ELSEVIER

MD Display: An interactive graphics program for visualization of molecular dynamics trajectories

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MD Display was developed as a means of visualizing molecular dynamic trajectories generated by Amber.[1] The program runs on Silicon Graphics workstations, and features a simple user interface, and convenient display and analysis options. The program has now been extended to accept input from several other molecular dynamics programs.

Keywords: *molecular graphics, molecular dynamics animation*

INTRODUCTION

Macromolecular molecular dynamics (MD) calculations generate a large amount of data, in the form of trajectories consisting of hundreds or thousands of frames of atomic coordinates. Graphical display of such trajectories is very helpful, both as a visual check of the validity of the dynamics calculation, and as a means of focusing on particular regions, motions, or properties of interest. Visualization is complementary to various numerical analyses, such as calculation of energies and thermodynamic quantities, and may assist the investigator in relating calculated quantities to molecular motions.

We describe here a program, MD Display, which was initially written for the purpose of viewing MD trajectories calculated using Amber.[1] Amber MD calculations are typically performed in batch mode, possibly on a remote compute server. Therefore, it has always made sense to separate the calculation from the display functions; furthermore this allows the display program to move freely in the time coordinate. MD Display was written in C, and takes advantage of the 3D graphics capabilities of Silicon Graphics IRIS workstations, and runs on this platform under IRIX versions 4.0 through 5.3. Dynamic memory allocation is used, avoiding fixed limits on the number of dynamics frames that may be displayed. The program now includes interfaces allowing it to read MD trajectories from CHARMM,[2] Discover,[3] and GROMOS.[4] A variant of the program (NM Display) may be used to view normal mode calculations computed by the Amber "nmode" program.

The Color Plate for this article is on p. 32.

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USER INTERFACE

The objectives in the design of the user interface to MD Display were (1) clear presentation of the molecular structures, with an uncluttered display and use of antialiasing, z-buffering, depth cueing, and support for stereo viewers, (2) intuitive manipulation of views through a virtual trackball and on-screen scale and clipping plane controls, (3) flexible control of frame animation, and (4) simple control of display options and other features. MD Display allows the user to concentrate on the models, rather than details of program operation. The screen layout is shown in Color Plate 1. A column of buttons at the left of the display may be used to control the display options, either with immediate effect, or in certain cases after an atom selection is entered. This selection may be accomplished either by picking atoms from the screen or by typing a selection using a molecule:residue@atom syntax akin to that used by Midas.[5] While in stereo viewer mode, atom picking may be done using a 3-D cursor, which can be moved on all three axes; when activated by an on-screen button the cursor can be translated by pressing the middle mouse button and moving the mouse. Atom picks are restricted to atoms that are fairly close to the cursor's Z location while the usual X–Y selectivity applies. (Programmers will realize that this 3-D cursor is actually a graphical object in 3-space, and the system cursor is blanked while in this mode. The program examines the transformed Z coordinates of picked atoms to enforce Z selectivity. The 3-D cursor is constrained to remain within the clipping planes to prevent its becoming "lost" in the Z dimension.) Z-Clipping controls, which are presented as a view from the top ($+y$) direction in a small region at the

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lower left when needed, provide both individual clipping plane adjustment and slicing with constant z thickness. Another button allows selection of mono, pair, stereo viewer, and 3-axis views. Scaling and frame animation are handled by sliders near the bottom of the window. Labels may be displayed at the residue and atom level. The window may be resized in the usual manner for X Windows. The simplicity of the user interface is in contrast to many user interfaces to multipurpose modeling programs, which involve layered menus with a plethora of options. We feel that these aspects of MD Display can easily be learned in the first session simply by experimenting with the options.

INPUT

A preprocessor is included with MD Display, in order to handle various output files from the computational programs, and produce a consistent input for the display program. Specifically, the preprocessor can read: Amber-formatted topology files (from PARM) together with formatted coordinate sets (from MINMD, SANDER, or GIBBS), CHARMM 22-formatted PSF files, Discover history files, or GROMOS molecular topology files together with GROMOS trajectory files. The preprocessor can also read structures from Brookhaven Protein Data bank[6] files, as single frames, together with an optional molecular surface file such as that generated by the Connolly MS program.[7] A utility is also provided that allows a pseudotrajectory to be constructed from a collection of PDB files. The preprocessor allows selection of starting and ending frames from a trajectory, and allows selection of every Nth frame. Periodic boundary conditions are handled, and there is an option to prevent solvent molecules from jumping from one edge to the opposite, which can be a visually annoying consequence of periodic boundary conditions. Output from the preprocessor is a set of three compact binary files that become inputs to the display program. It typically takes a few seconds to a couple of minutes to preprocess MD trajectories. For example, a system with ~10000 atoms and 100 frames in the trajectory will require less than 1 min on a current RISC workstation.

FEATURES

In addition to standard display options such as coloring and labeling, MD Display has several features suited to analysis of atomic motions.

Animation control

The speed and direction of animation are controlled by the user with a slidebar at the lower right of the window. It is possible to freeze the display on one frame and single step in either direction through the frame sequence. Frame animation is also frozen when translation or rotation are performed via the virtual trackball. All other controls remain available during frame animation. It is possible to superimpose several frames on the screen at one time, creating a "smear" image. This is useful for comparing several conformations or for estimating the amplitudes of atomic motions. There is also a "hyperspeed" mode, in which only every Nth frame is displayed, where the increment N is selectable.

Low-pass filtering

If the user is interested only in the low-frequency motions of the atoms, a low-pass filtering option can be utilized. This filtering is accomplished by treating each atomic coordinate as an independent, time-varying "signal." Each signal is filtered in the time domain with a finite impulse response (FIR) filter, and the resulting atomic trajectories are then displayed. The FIR filters are implemented with a simple convolution routine that calculates

$$x_f[n] = x_u[n] * h[n]$$

where $x_f[n]$ is the filtered coordinate trajectory, $x_u[n]$ is the unfiltered coordinate trajectory, $h[n]$ is the impulse response for the filter, and the asterisk ($*$) represents convolution.

With convolution, each element of $x_f[]$ is calculated as

$$x_f[n] = \sum_{k=0}^{N-1} (h[k]\, x_u[n-k])$$

where N is the length of $h[n]$.

Basically, each value $x_f[n]$ is a weighted average of a finite number of values from $x_u[]$, with the weighting coefficients specified by $h[]$. The $h[n]$ coefficients are calculated as the inverse Fourier transform of the desired frequency response for the filtering, in this case a low-pass filter. Unfortunately, the inverse Fourier transform of an "ideal" low-pass filter extends to infinity (i.e., we would have an infinite number of weighting coefficients). However, the magnitude of the coefficients quickly approaches zero, so at the cost of a small amount of error, we can truncate the impulse response function $h[]$ to a finite number of elements N; hence the name *finite impulse response filter*. In practice, the $h[]$ coefficients can be calculated directly and easily from the desired low-pass cutoff frequency (which is specified by the user when the filtering option is chosen in the DISPLAY program); no inverse Fourier transform is actually performed. Detailed information about FIR filtering can be found in Oppenheim and Schafer.[8] FIR processing was chosen over fast Fourier transform processing because the two methods were roughly equivalent in terms of performance for this application, and the FIR code is much simpler, dealing only with real numbers.

Low-pass filtering is useful mainly for removing high-frequency (100 cm^{-1} and up) bond and angle vibrations, which can obscure low-frequency motions such as large-scale torsions and conformational changes. However, improper use of low-pass filtering can lead to physically unreasonable results. For example, if the trajectory of a rotating methyl group is averaged over one or more full rotations, the filtered trajectory of the hydrogen atoms will collapse toward the axis of rotation.

Geometry measurements

The user may monitor a reconfigurable number of interatomic distances, angles, and dihedrals, which are updated during frame animation. The numerical measures are reported at the upper right, while each distance, angle, or

dihedral is highlighted in the main display with dashed yellow lines, etc.

Hydrogen bonds

Hydrogen bonds can be identified (again, with dashed yellow lines) as they form and dissolve, based on donor–acceptor distances. The position of explicit hydrogen atoms is ignored, however, so it is possible to examine the position of a hydrogen in relation to the donor–acceptor vector.

Ramachandran plot

If the user is interested in observing the changes in the ϕ–ψ values for a protein throughout the trajectory, a resizable window containing a Ramachandran plot can be opened on top of the normal display. The Ramachandran plot is animated synchronously with the main display. The data points in the plot can be picked with the mouse to reveal what residue they represent. Data points that lie outside of the energetically reasonable regions in ϕ–ψ space are automatically labeled with their residue number to aid identification.

PostScript output

For hardcopy or presentations, a color or black-and-white PostScript file can be created that contains an image of the current frame. Depth cueing may be simulated via varying line thickness in the output if desired.

AVAILABILITY

The program (version 2.0) including full source code is available from the Quantum Chemistry Program Exchange,[9] and is also included with Amber releases from Oxford Molecular Group PLC.

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