criteria. If multiple criteria are specified, each one must be satisfied in order to assign the state. If the same state is defined multiple times, the state will be assigned if either criteria match.

<ID> Name to give each state index. State indices start at 0. -1 means "undefined state".

<dataset> Data set to use.

<min>,<max> Frames with data set value above <min> and below <max> will be assigned <ID>.

[out <state v time file>] File to write state index vs frame to.

[name <setname>] Data set name.

[curveout <curve file>] File to write state lifetime and transition curves to.

[stateout <states file>] File to write state lifetime data to.

[transout <transitions file>] File to write state transition data to.

[countout <state count file>] File to write state counts (i.e. how many frames each state was observed) to.

DataSets Created:

<setname> State index vs frame.

<setname>[Count] Number of frames each state was observed.

<setname>[Frac] Fraction of time each state was observed

<setname>[Nlifetimes] Number of times each state was reached.

<setname>[Avglife] Average lifetime length for each state.

<setname>[Maxlife] Maximum lifetime of each state.

<setname>[Name] Name (<ID>) of each state.

<setname>[Xlifetimes] Number of times each state transitioned to each other state.

<setname>[Xavglife] Average lifetime of each state before transitioning to each other state.

<setname>[Xmaxlife] Maximum lifetime of each state before transitioning to each other state.

<setname>[Xname] Name of each transition, format "StateA->StateB".

<setname>[sCurve]:X State curves; lifetime curve for transitions from given state to any other state.

<setname>[tCurve]:X Transition curves; lifetime curve for transitions from given state to other specific state.

Data for the specified data set(s) that matches the given criteria will be assigned a state index. State indices start from 0 and match the order in which **state** keywords were given. The -1 state index is reserved for "undefined state". For example, the following input:

```
parm DPDP.parm7
trajin DPDP.nc
distance d1 :19@O :12@N
angle a1 :19@O :12@H :12@N
calcstate state D,d1,3.0,4.0 state A,a1,100,120 out state.dat curveout curve.agr \
                stateout States.dat transout States.dat name d1_a1
run
```

Defines two states. State index 0 is defined as a state named "D" based on the distance from ':19@O' to ':12@N' (data set d1) being between 3 and 4 Angstroms. State index 1 is defined as a state named "A" based on the angle between ':19@O', ':12@H', and ':12@N' (data set a1) being between 100 and 120 degrees. The output in state.dat might look like:

```
#Frame          d1_a1
       1           -1
       2            0
       3            0
       4            0
       5           -1
       6            1
       7           -1
       8           -1
       9            0
      10           -1
```

where the values in column d1_a1 refer to state index: -1 is undefined, 0 is state "D", and 1 is state "A".

To define a state State1 as having a distance named "dist" between 2.5 and 5.0 Ang. and an angle named "ang" between 30 and 60 degrees OR having a distance named "distA" between 0.0 and 3.0 Ang.:

```
calcstate state State1,dist,2.5,5.0,ang,30,60 \
          state State1,distA,0.0,3.0
```

Lifetime curves (see 13.21 on page 276 for further explanation) are calculated for transitions from each state to any other state (aspect [sCurve]) and each state to each other state (aspect [tCurve]). In this case there will be 3 sCurves and 4 tCurves:

```
d1_a1[sCurve]:0 "Undefined" (double), size is 10
d1_a1[sCurve]:1 "D" (double), size is 3
```

```
d1_a1[sCurve]:2 "A" (double), size is 1
d1_a1[tCurve]:0 "Undefined->D" (double), size is 10
d1_a1[tCurve]:1 "D->Undefined" (double), size is 3
d1_a1[tCurve]:2 "Undefined->A" (double), size is 1
d1_a1[tCurve]:3 "A->Undefined" (double), size is 1
```

Lifetime analysis from each state to any other state is directed to the file specified by **stateout** and has format:

```
#Index N Average Max State
```

Where `#Index` is the state index, `N` is the number of lifetimes in that state, `Average` is the average lifetime while in that state (in frames), `Max` is the maximum lifetime while in that state (in frames) and `State` is the name of the state.

Finally, lifetime analysis of transitions from each state to each other state is directory to the file specified by transout and has format:

```
#N Average Max Transition
```

Where `#N` is the number of transitions, `Average` is the average lifetime (in frames) in the first state before transitioning to the second state, `Max` is the max lifetime (in frames) before transitioning to the second state, and `Transition` is the name of the transition.

13.5 cluster

```
cluster [crdset <crd set>] [data <dset0>[,<dset1>...]] [nocoords]
[<name>] [<Algorithm>] [<Metric>] [<Pairwise>] [<Sieve>] [<BestRep>]
[<Output>] [<Coord. Output>] [<Graph>]
    [readinfo {infofile <info file> | cnvtset <dataset>}]
    [useframesincache]
  Algorithm Args: [{hieragglo|dbscan|kmeans|dpeaks}]
[hieragglo [epsilon <e>] [clusters <n>] [linkage|averagelinkage|complete]
           [epsilonplot <file>]]
[dbscan minpoints <n> epsilon <e> [kdist <k> [kfile <prefix>]]]
[kmeans clusters <n> [randompoint [kseed <seed>]] [maxit <iterations>]]
[dpeaks epsilon <e> [noise] [dvdfile <density_vs_dist_file>]
        [choosepoints {manual | auto}]
        [distancecut <distcut>] [densitycut <densitycut>]
        [runavg <runavg_file>] [deltafile <file>] [gauss]]
  Metric Args:
[{dme|rms|srmsd|qrmsd} [mass] [nofit] [<mask>]] [{euclid|manhattan}] [wgt <list>]
  Pairwise Args:
[pairdist <name> [pairdistfile <file>]] [pwrecalc]
[loadpairdist] [savepairdist] [pairwisecache {mem|disk|none}]
```

```
  Sieve Args:
[sieve <#> [sieveseed <#>] [random] [includesieveincalc] [includesieved_cdist]
 [{sievetoframe|sievetocentroid|closestcentroid}] [repsilon <restore epsilon>]]
  BestRep Args:
[bestrep {cumulative|centroid|cumulative_nosieve}] [savenreps <#>]
  Output Args:
[out <cnumvtime> [gracecolor]] [noinfo|info <file>] [summary <file>]
[summarysplit <splitfile>] [splitframe <comma-separated frame list>]
[clustersvtime <file> [cvtwindow <#>]] [sil <prefix> [silidx {idx|frm}]]
[metricstats <file>] [cpopvtime <file> [{normpop|normframe}]] [lifetime]
  Coordinate Output Args:
[clusterout <trajfileprefix> [clusterfmt <trajformat>]]
[singlerepout <trajfilename> [singlerepfmt <trajformat>]]
[repout <repprefix> [repfmt <trajformat>] [repframe]]
[avgout <avgprefix> [avgfmt <trajformat>]]
[assignrefs [refcut <rms>] [refmask <mask>]]
  Graph Args:
[{drawgraph|drawgraph3d} [draw_tol <tolerance>] [draw_maxit <iterations]]
```

[crdset <crd set>] Name of COORDS data set to cluster on and/or use for coordinate output. If not specified the default COORDS set will be generated and used unless nocoords has been specified.

[data <dset0>[,<dset1>,...] Distance between frames calculated using specified data set(s). Currently 1D scalar sets and COORDS sets are supported.

[nocoords] Do not use a COORDS data set; distance metrics that require coordinates and coordinate output will be disabled.

[<name>] Data set Name for generated cluster data sets.

[readinfo] Use previous cluster results to set up initial clusters. Clustering will continue if possible (i.e. this can be used to restart clustering).

infofile <file> Cluster info file to read clusters from.

cnvtset <dataset> Cluster number vs time data set to use to generate initial clusters.

[useframesincache] If a pairwise cache is specified, cluster on the frames stored in the cache.

Algorithms:

hieragglo (Default) Use hierarchical agglomerative (bottom-up) approach.

[epsilon <e>] Finish clustering when minimum distance between clusters is greater than <e>.

[clusters <n>] Finish clustering when <n> clusters remain.

[linkage] Single-linkage; use the shortest distance between members of two clusters.

[averagelinkage] Average-linkage (default); use the average distance between members of two clusters.

[complete] Complete-linkage; use the maximum distance between members of two clusters.

[epsilonplot <file>] Write number of clusters vs epsilon to <file>.

dbscan Use DBSCAN clustering algorithm of Ester et al.[36]

minpoints <n> Minimum number of points required to form a cluster.

epsilon <e> Distance cutoff between points for forming a cluster.

[kdist <k>] Generate K-dist plot for help in determining DBSCAN parameters (see below).

[kfile <prefix>] Prefix for K-dist plot file.

dpeaks Use the density peaks algorithm of Rodriguez and Laio[37]

epsilon <e> Cutoff for determining local density in Angstroms.

[noise] If specified, treat all points within epsilon of another cluster as noise.

[dvdfile <density_vs_dist_file>] File to write density versus minimum distance to point with next highest density. This can be used to determine appropriate cutoffs for distance and density in a subsequent step with choosepoints manual.

[choosepoints {manual | auto}] Specify whether clusters will be chosen based on specified distance/density cutoffs, or automatically. If not specified only the density vs distance file will be written and no clustering will be performed. Currently manual is recommended.

[distancecut <distcut>] [densitycut <densitycut>] If choosepoints manual, points with minimum

distance greather than or equal to <distcut> and density greater than or equal to <densitycut> will be chosen.

[runavg <runavg file>] If choosepoints automatic, the calculated running average of density versus distance will be written to <runavg file>.

[deltafile <file>] If choosepoints automatic, distance minus the running average for each point will be written to this file.

[gauss] Calculate density with Gaussian kernels instead of using discrete density.

kmeans Use K-means clustering algorithm.

clusters <n> Finish clustering when number of clusters is <n>.

[randompoint] Randomize initial set of points used (recommended).

[kseed <seed>] Random number generator seed for randompoint.

[maxit <iteration>] Algorithm will run until frames no longer change clusters of <iteration> iterations are reached (default 100).

Distance Metric Options:

[{rms | srmsd} [<mask>]] (Default rms) For COORDS data, distance between coordinate frames calculated via best-fit coordinate RMSD using atoms in <mask>. If srmsd specified use symmetry-corrected RMSD (see 12.85 on page 226).

[mass] Mass-weight the RMSD.

[nofit] Do not fit structures onto each other prior to calculating RMSD.

qrmsd [<mask>] For COORDS data, distance between coordinate frames calculated using best-fit quaternion RMSD (can be 15-20% faster than regular RMSD) using atoms in <mask>.

[mass] Mass-weight the RMSD.

dme [<mask>] For COORDS data, distance between coordinate frames calculated using distance-RMSD (aka DME, *distrmsd*) using atoms in <mask>.

euclid Use Euclidean distance (sqrt(SUM(distance^2))) when more than one data set has been specified (default).

manhatttan Use Manhattan distance (SUM(distance)) when more than one data set has been specified.

wgt <**list**> Factor to multiply distances from each metric by in a comma-separated list. Can be used to adjust the contribution from each metric. Default is 1 for each metric. Output from the metricstats keyword can be used to determine the relative contribution of each metric to the distance.

Pairwise Distance Matrix Options:

[pairdist <**name**>**]** Pairwise cache DataSet/File name to use for loading/saving pairwise distances.

[pairdistfile <**file**>**]** File name to use for pairwise cache; if not specified and 'pairdist' specified, uses 'pairdist'.

[pwrecalc] If the loaded pairwise distance matrix does not match the current setup, force recalculation.

[loadpairdist] Load pairwise distances from file specified by pairdist (CpptrajPairDist if pairdist not specified).

[savepairdist] Save pairwise distances to file specified by pairdist (CpptrajPairDist if pairdist not specified). NOTE: If sieving was performed only the calculated distances are saved.

[pairwisecache {mem | **disk** | **none}]** Cache pairwise distance data in memory (default), to disk, or disable pairwise caching. No caching will save memory but be extremely slow. Caching to disk will likely be slow unless writing to a fast storage device (e.g. SSD) - data is saved to a file named 'CpptrajPairwiseCache'.

Sieving Options:

[sieve <#>**]** Perform clustering only for every <#> frame. After clustering, all other frames will be added to clusters.

[random] When sieve is specified, select initial frames to cluster randomly.

[sieveseed <#>**]** Seed for random sieving; if not set the wallclock time will be used.

[includesieved_cdist] Include sieved frames in final cluster distance calculation (may be very slow).

[includesieveincalc] Include sieved frames when calculating within-cluster average (may be very slow).

[sievetoframe] When restoring sieved frames, compare frame to every frame in a cluster using a cutoff of <restore epsilon> (default is algorithm epsilon when using DPeaks/DBscan) instead of the centroid; slower but more accurate.

[sievetocentroid] When restoring sieved frames, compare frame to cluster centroid using a cutoff of <restore epsilon> (default is algorithm epsilon when using DPeaks/DBscan). Default method for DPeaks/DBSCAN.

[closestcentroid] When restoring sieved frames, add each frame to its closest centroid. Default method for hieragglo/kmeans.

[repsilon <restore epsilon>] Epsilon to use for sievetoframe/sievetocentroid (default is algorithm epsilon when using DPeaks/DBscan).

Best Representative Options:

[bestrep {cumulative|centroid|cumulative_nosieve}] Method for choosing cluster representative frames.

cumulative Choose by lowest cumulative distance to all other frames in cluster. Default when not sieving.

centroid Choose by lowest distance to cluster centroid. Default when sieving.

cumulative_nosieve Choose by lowest cumulative distance to all other frames, ignoring sieved frames.

[savenreps <#>] Number of best representative frames to choose (default 1).

Output Options:

[out <cnumvtime>] Write cluster # vs frame to <cnumvtime>. Algorithms that calculate noise (e.g. DBSCAN) will assign noise points a value of -1.

[gracecolor] Instead of cluster # vs frame, write cluster# + 1 (corresponding to colors used by XMGRACE) vs frame. Cluster #s larger than 15 are given the same color. Algorithms that calculate noise (e.g. DBSCAN) will assign noise points a color of 0 (blank).

[summary <summaryfile>] Summarize each cluster with format '#Cluster Frames Frac AvgDist Stdev Centroid AvgCDist':

#Cluster Cluster number starting from 0 (0 is most populated).

Frames # of frames in cluster.

Frac Size of cluster as fraction of total trajectory.

AvgDist Average distance between points in the cluster.

Stdev Standard deviation of points in the cluster.

Centroid Frame # of structure in cluster that has the lowest cumulative distance to every other point. If multiple representatives are being saved this column is replaced with two columns for each representative, 'Rep' (representative frame #) and 'RepScore' (score according to current best representative metric).

AvgCDist Average distance of this cluster to every other cluster.

[info <infofile>] Write ptraj-like cluster information to <infofile>. This file has format:
#Clustering: <X> clusters <N> frames
#Cluster <I> has average-distance-to-centroid <AVG>
...
#DBI: <DBI>
#pSF: <PSF>
#SSR/SST: <SSR/SST>
#Algorithm: <algorithm-specific info>
<Line for cluster 0>
...
#Representative frames: <representative frame list>
Where <X> is the number of clusters, <N> is the number of frames clustered, <I> ranges from 0 to <X>-1, <AVG> is the average distance of all frames in that cluster to the centroid, <DBI> is the Davies-Bouldin Index, <pSF> is the pseudo-F statistic, <SSR/SST> is the SSR/SST ratio, and <representative frame list> contains the frame # of the representative frame (i.e. closest to the centroid) for each cluster. Each cluster has a line made up of characters (one for each frame) where '.' means 'not in cluster' and 'X' means 'in cluster'.

[noinfo] Suppress printing of cluster info.

[summarysplit <splitfile>] Summarize each cluster based on which of its frames fall in portions of the trajectory specified by splitframe with format '#Cluster Total Frac C# Color NumInX ... FracX ... FirstX ... RepX':

#Cluster Cluster number starting from 0 (0 is most populated).

Total # of frames in cluster.

Frac Size of cluster as a fraction of the total trajectory.

C# Grace color number.

Color Text description of the color (based on standard XMGRACE coloring).

NumInX Number of frames in Xth portion of the trajectory.

FracX Fraction of frames in Xth portion of the trajectory.

FirstX Frame in the Xth portion of the trajectory where the cluster is first observed.

RepX Best representative frame in the Xth portion of the trajectory for that cluster.

[splitframe <frame>] For summarysplit, frame or comma-separated list of frames to split the trajectory at, e.g. '100,200,300'.

[clustersvtime <filename>] Write number of unique clusters observed in a given time window to <filename>.

[cvtwindow <windowsize>] Window size for clustersvtime output.

[sil <prefix>] Write average cluster silhouette value for each cluster to '<prefix>.cluster.dat' and cluster silhouette value for each individual frame to '<prefix>.frame.dat'.

[silidx {idx|frm}] Choose what indices to write to the cluster silhouette frame file: idx (the default) specifies the sorted index (starting from 0), frm specifies the actual frame number.

[metricstats <file>] When more than one metric in use, print the fraction contribution of each metric to the total distance. This information can be used in conjunction with the wgt keyword to adjust the contribution of each metric to the total distance. It is written to <file> with format:

#Metric FracAv FracSD Avg SD Min Max Description Where #Metric is the metric number, FracAv and FracSD are the average and standard devation of the fraction contribution of that metric to the total distance (taking into account distance type and weights), Avg, SD, Min, and Max are the average, standard devation, minimum, and maximum of the unmodified distance contribution from that metric, and Description is the metric description. This may be slow for large numbers of frames, so it is advisable to run this on a smaller (potentially sieved) number of frames.

[cpopvtime <file> [normpop | normframe]] Write cluster population vs time to <file>; if normpop specified normalize each cluster to 1.0; if normframe specified normalize cluster populations by number of frames.

[lifetime] Create a DataSet with aspect *[Lifetime]* for each cluster; for each frame, have 1 if the cluster is present and 0 otherwise. Can be used with *lifetime* analysis (13.21 on page 276).

Coordinate Output Options:

clusterout <trajfileprefix> Write frames in each cluster to files named <trajfileprefix>.cX, where X is the cluster number.

clusterfmt <trajformat> Format keyword for clusterout (default Amber Trajectory).

singlerepout <trajfilename> Write all representative frames to single trajectory named <trajfilename>.

singlerepfmt <trajformat> Format keyword for singlerepout (default Amber Trajectory).

repout <repprefix> Write representative frames to separate files named <repprefix>.X.<ext>, where X is the cluster number and <ext> is a format-specific filename extension.

repfmt <trajformat> Format keyword for repout (default Amber Trajectory).

repframe Include representative frame number in repout filename.

avgout <avgprefix> Write average structure for each cluster to separate files named <avgprefix>.X.<ext>, where X is the cluster number and <ext> is a format-specific filename extension.

avgfmt <**trajformat**> Format keyword for avgout.

assignrefs In summary/summarysplit, assign clusters to loaded reference structures if RMSD to that reference is less than specified cutoff. This will be printed in summary and summarysplit files as 2 extra columns: 'Name' (reference name) and 'RMS' (RMS to cluster centroid).

[refcut <**rms**>**]** RMSD cutoff in Angstroms.

[refmask <**mask**>**]** Mask to use for RMSD calculation. If not specified the default mask is all heavy atoms.

DataSets Created:

<**name**> Cluster number vs time (color number if gracecolor specified).

<**name**>**[DBI]** Hold final Davies-Bouldin index.

<**name**>**[PSF]** Hold final pseudo-F value.

<**name**>**[SSRSST]** Hold final SSR/SST value.

<**name**>**[NCVT]** (clustersvtime only). Number of unique clusters observed over time.

<**name**>**[Pop]:**<**X**> Cluster X population vs time; index X corresponds to cluster number.

<**name**>**[Lifetime]:**<**X**> (lifetime only). For each cluster X, contain 1 if cluster present that frame, 0 otherwise.

Note cluster population vs time data sets are not generated until the analysis has been run.

Cluster input frames using the specified input data sets (can be any combination of coordinates/COORDS and/or 1D scalar data) with the specified clustering algorithm. For COORDS sets, the distance metric can be RMSD, symmetry-corrected RMSD, or DME. When multiple data sets are present, the total distance can be determined either via the Euclidean (default) or Manhattan method.

In order to speed up clustering of large trajectories, the **sieve** keyword can be used. In addition, subsequent clustering calculations can be sped up by writing/reading calculated pair distances between each frame to/from a file specified by **pairdist** (or "CpptrajPairDist" if **pairdist** not specified).

Example: cluster on a specific distance:

```
distance endToEnd :1 :255
cluster data endToEnd clusters 10 epsilon 3.0 summary summary.dat info info.dat
```

Example: two clustering commands on the CA atoms of residues 2-10 using average-linkage, stopping when either 3 clusters are reached or the minimum distance between clusters is 4.0 for the first, and 8 clusters or minimum distance 2.0 for the second. The first command will write the cluster number vs time to "cnumvtime.dat" and a summary of each cluster to "avg.summary.dat". The second clustering command will use the pairwise distance matrix from the first to speed things up:

```
cluster C1 :2-10 clusters 3 epsilon 4.0 info C1.info out cnumvtime.dat summary avg.summ
cluster C2 :2-10 clusters 8 epsilon 2.0 info C2.info pairdist PW
```

Clustering Success Metrics

The Davies-Bouldin Index (DBI, reported in the **info** file) measures sum over all clusters of the within cluster scatter to the between cluster separation; **the smaller the DBI, the better**. The DBI is defined as the average, for all clusters X, of fred, where fred(X) = max, across other clusters Y, of (Cx + Cy)/dXY. Here Cx is the average distance from points in X to the centroid, similarly Cy, and dXY is the distance between cluster centroids.

The pseudo-F statistic (pSF, reported in the **info** file) is another measure of clustering goodness. It is intended to capture the 'tightness' of clusters, and is in essence a ratio of the mean sum of squares between groups to the mean sum of squares within group. **Higher values of pseudo-F are good**. Generally, one selects a cluster-count that gives a peak in the pseudo-f statistic. Formula: A/B, where A = (T - P)/(G-1), and B = P / (n-G). Here n is the number of points, G is the number of clusters, T is the total distance from the all-data centroid, and P is the sum (for all clusters) of the distances from the cluster centroid.

The SSR/SST (reported in the **info** file) is the ratio of the sum of squares regression (SSR or between sum of squares) and the total sum of squares (SST). The SSR is calculated via the sum of the squared distances of all points within a given cluster to its centroid, and summed together for all clusters. The total sum of squares is the sum of squared distances for all frames to the overall mean. The ratio lies between 0 and 1 and is supposed to give the fraction of explained variance by the data. The ratio should increase with cluster count. **There should be a point at which adding more clusters does not substantially increase SSR/SST**, i.e. the point where increasing the cluster count does not add new information and should not increase further.

The cluster silhouette (**sil**/**silidx** keywords) is a measure of how well each point fits within a cluster. Values of 1 indicate the point is very similar to other points in the cluster, i.e. it is well-clustered. Values of -1 indicate the point is dissimilar and may fit better in a neighboring cluster. Values of 0 indicate the point is on a border between two clusters. The **sil** <**prefix**> keyword will write two files. The first, <prefix>.cluster.dat, which has the format:

```
#Cluster <Si> StdDev
```

Where #Cluster is the cluster number, <Si> is the average silhouette value for all frames in the cluster, and StdDev is the standard deviation of the silhouette value for all frames in the cluster. The second, <prefix>.frame.dat, will contain the silhouette value for each frame grouped by cluster, with indices controlled by the **silidx** keyword (default sorted by ascending silhouette value), e.g.:

```
#C0 Silhouette
#C0      Silhouette
       0 -0.135988
       1 -0.0266746
       2 -0.0167628
       3 0.0609673
       4 0.0649603
       5 0.0835595
#C1      Silhouette
       6 0.319039
       7 0.319785
       8 0.348833
       9 0.358286
       0 0.1376
       9 0.1376
```

The last two lines will contain the overall average silhouette value twice, one at the lowest index and one at the highest. The file is formatted in this way to make it easy to visualize each cluster silhouette relative to the average value in e.g. the XMGRACE plotting program. If the clustering results in one or more cluster with silhouette values completely below the average line, the clustering is likely poor.

Hints for setting DBSCAN parameters with 'kdist'

It is not always obvious what parameters to set for DBSCAN. You can get a rough idea of what to set 'mindist' and 'epsilon' to by generating a so-called "K-dist" plot with the 'kidst <k>' option. The K-dist plot shows for each point (X axis) the Kth farthest distance (Y axis), sorted by decreasing distance. You supply the same distance metric and sieve parameters you want to use for the actual clustering, but nothing else. For example:

```
cluster C0 dbscan kdist 4 rms :1-4@CA sieve 10 loadpairdist pairdist CpptrajPairDist
```

The K-dist plot will be named <prefix>.<k>.dat, with the default prefix being 'Kdist' (in this case the file name would be Kdist.4.dat). The K-dist plot usually looks like a curve with an initially steep slope that gradually decreases. Around where the initial part of the curve starts to flatten out (indicating an increase in density) is around where epsilon should be set; minpoints is set to whatever <k> was. It has been suggested that the shape of the K-dist curve doesn't change too much after Kdist=4, but users are encouraged to experiment.

Using 'dpeaks' clustering

The 'dpeaks' (density peaks) algorithm attempts to find clusters by identifying points in high density regions which are far from other points of high density[37]. There are two ways these points can be chosen. The first and recommended way is manually. In this method, clustering if first run with **choosepoints** not specified to generate a plot containing density versus minimum distance to point with next highest density (the decision graph). Appropriate cut offs for distance and density can then be chosen based on visual inspection; cutoffs should be chosen so that they select points that have both a high density and a high distance to point with next highest density. Clustering can then be run again with **distancecut** and **densitycut** set.

The second way is automatically; cpptraj will attempt to identify outliers in the density vs distance plot based on distance from the running average. Although this only requires a single pass, this method of choosing points is not well-tested and currently not recommended.

The Binary pairwise matrix file format

When NetCDF is not present, the pairwise matrix file will be written in binary. The exact format depends on what version of cpptraj generated the file (since earlier versions had no concept of 'sieve'). The CpptrajPairDist file starts with a 4 byte header containing the characters 'C' 'T' 'M' followed by the version number. A quick way to figure out the version is to use the linux 'od' command to output the first 4 bytes as hexadecimal, e.g.:

```
$ od -t x1 -N 4 CpptrajPairDist 0000000 43 54 4d 02
```

So the CpptrajPairDist file version in the above example is 2.

The next few numbers describe the matrix size and depend on the version.

Version 0: Two 4-byte integers: # of rows and # of elements.

Version 1: Two 8-byte unsigned integers (equivalent to size_t on most systems): # of rows and # of elements.

Version 2: Three 8 byte unsigned integers: original # of rows, actual # of rows, and sieve value.

This is followed by the actual matrix data, stored as a single array of floats (4 bytes). For versions 1 and 2 the number of elements is explicitly stored. For version 2, to calculate the number of matrix elements you need to read:

```
Elements = (actual_rows * (actual_rows - 1)) / 2
```

The cluster pair-distance matrix is an upper-right triangle matrix without the diagonal (in row-major order), so the first element is the distance between elements 0 and 1, the second is between elements 0 and 2, etc.

In version 2 files, if the sieve value is greater than 1 that means original_rows > actual_rows and there is an additional array of characters original_nrows long, with 'T' if the row is being ignored (i.e. it was sieved out) and 'F' if the row is active (i.e. is active in the actual pairwise-distance matrix).

The code that cpptraj uses to read in CpptrajPairDist files is in ClusterMatrix::LoadFile() (ClusterMatrix.cpp).

The NetCDF pairwise matrix format

The default way to write pairwise matrix files as of version 6.0.0 is with NetCDF. This will be set up with the following parameters:

Attributes:

Conventions "CPPTRAJ_CMATRIX"

Version <version string>

MetricDescription <description of the distance metric used to create matrix>

Dimensions:

n_original_frames Number of frames originally in the set (i.e. before sieving).

n_rows Number of rows in the upper-triangle pairwise matrix.

msize Actual size of the matrix; should be (nRows_ * (nRows_-1)) / 2;

Variables:

sieve (integer, no dimension). Sieve value.

matrix (float, dimension msize). The pairwise matrix, flattened to 1 dimension. Index calc is: i1 = i + 1; index = (((nRows_ * i) - ((i1 * i) / 2)) + j - i1);

actual frames (integer, dimension n_rows). The actual frame numbers for which pairwise distances were calculated.

13.6 cphstats

cphstats <pH sets> [name <name>] [statsout <statsfile>] [deprot] [fracplot [fracplotout <file>]]

<**pH sets**> Previously read in pH data sets.

name <**name**> Output set name.

statsout <**statsfile**> Write pH statistics to <statsfile>

deprot If specified, calculate fraction deprotonated instead of protonated.

fracplot If specified, calculate fraction protonated/deprotonated vs pH.

fracplotout <**file**> File to write fraction plots to.

Data Sets Generated

<**name**>**[Frac]:**<**idx**> Fraction protonated/deprotonated for residue <idx>.

Calculate statistics for constant pH simulation data previously read in with ***readdata*** (see 6.11 on page 34). Statistics are calculated for each residue at each input pH. Output format is as follows:

```
Solvent pH is <pH>
<res name> <res num> : Offset <off> Pred <pred> Frac Prot <frac> Transitions <#trans>
...
Average total molecular protonation: <avg>
```

Where <**off**> is offset from predicted, <**pred**> is predicted pH, and <#trans> is the number of transitions. A line is printed for each residue. This functionality is similar to the **cphstats** utility that comes with Amber (see **??** on page ??).

Note that data from constant pH REMD must be sorted prior to use with ***cphstats***. See the ***readensembledata*** (9.23 on page 74) and ***sortensembledata*** (9.30 on page 76) commands for more details.

For example, to read in constant pH data from constant pH REMD, sort and analyze:

```
readensembledata ExplicitRemd/cpout.001 cpin ExplicitRemd/cpin name PH
sortensembledata PH
runanalysis cphstats PH[*] statsout stats.dat fracplot fracplotout frac.agr deprot
```

13.7 corr | correlationcoe

```
corr out <outfilename> <dataset1> [<dataset2>]
     [lagmax <lag>] [nocovar] [direct]
```

out <**outfilename**> Write results to file named <outfilename>. The datasets must have the same # of data points.

<**dataset1**> **[**<**dataset2**>**]** Data set(s) to calculate correlation for. If one dataset or the same dataset is given twice, the auto-correlation will be calculated, otherwise cross-correlation.

[lagmax] Maximum lag to calculate for. If not specified all frames are used.

[nocovar] Do not calculate covariance.

[direct] Do not use FFTs to calculate correlation; this will be much slower.

DataSet Aspects:

[<dataset1>] (Auto-correlation) The aspect will be the name of each of the input data set.

[<dataset1>-<dataset2>] (Cross-correlation) The aspect will be the names of each of the input data sets joined by a dash ('-').

DataSet Aspects:

[coeff] Correlation coefficient.

Calculate the auto-correlation function for data set named <dataset1> or the cross-correlation function for data sets named <dataset1> and <dataset2> up to <lagmax> frames (all if **lagmax** not specified), writing the result to file specified by **out**. The two datasets must have the same # of datapoints.

13.8 crank | crankshaft

```
crank {angle | distance} <dsetname1> <dsetname2> info <string>
      [out <filename>] [results <resultsfile>]
```

angle Analyze angle data sets.

distance Analyze distance data sets.

<dsetname1> Data set to analyze.

<dsetname2> Data set to analyze.

info <string> Title the analysis <string>.

[out <filename>] Write frame-vs-bin to <filename>.

[results <resultsfile>] Write results to <resultsfile>.

Calculate crankshaft motion between two data sets.

13.9 crdfluct

```
[crdset <crd set>] [<mask>] [out <filename>] [window <size>] [bfactor]
```

Calculate atomic positional fluctuations for atoms in **<mask>** over windows of size **<size>**. If **bfactor** is specified, the fluctuations are weighted by $\frac{8}{3}\pi^2$(similar but not necessarily equivalent to crystallographic B-factor calculation). Units are Å, or $Å^2 x \frac{8}{3}\pi^2$ if **bfactor** specified.

13.10 crosscorr

```
crosscorr [name <dsetname>] <dsetarg0> [<dsetarg1> ...] [out <filename>]
```

[name <dsetname>] The resulting upper-triangle matrix is stored with name <dsetname>.

<dsetarg0> [<dsetarg1> ...] Argument(s) specifying datasets to be used.

[out <filename>] Write results to file named <filename>.

Calculate the Pearson product-moment correlation coefficients between all specified datasets.

13.11 curvefit

```
curvefit <dset> { <equation>  |
                  name <dsname> {gauss | nexp <m> [form {mexp|mexpk|mexpk_penalty}} }
         [AX=<value> ...] [out <outfile>] [resultsout <results>]
         [maxit <max iterations>] [tol <tolerance>]
         [outxbins <NX> outxmin <xmin> outxmax <xmax>]
```

<dset> Data set to fit.

<equation> Equation to fit of form <Variable> = <Equation>. See 5.2 on page 26 for more details on equations *cpptraj* understands.

name <dsname> Final data set name (required if using nexp or gauss).

gauss Fit to Gaussian of form A0 * exp(-((X - A1)^2) / (2 * A2^2))

nexp <m> Fit to specified number of exponentials.

form <type> Fit to specified exponential form:

mexp Multi-exponential, SUM(m)[An * exp(An+1 * X)]

mexpk Multi-exponential plus constant, A0 + SUM(m)[An * exp(An+1 * X)]

mexpk_penalty Same as mexpk except sum of prefactors constrained to 1.0 and exponential constants constrained to < 0.0.

AX=<value> Value of any constants in specified equation with X starting from 0 (can specify more than one).

out <outfile> Write resulting fit curve to <outfile>.

resultsout <**results**> Write details of the fit to <results> (default STDOUT).

maxit <**max iterations**> Number of iterations to run curve fitting algorithm (default 50).

tol <**tolerance**> Curve-fitting tolerance (default 1E-4).

outxbins <**NX**> Number of points to use when generating final curve (default same number of points as input data set).

outxmin <**xmin**> Minimum X value to use for final curve (default same number of points as input data set).

outxmax <**xmax**> Maximum X value to use for final curve (default same number of points as input data set).

Perform non-linear curve fitting for the specified data set using the Levenberg-Marquardt algorithm. Any equation form that cpptraj understands (see 5.2 on page 26) can be used, or several preset forms can be used. Similar to Grace (http://plasma-gate.weizmann.ac.il/Grace/), an equation can contain constants for curve fitting termed AX (with X being a numerical digit, one for each constant), and is assigned to a variable which then becomes a data set. For example, to fit a curve to data from a file named Data.dat to a data set named 'FitY':

```
readdata Data.dat
runanalysis curvefit Data.dat \
  "FitY = (A0 * exp(X * A1)) + (A2 * exp(X * A3))" \
  A0=1 A1=-1 A2=1 A3=-1 \
  out curve.dat tol 0.0001 maxit 50
```

To perform the same fit but to a multi-exponential curve with two exponentials:

```
readdata Data.dat
runanalysis curvefit Data.dat nexp 2 name FitY \
  A0=1 A1=-1 A2=1 A3=-1 \
  out curve1.dat tol 0.0001 maxit 50
```

13.12 diagmatrix

```
diagmatrix <matrix name> [out <filename>] [thermo [outthermo <filename>]]
           [vecs <#>] [name <modesname>] [reduce]
           [nmwiz [nmwizvecs <#>] [nmwizfile <filename>]]
```

<**matrix name**> Name of symmetric matrix to diagonalize.

[out <**filename**>**]** Write results to <filename>.

[thermo [outthermo <filename>]] Mass-weighted covariance (mwcovar) matrix only. Calculate entropy, heat capacity, and internal energy from the structure of a molecule (average coordinates, see above) and its vibrational frequencies using standard statistical mechanical formulas for an ideal gas. Results are written to <filename> if specified, otherwise results are written to STDOUT. Note that this converts the units of the calculated eigenvalues to frequencies (cm^{-1}).

[vecs <#>] Number of eigenvectors to calculate. Default is 0, which is only allowed when 'thermo' is specified.

[name <modesname>] Store resulting modes data set with name <modesname>.

[reduce] Covariance (covar/mwcovar/distcovar) matrices only. For coordinate covariance (covar/mwcovar) matrices, each eigenvector element is reduced via Ei = Eix^2 + Eiy^2 + Eiz^2. For distance covariance (distcovar) the eigenvectors are reduced by taking the sum of the squares of each row. See Abseher & Nilges, JMB 1998, 279, 911-920 for further details. They may be used to compare results from PCA in distance space with those from PCA in cartesian-coordinate space.

[nmwiz] Generate output in *.nmd* format file for viewing with NMWiz[38]. See http://prody.csb.pitt.edu/tutorials/nmwiz_tutorial/ for further details.

[nmwizvecs <#>] Number of vectors to write out for nmwiz output, starting with the lowest frequency mode (default 20).

[nmwizfile <filename>] Name of nmwiz file to write to (default 'out.nmd').

[nmwizmask <mask>] Mask of atoms corresponding to eigenvectors - should be the same one used to generate the matrix.

Calculate eigenvectors and eigenvalues for the specified symmetric matrix. This is followed by Principal Component Analysis (in cartesian coordinate space in the case of a covariance matrix or in distance space in the case of a distance-covariance matrix), or Quasiharmonic Analysis (in the case of a mass-weighted covariance matrix). Diagonalization of distance, correlation, idea, and ired matrices are also possible. Eigenvalues are given in cm^{-1} in the case of a mass-weighted covariance matrix and in the units of the matrix elements in all other

cases. In the case of a mass-weighted covariance matrix, the eigenvectors are mass-weighted.

For quasi-harmonic analysis the input must be a mass-weighted covariance matrix. Thermodynamic quantities are calculated based on statistical mechanical formulae that assume the input system is oscillating in a single energy well: see Statistical Thermodynamics by D. A. McQuarrie, particularly chapters 4, 5, and 6 for more details.[39] For an in-depth discussion of the accuracy of thermodynamic parameters obtained via quasi-harmonic analysis see Chang et al..[40]

Note that the maximum number of non-zero eigenvalues obtainable depends on the number of frames used to generate the input matrix; the number of frames should be equal to or greater than the number of columns in the matrix in order to obtain all eigenmodes.

Results may include average coordinates (in the case of covar, mwcovar, correl), average distances (in the case of distcovar), main diagonal elements (in the case of idea and ired), eigenvalues, and eigenvectors.

For example, in the following a mass-weighted covariance matrix of all atoms is generated and stored internally with the name mwcvmat; the matrix itself is written to mwcvmat.dat. Subsequently, the first 20 eigenmodes of the matrix are calculated and written to evecs.dat, and quasiharmonic analysis is performed at 300.0 K, with the results written to thermo.dat.

```
matrix mwcovar name mwcvmat out mwcvmat.dat
diagmatrix mwcvmat out evecs.dat vecs 20 \
           thermo outthermo thermo.dat temp 300.0
```

Output Format

The "modes" or "evecs" output file is a text file with the following format:

```
[Reduced] Eigenvector file: <Type> nmodes <#> width <width>
  <# Avg Coords> <Eigenvector Size>
<Average Coordinates>
```

Where <Type> is a string identifying what kind of matrix the eigenvectors/eigenvalues were determined from, nmodes is how many eigenvectors are in the file, and <Average Coordinates> are in lines 7 columns wide, with each element having width specified by <width>. Then for each eigenvector:

```
 ****
<Eigenvector#> <Eigenvalue>
<Eigenvector Coordinates>
...
```

Where <Eigenvector Coordinates> are in lines 7 columns wide, with each element having width specified by <width>.

13.13 divergence

```
divergence ds1 <ds1> ds2 <ds2>
```

Calculate Kullback-Leibler divergence between specified data sets.

13.14 evalplateau

```
evalplateau [name <set out name>] [tol <tol>] [valacut <valacut>]
        [initpct <initial pct>] [finalpct <final pct>]
        [chisqcut <chisqcut>] [slopecut <slopecut>] [maxit <maxit>]
        [out <outfile>] [resultsout <resultsfile>] [statsout <statsfile>]
        <input set args> ...
```

name <set out name>] Name for output data sets.

tol <tol> Curve fitting tolerance. Default 0.00001.

valacut <valacut> ("Value A cutoff") Cutoff for last half average vs estimated long term value. Default 0.01.

initpct <initial pct> The initial percentage of data to use for the initial density guess. Default 1%.

finalpct <final pct> The final percentatge of data to use for the final density guess. Default 50%.

chisqcut <chisqcut> Curve fit chi-squared cutoff. Defualt 0.5.

slopecut <slopecut> Final slope of fitted curve cutoff. Default 0.000001.

maxit <maxit> Maximum number of iterations to perform during curve fit.

out <outfile> File to write data and fitted curve to.

resultsout <resultsfile> File to write plateau results to.

statsout <statsfile> File to write curve fitting stats to.

<input set args> Data sets to evaluate plateau for.

Data Sets Created

<name>[A0] The A0 (initial density) values.

<name>[A1] The A1 (rate constant) values.

<name>[A2] The A2 (final density) values.

<name>[OneA1] One over the A1 (rate constant) values.

<name>[corr] Curve fit correlation.

<name>[vala] Difference between last half average of data vs final density (A2).

<name>[chisq] Chi-squared of the curve fit.

<name>[pltime] Plateau time (time at which all cutoffs satisfied).

<name>[fslope] Final slope of fitted curve.

<name>[name] Input set legend.

<name>[result] Final result: yes, no, err (error).

Attempt to determine if data has "plateaued", i.e. stopped changing significantly by the end of the set. Currently the defaults are set up to evaluate density data as part of the system preparation protocol described by Roe & Brooks.[41]

13.15 fft

```
fft <dset0> [<dset1> ...] [out <outfile>] [name <outsetname>] [dt <samp_int>]
```

<dset0> [<dset1 ...] Argument(s) specifying datasets to be used.

[out <outfile>] Write results to file named <outfile>.

[name <outsetname>] The resulting transform will be stored with name <outsetname>.

[dt <samp_int>] Set the sampling interval (default is 1.0).

Perform fast Fourier transform (FFT) on specified data set(s). If more than 1 data set, they must all have the same size.

13.16 hausdorff

```
hausdorff <set arg0> [<set arg1> ...]
          [outtype {basic|trimatrix nrows <#>|fullmatrix nrows <#> [ncols <#>]}]
       [name <output set name>] [out <file>] [outab <file>] [outba <file>]
```

<set arg0> ... Input matrix data set(s) to calculate Hausdorff distance(s) for.

[outtype] Specify the output type.

basic Output the Hausdorff distance for each input matrix as scalar 1D data.

trimatrix nrows <#> Output Hausdorff distances for each input matrix as a 2D upper-triangular matrix with the given number of rows. Must have (nrows * (nrows-1)) / 2 input sets.

fullmatrix nrows <#> **ncols** <#> Output Hausdorff distances for each input matrix as a full matrix with the given number of columns and rows. If ncols is not given, use nrows. Must have nrows * ncols input sets.

[name <output set name>] Name of output data sets.

[out <file>] File to write Hausdorff distances to.

[outab <file>] File to write directed A->B Hausdorff distances to.

[outba <file>] File to write directed B->A Hausdorff distances to.

Calculate the symmetric Hausdorff distance for one or more matrices. The results can be saved as an array or as a full or upper-triangular matrix with the specified dimensions. The Hausdorff distance H is determined from:

```
H = max{dH(A,B), dH(B,A)]
```

Where dH(A,B) is the directed Hausdorff distance between sets A and B, etc. Colloquially speaking, the directed Hausdorff distance between A and B is determined as follows:

1. What is the closest approach (distance) of each point in A to any point in B?

2. Choose the largest distance from among those distances.

If desired, the output can be formed into a matrix, which can be useful e.g. when doing multiple 2D rms calculations on different regions of a trajectory. For example, the following input divides a 100 frame trajectory into 10 frame chunks, calcultes the 2D RMS matrix for each chunk, then performs Hausdorff analysis on the resulting matrices and forms a full output matrix.

```
parm ../DPDP.parm7
for beg=1;beg<100;beg+=10 end=10;end+=10 i=1;i++
  loadcrd ../DPDP.nc \$beg \$end name Chunk\$i
done
# Do the 2drms in chunks
for i=1;i<11;i++
  for j=1;j<11;j++
    2drms crdset Chunk\$i reftraj Chunk\$j M\$i.\$j
  done
done
hausdorff M* out hausdorff.fullmatrix.gnu title hausdorff.matrix.gnu \
  outtype fullmatrix nrows 10
runanalysis
```

This type of calculation lends itself well to parallelization. The **parallelanalysis** command can be used to run all the **2drms** calculations in parallel with MPI-enabled cpptraj:

```
parm ../DPDP.parm7
for beg=1;beg<100;beg+=10 end=10;end+=10 i=1;i++
  loadcrd ../DPDP.nc \$beg \$end name Chunk\$i
done
# Do the 2drms in chunks
for i=1;i<11;i++
  for j=1;j<11;j++
    2drms crdset Chunk\$i reftraj Chunk\$j M\$i.\$j
  done
done
parallelanalysis sync
runanalysis hausdorff M* out hausdorff.fullmatrix.gnu title hausdorff.matrix.gnu \
  outtype fullmatrix nrows 10
```

13.17 hist | histogram

```
hist <dataset_name>[,<min>,<max>,<step>,<bins>] ...
[free <temperature>] [norm | normint] [gnu] [circular] out <filename>
[amd <amdboost_data>] [name <outputset name>]
    [traj3d <file> [trajfmt <format>] [parmout <file>]]
[min <min>] [max <max>] [step <step>] [bins <bins>] [nativeout]
```

<dataset_name>[,<min>,<max>,<step>,<bins>]
Dataset(s) to be histogrammed. Optionally, the min, max, step, and/or number of bins can be specified for this dimension after the dataset name separated by commas. It is only necessary to specify the step or number of bins, an asterisk '*' indicates the value should be calculated from available data.

[free <temperature>] If specified, estimate free energy from bin populations using $G_i = -k_B T \ln\left(\frac{N_i}{N_{Max}}\right)$, where K_B is Boltzmann's constant, T is the temperature specified by <temperature>, N_i is the population of bin i and N_{Max} is the population of the most populated bin. Bins with no population are given an artificial barrier equivalent to a population of 0.5.

[norm] If specified, normalize bin populations so the sum over all bins equals 1.0.

[normint] Normalize bin populations so the integral over them is 1.0.

[gnu] Internal output only; data will be gnuplot-readable, i.e. a space will be printed after the highest order coordinate cycles.

[circular] Internal output only; data will wrap, i.e. an extra bin will be printed before min and after max in each direction. Useful for e.g. dihedral angles.

out <**filename**> Write results to file named <filename>.

[amd <**amdboost_data**>**]** Reweight bins using AMD boost energies in data set <amdboost_data> (in KT).

[name <**outputset name**>**]** Output histogram data set name.

[traj3d <**file**>**]** **[trajfmt** <**format**>**]** (3D histograms only) Write a pseudo-trajectory of the 3 data sets (1 atom) to <file> with format <format>.

[parmout <**file**>**]** (3D histograms only) Write a topology corresponding to the pseudo-trajectory to <file>.

[min <**min**>**]** Default minimum to bin if not specified.

[max <**max**>**]** Default max to use if not specified.

[step <**step**>**]** Default step size to use if not specified.

[bins <**bins**>**]** Default bin size to use if not specified.

[nativeout] Do not use cpptraj data file framework; only necessary for writing out histograms with > 3 dimensions.

Create an N-dimensional histrogram, where N is the number of datasets specified. For 1-dimensional histograms the xmgrace '.agr' file format is recommended; for 2-dimensional hisograms the gnuplot '.gnu' file format is recommended; for all other dimensions plot formatting is disabled and the routine uses its own internal output format; this is also enabled if **gnu** or **circular** is specified.

For example, to create a two dimensional histogram of two datasets 'phi' and 'psi':

```
dihedral phi :2@C :3@N :3@CA :3@C
dihedral psi :3@N :3@CA :3@C :4@N
hist phi,-180,180,*,72 psi,-180,180,*,72 out hist.gnu
```

In this case the number of bins (72) has been specified for each dimension and '*' has been given for the step size, indicating it should be calculated based on min/max/bins. The following 'hist' command is equivalent:

```
hist phi psi min -180 max 180 bins 72 out hist.gnu
```

13.18 integrate

```
integrate <dset0> [<dset1> ...] [out <outfile>] [intout <intfile>]
          [name <name>]
```

<dset0> [<dset1> ...] Data set(s) to integrate.

[out <outfile>] If specified, write cumulative sum curves to <outfile>.

[intout <intfile>] If specified, write final integral values to <intfile>.

[name <name>] Output data set(s) name.

DataSets Created:

<name> Final integral values, 1 for each input data set (indexed from 0).

<name>[Sum]:<idx> Cumulative sum curves if out was specified, 1 for each input data set (indexed from 0).

Integrate specified data set(s) using trapezoid integration. If **'out'** is specified write cumulative sum curves to <outfile>. If **'intout'** is specified write final integral values for each set to <intfile>.

13.19 ired

```
ired [relax freq <MHz> [NHdist <distnh>] [noefile <noefilename>]]
     [order <order>] [orderparamfile <orderfilename>]
  tstep <tstep> tcorr <tcorr> out <filename> [norm] [drct]
  modes <modesname> [name <output sets name>] [ds2matrix <file>]
```

[relax freq <MHz>] Should only be used when ired vectors represent N-H bonds; calculate correlation times τ_m for each eigenmode and relaxation rates and NOEs for each N-H vector. 'freq <MHz>' (required) is the Lamor frequency of the measurement.

[NHdist <distnh>] Specifies the length of the NH bond in Angstroms (default is 1.02).

[noefile <noefilename>] File to write the T1, T2, and NOE data to.

[order <order>] Order of the Legendre polynomials to use when calculating spherical harmonics (default 2).

[orderparamfile <orderfilename>] File to write the S2 data to.

[tstep <tstep>] Time between snapshots in ps (default 1.0).

[tcorr <tcorr>] Maximum time to calculate correlation functions for in ps (default 10000.0).

[out <filename> Name of file to write plateau and TauM data. Also the prefix for the .cmt and .cjt files (see below).

[norm] Normalize all correlation functions, i.e., $C_l(t=0) = P_l(t=0) = 1.0$.

[drct] Use the direct method to calculate correlations instead of FFT; this will be much slower.

modes <modesname> Name of previously calculated eigenmodes corresponding to IRED vectors.

[name <name>] Output data set name.

[ds2matrix <file>] If specified, write full delta*S^2 matrix (# IRED vector rows by # eigenmodes columns) to <file>.

DataSets Created:

<name>[S2] S2 order parameters for each vector.

<name>[Plateau] Plateau values for each vector.

<name>[TauM] TauM values for each vector.

<name>[dS2] Full delta*S^2 matrix.

<name>[T1] T1 relaxation values for each vector.

<name>[T2] T2 relaxation values for each vector.

<name>[NOE] NOEs for each vector.

<name>[Cm(t)]:X Cm(t) function for vector X.

<name>[Cj(t)]:X Cj(t) function for vector X.

Peform IRED[17] analysis on previously defined IRED vectors (see vector ired) using eigenmodes calculated from those vectors with a previous 'diagmatrix' command. The number of defined IRED vectors should match the number of eigenmodes calculated. Autocorrelation functions for each mode and the corresponding correlation time τ_m will be written to <filename>.cmt. Autocorrelation functions for each vector will be written to <filename>.cjt. Relaxation rates and NOEs for each N-H vector will be written to <filename> or added to the the end of the standard output. For the calculation of τ_m the normalized correlation functions and only the first third of the analyzed time steps will be used. For further information on the convergence of correlation functions see [Schneider, Brünger, Nilges, *J. Mol. Biol.* **285**, 727 (1999)].

Example of IRED in Cpptraj

In *cpptraj*, IRED analysis[17] can now be performed in one pass (as opposed to the two passes previously required in *ptraj*). First, IRED vectors are defined (in this case for N-H bonds) and an IRED matrix is calculated and analyzed. The IRED vectors are then projected onto the calculated IRED eigenvectors in the ***ired*** analysis command to calculate the time correlation functions. If the parameter *order* is specified, order parameters based on IRED are calculated. By specifying the *relax* parameter, relaxation rates and NOEs can be obtained for each N-H vector. Note that the order of the IRED matrix should be the same as the one specified for IRED analysis.

```
# Define N-H IRED vectors
vector v0 @5 ired @6
vector v1 @7 ired @8
...
vector v5 @15 ired @16
vector v6 @17 ired @18‘
# Define IRED matrix using all previous IRED vectors
matrix ired name matired order 2
# Diagonalize IRED matrix
diagmatrix matired vecs 6 out ired.vec name ired.vec
# Perform IRED analysis
ired relax NHdist 1.02 freq 500.0 tstep 1.0 tcorr 100.0 out v0.out \
     noefile noe order 2
```

13.20 kde

```
kde <dataset> [bandwidth <bw>] [out <file>] [name <dsname>]
    [min <min>] [max <max] [step <step>] [bins <bins>] [free]
    [kldiv <dsname2> [klout <outfile>]] [amd <amdboost_data>]
```

[bandwidth <bw>] Bandwidth to use for KDE; if not specified bandwidth will be estimated using the normal distribution approximation.

[out <file>] Output file name.

[name <dsname>] Output data set name.

[min <min>] Minimum bin.

[max <max>] Maximum bin.

[step <step>] Bin step.

[bins <bins>] Number of bins.

[free] Calculate free energy from bin population.

[kldiv <dsname2> [klout <outfile>]] Calculate Kullback-Leibler divergence over time of <dataset> distribution to <dsname2> distribution. Output to <outfile> if klout specified.

[amd <amdboost_data>] Reweight histogram using AMD boost data from data set <amdboost_data> (in KT).

Histogram 1D data set using a Gaussian kernel density estimator.

13.21 lifetime

```
lifetime [out <filename>] <dsetarg0> [ <dsetarg1> ... ]
      [window <windowsize> [name <setname>]] [averageonly]
      [cumulative] [delta] [cut <cutoff>] [greater | less] [rawcurve]
         [fuzz <fuzzcut>] [nosort]
```

[out <filename>] Write results to file named <filename>, and lifetime curves to 'crv.<filename>'. If performing windowed lifetime analysis, <filename> contains the fraction present over time windows, and 2 additional files are written: 'max.<filename>', containing max lifetime over windows, and 'avg.<filename>', containing average lifetime over windows.

<dsetarg0> [<dsetarg1> ...] Argument(s) specifying datasets to be used.

[window <windowsize>] Size of window (in frames) over which to calculate lifetimes/averages. If not specified lifetime/average will be calculated over all frames.

[name <setname>] Store results in data sets with name <setname>.

[averageonly] Just calculate averages (no lifetime analysis).

[cumulative] Calculate cumulative lifetimes/averages over windows.

[delta] Calculate difference from previous window average.

[cut <cutoff>] Cutoff to use when determining if data is 'present' (default 0.5).

[greater] Data is considered present when above the cutoff (default).

[less] Data is considered present when below the cutoff.

[rawcurve] Do not normalize lifetime curves to 1.0.

[fuzz <fuzzcut>] Ignore changes in lifetime state that are less than <fuzzcut> frames.

[nosort] Do not sort data sets by name.

Data Sets Created:

<**setname**> Number of lifetimes for each set, or if window specified fraction present over time windows.

<**setname**>**[max]** Maximum lifetime for each set, or if window specified maximum lifetime over time windows.

<**setname**>**[avg]** Average lifetime for each set, or if window specified average lifetime over time windows.

<**setname**>**[curve]** Lifetime curves.

The following are created only if window not specified:

<**setname**>**[frames]** Total number of frames lifetime present for each set.

<**setname**>**[name]** Name of each set.

Perform lifetime analysis for specified data sets. Lifetime data can either be determined for the entire set, or for time windows of specified size within the set if **window** specified.

A "lifetime" is defined as the length of time something remains 'present'; data is considered present when above or below a certain cutoff (the default is greater than 0.5, useful for analysis of ***hbond*** time series data). For example, in the case of a hydrogen bond **'series'** data set, if a hydrogen bond is present during a frame the value is 1, otherwise it is 0. Given the hbond time series data set {1 1 1 0 1 0 0 0 1 1}, the overall fraction present is 0.6. However, there are 3 lifetimes of lengths 3, 1, and 2 ({1 1 1}, {1}, and {1 1}). The maximum lifetime is 3 and the average lifetime is 2.0, i.e. (3 + 1 + 2) / 3 lifetimes = 2.0. One can also construct a "lifetime curve", which is constructed as the sum of all individual lifetimes. By default these curves are normalized to 1.0, but the raw curve can be obtained using the **rawcurve** keyword. For the example data set here the raw lifetime curve would be 3 frames long:

```
      1 1 1
      1
      1 1
Curve: 3 2 1
```

By default data sets are sorted by name unless **nosort** is specified. The lifetime command can calculate lifetimes over specific time windows by using the **window** keyword. This can be particularly useful if one wants to get a sense for how lifetimes are changing over the course of very long time series data. In addition, averages can be calculated instead of lifetimes by specifying **averageonly**.

Cumulative averages over windows can be obtained using the **cumulative** keyword, or the change from the average value in the previous window can be obtained using the **delta** keyword.

The **fuzz** keyword can be used to try and smooth the input data by ignoring changes in state that occur for fewer frames than <fuzzcut>. For example, in the above example hbond time series data set there is a one frame change in state between the first and second lifetimes which could be interpreted as a transient breaking of the hydrogen bond. Using a <fuzzcut> value of 1, this one frame change in state would be ignored, and the data set would effectively appear to lifetime as {1 1 1 1 1 0 0 0 1 1}. The state change between the second and third lifetimes is longer than <fuzzcut> (3 frames) and so it would remain.

If **window** is not specified, two files are output: <filename> and crv.<filename>. The file <filename> contains overall lifetime stats for each set with format:

```
#Set <setname> <setname>[max] <setname>[avg] <setname>[frames] <setname>[name]
```

where `<setname>` denotes the total number of lifetimes, `<setname>[max]` denotes the maximum lifetime, `<setname>[avg]` denotes the average lifetime, `<setname>[frames]` denotes the total number of frames present in all lifetimes, and `<setname>[name]` is the data set name. The file crv.<filename> contains the lifetime curves for each set.

If **window** is specified, four files are output: <filename>, max.<filename>, avg.<filename>, and crv.<filename>. <filename> contains the fraction "present" over each time window for each set, max.<filename> contains the maximum lifetime in each time window for each set, avg.<filename> contains the average lifetime over each window for each set, and crv.<filename> contains the overall lifetime curves for each set. For window output, Gnuplot format is recommended.

Example: hbond lifetime analysis

```
parm DPDP.parm7
trajin DPDP.nc
hbond HB out hbond.dat @N,H,C,O series uuseries solutehb.agr \
  avgout hbavg.dat printatomnum
# 'run' is used here to process the trajectory and generate hbond data
run
# Perform lifetime analysis
runanalysis lifetime HB[solutehb] out lifehb.dat
```

Calculate ion lifetimes from hbond over windows of size 100 frames:

```
hbond ION out ion.dat solventdonor :WAT solventacceptor :WAT@O series
run
lifetime HB[solventhb] out ion.lifetime.100.gnu window 100
```

13.22 lowestcurve

```
lowestcurve points <# lowest> [step <stepsize>] <dset0> [<dset1> ...]
                  [out <file>] [name <setname>]
```

<# lowest> Number of lowest points in each bin to average over.

[step <stepsize>] Bin step size

<dset0> [<dset1> ...] Data set(s) to use.

[out <file>] File to write lowest curve to.

[name <setname>] Output lowest curve set name.

Calculate a curve of the average of the # lowest points in bins of stepsize. Essentially each input data set is binned over bins of stepsize, then the lowest <#> points are averaged over for each bin.

13.23 meltcurve

```
meltcurve <dset0> [<dset1> ...] [out <outfile>] [name <outsetname>] cut <cut>
```

Calculate melting curve from input data sets (i.e. fraction 'folded' for each data set) assuming a simple 2-state transition model, using data below <cut>as 'folded' and data above <cut> as 'unfolded'.

13.24 modes

```
modes {fluct|displ|corr|eigenval|trajout|rmsip} name <modesname> [name2 <modesname>]
   [beg <beg>] [end <end>] [bose] [factor <factor>] [calcall]
   [out <outfile>] [setname <name>]
    Options for 'trajout': (Generate pseudo-trajectory)
   [trajout <name> parm <name> | parmindex <#>
     [trajoutfmt <format>] [trajoutmask <mask>]
    [pcmin <pcmin>] [pcmax <pcmax>] [tmode <mode>]]
    Options for 'corr': (Calculate dipole correlation)
   { maskp <mask1> <mask2> [...] | mask1 <mask> mask2 <mask> }
   parm <name> | parmindex <#>
Types of Calculations:
```

fluct RMS fluctuations (X, Y, Z, and total) for each atom across specified normal modes.

displ Displacement of cartesian coordinates in the X, Y and Z directions for each atom across specified normal modes.

corr Dipole-dipole correlation functions. Must also specify maskp (see below).

eigenval Calculate eigenvalue fractions.

trajout Create a pseudo-trajectory along the given mode from the average structure.

rmsip Calculate the root-mean-square inner product between modes specified by name and name2.

Options:

name <modesname> Previously read-in or generated Modes data set name.

[beg <beg>] [end <end>] If modes taken from datafile, beginning and end modes to read. Default for *beg* is 7 (which skips the first 6 zero-frequency modes in the case of a normal mode analysis); for *end* it is 50.

[bose] Use quantum (Bose) statistics in populating the modes.

[factor <factor>] multiplicative constant on the amplitude of displacement/pseudo-trajectory, default 1.0.

[calcall] If specified use all eigenvectors; otherwise eigenvectors associated with zero or negative eigenvalues will be skipped.

[out <outfile>] File to write data results to. If not given results are written to STDOUT.

[setname <name>] Output data set name.

Options for 'trajout':

<name> Output trajectory file name.

[parm <parmfile/tag>|parmindex <#>] Topology file to use (default first Topology loaded).

[trajoutfmt <format>] Output trajectory format.

[trajoutmask <mask>] Mask of atoms that correspond to how modes were originally generated.

[pcmin <pcmin>] Lowest principal component projection value to use for output trajectory.

[pcmax <pcmax>] Highest principal component projection value to use for output trajectory.

[tmode <mode>] Mode to generate pseudo-trajectory for.

Options for 'corr':

[maskp <mask1> <mask2> [...]] If corr, pairs of atom masks (*mask1*, *mask2*; each pair preceded by "maskp" and each mask defining only a single atom) have to be given that specify the atoms for which the correlation functions are desired.

mask1 <mask> mask2 <mask> Instead of maskp, specify two masks; atoms from the first mask will be paired up with atoms from the second mask.

DataSets Created (fluct)

<name>[rmsX] RMS fluctuations in the X direction.

<name>[rmsY] RMS fluctuations in the Y direction.

<name>[rmsZ] RMS fluctuations in the Z direction.

<name>[rms] Total RMS fluctuations.

DataSets Created (displ)

<name>[displX] Displacement in X direction.

<name>[displY] Displacement in Y direction.

<name>[displZ] Displacement in Z direction.

DataSets Created (eigenval)

<name>[Frac] Fraction eigenvalue contributes to overall motion.

<name>[Cumulative] Cumulative fraction.

<name>[Eigenval] Value of eigenvlue.

DataSets Created (rmsip)

<name> Result of RMSIP calculation.

Analyze previously calculated eigenmodes obtained from principal component analyses (of covariance matrices) or quasiharmonic analyses (diagmatrix analysis command). Modes are taken from a previously generated data set (i.e. from ***diagmatrix***) or read in from a data file with ***readdata***. By default, classical (Boltzmann) statistics are used in populating the modes. A possible series of commands would be "**matrix** `covar | mwcovar` ..." to generate the matrix, "`diagmatrix` ..." to calculate the modes, and, finally, "`modes` ...".

For example, to calculate the RMS fluctuations or displacements of the first 3 eigenmodes caluclated from a mass-weighted covariance matrix:

```
matrix mwcovar name mwcvmat out mwcvmat.dat
diagmatrix mwcvmat name evecs vecs 5
modes fluct out rmsfluct.dat name evecs beg 1 end 3
modes displ out resdispl.dat name evecs beg 1 end 3
```

Additionally, dipole-dipole correlation functions for modes obtained from principle component analysis or quasiharmonic analysis can be computed.

```
modes corr out cffromvec.dat name evecs beg 1 end 3 \
      maskp @1 @2 maskp @3 @4 maskp @5 @6
```

or

```
mode corr out cffromvec.dat name evecs beg 1 end 3 mask1 @1,3,5 mask2 @2,4,6
```

If **eigenval** is specified, the fraction contribution of each eigenvector to the total motion is calculated and output with format:

```
#Mode Frac. Cumulative Eigenval
```

where `#Mode` is the eigenvector number, `Frac.` is the eigenvalue over the sum of all eigenvalues, `Cumulative` is the cumulative sum of `Frac.`, and `Eigenval` is the eigenvalue itself. Note that in order to get an idea for how much each eigenvector contributes to all motion, this is best used when all possible eigenvectors have been determined for a system.

In order to visualize eigenvectors, pseudo-trajectories along eigenvectors can be created using average coordinates with the **trajout** keyword. For example, to write a pseudo-trajectory of the first principal component from principal component value of -100 to 100 for a previously calculated Modes data set corresponding to heavy atoms (no hydrogens) for residues 1 to 36:

```
parm ../GAAC.nowat.parm7
readdata evecs.dat
runanalysis modes name evecs.dat trajout test.nc trajoutfmt netcdf \
            trajoutmask :1-36&!@H= pcmin -100 pcmax 100 tmode 1
```

13.25 multicurve

```
multicurve set <dset> [set <dset> ...]
           <dset> { <equation> |
                    name <dsname> nexp <m> [form {mexp|mexpk|mexpk_penalty} }
           [AX=<value> ...] [out <outfile>] [resultsout <results>]
           [maxit <max iterations>] [tol <tolerance>]
           [outxbins <NX> outxmin <xmin> outxmax <xmax>]
```

set <**dset**> **[set** <**dset**> **...]** Data set(s) to fit.

<**equation**> Equation to fit of form <Variable> = <Equation>. See 5.2 on page 26 for more details on equations *cpptraj* understands.

name <**dsname**> Name of output data sets (required if using nexp).

nexp <**m**> Fit to specified number of exponentials.

form <**type**> Fit to specified exponential form:

mexp Multi-exponential, SUM(m)[An * exp(An+1 * X)]

mexpk Multi-exponential plus constant, A0 + SUM(m)[An * exp(An+1 * X)]

mexpk_penalty Same as mexpk except sum of prefactors constrained to 1.0 and exponential constants constrained to < 0.0.

AX=<value> Value of any constants in specified equation with X starting from 0 (can specify more than one).

out <outfile> Write resulting fit curve to <outfile>.

resultsout <results> Write details of the fit to <results> (default STDOUT).

maxit <max iterations> Number of iterations to run curve fitting algotrithm (default 50).

tol <tolerance> Curve-fitting tolerance (default 1E-4).

outxbins <NX> Number of points to use when generating final curve (default same number of points as input data set).

outxmin <xmin> Minimum X value to use for final curve (default same number of points as input data set).

outxmax <xmax> Maximum X value to use for final curve (default same number of points as input data set).

Fit each input data set <dset> to <equation>. See the ***curvefit*** command on page 264 for more details.

13.26 multihist

```
multihist [out <filename>] [name <dsname>] [norm | normint] [kde]
          [min <min>] [max <max>] [step <step>] [bins <bins>] [free <T>]
          <dsetarg0> [ <dsetarg1> ... ]
```

out <filename> Output file.

name <dsname> Name for resulting histogram data sets.

norm (Only used if not kde) Normalize so that max bin is 1.0.

normint (Default for kde) Normalize integral over histogram to 1.0.

kde Use kernel density estimator to construct histogram.

min <**min**> Histogram minimum (default data set minimum).

max <**max**> Histogram maximum (default data set maximum).

step <**step**> Histogram step.

bins <**bins**> Number of histogram bins.

free <**T**> Calculate free energy from bin populations as G = -R * <T> * ln(Ni / Nmax).

<**dsetargX**> Data set argument - may specify more than one.

Histogram each data set separately in 1D. Must specify at least **bins** or **step**.

13.27 phipsi

```
phipsi <dsarg0> [<dsarg1> ...] resrange <range> [out <file>]
```

<**dsargX**> Argument selecting data sets. Can specify more than 1.

resrange <**range**> Residue range to use (actually uses data set index).

[out <**file**>**]** Output file.

Calculate the average and standard deviation of [phi] and [psi] data set pairs, write to <file> with format:

```
#Phi Psi SD(Phi) SD(Psi) Legend
```

Where Phi is the average value of phi, Psi is the average value of psi, SD(Phi) is the standard deviation of phi, SD(psi) is the standard deviation of psi, and Legend contains text describing the phi and psi data sets used in the calculation. Periodicity is taken into account during averaging. The data sets must have been internally labeled as type 'phi'/'psi' and must have a data set index set (actions like dihedral and multidihedral do this automatically). For example:

```
parm ../DPDP.parm7
trajin ../DPDP.nc
multidihedral DPDP phi psi
run
phipsi DPDP[phi] DPDP[psi] out phipsi.dat resrange 1-22
```

13.28 projectdata

```
projectdata evecs <evecs dataset> [name <name>] [out <outfile>] [beg <beg>] [end <end>]
            {[dihedrals <dataset arg>] | [data <dataset arg> ...]}
```

evecs <**dataset name**> Data set containing eigenvectors (modes).

[name <**name**>**]** Output data set name.

[out <**outfile**>**]** Write projections to <outfile>.

[beg <**beg**>**]** First eigenvector/mode to use (default 1).

[end <**end**>**]** Final eigenvector/mode to use (default 2).

[dihedrals <**dataset arg**>**]** (Dihedral covariance only) Dihedral data sets to use in projection; MUST CORRESPOND TO HOW EIGENVECTORS WERE GENERATED.

[data <**dataset arg**>**]** (Data covariance only, e.g. from TICA). 1D data sets to use in projection; MUST CORRESPOND TO HOW EIGENVECTORS WERE GENERATED.

Data Sets Created:

<**name**>:<#> Projection data set for mode <#>.

Project data along previously generated eigenmodes from e.g. PCA or TICA. This is a faster alternative to the ***projection*** command (12.63 on page 204) if only 1D data sets need to be projected.

13.29 regress

```
regress <dset0> [<dset1> ...] [name <name>] [nx <nxvals>]
     [out <filename>] [statsout <filename>]
```

dsetX Data set(s) to perform linear regression for.

name <**name**> Data set name for resulting linear fits.

nx <**nxvals**> Number of X values to use in output data set(s) (ranging from input set min to max X). If not specified, input X values used.

out <**filename**> File to write fit lines to.

statsout <**filename**> File to write fit statistics to.

DataSets Generated:

<**name**>:<**idx**> Output fit line(s) (indexed by input set order if more than one input set).

<**name**>**[slope]**:<**idx**> Output fit line slope(s).

<**name**>**[intercept]**:<**idx**> Output fit line intercept(s).

Perform linear regression on the specified data set(s). The fit line is calculated using either the input X values or <**nxvals**> values ranging from the input set minimum to maximum X. Statistics for the fit(s) are saved to the file specified by **statsout** or reported to STDOUT.

For example, to fit data read in from a file and then create a set using the fit parameters:

```
readdata esurf_vs_rmsd.dat.txt index 1 name XY
runanalysis regress XY name FitXY statsout statsout.dat
createset "Y = FitXY[slope] * X + FitXY[intercept]" xstep .2 nx 100
writedata Y.dat Y
```

13.30 remlog

```
remlog {<remlog dataset> | <remlog filename>} [out <filename>] [crdidx | repidx]
    [stats [statsout <file>] [printtrips] [reptime <file>]] [lifetime <file>]
    [reptimeslope <n> reptimeslopeout <file>] [acceptout <file>] [name <setname>]
       [edata [edataout <file>]]
```

<**remlog dataset**> Previously read-in REM log data.

<**remlog filename**> REM log file name to read in.

[out <**filename**>**]** Write replica/coordinate index versus time to <filename>.

crdidx Print coordinate index vs exchange; output sets contain replica indices.

repidx Print replica index vs exchange; output sets contain coordinate indices.

stats [statsout <**file**>**]** Calculate round-trip statistics and optionally write to <file>.

printtrips Print details of each individual round trip.

[reptime <**file**>**]** Write time spent at each replica to <file>.

[lifetime <**file**>**]** Print lifetime data at each replica to <file>.

[reptimeslope <**n**>**]** Calculate the slope of time spent at each replica every <n> exchanges.

[reptimeslopeout <**file**>**]** File to write reptimeslope output to.

[acceptout <**file**>**]** Write overall exchange acceptances to <file>.

[name <**setname**>**]** Output data set name.

[edata [edataout <file>]] Extract energy data from replica log, optionally write to file.

DataSets created:

<**setname**>:<**idx**> Replica/coordinate index vs exchange.

<**setname**>**[E]**:<**idx**> If 'edata' specified, energy data from replica log.

Analyze previously read in (via ***readdata***) M-REMD/T-REMD/H-REMD replica log data. Statistics calculated include round-trip time, which is the time needed for a coordinate set to travel from the lowest replica to the highest and back, and the number of exchanges each coordinate spent at each replica. For example, to read in REM log data from an Amber M-REMD run and analyze it:

```
readdata rem.log.1.save rem.log.2.save dimfile remd.dim as remlog nosearch
remlog rem.log.1.save stats reptime mremdreptime.dat
```

For an example of ***remlog*** analysis applied to actual REMD data, see Roe et al.[42].

13.31 rms2d | 2drms

```
rms2d [crdset <crd set>] [<name>] [<mask>] [out <filename>]
      [{dme | nofit | srmsd | qrmsd}] [mass]
      [reftraj <traj> [parm <parmname> | parmindex <parm#>] [<refmask>]]
      [corr <corrfilename>]
```

[crdset <crd set>] Name of previously generated COORDS DataSet. If not specified the default COORDS set will be used.

[<mask>] Mask of atoms to calculate 2D-RMSD for. Default is all atoms.

[out <filename>] Write results to <filename>.

[dme] Calculate distance RMSD instead of coordinate RMSD; this is substantially slower.

[nofit] Calculate RMSD without fitting.

[srmsd] Calculate symmetry-corrected RMSD (see 12.85 on page 226).

[qrmsd] Use quaternion RMSD calculation (can be 15-20% faster).

[mass] Mass-weight RMSD.

[reftraj <traj>] Calculate 2D RMSD to frames in trajectory <traj> instead (can also be another COORDS set).

[parm <parmname> | parmindex <#>] Topology to use for <traj>; only useful in conjunction with reftraj.

[<refmask>] Mask of atoms in reference; only useful in conjunction with reftraj.

[corr <corrfilename>] Calculate pseudo-auto-correlation C for 2D-RMSD as $C(i) = \frac{\sum_{j=0}^{j<N-i} \exp(-RMSD(j,j+i))}{N-i}$, where i is the lag, j is the frame #, and N is the total number of frames. An exponential is used to weight the RMSD since 0.0 RMSD is equivalent to correlation of 1.0. This can only be done if reftraj is not used.

DataSet Aspects:

[Corr] (corr only) Pseudo-auto-correlation.

Note: For backwards compatibility with ptraj the command '2drms' will also work.

Calculate the best-fit RMSD of each frame in <crd set> (the default COORDS set if none specified) to each other frame. This creates an upper-triangle matrix named <name> (or a full matrix if **reftraj** specified). The output of the rms2d command can be best-viewed using gnuplot; a gnuplot-formatted file can be produced by giving <filename> a '.gnu' extension. For example, to calculate the RMSD of non-hydrogen atoms of each frame in trajectory "test.nc" to each other frame, writing to a gnuplot-viewable file "test.2drms.gnu":

```
trajin test.nc
rms2d !(@H=) out test.2drms.gnu
```

To calculate the RMSD of atoms named CA of each frame in trajectory "test.nc" to each frame in "ref.nc" (assuming test.nc and ref.nc are using the default topology file):

```
trajin test.nc
rms2d @CA out test.2drms.gnu reftraj ref.nc
```

13.32 rmsavgcorr

```
rmsavgcorr [crdset <crd set>] [<name>] [<mask>] [out <filename>] [mass]
        [stop <maxwindow>] [offset <offset>]
        {reference <ref file> parm <parmfile> | first}
```

[crdset <crd set>] COORDS data set to use (if not specified the default COORDS set will be used).

[<name>] Output data set name.

[<mask>] Atoms to calculate RMS average correlation for.

[out <filename>] Output filename.

[mass] Mass weight the RMSD calculation.

[stop <maxwindow>] Only calculate RMS average correlation up to <maxwindow>.

[offset <offset>] Skip every <offset> windows in calculation.

[first] Use first averaged frame as reference for each window (default).

[reference <ref file> [parm <parmfile>] Use reference file (with specified parm) as reference for each window.

The RMS average correlation[1] (RAC) is calculated as the average RMSD of running-averaged coordinates over increasing window sizes (or lag). Output has format:

```
<WindowSize> <RAC>
```

The first entry has a window size of 1, and so is just the average RMSD of all frames to the specified reference structure. The second entry has a window size of two, so it is the average RMSD of all frames averaged over two adjacent windows to the specified reference, and so on. The RAC will be calculated up to the number of frames minus 1 or the value specified by **stop**, whichever is lower. The offset can be used to speed up the calculation by skipping window sizes. To calculate mass-weighted RMSD specify **mass**. Note that to reduce memory costs it can be useful to strip all coordinates not involved in the RMS fit from the system prior to specifying 'rmsavgcorr'. For example, to calculate the correlation of C-alpha RMSD of residues 2 to 12:

```
strip !(:2-12@CA)
rmsavgcorr out rmscorr.dat
```

The curve generated by RAC decays towards zero due to the way RAC is defined. By the time the "lag" is N-1 (where N is the total number of frames) you have only two averaged coordinates: call them Avg1 (averaged over 1 though N-1 frames) and Avg2 (averaged over 2 through N frames). Barring any extraordinary circumstances the RMSD between Avg1 and Avg2 will almost certainly be quite low.

The RAC is a way to probe the time scales of interesting events. Any deviation from a smoothly decaying curve is an indication that there are some significant structural differences occurring over that time interval. RAC curves can be particularly useful when comparing independent simulations of the same system.

One thing to keep in mind that since the underlying metric is RMSD, it can be sensitive to the reference frame you choose. It may be useful to try looking at both RAC from the first frame, as well as an averaged reference frame. For an example of use see Galindo-Murillo et al.[43], in particular Figure 2.

13.33 rotdif

```
rotdif [outfile <outfilename>] [usefft]
  Options for generating random vectors:
[nvecs <nvecs>] [rvecin <randvecIn>] [rseed <random seed>]
[rvecout <randvecOut>] [rmatrix <set name> [rmout <rmOut>]]
  Options for calculating vector time correlation functions:
[order <olegendre>] [ncorr <ncorr>] [corrout <corrOut>]
  *** The options below only apply if 'usefft' IS NOT specified. ***
  Options for calculating local effective D, small anisotropy:
[deffout <deffOut>] [itmax <itmax>] [tol <tolerance>] [d0 <d0>]
[nmesh <NmeshPoints>] dt <tfac> [ti <ti>] tf <tf>
  Options for calculating D with full anisotropy:
[amoeba_tol <tolerance>] [amoeba_itmax <iterations>]
[amoeba_nsearch <n>] [scalesimplex <scale>] [gridsearch]
  *** The options below only apply if 'usefft' IS specified. ***
  Options for curve-fitting:
[fit_tol <tolerance>] [fit_itmax <max # iterations>]
```

outfile <**outfilename**> File to write all output from rotdif command to.

Options for generating random vectors:

nvecs <**nvecs**> Number of random vectors to generate (default 1000).

rvecin <**randvecIn**> File to read random vectors from (format is 1 per line, 4 columns, <#> <VX> <VY> <VZ>).

rseed <**random seed**> Seed for random number generator (default 80531). Specify -1 to use wallclock time.

rvecout <**randvecOut**> File to write random vectors to (format is 1 per line, 4 columns, <#> <VX> <VY> <VZ>).

rmatrix <**set name**> Data set to read rotation matrices from. Rotation matrices will be used to rotate random vectors.

rmout <**rmOut**> Write rotation matrices to file, 1 per line, frame # followed by matrix in row-major order.

Options for calculating vector time correlation functions:

order <**olegendre**> The order of Legendre polynomials to use when calculating vector time correlation functions (default 2).

ncorr <**ncorr**> Maximum length of time correlation functions in frames. If this is not specified it will be set to (tf - ti) / dt (recommended).

corrout <**corrOut**> If specified write vector time correlation functions to <corrOut>.X with format: <Time> <Px>

Options for calculating local effective D, small anisotropy:

deffout <**deffOut**> File to write out local effective diffusion constants determined in the limit of small anisotropy.

itmax <**itmax**> Maximum number of iterations to determine each local effective diffusion constant (small anisotropy) assuming fit to single exponential form (default 500).

tol <**tolerance**> Tolerance for determining local effective diffusion constant (small anisotropy) assuming fit to single exponential form (default 1E-6).

d0 <**d0**> Initial guess for small anisotropy diffusion constant in radians^2/ns (default 0.03).

nmesh <**NmeshPoints**> Number of points per frame to use when creating cubic-splined-smoothed forms of vector time correlation curves (default 2).

dt <**tfac**> Time interval between frames (used in integrating vector time correlation curves) in ns.

ti <**ti**> Initial time value in ns for integrating the time correlation functions (default 0.0).

tf <**tf**> Final time value in ns for integrating the time correlation functions. It is recommended this be less than the maximum simulation time since the tails of time correlation functions tend to be noisy.

Options for calculating D with full anisotropy:

amoeba_tol <**tolerance**> Tolerance for downhill-simplex minimizer (default 1E-7).

amoeba_itmax <**iterations**> Number of iterations to run downhill-simplex minimizer (default 10000).

amoeba_nsearch <**n**> Number of searches to perform with downhill-simplex minimizer (default 1).

scalesimplex <**scale**> Factor to use when scaling simplexes (default 0.5).

gridsearch If specified, perform a brute-force grid search to attempt to find a better solution for diffusion tensor with full anisotropy (may be expensive).

Evaluate rotational diffusion properties of a molecule over a trajectory according to an expanded version of the procedure laid out by Wong & Case[44]. Briefly, random vectors (representing the orientation of the molecule) are rotated according to rotation matrices obtained from an RMS fit to a reference structure (typically an averaged structure). For each random vector the time correlation function of the rotated vector is calculated using Legendre polynomials of the specified order. The integral over this time correlation function (which may be smoothed using cubic splines to improve the integration) is then used to find the effective diffusion constant (D) in the limit of small anisotropy. Then, using each calculated D, the diffusion tensor is determined with full anisotropy. Finally, a downhill simplex minimizer is used to optimize D with full anisotropy; (this last step is not described in the original paper).

Rotation matrices are generated via an RMS fit to a reference structure (see 12.70 on page 211). It is recommended that the RMS fit be done to an average structure (see 12.9 on page 124). These rotation matrices are used to rotate each random vector M times (where M is the total number of frames), which creates a time series for each random vector. The time correlation functions are calculated for each random vector time series using Legendre polynomials of the specified order (default 2). Calculation of time correlation functions can be sped up by using the OpenMP version of CPPTRAJ. The maximum length of the correlation function (or lag) can be specified by **ncorr** (in frames). If **ncorr** is not specified it will be set internally based on the specified values of **ti**, **tf**, and **dt**; this is recommended. Note that if **ncorr** is specified it should be set to a number less than the total number of frames since noise in time correlation functions increases as **ncorr** approaches the # of frames. The integration over the correlation function is from **ti** (in whatever units are used of **dt**, generally ns; 0.0 ns if not specified) to **tf** (same units as **ti**), with the time between frames specified by **dt**; the final time should be less than the total simulation time (see example below). The relative size of the mesh used with cubic spline interpolation for integration is controlled by **nmesh** (size of the mesh is **ncorr** points * **nmesh**); **nmesh** = 1 means no interpolation, default is 2. Note that if the integral of the correlation function for a vector is negative, that vector will be skipped in subsequent calculations (since it would imply a negative value for effective diffusion).

The iterative solver for effective value of the diffusion constant from the correlation functions is controlled by **itmax**, **tol**, and **d0**, where **itmax** specifies

the number of iterations to perform (default 500), **tol** specifies the tolerance (default 1E-6), and **d0** specifies the initial guess for the diffusion constant in radians^2 / ns (default 0.03). Effective diffusion constants for each random vector can be written out to a file specified by **deffout**. Results are printed to the file specified by **outfile**. Details on the Q and D tensors are given, as well as observed and calculated tau for each random vector. First, results are printed for analysis in the limit of small anisotropy. Next, results are printed for analysis with full anisotropy. The results of the full anisotropic calculation are first given using results from the small anisotropic analysis as an initial guess, followed by the final results after minimization using the downhill simplex (amoeba) minimizer.

Example

There are two important things to keep in mind when using rotdif analysis:

1. When calculating any kind of diffusive property it is best to simulate in the microcanonical (NVE) ensemble with a shorter time step and increased SHAKE tolerance; thermostats and barostats will effect diffusion calculations.

2. Time correlation functions become noisier as the length of the function approaches the maximum. Therefore in general one should choose parameters for the time correlation function that are much shorter than the total simulation length.

For example, given a trajectory 'mdcrd.nc' containing 10000 frames with a total simulation time of 200 ns (so the time between frames is 0.02 ns), to calculate rotational diffusion using 100 vectors using rotation matrices generated via an RMS fit to 'avgstruct.pdb', computing and integrating the time correlation function for each vector from 0 to 5 ns (1/40th of the simulation), and writing out the effective diffusion constants and results to 'deffs.dat' and 'rotdif.out' respectively:

```
reference avgstruct.pdb [avg]
rms R0 @CA,C,N,O ref [avg] savematrices
trajin mdcrd.nc
rotdif nvecs 100 rmatrix R0[RM] \
       ti 0.0 tf 5.0 dt 0.02 deffout deffs.dat \
       outfile rotdif.out
```

13.34 runningavg

```
runningavg <dset1> [<dset2> ...] [name <dsetname>] [out <filename>]
                   [ [cumulative] | [window <window>] ]
```

<dset1> [<dset2> ...] Data set(s) to calculate running average for.

[name <dsetname>] Output running average data set name.

[out <filename>] File to write results to.

[cumulative] Calculate cumulative running average instead.

[window <window>] Size in frames of window over which to calculate running average.

Calculate running average over windows of given size for data in selected data set(s).

13.35 slope

```
slope <dset0> [<dset1> ...] [out <outfile>] [name <name>]
   [type {forward|backward|central}]
```

<dset0> [<dset1> ...] Data set(s) to calculate finite difference for.

[out <outfile>] File to write finite difference curves to.

[name <name>] Output data set(s) name.

[type {forward|backward|central}] Specify type of finite difference to calculate (default forward).

DataSets generated:

<name>:<idx> Output finite difference curves for each input data set (indexed from 0).

Calculate finite differences for each input data set.

13.36 spline

```
spline <dset0> [<dset1> ...] [out <outfile>] [meshsize <n> | meshfactor <x>]
[meshmin <mmin>] [meshmax <mmax>]
```

<dsetX> Data set(s) to perform splining on.

[out <outfile>] Write splined data to <outfile>.

[meshsize<n>] Size of the mesh to use for splining.

[meshfactor <x>] If meshsize is not given, use a mesh of data set size * <x>.

[meshmin <mmin>] Mesh X minimum value.

[meshmax <mmax>] Mesh X maximum value.

Apply cubic splines to the given input data sets to create new data sets.

13.37 statistics | stat

`stat {<name> | ALL} [shift <value>] [out <filename>] [noeout <filename>] [ignorenv] [name <noe setname>]`

<name> Name of data set to analyze.

ALL analyze all data sets.

shift <value> Subtract <value> from all elements in each data set.

[out <filename>] Write analysis results to <filename> (STDOUT if not specified).

[noeout <filename>] (Type 'noe' only) Write summary of NOE results to <filename>.

[ignorenv] (Type 'noe' only) Ignore negative NOE violations (i.e. shorter-than-expected distances).

[name <noe setname>] (Type 'noe' only) Name for output NOE data sets.

DataSet Aspects for type 'noe' output:

[R6] Averaged $1/r^6$distance for each set.

[NViolations] Number of violations based on given bounds for each set.

[AvgViolation] $1/r^6$ averaged distance minus expected distance for each set.

[NOEnames] Name of each set.

Analyze angles, dihedrals, distances, and/or puckers and calculate various properties. More specific analyses can be obtained by labelling distances/dihedrals/puckers (from e.g. the ***distance***, ***dihedral***, ***pucker*** commands or with the ***dataset*** command) with the 'type <label>' keyword:

dihedral type labels: alpha, beta, gamma, delta, epsilon, zeta, chi, c2p h1p, phi, psi, omega, pchi

distance type labels: noe

pucker type labels: pucker

For each input data set, the average, standard deviation, initial and final values will be reported. The cyclic nature of dihedral/pucker data sets is taken into consideration when averaging.

13.37.1 Torsion Analysis

A table will be written in ASCII format showing the distribution of torsion values for each data set. More specific information may be printed based on the set type. Values in the output marked SNB are from those defined by Schneider, Neidle, and Berman.[45] For more information on nucleic acid torsion as pertains to RNA see further work by Schneider et al..[46]

For example, to perform in-depth analysis on some nucleic acid dihedral angles:

```
dihedral g0 out dihedrals.dat :1@O5' :1@C5' :1@C4' :1@C3' type gamma
dihedral d0 out dihedrals.dat :1@C5' :1@C4' :1@C3' :1@O3' type delta
dihedral c0 out dihedrals.dat :1@O4' :1@C1' :1@N9 :1@C4 type chi
analyze statistics all out stat.dat
```

13.37.2 Distance Analysis

A table will be written in ASCII format showing the distribution of distance values < 6.5. If a distance is labled as 'type noe' a compact time series will be printed in ASCII format showing the NOE as strong, medium, or weak. In addition the <r^-6>^(-1/6) averaged value will be reported, as well as the number of upper/lower bound violations. If **'noeout'** is specified, a summary of these results will be written with format:

```
<#NOE> <R6> <Nviolation> <AvgViolation> <Name>
```

Where <#NOE> is an index, <R6> is the <r^-6>^(-1/6) averaged distance, <Nviolation> is the total number of bounds violations, <AvgViolation> is the average difference from expected distance *Rexp* when the distance is violated (note that if not explicitly set, *Rexp* is set to the upper bound when the lower bound is 0.0, or the average of upper and lower bounds otherwise), and <Name> is the data set legend.

For example, the following input could be used to check certain distances for NOE violations:

```
distance :3@HB= :10@HG= type noe noe_medium
distance :3@HE= :10@HG= type noe noe_strong
distance :3@HA :12@HA type noe noe_medium
distance :3@HD= :12@HG= type noe noe_medium
distance :3@HE= :12@HA type noe noe_strong
analyze statistics all out dpdp.noe.dat noeout noe_graph.dat name Res3_NOE
```

13.37.3 Pucker Analysis

A table will be written in ASCII format showing the distribution of pucker phases for each data set.

13.38 ti

```
ti <dset0> [<dset1> ...] {nq <n quad pts> | xvals <x values>}
[name <set name>] [out <file>] [curveout <ti curve file>]
[nskip <#s to skip>]
[avgincrement <#> [avgmax <#>] [avgskip <#>]]
[bs_samples <samples> [bs_points <points>] [bs_seed <#>]
 [bs_fac <factor>]]
```

<dset0> [<dset1> ...] Data set arguments specifying input DV/DL values.

nq <n quad pts> Number of points for Gaussian quadrature integration. Expect one data set per point.

xvals <x values> Comma-separated list of X values for integration. Expect one data set per value.

name <set name> Output data set name.

out <file> File to write results of integration to.

curveout <ti curve file> File to write TI curves to.

nskip <#s to skip> Comma separated list of number of points to skip. For each number given, the TI integration will be repeated.

avgincrement <#> [avgmax <#>] [avgskip <#>] Starting from point 'avgskip' (default 0), repeat the TI integration calculation in increments of <#> up to 'avgmax' (default all points), so 'avgincrement 10' will do points 0-10, 0-20, etc.

bs_samples <samples> [bs_points <points>] [bs_seed<#>] [bs_fac <factor>] Estimate error via bootstrap analysis, repeating the TI integration <samples> times using <points> points or <factor> times the total number of points. Randomize with given seed.

DataSet Aspects:

[TIcurve] Raw TI curve. If 'nskip' index is number of points skipped. If bootstrapping, index is sample index. If 'avgincrement' the index is the number of points.

[SD] For bootstrap analysis, standard deviation of average free energy over samples.

Calculate free energy using DV/DL energies from thermodynamic integration. The results of integration of the DV/DL curve will be written to <**file**>, while the curves themselves will be written to <**ti curve file**>. Use **nq** to specify

number of Gaussian quadrature points; otherwise the lambda values should be specified by **xvals**, where <**x values**> is a comma-separated list.

For example, to perform Gaussian quadrature integration using data sets named 'TIdata', repeating the calculation for various number of skipped data points:

```
ti TIdata nq 9 name Curve out skip.agr curveout curve.agr nskip 0,5,10,15,20,30,40,50
```

13.39 tica

```
tica { crdset <COORDS set name> [mask <mask>] |
       data <input set arg1> ... }
     [lag <time lag>] [map {kinetic|commute|none}]
     [name <output set name>] [out <file>] [cumvarout <file>]
```

crdset <**COORDS set name**> Input coordinates (COORDS) data set.

mask <**mask**> Selected atoms in input coordinates (COORDS) data set.

data <**input set arg1**> Input 1D data set name(s), may specify more than once. If any data set is periodic, all need to be periodic.

lag <**time lag**> TICA lag time in frames.

map {kinetic|commute|none} How to transform the resulting eigenvectors.

kinetic (default) Scale eigenvectors by eigenvalues so that distances in the transformed data approximate kinetic distances; particularly useful if using the projections to cluster.

commute Scale eigenvectors by regularized time scales, sqrt(timescale_i / 2), so that distances in the transformed data will approximate commute distances. Timescales smaller than the lag time are dampened.[47]

none Do not scale eigenvectors.

name <**output set name**> Output data set name.

out <**file**> File to write TICA modes to.

cumvarout <**file**> File to write eigenvalue cumulative variance to.

Perform time-independent correlation analysis (TICA). Similar to principal component analysis (PCA), TICA calculates eigenvectors/eigenvalues (i.e. eigenmodes) from input data sets (either coordinates or a combination of other 1D

data sets). Whereas the eigenvectors from PCA describe the variance in the input data, the eigenvectors from TICA describe the maximal autocorrelation in the input data at the given lag time.[48] The analysis can be performed on either coordinates or 1D data sets; the data sets can either be all periodic (in which case they will be converted to cos/sin form) or not.

13.40 timecorr

```
timecorr vec1 <vecname1> [vec2 <vecname2>] out <filename> [name <dsname>]
          [order <order>] [tstep <tstep>] [tcorr <tcorr>]
          [dplr] [norm] [drct] [dplrout <dplrfile>] [ptrajformat]
```

vec1 <**vecname1**> **[vec2** <**vecname2**>**]** Vector(s) on which to operate. By default the auto-correlation function will be calculated if one vector is specified, and the cross-correlation function will be calculated if two vectors are specified.

out <**filename**> Name of file to write output to.

[name <**dsname**>**]** Name of output vector data sets.

[order <**order**>**]** Order of Legendre polynomials to use; default 2.

[tstep <**tstep**>**]** Time between snapshots (default 1.0).

[tcorr <**tcorr**>**]** Maximum time to calculate correlation functions for (default 10000.0).

[dplr] Output correlation functions $C_l \equiv < P_l/(r(0)^3 r(\tau)^3) >$ and $< 1/(r(0)^3 r(\tau)^3) >$ in addition to the P_l correlation function.

[norm] Normalize all correlation functions, i.e., $C_l(t=0) = P_l(t=0) = 1.0$.

[drct] Use the direct method to calculate correlations instead of FFT; this will be much slower.

[dplrout] (dplr only) Write extra information for each vector related to dplr option to <dplrfile>.

[ptrajformat] Write output in ptraj style (prevents use of data formatting options).

DataSet Aspects:

[P] P<order> correlation function.

[C] C<order> correlation function (dplr only).

DataSet Aspects for dplr only:

[R3R3] <1/(r(0)^{3}r(t)^3> correlation function.

[R] Average magnitude (<R>).

[RRIG] Sqrt(<R^2>).

[R3] <1/R^3>.

[R6] <1/R^6>.

[Name] Vector name.

Calculate time auto/cross-correlation functions for vectors using spherical harmonics theory. NOTE: To calculate direct correlation functions for vectors just use the ***corr*** analysis command. The **norm** keyword will normalize the resulting correlation functions. Note that if **dplr** is specified, several additional data sets with aspects [R], [RRIG], [R3], [R6], and [Name] will be created containing either 1 or 2 values depending on how many vectors were specified.

Examples

Vectors between atoms 5 and 6 as well as 7 and 8 are calculated below, for which auto and cross time correlation functions are obtained.

```
vector v0 @5 @6
vector v1 @7 @8
timecorr vec1 v0 tstep 1.0 tcorr 100.0 out v0.out order 2
timecorr vec1 v1 tstep 1.0 tcorr 100.0 out v1.out order 2
timecorr vec1 v0 vec2 v1 tstep 1.0 tcorr 100.0 out v0_v1.out order 2
```

Similarly, a vector perpendicular to the plane through atoms 18, 19, and 20 is obtained and further analyzed.

```
vector v2 @18,@19,@20 corrplane
timecorr vec1 v3 tstep 1.0 tcorr 100.0 out v2.out order 2
```

13.41 vectormath

```
vectormath vec1 <vecname1> vec2 <vecname2> [out <filename>] [norm] [name <setname>]
           [ dotproduct | dotangle | crossproduct | magnitude | average ]
```

vec1 <**vecname1**> **vec2** <**vecname2**> Vector(s) on which to operate.

[out <**filename**>**]** Name of file to write output to.

[norm] Normalize the vectors; this will affect any subsequent calculations with the vectors. This is turned on automatically if dotangle/magnitude specified.

[name <**setname**>**]** Output data set name.

[dotproduct] (Default) Calculate the dot-product of the two vectors.

[dotangle] Calculate angle from dot-product between the two vectors; vectors will be normalized.

[crossproduct] Calculate cross-product of the two vectors.

[magnitude] Calculate the magnitude of the vectors selected by vec1 (no need to specify vec2).

[average] Calculate the average (over frames) of vectors selected by vec1 (no need to specify vec2).

DataSets created:

<**setname**>**[Dot]** (double) Vector dot product (dotproduct only).

<**setname**>**[Angle]** (double) Angle in degrees from vector dot product (dotangle only).

<**setname**>**[Cross]** (vector) Cross product (crossproduct only).

<**setname**>**[Mag]** (double) Magnitude (magnitude only).

<**setname**>**[Avg]** (vector) Average vector (average only).

Calculate dot product, angle from dot product (degrees), or cross product for specified vectors. Note that **norm** normalizes the vectors themselves; the vectors will remain normalized for subsequent calculations or output. Either **vec1** or **vec2** can be of size 1; in that case each vector in the set with N frames operates on the single vector. For example, if **vec1** is size N and **vec2** is size 1, then each frame of vec1 is operated on the single vector from vec2.

For example, to get the angles between two previously calculated vectors v1 and v2:

```
vectormath vec1 v1 vec2 v2 dotangle out dotproduct.dat name acos(|V1|*|V2|)
```

13.42 wavelet

```
wavelet [crdset <set name>] nb <n scaling vals> [s0 <s0>] [ds <ds>]
        [correction <correction>] [chival <chival>] [type <wavelet>]
        [out <filename>] [name <setname>]
        [cluster [minpoints <#>] [epsilon <value>] [clusterout <file>]
           [clustermapout <file>] [cmapdetail] [kdist] [cprefix <PDB prefix>]
           [overlay <trajfile>] [overlayparm <parmfile>]]
```

[crdset <set name>] COORDS data set to use

nb <n scaling vals> Number of scales. The smaller the number the better resolution, but slower to plot.

[s0 <s0>] The smallest scale of the wavelet function (default 2dt where dt is time between snapshots in ps)

[ds <ds>] Spacing between discrete scales. (Default is 0.25. Smaller value of ds gives finer resolution. The largest values that give adequate sampling in scale for Morlet and Paul are 0.5 and 1.5, respectively)

[correction <correction>] The scale-to-wavelength parameter (1.01 for Morlet, 1.389 for Paul). Automatically set based on wavelet if not otherwise specified.

[chival <chival>] The value of χ^2_2at a particular confidence level

[type <wavelet>] Type of wavelet function to use <morlet> or <paul>

[out <filename>] Write results to file named <filename>

[name <setname>] Store results in data set with name <setname>

[cluster] Perform wavelet clustering i.e. wavelet feature extraction analysis.

- **[minpoints <#>]** Minimum number of points necessary to form a region of interest.
- **[epsilon <value>]** Minimum region of interest size.
- **[clusterout <file>]** Output for clustering (see below).
- **[clustermapout <file>]** Output cluster map (recommended gnuplot format, see below).
- **[cmapdetail]** Instead of the map being smoothed to cluster regions, show full detail.
- **[kdist]** Can be used to determine minpoints and epsilon - see below.
- **[cprefix <PDB prefix>]** Output cluster region PDBs (only containing from minimum to maximum atom and minimum to maximum frame) with given prefix.
- **[overlay <trajfile>]** Create a trajectory that can be overlaid with the original trajectory to highlight atoms of interest. Atoms in cluster regions will get their normal coordinates - all others are set to the common center of mass.
- **[overlayparm <parmfile>]** Topology that can be used with the overlay trajectory.

`<wavelet>: morlet, paul`

Perform the wavelet analysis using fast Fourier transform (FFT) algorithm on specified trajectory and write out to a gnuplot-formatted file named <name.gnu>. The created Wavelet map provides a clear picture of the significant motions which are characterized both in time and space. Note that typically the trajectory in question should have rotational and translational movement removed (via e.g. the ***rms*** command); otherwise these will be reflected in the wavelet analysis results.

Wavelet analysis contains two main steps which performs continues wavelet transform (CWT) and statistical significance testing as proposed by Torrence and Compo[49]. Analysis is executed on one dimensional (1-D) coordinate which is defined as the displacement from the starting position. For each atom, CWT is calculated over a specified range of scales from S_0up to $S_0 2^{(nb-1)ds}$. To obtain the CWT of the trajectory the Fourier transform of atom's displacement and wavelets which scaled by S (S is calculated from: $S = S_0 2^{jds}$; $j = 0, 1, 2, \ldots, nb-1$) is computed and then the inverse Fourier transform of the product of Fourier transforms will be calculated as the CWT. After calculating the wavelet coordinates for all atoms, a significance testing is performed to determine the significance of each wavelet coordinate. For doing this test we need to have an appropriate background spectrum to consider as a mean or expected spectrum and compare our wavelet coordinates against this background. In order to calculate the background spectrum since wavelet spectrum (according to the convolution theorem) follows the Fourier spectrum, the Fourier coefficients over every atom's displacement is calculated using the following formula and a model (μ_k) is constructed on average which Fourier coefficients fit (X_n) is the time series which is the atom's displacement and k is the frequency index[50].

$$f_{k=\frac{1}{N}} \sum_{n=0}^{N-1} \exp\left(\frac{-2\pi i k n}{N}\right) X_n$$

This test is implemented based on the null hypothesis that the assumption is that Fourier coordinates normally distributed around the expected value, then the wavelet coordinates should also be normally distributed. Assuming the expected background spectrum and since the square of a normally distributed variable is chi-square distributed, then the distribution for the square of the absolute values of wavelet coordinates ($|W_{i,k}|^2$ is as follows ($\sigma^2$is the variance of the atom's displacement).

$$\sigma^2 \mu_k \chi_2^2 / 2$$

Then choosing a confidence level we can determine the minimum acceptable value for $|W_{i,k}|^2$to be considered as a significant coordinates at that certain confidence level. In the final map the scales of only those wavelet coordinates which are significantly above the expected distribution are stored.

For example, to perform wavelet analysis on residues 1 to 17 with 40 scaling values starting from scaling of 0.2 with a spacing of 0.25 using the Morlet wavelet:

```
parm nowat.withions.parm7
trajin nowat.image.nc
rms :1-17@C*,N*,O*,P* first mass
wavelet nb 40 s0 0.2 ds 0.25 correction 1.01 chival 1.6094 type morlet \
        :1-17 out wavelet.gnu usemap
```

Wavelet Analysis Feature Extraction

Wavelet analysis feature extraction (WAFEX)[51] uses a density-based clustering algorithm (a modified version of the DBSCAN algorithm) to highlight physical and temporal regions that have significant motions from wavelet mapsand can extract the specific atoms and frames involved in these motions for further analysis. Cluster regions shown in the map will be smoother by default for easier visualization (unless **cmapdetail** is specified). Details of the clustering are provided via the **clusterout** keyword with format:

```
#Cluster [points] [minatm] [maxatm] [minfrm] [maxfrm] [avgval]
```

#**Cluster** Cluster region number.

points Number of points in the cluster.

minatm Starting atom of the region.

maxatm End atom of the region.

minfrm Starting frame of the region.

maxfrm End frame of the region.

avgval Average value of points in the region.

For example, to create a 2D gnuplot map highlight regions of interest called 'cluster.gnu' one could use the following input.

```
parm ../DPDP.parm7
trajin ../DPDP.nc
rms @C,CA,N first
wavelet nb 10 s0 2 ds 0.25 type morlet correction 1.01 chival 0.25 \
        :1-22 name DPDP \
        cluster clustermapout cluster.gnu clusterout cluster.dat \
          minpoints 66 epsilon 10.0
datafile cluster.gnu usemap palette kbvyw
```

Some experimentation with **kdist** may be required to obtain reasonable values for **minpoints** and **epsilon**. See 13.5 on page 259 as well as the Heidari et al paper for further discussion.

14 Analysis Examples

Please note that typically for principal component analysis (PCA) the trajectory needs to be aligned against a reference structure to remove overall global and translation motion. Use the ***rms*** command for this.

14.1 Cartesian covariance matrix calculation and projection (PCA)

After calculating modes, snapshots can be projected onto these in an additional pass through the trajectory. It is very important that the snapshots used when projecting are exactly the same as those used to generate the original covariance matrix. This example takes advantage of the COORDS data set functionality in cpptraj to save snapshots for the purposes of projection.

```
# Step one. Generate average structure.
# RMS-Fit to first frame to remove global translation/rotation.
parm myparm.parm7
trajin mytraj.nc
rms first !@H=
average crdset AVG
run
# Step two. RMS-Fit to average structure. Calculate covariance matrix.
# Save the fit coordinates.
rms ref AVG !@H=
matrix covar name MyMatrix !@H=
createcrd CRD1
run
# Step three. Diagonalize matrix.
runanalysis diagmatrix MyMatrix vecs 2 name MyEvecs
# Step four. Project saved fit coordinates along eigenvectors 1 and 2
crdaction CRD1 projection evecs MyEvecs !@H= out project.dat beg 1 end 2
```

14.2 Dihedral covariance matrix calculation and projection for backbone phi/psi (PCA)

```
parm ../1rrb_vac.prmtop
trajin ../1rrb_vac.mdcrd
# Generation of phi/psi dihedral data
multidihedral BB phi psi resrange 2
run
# Calculate dihedral covariance matrix and obtain eigenvectors
matrix dihcovar dihedrals BB[*] out dihcovar.dat name DIH
diagmatrix DIH vecs 4 out modes.dihcovar.dat name DIHMODES
run
# Project along eigenvectors
```

```
projection evecs DIHMODES out dih.project.dat beg 1 end 4 dihedrals BB[*]
run
```

References

[1] Daniel R. Roe and Thomas E. Cheatham, III. PTRAJ and CPPTRAJ: Software for Processing and Analysis of Molecular Dynamics Trajectory Data. *J. Chem. Theory Comput.*, 9:3084–3095, 2013.

[2] Daniel R. Roe and Thomas E. Cheatham III. Parallelization of CPPTRAJ enables large scale analysis of molecular dynamics trajectory data. *Journal of Computational Chemistry*, 39(25):2110–2117, 2018.

[3] Daniel R. Roe and Christina Bergonzo. PrepareForLeap: An Automated Tool for Fast PDB-to-Parameter Generation. *Journal of Computational Chemistry*, 43:930–935, may 2022.

[4] Melissa E. O'Neill. Pcg: A family of simple fast space-efficient statistically good algorithms for random number generation. Technical Report HMC-CS-2014-0905, Harvey Mudd College, Claremont, CA, September 2014.

[5] Sebastiano Vigna. Further scramblings of Marsaglia's xorshift generators. *Journal of Computational and Applied Mathematics*, 315:175–181, may 2017.

[6] Daniel R. Roe and Bernard R. Brooks. Quantifying the Effects of Lossy Compression on Energies Calculated from Molecular Dynamics Trajectories. *Protein Science*, 2022.

[7] S. Chatterjee, P. G. Debenedetti, F. H. Stillinger, and R. M. Lynden-Bell. A Computational Investigation of Thermodynamics, Structure, Dynamics and Solvation Behavior in Modified Water Models. *J. Chem. Phys.*, 128:124511, 2008.

[8] T. Lazaridis. Inhomogeneous Fluid Approach to Solvation Thermodynamics. 1 Theory. *J. Phys. Chem. B*, 102:3531–3541, 1998.

[9] C. N. Nguyen, T. Kurtzman Young, and M. K. Gilson. Grid Inhomogeneous Solvation Theory: Hydration Structure and Thermodynamics of the Miniature Receptor cucurbit[7]uril. *J. Chem. Phys.*, 137:044101, 2012.

[10] Lieyang Chen, Anthony Cruz, Daniel R. Roe, Andrew C. Simmonett, Lauren Wickstrom, Nanjie Deng, and Tom Kurtzman. Thermodynamic Decomposition of Solvation Free Energies with Particle Mesh Ewald and Long-Range Lennard-Jones Interactions in Grid Inhomogeneous Solvation Theory. *Journal of Chemical Theory and Computation*, page acs.jctc.0c01185, apr 2021.

[11] W. Humphrey, A. Dalke, and K. Schulten. VMD Visual Molecular Dynamics. *J. Molec. Graph.*, 14:33–38, 1996.

[12] D. J. Sindhikara, N. Yoshida, and F. Hirata. Placevent: An Algorithm for Prediction of Explicit Solvent Atom Distribution-Application to HIV-1 Protease and F-ATP Synthase. *J. Comput. Chem.*, 33:1536–1543, 2012.

[13] J.J. Chou, D.A. Case, and A. Bax. Insights into the mobility of methyl-bearing side chains in proteins. *J. Am. Chem. Soc.*, 125:8959–8966, 2003.

[14] C. Perez, F. Lohr, H. Ruterjans, and J.M. Schmidt. Self-Consistent Karplus Parameterization of (3)J couplings depending on the polypeptide side-chain torsion chi(1). *J. Am. Chem. Soc.*, 123:7081–7093, 2001.

[15] P.H. Hunenberger, A.E. Mark, and W.F. van Gunsteren. Fluctuation and Cross-correlation Analysis of Protein Motions Observed in Nanosecond Molecular Dynamics Simulations. *J. Mol. Biol.*, 252:492–503, 1995.

[16] J.J. Prompers and R. Brüschweiler. Dynamic and structural analysis of isotropically distributed molecular ensembles. *Proteins*, 46:177–189, 2002.

[17] J.J. Prompers and R. Brüschweiler. General framework for studying the dynamics of folded and nonfolded proteins by NMR relaxation spectroscopy and MD simulation. *J. Am. Chem. Soc.*, 124:4522–4534, 2002.

[18] M.L. Connolly. Analytical molecular surface calculation. *J. Appl. Cryst.*, 16:548–558, 1983.

[19] Doree Sitkoff, Kim A. Sharp, and Barry Honig. Accurate Calculation of Hydration Free Energies Using Macroscopic Solvent Models. *J. Phys. Chem.*, 98:1978–1988, 1994.

[20] XJ Lu and WK Olson. 3dna: a software package for the analysis, rebuilding and visualization of three-dimensional nucleic acid structures. *NUCLEIC ACIDS RESEARCH*, 31:5108–5121, 2003.

[21] M.S. Babcock, E.P.D. Pednault, and W.K. Olson. Nucleic Acid Structure Analysis. *J. Mol. Biol.*, 237:125–156, 1994.

[22] M. A. El Hassan and C. R. Calladine. Two distinct modes of protein-induced bending in dna. *J. Mol. Biol.*, 282:331–343, 1998.

[23] Wilma K. Olson, Manju Bansal, Stephen K. Burley, Richard E. Dickerson, Mark Gerstein, Stephen C. Harvey, Udo Heinemann, Xiang-Jun Lu, Stephen Neidle, Zippora Shakked, Heinz Sklenar, Masashi Suzuki, Chang-Shung Tung, Eric Westhof, Cynthia Wolberger, and Helen M. Berman. A standard reference frame for the description of nucleic acid base-pair geometry. *J. Mol. Biol.*, 313:229–237, 2001.

[24] C Altona and M Sundaralingam. Conformational analysis of the sugar ring in nucleosides and nucleotides. a new description using the concept of pseudorotation. *J Am Chem Soc*, 94:8205–8212, 1972.

[25] SC Harvey and M Prabhakaran. Ribose puckering - structure, dynamics, energetics, and the pseudorotation cycle. *J Am Chem Soc*, 108:6128–6136, 1986.

[26] D Cremer and JA Pople. A general definition of ring puckering coordinates. *J Am Chem Soc*, 97:1354–1358, 1975.

[27] W. Kabsch and C. Sander. Dictionary of protein secondary structure: pattern recognition of hydrogen-bonded and geometrical features. *Biopolymers*, 22:2577–2637, 1983.

[28] G. Cui, J. M. Swails, and E. S. Manas. SPAM: A Simple Approach for Profiling Bound Water Molecules. *J. Chem. Theory Comput.*, 9:5539–5549, 2013.

[29] J. Weiser, P.S. Shenkin, and W.C. Still. Approximate Atomic Surfaces from Linear Combinations of Pairwise Overlaps (LCPO). *J. Comput. Chem.*, 20:217–230, 1999.

[30] F. P. Buff, R. A. Lovett, and F. H. Stillinger. Interfacial Density Profile for Fluids in the Critical Region. *Phys. Rev. Lett.*, 15:621–623, 1965.

[31] S. W. Sides, G. S. Grest, and M.-D. Lacasse. Capillary waves at liquid-vapor interfaces: A molecular dynamics simulation. *Phys. Rev. E*, 60:6708–6713, 1999.

[32] A. P. Willard and D. Chandler. Instantaneous Liquid Interfaces. *J. Phys. Chem. B*, 114:1954–1958, 2010.

[33] L. B. Pártay, G. Hantal, P. Jedlovszky, Á. Vincze, and G. Horvai. A new method for determining the interfacial molecules and characterizing the surface roughness in computer simulations. Application to the liquid–vapor interface of water. *J. Comput. Chem.*, 29:945–956, 2008.

[34] W. Helfrich. Elastic Properties of Lipid Bilayers: Theory and Possible Experiments. *Z. Naturforsch. C*, 28:693–703, 1973.

[35] Daniel R. Roe and Bernard R. Brooks. Improving the Speed of Volumetric Density Map Generation via Cubic Spline Interpolation. *Journal of Molecular Graphics and Modelling*, 104:107832, 2021.

[36] M. Ester, H. Kriegel, J. Sander, and X. Xu. A Density-Based Algorithm for Discovering Clusters in Large Spatial Databases with Noise. *Proc. Second Int. Conf. Knowledge Disc. Data Mining (KDD-96)*, pages 226–231, 1996.

[37] Alex Rodriguez and Alessandro Laio. Clustering by fast search and find of density peaks. *Science*, 344:1492–1496, 2014.

[38] A. Bakan, L.M. Meireles, and I. Bahar. ProDy: Protein Dynamics Inferred from Theory and Experiments. *Bioinformatics*, 27(11):1575–1577, 2011.

[39] Donald A. McQuarrie. *Statistical Thermodynamics*. Harper and Row, New York, 1973.

[40] Chia-En Chang, Wei Chen, and Michael K. Gilson. Evaluating the Accuracy of the Quasiharmonic Approximation. *Journal of Chemical Theory and Computation*, 1(5):1017–1028, 2005. PMID: 26641917.

[41] Daniel R. Roe and Bernard R. Brooks. A protocol for preparing explicitly solvated systems for stable molecular dynamics simulations. *The Journal of Chemical Physics*, 153(5):054123, aug 2020.

[42] Daniel R. Roe, Christina Bergonzo, and Thomas E. Cheatham III. Evaluation of enhanced sampling provided by accelerated molecular dynamics with hamiltonian replica exchange methods. *J. Phys. Chem. B*, 118(13):3543–3552, 2014.

[43] Rodrigo Galindo-Murillo, Daniel R. Roe, and Thomas E. Cheatham, III. Convergence and reproducibility in molecular dynamics simulations of the DNA duplex d(GCACGAACGAACGAACGC). *Biochim. Biophys. Acta*, 1850:1041–1058, 2015.

[44] V. Wong and D.A. Case. Evaluating rotational diffusion from protein md simulations. *J. Phys. Chem. B*, 112:6013–6024, 2008.

[45] B. Schneider, S. Neidle, and H. M. Berman. Conformations of the sugar-phosphate backbone in helical dna crystal structures. *Biopolymers*, 42(1):113–124, 1997.

[46] B. Schneider, Z. Moravek, and H. M. Berman. Rna conformational classes. *Nucleic Acids Res.*, 32(5):1666–1677, 2004.

[47] Frank Noé, Ralf Banisch, and Cecilia Clementi. Commute maps: Separating slowly mixing molecular configurations for kinetic modeling. *Journal of Chemical Theory and Computation*, 12(11):5620–5630, 2016.

[48] Guillermo Pérez-Hernández, Fabian Paul, Toni Giorgino, Gianni De Fabritiis, and Frank Noé. Identification of slow molecular order parameters for Markov model construction. *The Journal of Chemical Physics*, 139(1):015102, 07 2013.

[49] C. Torrence and G. P. Compo. A practical guide to wavelet analysis. *Bull. Am. Meteorol. Soc.*, 79(1):61–78, 1998.

[50] N. C. Benson and V. Dagget. Wavelet analysis of protein motion. *Int. J. Wavelets Multi.*, 10(4), 2012.

[51] Z. Heidari, D. R. Roe, R. Galindo-Murillo, J. B. Ghasemi, and T. E. Cheatham, III. Using Wavelet Analysis To Assist in Identification of Significant Events in Molecular Dynamics Simulations. *J. Chem. Inf. Model.*, 56:1282–1291, 2016.