VMD User's Guide

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Description

The VMD User's Guide describes how to run and use the molecular visualization and analysis program VMD. This guide documents the usage of both the graphical user interface and the text console interface for displaying and grapically manipulating molecules, and describes how to customize the appearance and behavior of VMD for each user.

[1] http://www.ks.uiuc.edu/

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Chapter 1

Introduction

VMD is a molecular graphics program designed for the interactive visualization and analysis of biopolymers such as proteins, nucleic acids, lipids, and membranes. Currently VMD runs on SGI workstations with IRIX 5.3 or higher, Hewlett-Packard workstations with HP-UX 10.20, Sun workstations with Solaris 2.6 or higher, IBM RS/6000 workstations with AIX 4.3 or higher, Compaq Alpha workstations running Tru64 Unix 4.0E or higher, PC's running Linux, and PC's running Windows 95/98/NT/ME/2000. Online information about VMD is available from:
`http://www.ks.uiuc.edu/Research/vmd/`

List of key VMD features:

- **General molecular visualization**
  At its heart, this program is a general application for displaying molecules containing any number of atoms. It is similar in basic capabilities to commercial programs such as Quanta and non-commercial programs such as RasMol, XMol, and Ribbons. It can read PDB files or use Babel (if available) to convert other formats automatically. Once loaded, user-defined subsets of the molecule can be displayed in various ways including licorice, ribbons, van der Waal spheres, and molecular surfaces. The display can be saved directly to a postscript file or in a format suitable for use by ray tracing programs such as Raster3D, POV, and Rayshade.

- **Visualization of dynamic molecular data**
  VMD can read molecular trajectories from Charmm DCD, X-PLOR DCD, Gromacs, and Amber files, or it can acquire timesteps from a running molecular dynamics program. The data can be used to animate the molecule or to plot the change in molecular properties such as interatomic distances, angles, or dihedrals over time.

- **Display and control of molecular dynamics simulations**
  VMD can be used as a graphical front end to a molecular dynamics (MD) program running on a remote supercomputer or high-performance workstation. VMD can interactively display and control the MD simulation as the simulation is running. The user can disconnect from the simulation and let it continue, reattach to a running simulation, or halt the MD program.

- **Support for several input and display (output) devices**
  A number of different visual display and control systems are supported in addition to the usual monitor, keyboard, and mouse. The VRPN tracker library is used to get position and orientation information from a wide variety of spatial input devices, including magnetic

trackers, haptic feedback devices, wands, dial boxes, etc. An interface to the CAVE library has been developed for use in many different types of stereo projection facilities.

- **Tcl scripting language**
  VMD uses the freely available Tcl scripting language for processing text commands. This is a very common and popular language which contains variables, loops, subroutines, and much more.

- **Molecular analysis commands**
  Many new Tcl commands have been added for doing molecular analysis. These include methods to extract information about a set of atoms and molecules, vector and matrix routines for coordinate manipulation, and functions for computing values like the center of mass and radius of gyration.

1.1 For more information on BioCoRE, MDTools, NAMD, and VMD

VMD is part of a suite of tools developed by the Theoretical Biophysics group at the University of Illinois.

- BioCoRE
  BioCoRE is a web-based collaborative environment for structural biology which provides tools to allow collaboration between researchers down the hall or around the world. Anyone with access to the internet and a standard web browser can join BioCoRE and create or be added to research projects, and information about a particular project is shared among all members of that project. BioCoRE is accessed through a Java applet which includes instant messaging and notification of project updates.

  BioCoRE currently provides tools in three toolboxes. The Workbench toolbox provides access to structural biology applications such as simulation and visualization programs. The Notebook toolbox supplies a message board where users store project notes. The Conferences toolbox allows interactive text-based chats, which are also archived to the message board for future reference. Soon, the Documents toolbox will provide tools to assist in joint preparation of publications.

  BioCoRE is currently accessible to users through the BioCoRE server at UIUC, and a code release is planned which will allow sites to run their own servers. Because BioCoRE is web-based, updates and new features are automatically available every time the user logs in. More information is available at the BioCoRE home page[1]

- MDTools
  JMV is an easy-to-use Java-based molecular viewer which uses Java3D to provide hardware accelerated 3D rendering of molecules. JMV is designed as component software, and can be used within other programs, or as a standalone application. JMV is implemented as a Java Bean, and can be used in the standard Bean-capable development tools. JMV can be used as an applet to provide in-browser molecular visualization capabilities, in situations where VMD is overkill for the task. More information is available at the JMV home page[2]

[1] http://www.ks.uiuc.edu/Research/biocore
[2] http://www.ks.uiuc.edu/Development/jmv

- MDTools
  MDTools is a collection of programs, scripts, and utilities provided for researchers to make various modeling and simulation tasks easier, and to provide basic code and utilities which can be built up into larger toolsets. Each tool, script, or library has its own separate distribution, documentation, etc. The programs in this collection are provided for the benefit of the research community, but are not officially supported unless otherwise stated. Each program may have a software license and/or citation suggestions which should be listed on its web page. More information is available at the MDTools home page[3]

- NAMD
  A parallel, object-oriented molecular dynamics code designed for high-performance simulation of large biomolecular systems. NAMD uses the CHARMM force field and file formats compatible with both CHARMM and X-PLOR. NAMD supports both periodic and non-periodic boundaries with efficient full electrostatics, multiple timestepping, constant pressure and temperature ensemble simulation methods. NAMD provides several methods of steering a simulation through the application of additional forces, including the ability to connect directly to VMD for interactive steering of a live simulation. NAMD is distributed free of charge and includes source code. More information is available at the NAMD home page[4]

- Structural Biology Software Database
  The Structural Biology Software Database contains programs which are thought to be of interest to researchers in the fields of structural biology, quantum chemistry, and bioinformatics. The database entries are contributed by users, and are moderated to provide a high quality resource. More information is available at the Structural Biology Software Database home page[5]

- VMD
  A general molecular visualization program capable of interactive display and concurrent control of a molecular dynamics simulation running on a remote computer. VMD uses an object-oriented design, and is written in C++. This document describes VMD. More information is available at the VMD home page[6]

For more on any of the individual software efforts, BioCoRE, MDTools, NAMD, or VMD, see the Theoretical Biophysics Group WWW home page[7].

1.2 Contacting the authors

The current authors of VMD are Justin Gullingsrud, David Norris, and John Stone. We are very interested in and grateful for any user comments and reports of program bugs or inaccuracies. If you have any suggestions, bug reports, or general comments about VMD, please send them to us at `vmd@ks.uiuc.edu`.

[3] http://www.ks.uiuc.edu/Development/MDTools
[4] http://www.ks.uiuc.edu/Researach/namd
[5] http://www.ks.uiuc.edu/Development/biosoftdb/
[6] http://www.ks.uiuc.edu/Researach/vmd
[7] http://www.ks.uiuc.edu/

1.3 Credits and Program Reference

The authors request that any published work or images created using VMD include the following reference:

Humphrey, W., Dalke, A. and Schulten, K., "VMD - Visual Molecular Dynamics" *J. Molec. Graphics* **1996**, *14.1*, 33-38.

VMD has been developed by the Theoretical Biophysics group at the University of Illinois and the Beckman Institute. The main authors of VMD are A. Dalke, J. Gullingsrud, W. Humphrey, B. Isralewitz S. Izrailev, D. Norris, J. Stone, J. Ulrich. This work is supported by grants from the National Institutes of Health (grant number PHS 5 P41 RR05969-04), the National Science Foundation (grant number BIR-9423827 EQ), and the Roy J. Carver Charitable Trust.

1.4 Copyright and Disclaimer

VMD is Copyright © 1995-2001 Theoretical Biophysics Group and the Board of Trustees of the University of Illinois

Portions of this code are copyright © 1997-1998 Andrew Dalke.

The terms for using, copying, modifying, and distributing VMD are specified by the VMD License. The license agreement is distributed with VMD in the file LICENSE. If for any reason you do not have this file in your distribution, it can be downloaded from:
`http://www.ks.uiuc.edu/Research/vmd/current/LICENSE.html`
Some of the code and executables used by VMD have their own usage restrictions:

- STRIDE
  STRIDE, the program used for secondary structure calculation, is free to both academic and commercial sites provided that STRIDE will not be a part of a package sold for money. The use of STRIDE in commercial packages is not allowed without a prior written commercial license agreement. See `http://www.embl-heidelberg.de/argos/stride/stride_info.html`

- SURF
  The source code for SURF is copyrighted by the original author, Amitabh Varshney, and the University of North Carolina at Chapel Hill. Permission to use, copy, modify, and distribute this software and its documentation for educational, research, and non-profit purposes is hereby granted, provided this notice, all the source files, and the name(s) of the original author(s) appear in all such copies.
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  This software was developed and is made available for public use with the support of the National Institutes of Health, National Center for Research Resources under grant RR02170.
  See `ftp://ftp.cs.unc.edu/pub/projects/GRIP/SURF/surf.tar.Z`

- url_get
  The Perl script url_get, was written by Jack Lund at the University of Texas as Austin. There appear to be no restrictions on its use.

- Python
  Python is made available subject to the terms and conditions in CNRI's License Agreement. This Agreement together with Python may be located on the Internet using the following unique, persistent identifier (known as a handle): 1895.22/1012. This Agreement may also be obtained from a proxy server on the Internet using the following URL: `http://hdl.handle.net/1895.22/1012`

- PCRE
  The Perl Compatible Regular Expressions (PCRE) library used in VMD was written by Philip Hazel and is Copyright (c) 1997-1999 University of Cambridge.
  Permission is granted to anyone to use this software for any purpose on any computer system, and to redistribute it freely, subject to the following restrictions:
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  3. Altered versions must be plainly marked as such, and must not be misrepresented as being the original software.
  4. If PCRE is embedded in any software that is released under the GNU General Purpose Licence (GPL), then the terms of that licence shall supersede any condition above with which it is incompatible.

- Tachyon
  The Tachyon ray tracing system distributed with VMD was written by John E. Stone and is Copyright (c) 1994-2001 by John E. Stone. Please see the current distribution of Tachyon for redistribution and or licensing information outside of VMD use. Permission is granted to use Tachyon freely along with VMD.

1.5 Registering VMD

VMD is made available free of charge for all interested end-users of the software (but please see the Copyright and Disclaimer notices). Redistribution of the software to third parties may require a special license, please check the current VMD license agreement for details. We would like to request that you register with us that you are using VMD. This is so that we can maintain some idea of the number of users of the program and so that we know who to contact about program updates, bug fixes, etc. Registration is now part of our software download procedure, so once you've filled out the forms on the VMD download area you are finished.

1.6 Acknowledgments

The authors would particularly like to thank those individuals who have contributed improvements to VMD in the form of new features or entire replacement codes for old features. Special thanks go to Andrew Dalke, Paul Grayson, and Charles Schwieters for their VMD contributions. The entire VMD user community now benefits from your contributions.

The authors would like to thank the members of the Theoretical Biophysics group, past and present, who have helped tremendously in making suggestions, pushing for new features, and trying out bug-ridden code. Thanks go to Alexander Balaeff, Daniel Barsky, Tom Bishop, Ivo Hofacker, Xiche Hu, Barry Israeliwitz, Dorina Kosztin, Ilya Logunov, Jim Phillips, Ari Shinozaki, Svilen Tzonev, Willy Wriggers, Dong Xu, Feng Zhou. Thanks also to all of you who have tried out the program.

Many external libraries and packages are used in VMD, and the program would not be possible without them. The authors wish to thank Jon Leech for the code to compute the uniform point distributions; John Ousterhout and the other authors of the Tcl and Tk packages; the authors of the VRPN library from the University of North Carolina; Amitabh Varshney, author of SURF, also from UNC; Dmitrij Frishman at EMBL for developing STRIDE; Jack Lund for the url_get perl script; and Ethan Merrit from the University of Washington for developing the algorithm for drawing ribbons.

We also received invaluable assistance from people who got the source code and sent in patches and explicit bug reports. The VMD developers would like to thank Axel Berg, Andrew Dalke, Rick Kufrin, Joe Landman, Clare Macrae, Lukasz Salwinski, Stephen Searle, Charles Schwieters, Michael Tiemann, Raymond de Vries, and Simon Warfield for their bug fixes and correspondence.

1.7 Future Plans

Following is a list of features we would like to add. They will be implemented as they are needed, but some will not be done until the next major version.

- Improve PDB reader to use more of the information present in the PDB file, especially secondary structure information.
- append and delete specific atoms
- provide improved user control of automatic bond determination
- text for raster outputs

- continue to improve rendering speed
- save more information about current setup (see section § 2.8 for the script commands to save the current setup)
- add bioinformatics functionality, sequence-based coloring, etc.
- add several new coloring methods
- faster calculation of hydrogen bonds
- implement "correct" transparency
- be able to select bonds
- improve the IMD features
- read in the electron density maps made by X-PLOR and display isosurfaces
- display electron orbitals

Chapter 2

Tutorials

2.1 Rapid Introduction to VMD

For those of you who don't like reading manuals, here is a quick introduction to VMD. To start it type `vmd` on the command line of your shell (Unix), or start it by clicking the VMD icon in your desktop or Start menu (Microsoft Windows). VMD should start up in a window titled vmd console, a display window entitled OpenGL Display, and a button bar entitled main. Text commands are typed in the console window, graphics are displayed and manipulated in the display window, and most commands are available from the menu interface, accessible through the button bar. (The menus are built on the Forms or FLTK library so all future references in the documentation will refer to them as *forms* and not *menus*.) All the forms except the main form can be turned off by pressing the button in the center top. There are two ways to perform almost all functions in VMD, either use the forms or the text console. Some of the more sophisticated commands, such as Tcl scripting, are only available in the text interface.

2.2 Viewing a molecule: Myoglobin

You have probably obtained VMD in order to visualize molecules, so we'll load up one of the provided molecular structures to demonstrate the capabilities of VMD. On the button bar, click on the Mol button. This brings up the Molecules form [§4.4.3]. (As before, this form may be turned off by clicking the button in the center top of the form, labeled Molecules). Select Load From Files on the Molecules form to bring up the Files form [§4.4.5].

We will load a PDB (Protein Data Bank) file containing the coordinates of the atoms in myoglobin (compliments of Joel Berendzen from the Biophysics Group at Los Alamos National Laboratory). In the browser on the left, select the line that says pdb only then click on the button labeled Select pdb. Use the file browser that appears to go to the subdirectory `proteins/` of the VMD distribution (you may have to ask where this is located; On Unix systems try `/usr/local/lib/vmd`. On Microsoft Windows systems, try `C:/Program Files/University of Illinois/VMD`. Once there, select the file `mbco.pdb`. Once the PDB file is selected, click on the Load Molecule button in the center of the Files form. You have loaded a myoglobin structure. Figure 2.1 shows an example of VMD displaying this protein.

You can use the mouse to manipulate the structure in the display window. There are three basic mouse modes [§4.1.1]: rotation[§4.1.1], translation [§4.1.1], scaling[§4.1.1]. The mode can be changed from the Mouse form, or by pressing `r`, `t`, or `s` on the keyboard. Experiment with these

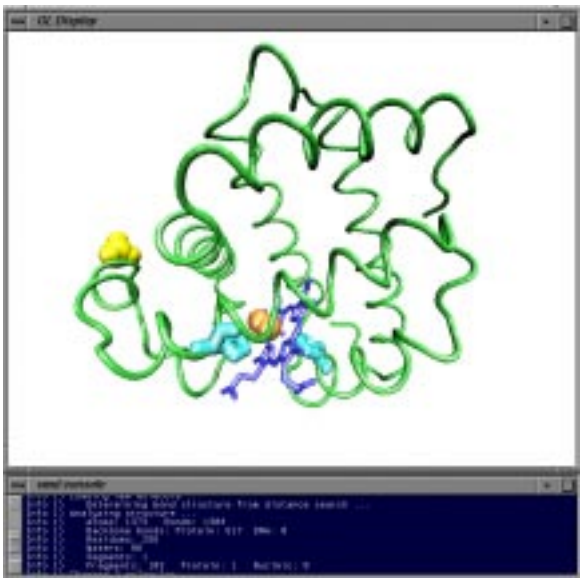

Figure 2.1: Sample VMD session displaying myoglobin.

modes, and note how the cursor changes to indicate the current mode. In rotation mode, the left mouse button controls rotation about axes parallel to the screen, and the middle button controls rotation about the axis perpendicular to the screen. In translation mode, the left mouse button controls translation parallel to the screen, while the middle button controls translation in and out of the screen. Finally, in scaling mode, both the left and middle buttons control global scaling when the mouse is moved left or right, but the middle button causes larger changes.

By default the myoglobin bonds are represented as lines and non-bonded atoms as points, with the color in both cases representing the atom type. This representation is easy for the computer to draw but is not always informative, especially when there are a large number of atoms. VMD allows you to display many of the common molecular representations. To access these, open the Graphics form [§4.4.6] using the button bar.

Suppose you would like to view the myoglobin structure with its protein backbone represented as a tube, the heme represented as licorice, the SO_4 ion and CO molecule represented as van der Waals spheres, and histidines 64 and 93 represented as CPK models. First, type `backbone` in the atom selection text entry area and press 'enter' to select the myoglobin backbone. All of the protein except for the backbone will disappear. Choose drawing method 'Tube' from the drawing method chooser to render the backbone as a tube, and chose coloring method 'Backbone' from the coloring method chooser to color the tube with the predefined backbone color. Click on the Create New button. This causes a new line to appear on the browser identical to the first line. The new line can be changed without affecting the first one, so clear the atom selection text area and then enter `resname HEM` to select the heme. At this point the heme isn't visible because it cannot be drawn as a tube, so choose the 'Licorice' drawing method to make it appear. Click on Create New again to make a new view, and enter `resname SO4 CO` to select the SO_4 ion and the CO molecule, and choose the drawing method 'VDW' to render them as Van der Waal spheres. Once again, press the Create New button and enter `resid 93 64` to select the two histidines, and render them as 'CPK'. If you followed all that, then congratulations, you have made a beautiful image of

myoglobin! Many more ways to represent atoms are possible. Please experiment with the options available in the Graphics form.

2.3 Rendering an Image

This tutorial assumes Raster3D is installed on your system and the executable `render` is in your path.

Find an interesting view of the molecule from the previous tutorial. Suppose you want to publish this view in a journal and want a high quality image, or you want to make a large poster. Taking the image from a screen capture results in a rather grainy image as the size of the pixels becomes apparent, so you want something with more resolution. There are several programs available which can render a high-quality raster image, based on an input script. VMD has the option to create input scripts for many of these image processing programs, which may then be processed to create a higher quality image of the scene displayed by VMD at the time the script was created. See the section on rendering [§ 6] for a further description of how this works.

Open the Render form [§ 4.4.13] and click on the 'Raster3D' Output Format. Both of the text boxes will fill with default values and do not need to be changed. Press the Go button. If everything works correctly, a message starting with:

```
Info 1) Rendering current scene to 'plot.r3d' ...
Info 1) Raster3D file generation finished
Info 1) Executing post-render cmd ' render < %s -sgi %s.rgb; ipaste %s.rgb' ...
 Raster3D V2.4j
```

will appear in the text console. After a few moments, a window should open with an image similar to the one in the VMD display. This image is in the RGB graphics format and can be read by many programs (such as `xv` and `ipaste`).

2.4 A Quick Animation

Another strength of VMD lies in its ability to playback trajectories resulting from molecular dynamics simulations. A sample trajectory, `alanin.DCD` is provided in the `proteins` directory included with VMD. To load it, click on the Mol button of the button bar to bring up the Molecules form [§4.4.3]. Next click on the Load From Files button and select the `psf and dcd` option under the Molecule File Types listing. Select `alanin.psf` for the psf file and `alanin.DCD` for the DCD by clicking on the Select psf and Select dcd buttons respectively. After this, you need only click the Load Molecule button in order to begin reading the trajectory. In the display window you should see a simulation of an alanin residue in vacuo. It isn't particularly informative, but you can easily see that the structure is quite unstable in an isolated environment. After the DCD file has loaded, it will by default stop. To see it again or to fine- tune playback, open the Animate form [§4.4.7] by clicking on the appropriate button in the button bar. Press the button that looks like >> to play the animation. Use the slider at the bottom of the form to change the speed of playback. By rotating the molecule around, etc. you should get an idea about how the system destabilizes over the course of the simulation.

2.5 An Introduction to Atom Selection

In this section it is assumed that you have the myoglobin structure `mbco.pdb` loaded and the views discussed in 2.2 created. If this is not true, go back to 2.2 and repeat the process described there.

VMD has a powerful atom selection method which is very helpful when generating attractive, informative, and complex graphics. In the previous section you used a few of these atom selection tools. This tutorial assumes that you have already loaded the myoglobin molecule, but it isn't necessary to recreate all the graphical representations.

To change which atoms are used to display each representation of the molecule shown in the display window, open the Graphics form [§ 4.4.6] and select the representation you want to change. You can then either edit the different fields (selection, coloring method, or drawing method) or use the Delete button to delete the view entirely. Try changing or deleting some of the views. When finished, delete all representations for the myoglobin structure. To get the basic line drawing view back, clear the atom selection text entry area (press `Esc`), enter `all` and press the Create New button.

Atoms may be selected on the basis of a property, i.e. `protein` or `not protein`, `water`, or `nucleic backbone`. They may also be selected by atom name, such as `atom C`, by residue name, such as `resname HEM`, or by many other identifiers. Multiple atoms may be specified with one keyword. For example, the selection `name C CA N O` will select the backbone atoms. (A similar effect may be obtained with the command `protein backbone`.) VMD can handle regular expressions, so that `name "C.*"` will select all atoms with names starting with C. VMD also understands the boolean operators `and`, `or`, and `not`, so the selection `resname HEM and not name "N.*"` selects all non-nitrogen atoms in the heme group of myoglobin.

Several more abstract selection criteria are available. For instance, the selection `x > 5` finds all atoms with an x coordinate greater than 5, while `mass >12 and mass < 14` selects all atoms with mass greater than 12 and less than 14 atomic mass units. Many math functions are also provided, so the selection `sqrt( sqr(x) + sqr(y) + sqr(z) ) < 10` will select atoms in a spherical region of radius 10 Å centered about the origin of the coordinate space. You can pick atoms nearby a selection with the phrase "within <distance> of <selection>" and all residues with the same property as a given selection as "same <property> as <selection>".

See section § 5.3 for a full description of the selection command.

2.6 Comparing Two Structures

Let's start from scratch by deleting everything: open the Mol form [§ 4.4.3], select every line in the browser (there should be only one), and press the Delete button.

Start by loading the `mbco.pdb` structure with the Files form. Turn on just the heme, CO, and histidines by using the selection commands `resname HEM CO or resid 64 93`. The dot (probably green) in the middle is the iron and you can verify that by picking it with the mouse. Do this by changing the "Object Mode" pull-down to "Pick", and selecting "Atoms" for the pick mode in the Mouse form. The label `HEM154:FE` should appear both on the display and in the text console.

Change the pick mode in the Mouse form to "Bonds". To get the distance between the iron and the oxygen of the CO, click with the left mouse button first on the iron and then on the oxygen. The first click turned the FE label on and the second turned the O label on and drew a line between the two atoms with the distance drawn in the middle and a bit to the right. The distance between the two atoms is 2.94 Å, as compared to 2.93 Å in the paper; not bad. However, picking

the distance between the FE and the C of the CO reveals a distance of 1.91 Å as compared to 1.85 Å in the paper. The difference is that the structures in the VMD distribution are actually preliminary structures obtained before the final coordinates were determined.

In order to experiment with more complex picking modes, consider the angle made by the O of the CO with the FE of the heme and the NE2 of residue 93 (you can click on the atoms to find which ones are which). Using the Mouse form, change the pick mode to "Angles". This should cause the cursor to become a red crosshair. Click on each of the three atoms using the left mouse button. After the third pick, a shallow angle will appear indicating an 8.71 degree angle between the three atoms.

Now load the intermediate `star.pdb` file which can also be found in the `proteins` directory of your distribution. Again use the Files form to do this. Both of the molecules will be loaded side by side. Go to the Graphics form and change the selection so it the same as the first, i.e. `resname HEM CO or resid 64 93`. The two molecules are almost atop each other, making it hard to distinguish the two, so change the colors to simplify things.

First, in the Graphics form, change the Coloring method to 'Molecule'. Use the Selected Molecule chooser to change the `mbco.pdb` Coloring method to 'Molecule' as well. Open the Color form [§4.4.11] and scroll the Category browser down until the line 'Molecule' is visible. Click on it then click on the line which says `mbco.pdb`. (There may be two `mbco` lines if the file had been loaded before in this session.) Scroll the Colors browser up to click on 'blue'. This should change one of the molecules in the display to blue.

Next, click on the last line in the Names chooser, which says `star.pdb`. This time, choose 'red' from the Colors chooser. The display should be much easier to understand. The myoglobin with the bound CO is in blue and the intermediate state is in red. At this point it is easy to measure the change in position between the two different states by using the middle mouse button to pick the same atom in the two conformations.

Once that is done, it is easy to point out one interesting aspect of the way VMD handles the graphics. Go to the Mol form, select one of the two molecules, and press Toggle Fixed. Enter translation mode and move the other molecule around. Notice that the number which lists the distance between the two atoms never changes. That's because the mouse only affects the way the coordinates are translated to the screen image. It does not affect the real coordinates at all. It is possible to change the coordinates in a molecule using the text command interface, or by using the atom move pick modes [§4.1.2]).

By the way, unfix the molecules and do a 'Reset View' from the right pull-down menu to reset everything. Load up the third structure, `deoxy.pdb` and give it the same selection as the other two molecules. However, color this one green. Pull out Nature v. 371, Oct. 27, 1994 and turn to page 740. With a bit of manipulation you should be able to recreate the image that appears there.

2.7 Some Nice Represenations

The following views are quite nice for displaying proteins and nucleic acids:

```
selection: all
drawing method: tube
coloring method: segname (or chain)
why?  This show the backbone of the protein and nucleic acid strands

selection: protein and (name CA or not backbone)
```

```
drawing method: lines
coloring method: segname (or chain)
why? shows where the side chains are located, but they are thin so the
  backbone is still visible and the scene is quickly drawn

selection: (numbonds = 0) and not waters
drawing method: vdw
coloring method: name
why? shows ions.  The "not waters" omits cases where a water's oxygen is
  known but not the hydrogen.

selection: not (waters or protein or nucleic)
drawing method: lines
coloring method: name
why? shows whatever is left; usually ligands and crystallizing agents
```

2.8 Saving your work

After creating a set of attractive and informative representations of your molecule, you may want to save your work so that you can regenerate the scene later. There are two ways to do this in VMD:

- In the Mouse form, press the "Save Config" button; this will bring up a window where you can enter a file name in which to save your work.
- In the text console, type "save_state *filename*", where *filename* is the name of the file in which to save your work.

To restore your scene, you also have two choices:

- From the command line, start VMD with the options "vmd -e *filename*", where *filename* was the name of the file you saved before. (Currently works for Unix version of VMD only).
- After starting VMD, from the text console, type "play *filename*".

The most common source of problems is when VMD can't find the files you used to load the molecule. If this happens, try changing to the directory you were in when you first loaded the molecule, or edit the state file and use the full path names where you see a "mol load" command.

Chapter 3

Loading A Molecule

The Files form is the primary means for loading a new molecule into VMD from one or more data files. VMD natively understands six molecular data file formats: PDB coordinate files, CHARMM and X-PLOR style PSF (topology) files, CHARMM and X-PLOR style DCD trajectory files, Amber structure and trajectory files (i.e. PARM and CRD), and Gromacs (i.e. GRO, G96, XTC, TRR) structure and trajectory files. These files may contain some redundant information and can be loaded in different combinations.

VMD can also load a PDB file directory from the Protein Data Bank, provided a network connection is present. Choose "pdb databank" from the list file types and enter the four-character accession code.

The PDB file contains data about the atom, residue, and segment names, the occupancy and beta factor, and one coordinate set. The PSF and PARM files list the atom, residue, and segment names, the residue type, atomic mass and charge, and the bond connectivity. The DCD and CRD files contain only the atomic coordinates over multiple frames (timesteps). VMD supports four file formats used by Gromacs: GRO, G96, TRR and XTC. GRO and G96 files contain only structure information, including atom, residue and segment data with one coordinate set. TRR and XTC files contain only coordinate data. It should be noted that while PDB, GRO and G96 files were designed to only contain one coordinate set, multiple files can be concatenated into one larger file to create a makeshift trajectory which is recognized by VMD.

When VMD loads a file it requires information about atom names and coordinates and tries to fill in the rest. Since the PDB file contains all this information, it does not need to be loaded with any other data files. However, the PDB file doesn't contain the atom types, masses, and charges, so these are guessed.

A PSF file does not contain coordinate information so it must be loaded along with a PDB or DCD file. If a PDB and PSF are given there is no missing data and VMD makes no assumptions. If a PSF and DCD are given then only the chain identifier and occupancy and beta values are missing so they are given a default value.

A PARM file is similar to a PSF in that it too contains no coordinate information. It must be loaded along with an CRD trajectory file. If a PARM and CRD file are loaded together, then only the segname and chain ID for the atoms are left blank. VMD fills in the remaining fields explicitly, making no assumptions.

A CRD or DCD file can be specified along with the PDB, in which case the PDB file will be read as normal, and then coordinate sets are read from the DCD or CRD until the end of the file is reached.

Gromacs GRO and G96 files can be loaded on their own since they contain the necessary atom data and coordinates. They can also be loaded along with TRR and XTC files to obtain trajectory data.

Additional coordinates from a PDB, CRD, or DCD file can be appended to the current coordinate set using the Edit form [§4.4.8].

3.1 Babel interface

VMD can use the program Babel, if installed, to translate a wide variety of different molecular data files into the PDB format. Babel, written by Pat Walters and Matt Stahl, can convert between many types of molecular data files. Not all of these have been tested for use with VMD, so your results may vary. Some data formats, such as XYZ, contain a series of coordinates. Babel converts these to a series of PDB files which VMD then reads as an animation. For more information about Babel, see `http://www.eyesopen.com/babel.html` VMD supports version 1.6 of Babel. Older versions of Babel will not work correctly with VMD.

VMD at present has no provision for using Babel to convert the output PDB CRD, or DCD files to anything else (see sections §4.4.8, § 8.3.1 and § 12.2 for information on writing output files).

The Babel-VMD interface uses two environment variables [§13.3], `VMDBABELBIN` and `VMDTMPDIR`. The first specifies the absolute location for the Babel binary (i.e. it must include the name of the executable itself, such as /usr/local/bin/babel (Unix), or `C:\Program Files\Babel\babel.exe` (Windows)). The second defines the location for the temporary PDB files made by Babel.

3.2 What happens when a file is loaded?

(See the Files form §4.4.5 for instructions on how to specify input files. See the the Edit form [§4.4.8] for instructions on how to save data as either a PDB, DCD, or CRD file. The Edit form can also be used to append [§4.4.8] PDB and DCD files to a loaded molecule.)

If only a coordinate file (i.e. just a PDB, with no PSF) is given, two passes are made through the file. The first pass determines how many atoms exist and the second reads them in. VMD then uses internal defaults to fill in the missing values. It then does a distance search to determine the bond connectivity, which will make some strange bonds if atoms are too close. If both a PSF and a PDB file are given, no approximations or guesses are made. For those interested in the details, when VMD is forced to guess the connectivity, it considers a bond to be formed whenever two atoms are within $R_1 * R_2 * 0.6$ of each other, where R_1 and R_2 are the respective radii of candidate atoms.

After the molecule is read, VMD checks to see if any new names are needed for the various coloring categories [§5.2.3]. If so, they are created and assigned a new color. (When the end of the color list is reached, the color starts again at the beginning.) Next, the bond connectivity is established and the molecule is analyzed to identify the various components, i.e., determine which residues are protein, nucleic acids, and waters, which atoms are backbone atoms, etc. A search is then made to connect these different types into larger fragments of the same type. As these searches take place, the information is printed to the screen. An example output for BPTI is:

```
Info 1) Analyzing structure ...
Info 1)    Atoms: 898   Bonds: 909
Info 1)    Backbone bonds: Protein: 231  DNA: 0
```

```
Info 1)    Residues: 58
Info 1)    Waters: 0
Info 1)    Segments: 1
Info 1)    Fragments: 1   Protein: 1   Nucleic: 0
```

There are actually several types of fragments. Protein and nucleic fragments are homogeneous; either all proteins or all nucleic acids. However, it is quite possible for a protein to be connected to a nucleic acid or some other non-protein. When this occurs, a warning message is printed, as in:

```
Warning 1) Unusual bond between residues 1 and 2
```

These warnings are known to occur with terminal amino acids, zinc fingers, myristolated residues, and poorly defined structures.

3.3 Raster3D file format

In addition to the molecular file formats, VMD can read the input file for Raster3D. (Raster3D converts an input file into a shaded raster image for use in making high quality pictures. It is often used with MolScript.) The ability to read Raster3D allows users to view MolScript files in 3D and incorporate special images into the display without having to edit the VMD code. If anyone has used this second option, we would be interested in knowing what was done.

The file format, which is part of the Raster3D documentation, describes a simple collection of triangles, spheres, and cylinders with either flat or spherical ends. Each shape is colored by an RGB triplet.

3.4 Raster3D Caveats

Certain newer Raster3D objects are ignored, such as quadrics. Also, nearly all of the header information is ignored—most notably, the viewing matrix.

Aside from quadrics, VMD can read and display all shapes in the format with one exception. Raster3D uses many cylinders with spherical (rounded) ends. VMD deliberately omits these rounded ends since the resultant image would be very slow.

Finally, since VMD uses a palette of 1024 colors, each triplet is converted into its "nearest" indexed color. This may cause images to be colored slightly differently than expected.

Chapter 4

User Interface Components

There are several methods available in VMD for the user to control and interact with the molecular display. The primary methods are by using the mouse, either in the VMD graphical display window (where the molecule is displayed) or in the different graphical user interface (GUI) *forms* provided by the program. In addition to the mouse, VMD also supports the use of a number of advanced input devices such as the Spaceball, Magellan, and Phantom, which provide the ability to manipulate molecules with six degrees of freedom. Some devices such as the Phantom can also provide haptic (sense of touch) force feedback. VMD also provides a text console interface, in which the user can enter and execute simple commands or more sophisticated VMD scripts. This chapter describes how to use the mouse-based user interface components and a subset of the more advanced input devices supported in VMD. This chapter describes the basic operation of the graphical user interface components, and gives a quick overview of each available form. The other primary user interface component, the text user interface, is described fully in chapter § 8.

4.1 Using the Mouse in the Graphics Window

The graphics display window is labeled OpenGL Display and contains a display of the various molecules and other graphical objects, like the axes, which make up the scene. When the mouse cursor is located inside the graphics display window, it may be used to perform the following actions:

- Rotate, translate, or scale the displayed molecules
- 'Pick' atoms or other objects. That is, select them in order to move them around, label them etc.
- Move the lights
- Translate and rotate a set of atoms
- Apply a force (acceleration) to a set of atoms

There are also *hot keys*, or keyboard accelerators, available when the mouse is in the graphics display window. These hot keys are bound to some VMD text commands, which are executed when a hot key is pressed. VMD has several built-in hot key commands (see Tables 4.1, 4.2, 4.3 and 4.4), and the user can add new ones as well (overriding the built-in ones if desired).

4.1.1 Mouse Modes

The mouse, while positioned within the graphics display window, is used to perform a variety of functions. There are several different *modes* which the mouse may be in at any time; the current mouse mode determines what the effect is when the user presses the left or middle button. Each mouse mode, except the lights mode (see below), causes the cursor to acquire a characteristic shape. The mouse mode is changed via the Mouse Form.

The available modes are as follows:

- **Mouse Mode → Rotation Mode**
  When the mouse is in this mode, holding the left mouse button down and moving the mouse rotates the molecules about axes parallel to the screen, in a 'virtual trackball' behavior. To get a rotation around the axes coming out of the screen (the 'z' axis), hold the middle button down and move the mouse left (clockwise) or right (counter-clockwise).

  You can keep the molecules rotating without continuously moving the mouse. Start the molecule moving with the mouse, as above, then release the mouse button before you stop moving the mouse. With some practice it becomes easy to impart a slight spin on the molecule, or whirl it about madly. To stop the rotation, either press and hold the left mouse button down until the molecule stops moving, or select 'Stop Rotation' in the Mouse form.

  The hot key to enter rotation mode is `r`. Also, pressing `r` or any of the other mouse mode hot keys causes the rotation to stop.

- **Mouse Mode → Translation Mode**
  When the mouse is in translation mode, holding the left button down allows you to move the molecules parallel to the screen plane, so, for example, moving the mouse left moves the system left. To move the molecule towards or away from you, hold the middle button down and move the mouse right or left, respectively.

  The translation hot key is `t`; pressing `t` while the mouse is in the graphics display window will change the mouse to translation mode.

- **Mouse Mode → Scaling Mode**
  The scaling mode has the simplest mouse controls as pressing either the left or middle button down and moving to the right enlarges the molecules, and moving the mouse left shrinks them. The difference is that the middle button scales faster than the left button.

  The scaling hot key is `s`.

- **Mouse Mode → Move Lights Mode**
  VMD provides up to four separate light sources to illuminate the graphics objects in the display window. These light sources act independently, and use the native lighting hardware acceleration available on the graphics workstation (if any). Thus, they do not cast shadows, and their effect is not calculated with any form of raytracing or similar algorithm. They do, however, add a nice realistic effect to the objects and help give the appearance of material characteristics to spheres, cylinders, and so forth. You can use the mouse to rotate each of the light sources in space to a new position; you can even set a specific light to rotate continuously about the origin. The light sources are located at infinity, so only their orientation is important. If the light is not currently on, moving that light source will not affect any change in the displayed image. To turn a light on or off, use the Lights browser in the upper right of the Display form [§4.4.10].

4.1.2 Pick Item Mode

The mouse can also be used to select things from the screen. As with many molecular graphics programs, an atom can be picked by moving the cursor over it and clicking the left mouse button. When an atom is picked for the first time, a text label appears which shows the atom residue name and number, and the atom name. Clicking on the atom again turns the label off.

Picking atoms with the mouse is used to turn on or off various types of labels, to query for information about an object, or to move items around on the screen. You can label an atom (and display the atom name), or you can label geometric values such as the distance between two atoms (a *bond* label), an angle between three atoms (an *angle* label), or the dihedral angle formed by four atoms (a *dihedral* label). This is done by setting the mouse into the proper picking mode and then selecting the relevant atoms with the mouse.

You first select the proper picking mode by using the Mouse form, and choosing the mode required to perform the desired action. The available actions when in pick item mode are:

- **Pick Item Mode → Query**
  Clicking with the left or middle mouse button on an item will print out the name of the item (e.g. the atom name) to the text console window. The hot key to set this mode is '0'.

- **Pick Item Mode → Center**
  This mode is used to change the point about which a molecule rotates when the molecule is rotated. To cause a molecule to rotate about a specific atom, select this mode and then click on that atom. The rotation point may be restored to its default position (the center of volume of the molecule) by executing the 'Reset View' option from the Mouse form. The hot key to set the mouse to Pick Item Mode → Centering mode is 'c'.

- **Pick Item Mode → Atom**
  Clicking on an atom will toggle on/off a label for the atom. The hot key to set this mode is '1'.

- **Pick Item Mode → Bond**
  Clicking on two atoms in a row will toggle on/off a bond distance label between the two atoms (a dotted line with the distance printed at the midpoint). The hot key to set this mode is '2'.

- **Pick Item Mode → Angle**
  Clicking on three atoms in a row will toggle on/off a label showing the angle formed by the three atoms. The hot key to set this mode is '3'.

- **Pick Item Mode → Dihedral**
  Clicking on four atoms in a row toggles on/off a label showing the dihedral angle formed by the four atoms. The hot key to set this mode is '4'.

- **Pick Item Mode → MoveAtom**
  In this mode, the position of an atom can be changed by clicking on the desired atom, and dragging with the mouse while the button is still pressed. This will change the atom coordinates. The hot key to set this mode is '5'.

- **Pick Item Mode → MoveResidue**
  This mode may be used to move all the atoms in a selected residue at the same time. Select an atom in a residue, and move it to a new position while keeping the mouse button pressed.

All the atoms in the same residue as the selected one will be moved the same amount. Holding down the ¡shift¿ key and the left mouse button while moving the mouse will rotate the atoms in the residue about the selected atom. If the middle mouse button is held down instead, the atoms in the residue will rotate about a line drawn through the picked atom and parallel to a line coming directly out of the screen. This behavior is similar to the usual Rotate mode, except that coordinates of atoms are changed.

The hot key to set this mode is '6'.

- **Pick Item Mode → MoveFragment**
  A *fragment* is a set of atoms all connected by a series of covalent bonds. This mode acts just like MoveResidue, except that the atoms which are moved are all in the selected fragment rather than in the selected residue. This will change the atom coordinates. Holding down the ¡shift¿ key and the left mouse button while moving the mouse will rotate the atoms in the fragment about the selected atom. If the middle mouse button is held down instead, the atoms in the fragment will rotate about a line drawn through the picked atom and parallel to a line coming directly out of the screen. This behavior is similar to the usual Rotate mode, except that coordinates of atoms are changed.

  The hot key to set this mode is '7'.

- **Pick Item Mode → MoveMolecule**
  This mode may be used to move all the atoms in a selected molecule at the same time. Select an atom in a molecule, and move it to a new position while keeping the mouse button pressed. All the atoms in the same molecule as the selected one will be moved the same amount. Holding down the ¡shift¿ key and the left mouse button while moving the mouse will rotate the atoms in the molecule about the selected atom. If the middle mouse button is held down instead, the atoms in the molecule will rotate about a line drawn through the picked atom and parallel to a line coming directly out of the screen. This behavior is similar to the usual Rotate mode, except that coordinates of atoms are changed.

  The hot key to set this mode is '8'.

- **Pick Item Mode → MoveHighlightedRep**
  This mode may be used to move all the atoms in a selected representation at the same time. You select a representation by clicking on one of the reps in the browser window of the Graphics form. In order to move the atoms in this rep, the atom you pick with the mouse must be selected by that rep.

  When you have clicked on an atom in the rep, move the mouse to a new position while keeping the mouse button pressed. All the atoms selected by the highlighted rep will be moved the same amount. Holding down the ¡shift¿ key and the left mouse button while moving the mouse will rotate the atoms in the rep about the selected atom. If the middle mouse button is held down instead, the atoms in the rep will rotate about a line drawn through the picked atom and parallel to a line coming directly out of the screen. This behavior is similar to the usual Rotate mode, except that coordinates of atoms are changed.

  The hot key to set this mode is '9'.

4.1.3 Hot Keys

When the mouse is in the graphics window, several more commands are accessible via programmable hot keys. They allow you to do things like change mouse modes or advance the animation by a frame by simply pressing a key. The default key bindings are listed in the following tables. The commands listed are the text commands which are executed when the hot key is pressed; these text commands are explained in section §8.3.

VMD keeps a list of user hot keys, which when pressed will result in an associated text command being executed as if it had been typed at the console. There are a number of predefined hot keys, as listed in tables 4.1, 4.2, 4.3, and 4.4. The current state of these can be printed out with the command

- **user print keys**

The commands attached to these hot keys can be customized by the user.

To add/modify a hot key, use the command

- **user add key** *key command*

key must be a single character. When that key is pressed while the mouse cursor is in the graphics display window, the associated command will be executed.

Once you have discovered a set of commands which are particularly useful and familiar for you, you will want to have these hot key commands automatically available every time you run VMD. This can be done by placing the commands to add these items in your `.vmdrc` file, which is a file containing VMD text commands that is executed every time VMD starts up. The basic method for setting up this file is described in section §13.4.3. Once you have such a file, just put the `user add` commands in it, and you will have your own specialized version of VMD.

Hot Key	Command	Purpose
`r, R`	`mouse mode 0 0`	enter rotate mode; stop rotation
`t, T`	`mouse mode 1 0`	enter translate mode
`s, S`	`mouse mode 2 0`	enter scaling mode
`0`	`mouse mode 4 0`	query item
`c`	`mouse mode 4 1`	pick center
`1`	`mouse mode 4 2`	pick atom
`2`	`mouse mode 4 3`	pick bond (2 atoms)
`3`	`mouse mode 4 4`	pick angle (3 atoms)
`4`	`mouse mode 4 5`	pick dihedral (4 atoms)
`5`	`mouse mode 4 6`	move atom
`6`	`mouse mode 4 7`	move residue
`7`	`mouse mode 4 8`	move fragment
`8`	`mouse mode 4 9`	move molecule
`9`	`mouse mode 4 13`	move highlighted rep
`%`	`mouse mode 4 10`	force on atom
`^`	`mouse mode 4 11`	force on residue
`&`	`mouse mode 4 12`	force on fragment

Table 4.1: Mouse control hot keys.

Hot Key	Command	Purpose
x	`rock x by 1 -1`	spin about x axis
X	`rock x by 1 70`	rock about x axis
y	`rock y by 1 -1`	spin about y axis
Y	`rock y by 1 70`	rock about y axis
z	`rock z by 1 -1`	spin about z axis
Z	`rock z by 1 70`	rock about z axis
j, Cntl-n	`rotate x by 2`	rotate 2° about x
k, Cntl-p	`rotate x by -2`	rotate −2° about x
l, Cntl-f	`rotate y by 2`	rotate 2° about y
h, Cntl-b	`rotate y by -2`	rotate −2° about y
g	`rotate z by 2`	rotate 2° about z
G	`rotate z by -2`	rotate −2° about z
Cntl-a	`scale by 1.1`	enlarge 10 percent
Cntl-z	`scale by 0.9`	shrink 10 percent

Table 4.2: Rotation & scaling hot keys.

4.2 Using the Spaceball in the Graphics Window

VMD provides optional support for Spaceball six-degree-of-freedom input devices. The Spaceball may be used to rotate, translate, and scale molecules, using up to 6 control axes simultaneously (3 axes in translation, 3 in rotation). The Spaceball can be used both independently and simultaneously with the mouse. With the spaceball in one hand and the mouse in the other, a user can perform complex picking and identification operations more efficiently, since the mouse can be left in pick mode (for example) while the Spaceball is used to perform rotations, translations, and scaling operations with the other hand.

4.2.1 Spaceball Driver

VMD currently interfaces to the Spaceball in one of two ways; either by communicating directly with the Spaceball using Spaceball serial interface software written by John Stone, or through the use of operating system specific drivers supplied by the Spaceball vendor. Currently the Windows versions of VMD use the vendor driver and the

Unix versions of VMD currently use the serial interface software. At startup time, VMD checks for the existence of an environment variable *VMDSPACEBALLPORT*. This environment variable must be set to the Unix device name of the serial port to which the Spaceball is attached. The serial port device permissions must be set to allow the VMD user to open the device for reading and writing. In typical usage, this usually requires performing a `chmod 666 /dev/somettyname` on the appropriate device as root. Once serial port permissions are set correctly, VMD should be able to communcate with the Spaceball at startup. The serial interface software used in the Unix versions of VMD does not presently provide a means of controlling spaceball sensitivity, and the button functions are currently hard coded to reset the view and change the Spaceball mode. One restriction with the use of the Unix Spaceball software is that only one VMD process may safely use the Spaceball at a time. If multiple VMD sessions are started on the same machine and all are set to open the Spaceball, it will likely behave very erratically. The main advantage of the serial interface driver used on Unix over the vendor driver is that it is open source, and supports

Hot Key	Command	Purpose
Alt-M	menu main off;menu main on	Show main menu
Alt-m	menu mol off;menu mol on	Show mol menu
Alt-f	menu files off;menu files on	Show files menu
Alt-a	menu animate off;menu animate on	Show animate menu
Alt-e	menu edit off;menu edit on	Show edit menu
Alt-g	menu graphics off;menu graphics on	Show graphics menu
Alt-l	menu labels off;menu labels on	Show labels menu
Alt-r	menu render off;menu render on	Show render menu
Alt-d	menu display off;menu display on	Show display menu
Alt-c	menu color off;menu color on	Show color menu
Alt-s	menu sim off;menu sim on	Show sim menu
Alt-t	menu tracker off;menu tracker on	Show tracker menu
Cntl-r	display resetview	Reset display
Alt-q	quit confirm	Quit VMD with confirmation
Alt-Q	quit	Quit VMD
Alt-h	hyperref invert	Invert hyper text mode (NOT help)

Table 4.3: Menu control hot keys.

Hot Key	Command	Purpose
+,f,F	animate next	move to next frame
-,b,B	animate prev	move to previous frame
.,>	animate forward	play animation forward
,	animate reverse	play animation reverse
<	animate reverse	play animation reverse
/, ?	animate pause	stop animation

Table 4.4: Animation hot keys.

a much wider variety of machines and operating systems than the vendor drivers do, though its functionality is much more limited. Future Unix versions of VMD may provide support for both the serial interface and vendor-provided drivers.

The Windows version of VMD uses the vendor-provided SpaceWare driver exclusively, and operates somewhat differently from the serial interface software used on Unix. The SpaceWare software runs as a separate process from VMD and must be started and fully operational before VMD is run. At startup time VMD attempts to open the SpaceWare interface, displaying the success or failure of initialization as it occurs, with applicable diagnostic information. The SpaceWare driver provides detailed control over the sensitivity and configuration of the Spaceball. In order to use the Spaceball function keys with VMD the SpaceWare driver must be set to send button events as *Function 1* and *Function 2* at a minimum. Once set, it should be possible to cycle through the various VMD Spaceball operational modes as described below.

The Spaceball can be run in one of several modes within VMDṪhe Spaceball interface currently provides two methods of rotation and translation, and a scaling mode. The Spaceball interface currently uses *Button 1* (known as *Function 1* in the SpaceWare driver) to reset the view, and *Button 2* to cycle through the available Spaceball interface modes.

4.3 Using the Joystick in the Graphics Window

The Windows version of VMD provides support for the Windows joystick driver, and will enumerate all available joystick devices at startup time. The joystick interface employed in VMD is quite simple, allowing the use of three control axes to translate, rotate, and scale the molecule. The joystick interface assumes a device with at least two buttons. The first joystick button resets the view in the display window, and the second button cycles through each of the available joystick modes. When VMD first attaches to each of the joysticks, they are initially disabled so that miscalibrated joysticks do not adversely affect the VMD session. Each joystick is initially enabled by pressing its second button to switch modes. All joysticks are independently controlled such that multiple joysticks can control different control axes, and multiple users could interact with the program with separate controls.

4.4 Description of each VMD form

VMD uses several different GUI forms, each designed to control a specific aspect of the molecular display (e.g., to control the appearance of the graphics display window, or to change the colors of displayed objects). Each form has a unique name, includes a button with the name of the form near the top of the window. Pressing this button will hide the form from view. The following sections give a brief description of the forms available in VMD; the remaining chapters in this manual describe the actions which these forms make available in greater detail.

4.4.1 Main Form

Figure 4.1: The Main form

The Main form, also called the button bar, can turn most of the other forms on or off. It can also be used to start an HTML viewer to see the VMD quick help file, and to exit the program. The buttons with lights control which forms are turned on or off; if the light is on, the form is being displayed. Sometimes a form is turned on but is hidden behind other forms or windows. A quick way to bring the form to the top is to turn it off and then on again, as implemented for you using the Menu shortcut keys described in Table 4.3.

The Help button starts an HTML viewer (like Mosaic or Netscape) and displays on-line VMD help documents. The viewer is designated by the environment variable `VMDHTMLVIEWER` [§ 13.3]. Starting help multiple times will start multiple viewers. The default web browser is Netscape for Unix systems, and the built-in Explorer shell for Windows systems. Note, you may need to have Netscape or Mosaic up and running before successfully using the Help button. That is, if you obtain a message such as `‘‘netscape: not running on display :0.0’’`, then you will have to start up the program yourself, after which VMD will be able to direct you to the correct page. The help button brings up the VMD Quick Help page, which contains links to the current User's Guide, FAQ, and links to various helpful information and programs.

Press the Quit button to exit VMD. This will bring up another form which verifies that you do indeed wish to exit. Press Yes to quit, or No to return to VMD.

4.4.2 Mouse Form

The Mouse form indicates and controls the behavior of the mouse when the mouse moves and clicks within the graphics window. Mouse clicks and drags can affect VMD in one of two ways. It can change the *view* of the scene, either by rotating, translating, or scaling. It can also *pick* objects in the scene, causing some further action to be taken. These behaviors are all reflected in the state of the Mouse form.

Below, we describe the four main parts of the Mouse form.

Action buttons

The three buttons in the upper left corner of the Mouse form perform actions which affect the entire scene. The Reset View button cancels the effect of rotations, scalings, and translations performed by the user and returns the scene to its original orientation. The Stop Rotation button halts rotation induced by clicking and dragging the mouse across the scene. Finally, the Save Config button prompts the user to enter a filename in the vmd console window where the current state of VMD is saved. For example, assume the filename "mystate.vmd" has been entered. Subsequent VMD can be returned to this state by either starting VMD with the command "vmd -e mystate.vmd", or by starting VMD normally and typing "source mystate.vmd" in the vmd console.

Mouse mode

The two pulldown menus in the bottom left corner of the Mouse form are part of the controls for the mouse mode. The top menu, entitled "View Mode", selects whether the mouse will rotate, translate, or scale the scene when the user clicks and drags with the left mouse button. Below the "View Mode" menu is the "Object Mode" menu. This pulldown menu does not change the state of the mouse. Instead, it controls which of five submenus are displayed to the right of the mouse mode menus on the Mouse form. These submenus will be described in further detail below.

Pick information

The large region in the upper right corner of the Mouse form displays information about the last atom picked by the mouse. This information is also echoed to the vmd console. The data in the Pick information will remain on the Mouse form until a new atom is picked by the mouse. Information about the following fields is identified:

- Name - the name of the atom as it appeared in the coordinate file
- Type - the type of the atom, as determined by an internal VMD match-up of the given name to a likely atom type associated with that name
- Index - the internal VMD index used to identify the atom; this is useful for specifying selection syntax to generate different representation styles for particular atoms. For PDB files Index corresponds to the atom number listed in the file minus 1 (so that the index starts with 0).
- Resname - the type of the amino or nucleic acid to which this atom belongs

- ResId - the internal VMD ID number of the entire residue to which the particular atom belongs. E.g., ResId for an atom of a protein is the same as the residue number of that atom as listed in its PDB file.
- Chain - if the coordinate file contained data in the "Chain" field for this atom, then that data is given here.
- Segname - the name of the segment to which this atom belongs
- X, Y, Z - the position of the atom in 3D space

Object menus

The five object menus all appear in the bottom right corner of the Mouse form. Only the menu selected by the Object Mode pulldown menu is displayed. These menus control how the mouse affects objects in the scene (as opposed to how the mouse changes the *view* of these objects). Note that any time you choose a new object mode, the View Mode changes to "Rotate".

- **Pick Mode** generally adds labels to atoms in the scene. Labels include atoms, bonds, angles, and dihedrals. These labels require, respectively, one, two, three, and four atoms to be picked. For the latter three label types, the numerical value of the geometric label is displayed, along with a stippled line connecting the picked atoms. The units for "Bonds" corresponds to whatever units the coordinate file is written in. "Angles" and "Dihedrals" are measure in degrees.

  Labels can be temporarily hidden from view by pressing the "Show/Hide" light button to the right of the corresponding label type. Pressing the "Show/Hide" button again brings the label back into view. Labels can be removed by pressing the "Delete" button on the far right of the Pick menu.

  The button marked "Center" changes how VMD rotates and scales the scene. To get a feel for how this works, select "Center" from the Mouse form, then click on an atom in the scene. If you now rotate the scene by clicking and dragging with the left mouse button, the scene should rotate about the picked atom. If you change the view mode to "Scale" using the "View Mode" pulldown menu, the scene will expand while keeping the picked atom in view. The picked atom will remain the center atom until a new atom is selected as "Center", the "Reset View" button is pressed, or a new molecule is loaded.

- **Move Mode** changes the actual coordinates of atoms in the scene. Note that this is different from simply changing the view. Clicking on one of the buttons in the Mode Mode menu selects what group of atoms to move. "Atom" moves only the selected atom. "Residue" moves all atoms in the same residue (e.g., amino acid or nucleotide) as the selected atom. "Fragment" moves all atoms connected by a bond to the picked atom. "Molecule" moves every atom in the molecular structure. "Highlighted Rep" is the most flexible; it moves all atoms in the highlighted representation in the browser window of the Graphics form.

  Atoms are moved by clicking and dragging with the left mouse button. If the shift key is held while the mouse is moved, the affected atoms are *rotated* about the selected atom. Rotating atoms with the left button rotates about the x or y axis of the screen; rotating with the middle or right button rotates about an axis perpendicular to the screen.

Note that there is currently no way to undo Move operations, so the atom coordinates should first be saved using the Edit form.

- **Force Mode** applies a force to selected atoms. These forces will be visible only if an IMD connection has been established. Clicking and dragging with the left mouse button will apply a force to the selected Atom, Residue, or Fragment, as in Move Mode. Clicking with the middle or right button will cancel the force on the selected atoms.

- **Move Light Mode** allows the lights to be positioned around the scene. Individual lights are turned on or off in the Display form. Selecting one of the lights in the Move Light menu rotates the selected light about the origin. Pressing the "Done button" puts the mouse into "Pick Atoms" mode. The Move Light Mode can also be cancelled by changing into any other mouse mode.

4.4.3 Molecules (Mol) Form

Figure 4.2: The Molecules form

The Mol, or Molecules, form shows the global status of the loaded molecules. Any number of molecules may be displayed by VMD simultaneously. Each molecule can separately be hidden from view, fixed in place (e.g., prevented from being affected by mouse rotation commands). This form contains controls to change the status of the molecules individually or in groups.

Loading a New Molecule

The Load From Files button will activate the Files form [§4.4.5], which is used to read a new molecular structure in from a file or set of files.

The Setup Remote Connection does nothing at this time; future versions of VMD will use this button to activate a browser for running remote simulations. Chapter § 3 describes fully how to load a molecule and what file formats are supported.

The Molecule List browser

The browser at the center displays information about each molecule. The Name is the file name which contained the topology information, followed by a unique integer ID which is assigned to each molecule by VMD when it is loaded. Atoms shows the number of atoms in the molecule, Frames gives the number of timesteps associated with the file, and Source is either File or Remote, reflecting whether the information was acquired from a file or a remote simulation.

Next to each molecule is a set of status flags, which indicate the current Status of each molecule. Each molecule has the following characteristics, which can be *on* or *off*:

- **Top (T)**
  Top indicates the default molecule used in the text commands when nothing is specified for the `mol` text command. It is also used in some forms (like Graphics and Animate) to determine certain values. There can be only one top molecule at a time.

- **Active (A)**
  Several commands and actions in VMD operate on many molecules. These commands, unless specifically specified otherwise, will do their action for all the *active* molecules.

- **Drawn (D)**
  If a molecule is *Drawn* then it is being displayed in the graphics display window. This is useful for temporarily hiding a molecule from view without deleting it.

- **Fixed (F)**
  Fixed molecules do not undergo rotation, translation, or scaling. Note that while it may seem that one molecule has been moved relative to another, the difference is only apparent. The internal coordinates do not change when a standard rotation is applied by using, for example, the mouse. It is possible, however, to change the coordinates of atoms in a molecule, using the text command interface, and by using the atom move picking modes.

Changing the Molecule's Status

The status of a given molecule can be changed by selecting the molecule in the browser and pressing the toggle that controls the appropriate flag. The active, drawn, and fixed status values can be changed for several molecules at the same time by selecting several molecules before pressing the toggle. However, only one molecule can be top at any one time, so Make Top can only be applied to one selection. Pressing one of the All ... or No ... buttons either sets or unsets corresponding flag on all the loaded molecules.

The Single A/D/T button makes the selected molecule active, displayed, and top. It also resets the scene so the given molecule roughly fills the screen. It is a quick way to switch from viewing one molecule to another when it is desirable to only show one molecule within the graphics display window at a time.

Deleting a Molecule

The Delete button deletes all selected molecules. There is no prompt verifying the deletion, so take some care. If a deleted molecule was the top molecule, a new top molecule will be set from the remaining structures.

4.4.4 Canceling a Load of a Coordinate File

The Cancel button cancels the loading of coordinate files for all selected molecules. All coordinate files selected for that molecule are canceled, leaving only the timesteps that have already been loaded. VMD will report in the Text Console the names of the coordinate files which have been canceled.

Figure 4.3: The Files form

4.4.5 Files Form

The Files form is used to load a file from disk. It is not accessible via the button bar on the Main form. Instead, use the Load From Files button in the Molecules form.

To use this form, first select the appropriate file type from the browser on the left (the available file types are described in section §3). One or two text input lines (depending on the molecular structure and coordinate file formats selected) will be displayed in the center of the screen. These need to be filled with the appropriate file names, which can be done in two ways. The easiest is to press the button to the left of the text area to bring up the file browser. The other way is to type the name directly into the text area. To clear the file selection, press Reset; to cancel the operation press Cancel.

Once you've selected the correct file (or files), press the large button that says Load Molecule. The button will disappear and be replaced with a message that says Loading . . . Please Wait. After the files are completely processed, the structural information will be displayed in the text window, and the Files form will be closed automatically.

4.4.6 Graphics Form

The Graphics form is the most complicated form in VMD, which could be expected from a visualization program. The details of most of the subjects discussed below are covered in the special topics on selections [§ 5.3], drawing methods [§ 5], and coloring methods [§ 5.2]. In short, a molecule can have many different representation, also referred to as *views*. Each view consists of three parts: a selection, a drawing method (also called representation style, and a coloring method. The selection determines which part of the molecule is drawn, the drawing method defines which rendering representation is used, and the coloring method gives the the color of each part of the representation.

There are actually two parts to the graphics form. The Image Controls button brings up the controls used to alter the drawing and coloring methods. The Atom Name Lists button provides access to browsers which display the lists of atom names, residue names, and so forth for the selected molecule.

This form is used to control the appearance of one molecule at a time. The molecule it affects is selected in the 'Selected Molecule' chooser at the top of the form. The browser below this chooser lists the views available for the molecule. Each line of the browser shows information about the drawing method, the coloring method, and the selection which completely specify the view. To change the attributes of a given view, click on the view that should be changed. The atom selection for that view will appear in the Atom Selection text area and, if the Image Controls button is pressed, the drawing and coloring method choosers will also change to reflect the current view.

To add a new view of the molecule, enter the selection into the Atom Selection text area (or keep what is there) and press Create New. This adds the view to the currently selected molecule.

To delete a view, select the view in the browser and press the Delete button. Bear in mind that

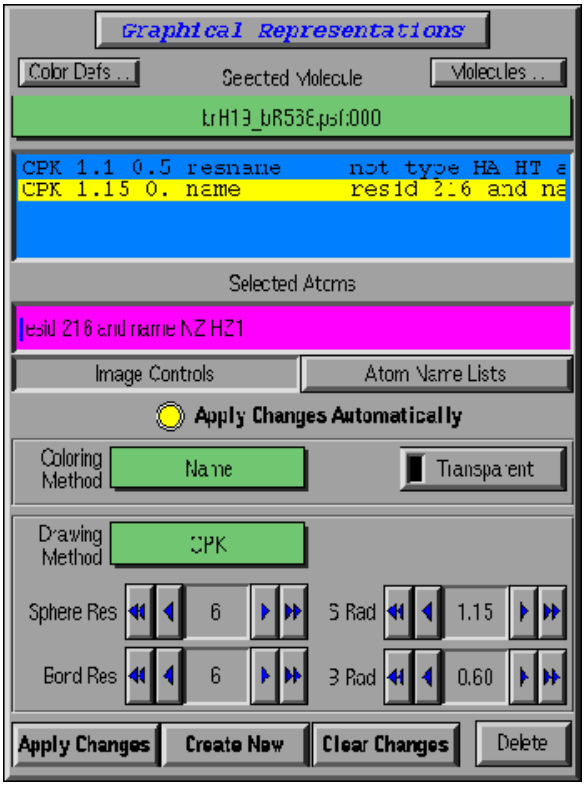

Figure 4.4: The Graphics form (in Image Controls mode)

this does not delete the molecule, it only deletes a view of the molecule. (To delete the molecule, use the Mol form [§ 4.4.3].)

Image Controls

The drawing method indicates how the view's selected atoms are displayed in the graphics display window, and the coloring method indicates how to color the displayed atoms. The selected view's drawing [§ 5] and coloring [§ 5.2] methods are changed via the corresponding chooser. Some of the methods have additional controls which will appear when that particular method (either drawing or coloring) is chosen. The controls for the drawing method are:

- Line Width – only works on some versions of IRIX (see section §11.1).
- Sphere Res – detail level for rendered spheres
- Sphere Rad – sphere radius scaling factor
- Cylinder Res – cylinder resolution (number of sides in the polygon approximation)
- Cylinder Rad – cylinder radius scaling factor

The Material pulldown menu allows you to select a material for the current drawing representation. There are two pre-defined materials, named "Opaque" and "Transparent". Materials can be created

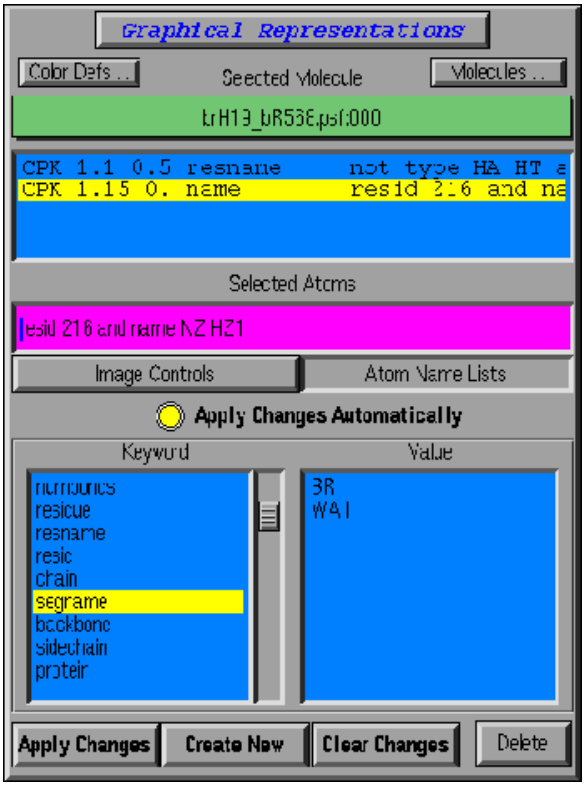

Figure 4.5: The Graphics form (in Atom Name Lists mode)

and modified using the Materials Form. Also, when 'ColorID' is chosen for the coloring method, a text entry box is shown allowing you to specify the index of a color to use for the selection, which may be a number from 0 to 15.

Atom Name Lists

When the Atom Name Lists button is pressed, two browsers appear in place of the drawing and coloring method controls. These are used to list the available keywords and values for use in choosing atoms for the selected views. The left browser contains a list of the keywords and functions understood by the selection command [§5.3]. If a keyword is selected which can take on a value (for instance, `name` and `index`), then the possible names will be displayed in the rightmost browser. The functions can be identified by the `(` to the right of the name. After selecting a keyword, the right browser will display all the names associated with the keyword. For example, selecting *resname* in the left browser will show all the three-letter residue names known for the selected molecule.

Clicking on a field in the value browser will add it to the selection text field. *Double* clicking a keyword field adds the keyword to the text field. A double click is used so that the single click is available for simple viewing of the possible keyword values.

Changing Views

In addition to adding or removing views from a molecule, this form is also used to change how an existing view is displayed. After selecting a view for a specific molecule, the form's controls are updated to show the current settings for that view. Changing the settings will automatically change the respective view, and the new format will be shown in the graphics display window. The display will be updated after every change, however, which is sometimes not always desirable (for example, if a number of different aspects need to be changed at once). The *Apply Changes Automatically* button may be toggled off to change this behavior – if it is turned off, selected changes will only be applied when the *Apply Changes* button is pressed. Selecting a different view, or pressing the *Clear Changes* button, before applying the changes will reset the form controls to the current settings of the selected view.

To clear the selection text for a given view *double* click on the *Clear Changes* button. The first (and every odd) click reverts the text to its previous setting, the second (and every even) click clears it completely.

A few details regarding the mechanism for 'selections' is in order. For beginners, it is best to use the `Atom Name Lists` and the `Image Controls` together in order to generate and organize views. For instance, load a molecule and choose the `Atom Name Lists` option. If you *double* click on the `name` keyword, you will notice that two things happen. First, a listing of values appears to the right of the keyword. Second, the word "name" appears in the text selection window. Now if you go ahead and *single* click on some of the available values, you will notice that they are also printed in the text selection box. In this way you can use the mouse to generate a description of your selection and then hit `Apply Changes` in order to have that description register with VMD. The moral is, if you want to create a complex description quickly with the mouse:

- Use the `Atom Name Lists` to see what your available options are.
- *Double* click on the keyword in order to enter it in the selection text box.
- *Single* click on each of the desired values for the keyword that you want to display.
- Hit the `Apply Changes` button.
- Go back to `Image Controls` and customize your style of presentation

As a final note, keep in mind that both the Color form [§4.4.6] and the Molecule form [§4.4.3] can be accessed from the Graphics form by clicking on the buttons located in the upper corners of the form.

The Tool Selection Button

Next to the `Apply Changes` button on the Graphics Form is the `Tool Selection` button. This button allows the tools defined in the Tracker form to affect certain atom selections, rather than simply a single atom or the entire molecule. Only one atom selection, if any, can be assigned to the tools. To make the assignment, click on the desired representation in the browser window so that it is highlighted, then press the `Tool Selection` button. If you have multiple representations or multiple molecules loaded, the button will be lighted only when the assigned representation is highlighted. To clear the assignment, again highlight the previously assigned representation in the browser window (when it is found, the `Tool Selection` button should be on) and press the button. Deleting the assigned representation also has the effect of clearing the assignment.

For information about how the Tools work with atom selections, see Tool descriptions [§4.4.14].

4.4.7 Animate Form

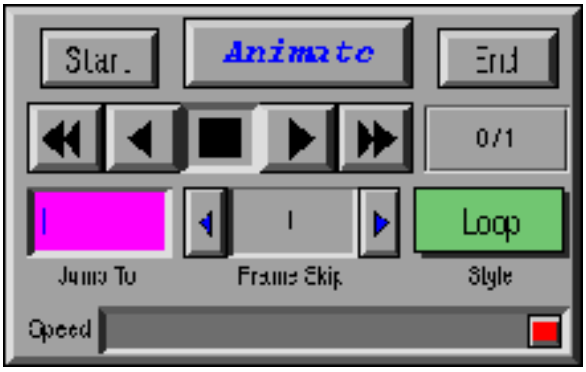

Figure 4.6: The Animate form

Each molecule displayed by VMD can contain multiple sets of atomic coordinates, which may be played back to animate the molecule and show its motion. The source of the coordinates can be, for example, from a molecular dynamics simulation, or simply multiple versions of the same molecular structure. The Animate form is one way to control the playback of these trajectories.

The Animate form handles the trajectory playback of the active molecules [§4.4.3]. The second line of controls contains five buttons which act like the buttons on a tape player or VCR. The center button (with the square) stops the animation. The button to the right of the stop button advances the animation one step forward in the trajectory, and the next button to the right continually steps the animation forward. Similarly, the buttons to the left of the stop button steps the animation backwards either once or continuously. (Just remember that the button that looks like fast-forward is really the play button, and that the one that looks like the play button is really the single step forward button.)

The molecular status shown in this form reflects the state of the *top* molecule. Commands entered via this form, however, affect all *active*, not just the top molecule. This makes it possible to position several different molecules at the same frame, and to start them in motion at the same time with one command. But, since it is not immediately obvious from the information shown in this form what molecules will be affected, some care must be taken to make sure you have the proper molecules active that you wish to animate.

Animation Speed

The rate of playback can be controlled in two ways. The Frame Skip controls change the step size. By default, the frame skip is 1, so each step of the playback increases (or decreases) the animation frame number by one. If the frame skip is 5 then the animation proceeds five times faster because only 1/5 of the frames are shown.

The Speed slider at the bottom of the form also affects the playback speed. Internally, this controls how many screen updates are needed between each step. By default, the slider is at the far right indicating that one step is performed for each screen redraw. Moving the slider to the left increases the minimum time required between updates.

Jumping to Specific Frames

The Start and End buttons are used to simplify the comparison between the initial and final structures - Start resets the current animation to the first frame, and End jumps to the last frame. If you need to jump to a specific frame, enter the frame number in the Jump To text area and press enter. One thing to bear in mind is that the frame number starts at 0, so to jump to the 5th frame, you must actually enter 4 here.

All of the controls affect the active molecules, but two parts of the animate menu use information from the top molecule [§4.4.3]. There is a display just below the End button which shows something like 0/1 or 23/59. The first number specifies the current frame number, starting at 0, and the second gives the total number of frames.

Looping Styles

When the animation is playing forward and reaches the end of the data available for the top molecule, one of three possible actions takes place, as specified in the Style chooser. The default is 'Loop', which will reset the active molecules to the first frame and continue playing forward. 'Once' will stop the animation when it reaches the last frame, and 'Rock' reverses the direction of animation. The actions are symmetrical when the animation is playing in reverse.

4.4.8 Edit Animation Form

Figure 4.7: The Edit Animation form

This form is used to add, save, or delete coordinates sets (also referred to here as *frames*) from a molecule. Usually these coordinates come from successive frames of a trajectory but, as shown in the tutorial **A Quick Animation** [§4.4.8], can also be distinct conformations of the same structure.

When this form is used, it will affect only the molecule selected in the Selected Molecule chooser. There are three types of actions which can take place; read frames from or write frames to a file (in the CRD, DCD or PDB format) or delete frames from the current animation.

Reading Frames

VMD can read in new coordinate sets from PDB files (to add a single new frame to the animation), from ascii CRD files (which may contain several frames), from binary DCD files (which may also contain several frames), or from Gromacs trajectory files. The new coordinate sets are appended to the end of the stored animation list for the selected molecule. At present, there is no way to use Babel to append non-natively-supported files. The format is determined by selecting the appropriate name in the File Type chooser. If you want to read in all the information from the file, make sure that the Amount chooser says 'All', then press the Read button in the bottom right corner. This will bring up the file browser so you can select the file. (Unlike the Files form, the file is loaded immediately after the filename is entered in the file browser.)

Sometimes you may not want to read in a whole CRD/DCD file. For example, you may only want the last frame, or every tenth frame. You can do this by choosing the 'Selected' option in the Amount chooser[§ 4.4.8]. This brings up the frame skip selection controls. Once you've chosen the appropriate values, press the Read button to bring up the file browser and finish as mentioned in the previous paragraph. The Amount options are ignored when reading in PDB files.

Writing Frames

Using the 'Write File' action, you can write the loaded frames to file in either the PDB or the CRD ASCII formats, or you may write to a binary file following the DCD format. This may be used to write out a new trajectory in a single file after assembling many frames from different sources (such as PDB CRD, DCD or Gromacs files, or even from a remote simulation). You can also use this, in combination with Read File, as a way to make PDB files from a DCD/CRD trajectory.

You can either save the entire stored trajectory, or a slice of the data by using the Amount chooser [§ 4.4.8]. Then select the appropriate output file type in the File Type chooser, and press the Write button in the bottom right corner. This brings up the file browser, which you can use to enter the new filename. Once you press the Write button in the browser, the file will be written without further confirmation. See section on `atomselect` command [§ 8.3.19] for information on how to write atom coordinates for an atom selection in a PDB file.

Deleting Frames

This provides a way to delete frames from memory. First, choose the frames you wish to delete with the Amount chooser and (possibly) the frame skip controls, then press the Delete button. There is no confirmation of deletions.

One problem with this mechanism is there is no way to delete every frame except for those given by the frame skip. You can get around this by writing the skip selection to a CRD/DCD file, deleting all the frames from memory, then reading the skip back in from disk.

Amount Chooser

The meaning of this option varies depending on the action. If 'All' is selected, then all the frames will be read from the file, or all the frames will be written to the file, or all the frames will be

deleted from memory.

The other option is 'Selected.' This will bring up three controls, labeled Begin, End, and Skip. These make it possible to use a subset of the frames, starting at frame Begin and selecting every Skip frames until the End is reached. For instance, to select every fifth frame between frames 14 and 98, set:

- Begin to 14
- End to 98
- Skip to 5

(Remember that frame numbers in VMD start at 0, so frame 0 is the first frame.) The value '-1' is a special number; setting Begin to -1 is the same as starting at the first frame, End = -1 is the same as ending at the last frame, and Skip = -1 is the same as taking one step.

When the Action is 'Read File', the selection is applied to the frames from the file to be read. When it is 'Write File', the selection determines the frames to be written, and when 'Delete Frames', the selection determines the frames to be deleted from memory.

4.4.9 Labels Form

Figure 4.8: The Labels form

This form is used to manipulate the labels which may be placed on atoms, and the geometry monitors which may be placed between atoms. Labels are selected with the mouse, as discussed in §4.1.2. Once selected, the Labels form can be used to turn different labels on or off or to delete them entirely. Also, labels displaying geometrical data such as bond lengths may be graphically displayed using this form.

Label categories

The Category chooser (in the upper left) is used to select which category of labels to manipulate. The different label categories include:

- Atoms, which are shown as a text string next to the atom listing the name and residue of the atom;
- Bonds, which are shown as dotted lines between the atoms with the bond length displayed at the bond midpoint;
- Angles, which are shown as dotted lines between the three atoms with the angle displayed at the center of the defined triangle;

- Dihedrals, which are shown as dotted lines between the four atoms with the dihedral angle (the angle between the planes formed by the first three atoms and the last three atoms) shown at the midpoint of the torsional bond.
- dihedrals

All the labels for the selected category which have been previously added are displayed in the browser in the center of the form. The line itself contains from 1 to 4 atom names, depending on the category; the atom names have the form `<residue name><residue id>:<atom name>` followed by either `(on)` or `(off)`. The last word indicates if the label is turned on or off.

Modifying or deleting a label

A label can be turned on or off without deleting it, by selecting the label in the central browser and pressing the Hide button. To turn it back on, select it again then press the Show button. Press the Delete button to delete it. This browser allows multiple selections, which, for example, allows you to delete several labels at once. To select everything in the current category, press Select All; to unselect them, press Unselect All. If nothing is selected, the action is applied to everything. Thus, one way to turn everything off is to press Unselect All then press Hide. (It may seem counterintuitive, but it was done this way so all the labels could be deleted by just pressing Delete.)

Plotting a label's value

If the label has a numeric value (such as a bond length geometry monitor), it is easy to graph the change of the value over time (for multiple frames in an animation). The Graph button creates a temporary file for use by a graphing program, then optionally starts such a program to display the data. Each line of the file contains the frame number (starting at zero and expressed as a floating point number) followed by the value of the label for that frame.

Once the file is created, the text in Graph Command is executed to plot the data. By default, the text is `xmgr %s`, where the `%s` is automatically replaced with the appropriate temporary file name. When the graphing program finishes, the temporary file is deleted.

The default setup causes VMD to freeze until the graphing program finishes. It is possible to get around this by including an `&` at the end of the graph command, as in:

```
xmgr %s &
```

This may sometimes cause a problem because VMD might delete the file before the program finishes reading it. If this is a problem, try:

```
csh -c "xmgr %s &; sleep 4"
```

to cause VMD to wait a few seconds before deleting the file. You may have to increase the delay depending on the file size and type of program used. You may also try variations on the theme; for instance

```
csh -c "xterm -e vi %s ; sleep 4"
```

will bring up a vi window with the data file.

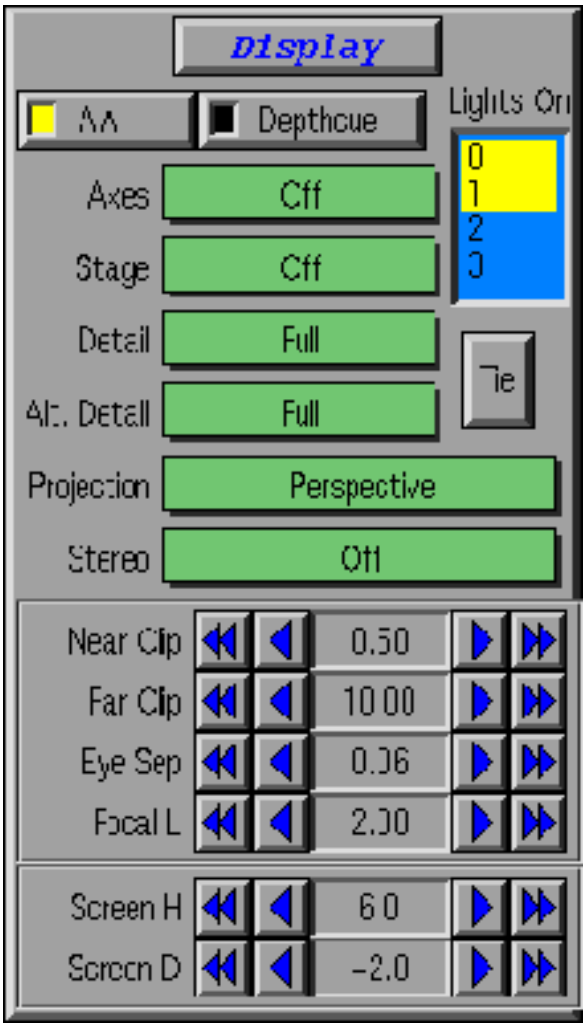

Figure 4.9: The Display form

4.4.10 Display Form

The Display form controls many of the characteristics of the graphics display window. The characteristics which may be modified include:

- **AA** – Turns antialiasing on or off. Antialiasing helps smooth out the jagged appearance of displayed geometry resulting from the inherently discrete pixels on the display device. The antialiasing feature is currently only available on platforms which support full-screen antialiasing, sometimes known as "multisample antialiasing". Several Silicon Graphics systems fully support this feature. On platforms lacking the multisample capability, there may be alternate ways to perform full-screen antialiasing by selecting an option in the display driver setup. Windows machines most commonly place these controls in the display driver configuration panel.

- **Depthcue** – Turns depth cueing on or off. Depth cueing causes the more distant objects to blend into the background color. This can help increase apparent the 3D effect for both stereo and non-stereo display modes. The depth cueing factors are currently fixed, with the depth cueing starting at the default front clipping plane ending at the default rear clipping plane. In order to get the desired visual effect, one may need to scale and translate the molecule for best effect. Scaling the molecule up (making it larger) will increase the amount of depth cueing effect that is visible on the molecule. Scaling the molecule size down decreases the depth cueing effect. Translating the molecule away from the camera will cause it to take on more of the background color, translating it toward the camera will cause it to take on less of the background color.

- **Axes** – A set of XYZ axes may be displayed at any one of five places on the screen (each of the corners or the center) or turned off. This is controlled by the Axes chooser.

- **Stage** – The Stage browser controls the stage, which is a checkerboard plane that can be located in any one of six places or turned off.

- **Detail** – The degree of detail in the displayed image. Nothing: show nothing; Points: show everything as points; Wireframe: show only wireframe representation for spheres, cylinders, etc.; Flat: show a flat image (no 3D effects); Full: show complete detail. The performance increases as the level of detail decreases.

- **Alt. Detail** – Same as Detail, but for the display during mouse operations on the displayed molecules, such as rotation, translation and scaling. Since VMD redraws the screen often while the molecule is rotated, it is sometimes beneficial to set lower level of detail for the time of rotation for better performance.

- **Perspective** – The view of the scene can be Perspective or Orthographic. In the perspective view (the default), objects which are far away are smaller than those near by. In the orthographic view, both objects appear at the same scale. Note that several of the supported external rendering programs do not support orthographic rendering. As such, it may be necessary to "fake it" by translating the scene far away from the camera, and apply a zoom factor. This has the effect of significantly reducing the perspective, while not truly an orthographic view.

- **Stereo, Eye Sep, and Focal L** – These controls set the stereo mode and parameters; stereo is discussed fully in chapter §7. The Stereo chooser changes the stereo mode, while the Eye Sep and Focal L controls change the eye separation distance and the focal length, respectively.

- **Lights** – The graphics display window can use up to four separate light sources to add a realistic effect to displayed graphical objects. The Lights On browser turns these light sources on or off. If the number is highlighted, the light is on, and clicking on it turns the light off. See sectin §4.1.1 for more discussion regarding lights.

- **Clipping Planes (Near Clip and Far Clip)** – Clipping occurs when only the part of an image within a certain region of space is drawn. Only those parts of graphical objects which are between the near and far clipping planes are drawn. This feature is useful for viewing a slice of the molecule. The clipping planes also affect the depth cueing, if it is turned on. Objects at the near clipping plane are distinct while objects at the far clipping plane are indistinguishable from the background color.

The positions of the clipping planes are changed with the Near Clip and Far Clip controls. It is not possible for the near clip to be farther away than the far clip. When using stereo, it may be useful to set the near clip plane much lower than the default value, or even set to zero. This makes the geometry "pop out of the screen" a bit more, and can be used for greater dramatic effect.

- **Screen Height (H) and Distance (D)** – The screen distance parameter determines the distance, in 'world' coordinates, from the origin to the display screen. If this is zero, the origin of the coordinate system in which molecules (and all other graphical objects) are drawn coincides with the center of the display. If it is less than 0, the origin is located between the viewer and the screen, while if it is greater than 0, the screen is located closer to the viewer than the origin. A negative value puts any stereo image in front of the screen, aiding the three-dimensional effect; a positive value results in a stereo image that is behind the screen, a less dramatic effect (but easier to see, for some people) stereo effect.

  The screen height, along with the screen distance, defines the geometry and position of the display screen relative to the viewer. The screen height is the vertical size of the display screen, in 'world' coordinates. Each molecule is initially scaled and translated to fit within a 2 x 2 x 2 box centered at the origin; so the screen height helps determine how large the molecule appears initially to the viewer. This parameter is used mainly to configure the VMD display to the dimensions and position of a large-screen display, such as a projector, that may be used as a stereo display.

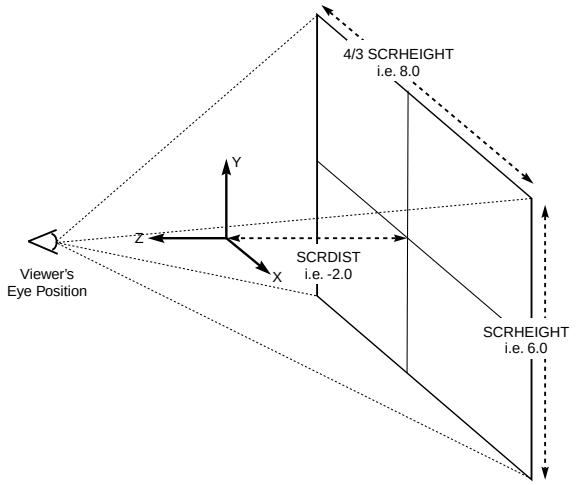

Figure 4.10: Relationship between screen height (SCRHEIGHT), screen distance to origin (SCRDIST), and the viewer

Figure 4.10 describes the relationship between the screen height, the screen distance, and the world coordinate space.

4.4.11 Color Form

VMD maintains a database of the colors used for the molecules and the other graphical objects in the display window. The database consists of several color *categories*; each color category contains

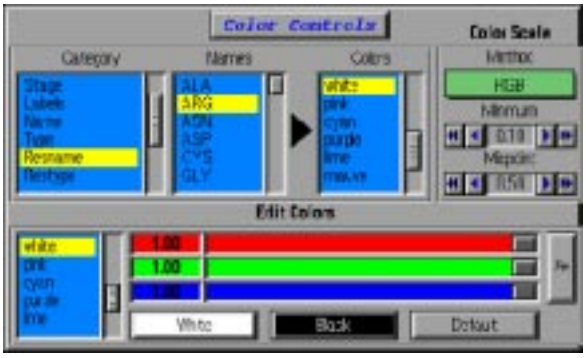

Figure 4.11: The Color form

a list of names, and each name is assigned a color. The assignment of colors to names can be changed with this form. There are 16 colors, as well as black (the VMD color *map*), and this form can also be used to modify the definitions of these 17 colors. For more about colors, see the chapter on Coloring [§5.2].

To see the names associated with a color category, click on the category in the Category browser located on the left side of the form. Click on the name to see the color to which it is mapped. To change the mapping, click on a new color in the browser to the right of the Category browser. For instance, to change the background to white, pick 'Display' in the left browser and 'Background' in the center one. The right browser will indicate the current color (which is initially `black` for the background). Scroll through the right browser and select `white` to change the background.

Changing the RGB Value of a Color

Sometimes you may want to change the RGB value of a color in the color map, instead of changing which color is assigned to a particular name. For example, you may need to make a black and white picture and need to emphasize the contrast between a red oxygen and a yellow sulphur. This is done with the Edit Colors part of the form. First, choose the color you want changed in the browser. Then move the red, green, and blue sliders until you get the desired color. There are a few additional buttons to help you do this. The white button makes the color white (red = blue = green = 1.0) and the black color makes it black (red = blue = green = 0.0). The default button restores the color to its original RGB values. The tie button is used to make grey colors; when the button is depressed, as you move one slider the rest will follow. Press the tie button again to untie the sliders.

For example, suppose, we don't really like the appearance of the green color and we want to make it darker. To see what is happening we'll change the color of the background, so choose Display in the category field of the upper part of the Color form, then choose Background, and, finally, choose green. The background should become green. The (default) RGB values are 0.20, 0.70, 0.20. To make the color darker, let's bring the RGB values down by moving the red, green and blue sliders to the left. You can see the color changing as you move the sliders, so this way you can easily pick the color you prefer to be named 'green'. The definition can be immediately brought back to the default values by pressing the 'Default' button on the form.

Color Scale

Several of the coloring methods in the graphics form are used to color a range of values, as compared to a list of names. The actual coloring is determined by the color scale [§5.2.4].

There is only one color scale available at any one time (out of the ten possible) and it is changed with the Color Scale Method chooser. Changing the values of Minimum and Midpoint change some of the proportionality values used in making the scale.

The colors used by the color scale are not the colors in the color map, so the Edit Colors part of the form will not affect the color scale colors.

4.4.12 Material Form

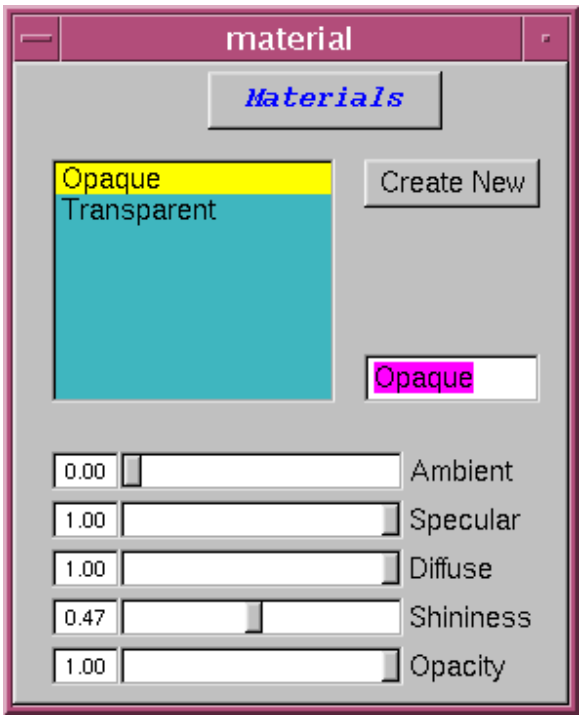

Figure 4.12: The Material Form

This form is used to create and modify material definitions. The material definitions created here will show up in the pulldown menu in the Graphics Form, allowing you to apply a material to a given representation.

The upper left corner of the Materials Form contains a browser listing all the currently defined materials. Below this browser is a set of five sliders which indicate the current materials settings for the material highlighted in the browser. Highlighting a different material in the browser by clicking with the mouse will update the settings of the sliders. Conversely, moving the sliders will change the definition of the the currently highlighted material in the browser. However, settings for the first two materials, named "Opaque" and "Transparent", cannot be changed.

To create a new material, press the "Create New" button in the upper right corner of the Form. A new material with a default name will be created and displayed in the browser window. This

name can be changed at any time to something more descriptive by typing in the input box to the right of the material browser and pressing ¡enter¿. You can now edit the properties of this material using the sliders at the bottom of the form. All materials in the materials browser, including those you create, will appear in the Material pulldown menu in the Graphics form.

To experiment with the material settings, first create a new material so that you can edit its values. Next, load any molecule, change its drawing method to VDW representation, and using the Material pulldown menu in the Graphics form, change the representation's material to the material you just created. Now, go back to the Materials form, highlight the new material in the browser, and change some of the values in the sliders. The effect of changing shininess should be especially dramatic.

4.4.13 Render Form

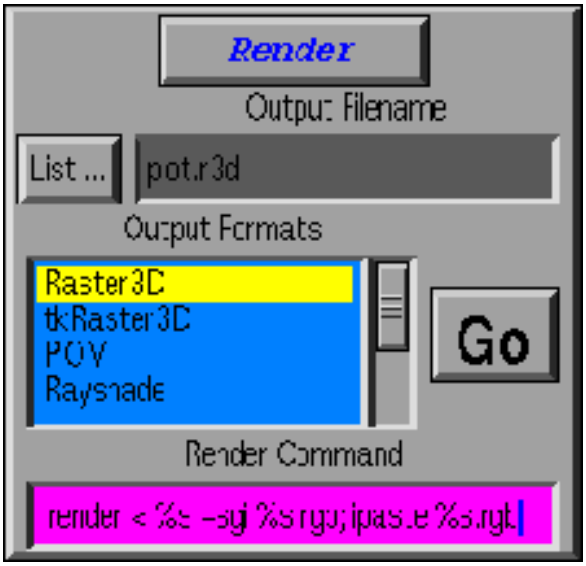

Figure 4.13: The Render form

This form is used to create a file with an image of the currently displayed graphics scene. VMD can write input script files for a number of external rendering packages. These packages are listed in table 6.1. Once VMD creates a scene description in one of the supported formats, the particular package can use this file to create a final output image. See Chapter § 6 for more information on how rendering is performed.

Rendering

The rendering process works in two stages. The first step writes an input file for the image processing program selected in the Output Formats browser, and the second (optionally) starts the rendering process. The file is given the name entered in the Output Filename field; a default name is given when a new format is selected, so it is best to hold off entering the filename until after the file format is selected. Another way to select the filename is available by pressing the List... button, which opens up a file browser.

Pressing the Go button writes the data file. After that, the Render Command is executed. The default command should start the appropriate rendering program if it is available.

The fastest of the currently supported programs are Raster3D and Tachyon . The rendering command for Raster3D has been set up to call the programs program `ipaste` or `xv` when the RGB output file is finished. VMD will wait for the rendering to finish, which causes VMD to freeze, so you may want to run the job in the background. This can be done by enclosing the existing text with `()`'s and putting an `&` at the end. For example, the way to make the Raster3D render command run in the background is:

```
(render < %s -sgi %s.rgb; ipaste %s.rgb)&
```

Caveats

There are some issues to consider when using the rendering commands, which can lead to discrepancies between the scene displayed in the VMD graphics display window and the image generated by external rendering applications. These issues include:

- Geometry may look slightly different; in VMD curved surfaces are polygonalized and drawn using a number of polygonal facets, curved surfaces may be rendered entirely smoothly in the final output (which is generally looked upon as an improvement!)
- The rendered object colors or intensities may be slightly different due to different colormaps, gamma values, or lighting models; This is particularly true with the material properties used for performing complex shading. VMD's real-time rendering of these material properties is often simplistic or limited compared to full-fledged photorealistic renderers, so there can potentially be big differences between implementations of transparency, specular highlights, etc.
- Many of the external renderers do not support true orthographic rendering. This can bed "faked" by translating the camera very far away from the molecule, followed by zooming the camera so that the image size is acceptable again. This will significantly decrease the perspective effect, but is not a true orthographic projection.
- The rendering commands do not currently support stereo output, so even if the display is currently in stereo mode, a non-stereo perspective will be used for the rendering program input script; Rendering in stereo is accomplished by setting the display mode to "left", then rendering an image, followed by "right", and rendering again. This will yield a stereo pair to the best of VMD's ability with the external rendering program.
- The near and far clipping planes are ignored by all external renderers;
- Text is generally not available as a graphics primitive in the renderer scene languages, so label text will not appear, although the lines of bond, angle, etc. labels will be drawn. The only exception is in Postscript output, which supports text output.
- Dotted spheres are not drawn with dots.
- The background color may be black, as not all output formats support a background color other than black;

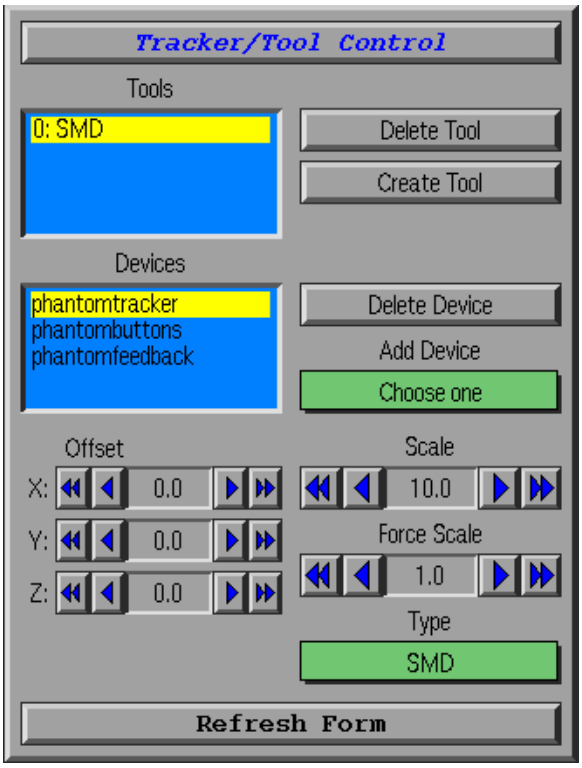

Figure 4.14: The Tracker form

4.4.14 Tracker Form

The Tracker form is used to set up external 3D pointers, buttons, force-feedback devices, and the VMD "tools" that they control.

Supported devices and how to configure them

VMD currently can only communicate with devices in two ways: through the CAVE software or using the Virtual Reality Peripheral Network (VRPN). VRPN is a system which allows workstations to use many types of devices over the network. This means that VMD does not have to be running on the same computer that the devices are plugged into. In the CAVE, VMD recognizes two types of devices: buttons and three-dimensional trackers. With VRPN, you may use buttons, trackers, and also force-feedback (haptic) devices such as the PHANToM. More types of devices may be added in the future.

To use these kinds of devices with VMD, you need to create a *sensor configuration file*, in your home directory, called `.vmdsensors`. In this file, any number of devices can be specified, using a *universal sensor locator* (USL). The format for a USL is as follows:

- *USL* – *type*`://`*place*`/`*name*`:`*nums*
- *type* – the type of sensor (`vrpntracker`, `vrpnbuttons`, `vrpnfeedback`, `cavetracker`, or `cavebuttons`)

- *place* – the machine that controls it. Devices that cannot yet be used on arbitrary computers over the network must have the keyword `local` here to be compatible with future versions.
- *name* – the name of the device within that machine. If multiple devices can't currently exist, such as with the CAVE, then a standard name should be used, such as `cave`, so that the same USL will make sense in the future, when multiple devices are allowed.
- *nums* – a comma-separated list of numbers of devices belonging to that names (optional, defaults to zero). Some devices demand only one number or a specific number but button devices should work correctly now.

The lines of a sensor configuration file come in four flavors:

- *Comments* begin with `#` and are ignored.
- *Empty lines* are also ignored.
- *Device lines* have the form `device` *name USL*, where *name* is the name that VMD will use to refer to the device, and *USL* is the device's USL.
- *Options* tell VMD how to use the most recently listed device. Currently, there are four supported options:
  - "`scale` x" scales the position of a tracker by a factor x.
  - "`offset` x y z" adds a constant vector to the position of a tracker.
  - "`rot right`—`left` A_{00} $A_{01} \ldots A_{33}$" multiplies the orientation matrix returned by a tracker on either the right or the left by the matrix A.
  - "`forcescale` x" multiplies the force applied to a force-feedback device by the amount x.

Here is an example, showing all the possible things you can do with a sensor configuration file:

```
# the PHANToM connected to the computer "odessa"
device phantomtracker vrpntracker://odessa/Phantom0
scale 10
rot left 0 0 -1 0 1 0 1 0 0

device phantombuttons vrpnbuttons://odessa/Phantom0
device   phantomfeedback vrpnfeedback://odessa/Phantom0

# Polhemus fastrak on titan
device fastrak1 vrpntracker://titan/Tracker0:0
rot right 0 0 1 1 0 0 0 1 0
rot left 0 0 -1 -1 0 0 0 -1 0
device fastrak2 vrpntracker://titan/Tracker0:1
rot right 0 0 1 1 0 0 0 1 0
rot left 0 0 -1 -1 0 0 0 -1 0

#### Configuration for the CAVE
# CAVE tracker
```

```
device cavetracker cavetracker://cave/cave
scale 0.32
offset 0 -3.03 0

# CAVE buttons
device cavebuttons cavebuttons://cave/cave:0,1,2,3

# CAVE buttons (for left-handers)
device cavebuttons cavebuttons://cave/cave:3,2,1,0
```

Using devices with VMD

There are several different "tools", each of which can be used with any of the input devices[1]:

- The **Grab Tool** mimics a pair of tweezers, and can be used to move molecules around on the screen without any keyboard or mouse commands. Pressing a button connects the 3d cursor to the nearest molecule. Then, moving or rotating the tracker will cause the molecule to move or rotate around on the screen.

- The **Rotate Tool** is a tool for precisely rotating molecules with haptic devices. When a button is pressed and released, the cursor is again connected to the molecule. With this tool, however, the center of the molecule is fixed, and the end of the haptic pointer is forced to lie on the surface of a sphere about this center. Moving the device around the surface of the sphere rotates the molecule, and another button click releases the molecule. There are detentes — like the clicks commonly felt in a 2d dial — on the surface of the sphere, arranged so that the user can rotate the molecule to precise 90-degree points. If the user holds down the button for a while initially, he can feel the sphere and the detentes, but do not affect the molecule. This "preview mode" allows the user to find a good point from which to start the rotation.

- The **Joystick Tool** is the three-dimensional equivalent of a Joystick, for haptic devices. Pressing the button creates a virtual "spring," holding the device to its current location. If it is pushed away from this point in some direction, the selected molecule starts sliding in that direction, with a velocity that is proportional to the displacement of the device. The joystick tool shows how a three dimensional input device can be used to supply relative (differential) coordinates instead of absolute coordinates.

- The **Tug Tool** is a tool that allows interaction with running molecular dynamics simulations. Pressing the button connects the device with a simulated spring to the nearest atom, and pulling on it adds a force to the simulation. If a haptic device is being used, the user will feel a force on his hand that is proportional to this force. In this way, the tug tool implements something like the click-and-drag that is commonly used with windowing systems.

  If an atom selection is assigned to the Tools, as described in section 4.4.6, the the Tug Tool will apply a force to all the atoms in the selection. The force applied will be proportional to the masses of the atoms in the selection, so that all atoms experience the same acceleration. When a Tool Selection has been assigned, the Tug Tool will always affect that selection, even

[1] The new tools have been designed to allow VMD to use haptic devices in many ways. All of the tools can give force-feedback to the user, but none of them actually require haptic devices to work.

if the button is pressed far from any atoms in the selection; this is intended to make it easier for the user to apply forces only on those atoms he/she intends to steer.

- The **Pinch Tool** is similar to the Tug Tool, except that force is applied only along the axis defined by the orientation of the tracker.
- The **SMD Tool** is a tool intended for use with steered molecular dynamics (SMD). It allows the user to pull on atoms in only one direction, so that the forces and motions of the molecule can be more easily analyzed. The user clicks at a "target point", drags the pointer back to the atom he wishes to pull on, then releases the button. The tool now behaves like a tug tool, but forces are restricted to lie parallel to the line through the atom and the target point. Using the SMD tool with a haptic device feels like pushing against a non-rotating, frictionless plane, since the forces applied to the user's hand must also all point parallel to this line. The force applied and the position of the atom are automatically recorded to the file `pull.txt`.

To add a new tool to a VMD session, open the tracker form and click the **Create Tool** button. The tool's number and type are displayed in the list to the left. Devices can be added to the tool by selecting them from the **Add Device** menu, or removed with the **Delete Device** button. Some of the options that can be specified in the sensor configuration file can be edited in using the controls below, and the tool's type can be changed with the **Type** menu.

4.4.15 Sim Form

Interactive Molecular Dynamics

VMD has the capability to work with a molecular dynamics program running on another computer, in order to display the results of a simulation as they are calculated; we refer to this capability as Interactive Molecular Dynamics (IMD). As new atomic coordinates are generated by the simulation process, they can be transferred directly over the network to VMD, which can then animate the molecule. A major feature in VMD is the ability to add perturbative steering forces to a running simulation, which are incorporated directly into the dynamics calculation.

In order for VMD to work in this fashion as a graphical front end and control console for a remote molecular dynamics simulation, it is necessary to have a version of a molecular dynamics program configured for IMD communication. The program NAMD, developed the the University of Illinois Theoretical Biophysics Group, will support IMD beginning with release 2.1. See the NAMD WWW home page[2] for information on obtaining a copy of NAMD. NAMD is a parallel molecular dynamics program written in C++, which implements the CHARMM energy function. It is compatible with X-PLOR style PSF files, but can use either X-PLOR or CHARMM parameter files. The rest of the discussion in this chapter assumes you are using NAMD.

IMD works by establishing a TCP connection between VMD and NAMD. NAMD, or whichever molecular dynamics program is being used, acts as the server. In order to prepare NAMD to accept VMD's connection request, NAMD must be instructed at the time the program starts to listen for incoming connections on a particular port. Once NAMD has started up, it will wait for the user to connect through VMD through that port. VMD and NAMD perform a handshake sequence to determine things such as the relative endianness of the machines, then the simulation commences.

Before connecting to the remote simulation, the VMD user must first load a molecule corresponding to the system being simulated. This can be done within the Load Files form by selecting

[2] http://www.ks.uiuc.edu/Research/namd/

"IMD" as the molecule type, then choosing a psf and pdb file for loading. It is not necessary that the coordinates in the pdb file bear any relation to the simulation coordinates, since they will immediately be replaced when VMD starts receiving coordinates from NAMD. However, the psf file should be the same file used in the NAMD configuration file. The pdb and psf files can also be loaded at the command line in the VMD console, using the command "mol load imd ¡psffile¿ pdb ¡pdbfile¿". Note that a molecule must be loaded in one of these two ways for a connection to be established.

Once the molecule is loaded and NAMD has been started and is listening for a connection, the user is ready to connect to the simulation and start receiving coordinates. To establish a connection, open the Sim form, enter the hostname on which NAMD is running and the port on which NAMD is listening for incoming connections, then press the Connect button to establish the connection. If NAMD is running on several distributed nodes, VMD must connect to the root node on which NAMD initially started out.

Using the Sim form

The Sim form allows you to control the behavior of a molecular dynamics simulations which has been previously connected to through use of the Remote form. This form contains controls to change parameters for the simulation and to affect how VMD displays the results of the simulation. The form also contains informative displays, which show the current status of the simulation connection, and such things as the current energy, temperature, and timestep of the molecular system being simulated.

At the top of the form are two entry fields and a button for establishing a connection to a running MD simulation. Enter both the hostname on which the simulation is running, and the port on which the simulation is listening, then press the Connect button to establish the connection. See the text console for possible error messages and status updates.

Below the connection display is a browser used to set some connection parameters. These include:

- **Transfer Rate**: How often a timestep is transferred from the remote simulation program to VMD. By default, this is 1, which means every calculated timestep is sent. If this is set to some value N, then only every Nth step will send from the remote computer. If you have the dubious misfortune of receiving coordinates faster than VMD can process them, or if you simply don't care to receive coordinates very often, setting this transfer period higher will improve the performance of both VMD and the simulation.

- **Keep Rate**: How often VMD saves the timestep in its animation list, instead of just discarding it after displaying it. By default, this is 0, which means that VMD does not save any frames. When this is 0, then when VMD receives a new frame it *replaces* the last frame in the animation list with the new frame, instead of *appending* it. When it is set to some number N larger than 0, then every Nth frame received from the remote simulation will be appended to the animation list, instead of being used to replace the last frame.

To change a parameter, select the line with the relevant parameter, and in the text entry area that appears enter the new value and press `<return>`. After you enter a new value, a command will be sent to the remote simulation to change it, and there may be some delay between when the simulation gets the command, acts on it, and the results propagate back to VMD.

In the central portion of the form is shown a *status message* for the chosen connection. A large browser near the bottom of the Sim form displays the different energy values for the system being

simulated (kinetic, electrostatic, etc.), as well as the current timestep and the temperature. It is automatically updated each time a new atomic coordinate set (timestep) is received and stored in the VMD animation loop.

At the bottom of the Sim form are two buttons:

- The Kill button, which when pressed will terminate the remote simulation which is currently selected in the connection chooser. This will not delete the molecule stored in VMD's internal lists, it will just stop the remote program from executing (and thus stop the transfer of new timesteps from that program to VMD). You must go to the Molecule form and delete the molecule from that list to completely remove the molecule from VMD memory.

- The Detach button, which when pressed will sever the connection between VMD and NAMD, but will NOT kill the NAMD process. Instead, the simulation will be left running.

Chapter 5

Molecular Drawing Methods

Each molecule in VMD is drawn as several *representations*, or *views*, of the molecule. A view is just one particular way of drawing the molecule, and consists of three characteristics:

- A *rendering* method (representation *style*), which determines what shape to draw the atoms, bonds, and other components of the molecule. Section § 5.2 describes the rendering methods available in VMD.
- A *coloring* method, which determines how to color each of the atoms and bonds included in the view. The Graphics form contains controls to set the coloring method at the right of the form. Section § 5.2 describes VMD's coloring methods.
- An *atom selection*, which determines which of the atoms in the molecule will be included in the view. This selection is entered in the text input field at the bottom of the Graphics form. Section § 5.3 describes the syntax used to select atoms.

A molecule can contain any number of different representations, and complex pictures of the molecule can be generated by creating views with different selections, coloring schemes, and rendering methods. For example, the protein backbone can be drawn as a smooth tube in one view, and important residues in the protein can be drawn as spheres or licorice bonds in other views. When a molecule is first loaded, it is given a 'default' view, which will draw all the atoms as lines and points, coloring each atom by what kind of element it is.

5.1 Rendering methods

All of the different rendering methods have various parameters which determine how they are drawn. For each method, there are controls in the Graphics form which modify the associated parameters, such as the line width and sphere resolution (the graphical controls are described in section §4.4.6). Table 5.1 lists the available rendering methods, and the following sections describe these methods and the parameters which modify their appearance.

5.1.1 Lines

The default representation is 'Lines', which is also known as 'wireframe'. It draws a line between each atom and the atoms to which it is bonded. Both atoms have to be selected before the bond

Representation styles	Description
Lines	simple lines for bonds, points for atoms
Bonds	lighted cylinders for bonds
CPK	scaled VDW spheres, with cylinders for bonds
Points	just points for atoms, no bonds
VDW	solid van der Waal spheres for atoms, no bonds
Dotted	dotted van der Wall spheres for atoms, no bonds
Solvent	dotted representation of the solvent accessible surface
Trace	connected cylindrical segments through C_α atoms
Licorice	spheres for atoms, cylinders for bonds, same radius
Ribbons	flat ribbon through the C_α atoms
Tube	smooth cylindrical tube through the C_α atoms
Cartoon	cartoon diagram (cylinders and ribbons) based on secondary structure
MSMS	molecular surface as determined by the program MSMS
HBonds	display hydrogen bonds
Surf	molecular surface as determined by SURF
Off	do not draw anything

Table 5.1: Molecular view representation styles.

will be drawn. The first half of each bond is colored appropriately for the first atom, while the color of the final half corresponds to the second atom.

The only parameter for this option is the line thickness. On some SGIs you will only notice a difference between settings of 0, 1, and 2. Anything beyond 2 looks the same as 2. To understand why, you should see the man page for `linewidth` (look at an excerpt from that man page in section §11.1).

5.1.2 Bonds

Nearly everything about this option is the same as lines except that instead of drawing a bond as a line between two atoms, a cylinder is drawn instead. To be more specific, it draws an n-sided prism, where the number of sides is determined in the Graphics form by the "Bond Res" control and the radius is given by the value of "Bond Rad," in Angstroms. If the radius or number of sides gets too small, the bonds are drawn as lines.

In order to fine tune the bond representation, VMD does a small amount of trickery to the prisms. That is, imagine two hollow cylinders coming together so that the center of the face of one cylinder is in the same position as the center of the face of the other cylinder. Also suppose these two cylinders come together at 90 degrees. Although most of these two cylinders will overlap, there will appear to be a gap at their intersection.

To correct for this problem, VMD extends both cylinders somewhat so that the far ends touch. If one looks closely, this produces more of an overlap, but it is much nicer looking than the gap. When three or more bonds join at one atom, VMD chooses the lowest numbered bond and extends all other bonds to meet with that one. It then extends that lowest numbered bond to meet with the second lowest numbered one. A bit technical, but not too difficult to do.

5.1.3 CPK

'CPK' is a combination of both 'Bonds' and 'VDW' in that it draws the atoms as spheres and the bonds as cylinders. The resolution and radius can be modified independently. The radius of the sphere drawn in CPK mode is by default smaller than the sphere drawn in VDW mode, but this radius can be made larger. Since a sphere is drawn for each atom, it will always be slower than the VDW option, but we will work on performance for future versions. If the values for a sphere or bond attribute are too small, then those objects will not be drawn.

5.1.4 Points

'Points' draws each atom as a point, and does not draw any of the bonds. This option is not terribly useful.

5.1.5 VDW

'VDW' draws the atoms as spheres. The radius used is the van der Waals radius multiplied by a user-selectable scaling factor. The sphere resolution determines how finely to tessellate the spheres that are drawn. Drawing spheres takes some time, since they are built from many polygons.

Note:: Due to variations in atom naming conventions, in rare instances VMD may improperly assign VDW radii to specific atoms, since VMD determines each atom type based on the first letter forming its name. For example, VMD would assume an atom named "HG" to be a hydrogen rather than a mercury. If this happens, you are always free to redefine the radii, using a syntax much like that below:

```
set sel [atomselect top ``name HG'']
$sel set radius 1.9
```

5.1.6 Dotted

Same as 'VDW' except that the spheres are drawn dotted instead of solid. That is, a dot is placed at each of the vertices of the triangle making up each sphere. This can be used, for instance, to imitate a surface representation.

5.1.7 Solvent

This method is similar in spirit to the Dotted representation in that it gives a quick estimate of the molecular surface with a collection of dots. However, it goes above and beyond the Dotted option by giving a more uniform coverage of the surface. The method that VMD uses to check for overlaps isn't technically correct, but it is fast and works quite well. A technical description of the algorithm is as follows:

For each point of the surface distribution (of radius r = atom radius + probe radius) of atom i, check each of the atoms j to which it is covalently bound. If the point is too close to j, don't display it. Also, if the point is too close to any neighbor k of j ($k \neq i$) then don't draw it. This is fast since there aren't that many neighbors to check, but it doesn't omit parts of the surface in contact with atoms which aren't one or two bonds away. This can be considered a good thing since you might get a better idea of the contact surface.

There are three parameters for this option. One is the probe radius, which was mentioned in the description. If the probe radius is too large, the problem of over-lapping surfaces between non-connected atoms becomes more apparent. The second is "Detail", which should probably be renamed "Density" as it determines the surface density of the distributions. The higher the detail, the higher the density. The final option is the "Method". By default the surface is drawn as a collection of points, but a point is a pixel in size regardless of the scale of the molecule, so when scaled small the surface density appears high, and when scaled large, the density appears low. Method 2 draws little plus signs instead of points, which does scale better so the density appears more contant. Method 3 draw lines between the surface points that are on the same atom, but makes no attempt to connect the two spheres.

Thanks to Jan Hermans for implementation pointers and thanks again to Jon Leech for the code to compute the uniform point distributions. That code was included as part of the 1.x distribution.

5.1.8 Tube

There are two ways to draw a 'Tube' representation, one for proteins and the other for nucleic acids. The protein tube is a smooth curve through the selected C_α positions, and the nucleic acid tube is a smooth curve through the backbone phosphates.

The protein tube is a spline curve that passes through all the C_αs in a protein fragment. Five evenly spaced interpolation points are found along the curve to break the curve connecting the two C_αs into six line segments. If the first C_α is selected, the first three segments are colored by the color assigned to that C_α. If the second C_α is selected, the last three segments are colored by the color of the second C_α. The nucleic acid tube is constructed in the same manner except that the phosphate atoms are used.

The two controls set the spline radius and resolution and have the same meaning as they did in the 'Bond' control. However, if the bond radius becomes 0 or the bond resolution is 2 or less then the spline is drawn as a simple line. This make moving and rotation the image much faster.

It is possible to pick with the mouse the C_α which defines the tube by clicking near the middle of the six tube segments which are associated with that atom.

5.1.9 Trace

This representation applies much of the procedure used to construct the Tube. In the end, it connects the alpha-carbon atoms of successive residues by cylindrical segments with adjustable width. In the case of nucleic acids, it is the P backbone atoms which are connected. As always, the segment pieces are colored according to the atom they are associated with. If the cylinder radius is made 0.00, then the cylinder segments are replaced with lines.

Note: the Trace option is useful for people doing threading or protein folding work who only look at the C_α coordinates and residue names, for then they don't have to build the sidechains necessary to see their structure. Also, people working on polymers can fake their structure by naming everything "CA." in the PDB file and then using Trace.

5.1.10 Licorice

'Licorice' draws the atoms as spheres and the bonds as cylinders. The difference between this and 'CPK' is that the sphere radius is not controllable; instead, it is made the same size as the bond. This makes for a nice, smooth transition and is one of the most often used representations. It can be rather slow for large molecules.

5.1.11 Ribbon

The 'Ribbon' representation is similar to 'Tube' in that it follows the same spline curve for both the protein and nucleic acids. However, it uses additional information (the O of the protein backbone or some of the phosphate oxygens for nucleic acids) to find a normal for drawing the oriented ribbon. (There may be some problems with the ribbon definition for nucleic acids as it is possible for the nucleic acid detection routine to label a residue as a nucleic acid even though it does not have phosphate oxygens.)

Given the coordinates of each atom and the offset vector for the ribbon vector, the drawing code finds the spline curves for the top and bottom of the ribbon. The two splines are connected by triangles and both splines are drawn as small tubes. As with the 'Tube' representation, the six ribbon segments nearest the given atom are drawn with the color assigned to that atom and the atom can be selected by clicking near the center of those six elements.

Bond radius and resolution modify the tubes that make up the top and bottom of the ribbon. If the radius or resolution get too small, the tubes are not drawn (this speeds up drawing time by an appreciable amount). The line thickness controls the width of the ribbon and make it look like everything from vermicelli to lasagna. Additionally, the sugars are drawn filled in with triangles. This helps highlight the pucker.

Thanks to Ethan Merrit for the ribbon drawing algorithm taken from Raster3D.

5.1.12 Surf

This option uses the molecular surface solver written by Amitabh Varshney when he was at the University of North Carolina. When this option is used, the radii and coordinates are written to a temporary file and the 'surf' executable is run with the probe radius as a parameter. When finished, the output is written to another temporary file which is then read by VMD and colored and displayed. The value of the probe radius is controlled by the sphere radius, and this is identical to the probe size in Å.

- Probe – Probe radius used to construct the molecular surface
- Wireframe – The surface can optionally be drawn using lines rather than solid triangles

This surface is rather slow in both generation and display for systems over several hundred atoms. The SURF calculation is quite exact and will show complete detail even when it isn't needed. The use of disk space as an interprocess communications medium takes up about half of the run time.

There is an environment variable which can affect the Surf display option:

- `SURF_BIN` – location of the SURF binary (defaults to `SURF_$ARCH` as defined in the vmd startup script)

A helpful trick when constructing surfaces is to use the "Apply Changes Automatically" toggle button on the graphics form wisely. That is, since surfaces often take a long time to build, changing viewing parameters such as the probe radius can cause long delays. By default, each time you hit the probe radius button, VMD rebuilds the surface. If you want to reduce or enlarge the probe radius by several increments, then you would end up rebuilding the surface multiple times. By toggling the afore-mentioned button, you can force VMD to update on your command only. This trick is sometimes helpful with other representations as well.

For a much faster but possibly less precise surface rendering method, see the description of MSMS later in this document.

5.1.13 Cartoon

The 'Cartoon' option produces a simplified representation of a protein based on its secondary structure. Helices are drawn as cylinders, beta sheets as solid ribbons, and all other structures (coils and turns) as a tube. If the secondary structure has not yet been determined, it will be calculated automatically by the program STRIDE.

A helix cylinder is constructed by finding the least squares linear fit along the coordinates of the helix's C_α atoms. If a given residue's C_α is selected, the small cylinder (found by linear interpolation along the line of best fit) is drawn with radius determined by the ??? parameter. Because this method computes a best fit, a helix must have at least 3 residues before it is drawn (those helicies with one or two residues are drawn as a coil). It is possible to pick the C_α for each cylinder segment, but they are at the location of the C_α, which is not near the axis cylinder. Interesting results occur when the whole protein is defined to be a helix and drawn as a cartoon.

The solid beta ribbon is constructed by building a spline along the center points between each beta sheet residue. Again, the spline is linearly interpolated to find the start and end points for each residue. Those are extended to construct the corners for a ribbon with rectangular cross section (the amount of extension is determined with the ??? parameter). A ribbon segment is used if the corresponding C_α atom is selected. Note that since this method assumes the protein is in a beta conformation, it draws a much smoother ribbon than the standard Ribbon option, which draw the ribbon with an oscillation along the sheet.

The other conformations are drawn as a tube. Since the endpoints of the helix cylinder and cartoon sheet are not at the C_α coordinate, the tube method was slightly changed to make the tube go to the new locations. This does not always work, resulting in a tube which does not quite connect to a cylinder.

5.1.14 MSMS

Another molecular surface renderer is MSMS, a program written by Michael Sanner of Olsen's lab at Scripps. This program is much faster than Surf, and can be a better choice depending on how it is used. See the web page http://www.scripps.edu/pub/olson-web/people/sanner/html/msms_home.html for more details. Available options include

- All Atoms – should the surface be of the selection (0) or of the contribution of this selection to the surface of all the atoms? (1)
- Density – triangle density on the surface (typical values are 1.0 for molecules with more than one thousand atoms and 3.0 for smaller molecules)
- Probe – Probe radius used to construct the molecular surface
- Wireframe – The surface can optionally be drawn using lines rather than solid triangles

There is an environment variable which can affect the MSMS display option:

- `MSMSSERVER` – location of the SURF binary (defaults to `msms` which is assumed to be in the user's path)

5.1.15 HBonds

The HBond representation will draw a dotted line between two atoms if there is a possible hydrogen bond between them. A possible hydrogen bond is defined by the following criteria:

```
Given an atom D with a hydrogen H bonded to it and an atom
A with no hydrogen bonded to it, a hydrogen bond exists between
A and H iff the distance ||D-A|| < dist and the angle D-H-A < ang,
where ang and dist are user defined.
```

Only the selected atoms are searched, so both the donor and acceptor must be selected for the bond to be drawn. Also, you'll note that the above doesn't check the atom type of the donor or acceptor; the only criterion is if it already has or doesn't have a hydrogen.

One downfall of the current implementation is that it does an n^2 search of the selected atoms so you probably don't want to show all the HBonds of a very large structure. Look for performance improvements in future versions of VMD.

If you choose an HBonds representation but fail to see any hydrogen bonds, it may be because the default angle and distance criterion in VMD are too small, so you might want to try increasing the angle value from 20 to 30 degrees and the distance value from 3 to 4.

The HBonds are drawn as dotted lines of a given width. The default is 1 but you should probably increase that to 2. On most SGIs you can't make it any wider than that, as described in the man page for linewidth. The bond is colored by the color associated with the acceptor.

5.1.16 Off

The 'Off' representation draws nothing. It is used in place of delete to hide a selection so it can be redisplayed quickly later.

5.2 Coloring Methods

VMD maintains a database of the colors used for the molecules and other graphical objects which are visible in the display window. It keeps track of

- color name definitions - its RGB value;
- mappings from a color category to color name - so residue name MET is colored yellow
- the current color scale - red to white to blue, and several related parameters

There are 1041 colors available in VMD, with color ids ranging from 0 to 1040. The first 17 are, in order: blue, red, gray, orange, yellow, tan, silver, green, white, pink, cyan, purple, lime, mauve, ochre, iceblue, and black.

The next group of 1024 colors (from 17 to 1040) are colors used in the color map, These can be set to one of several ranges with the Color form or the `color` text command: red→green→blue, red→white→blue, or black→white, etc. There are no names for the specific colors. The color map will be discussed in more detail in a section to follow.

5.2.1 Color categories

VMD maintains a database of the colors used for the molecules and the other graphical objects in the display window. The database consists of several color *categories*; each color category contains a list of names, and each name is assigned a color. For example, there is a Resname color category, and within this category there are many names; one for each of the available residue names. Some of these are `ALA`, `CYS`, and `PRO`. Each name can be assigned a color from a list of 17 available colors called the *color map*. The RGB value of each color can be modified directly in the Color form [§4.4.11]. To color items in a gradation manner, there are additional 1024 colors used in the color scale [§5.2.4].

The different color categories in VMD are listed in table 5.2. The Color form can be used to change the assignment of colors to the names in each of these categories. For example, to change the color used to draw Arginine residues when molecules are colored by residue, you would use the Color form, select the 'Resname' category, select the 'Arg' name there, and then pick the color to use for Arginine's from the list of colors next to the names.

Category	Contents
Display	The background color
Axes	The components of the axes
Stage	The colors for the checkboard stage
Name	The available atom names (color by Name)
Type	The available atom types (color by Type)
Resname	The residue names (color by ResName)
Chain	The one-character chain identifier.
Segname	The segment names (color by SegName)
Molecule	The names assigned to each molecule (color by Molecule)
Highlight	The protein, nucleic, and non-backbone colors
Restype	The residue types (color by ResType)
Structure	The secondary structure type (helix, sheet, coil) (color by Structure)
Labels	The different labels (atoms, bonds, etc.)

Table 5.2: Color categories used in VMD.

5.2.2 Coloring Methods

As described in chapter 5, each representation for a molecule has a specific *coloring method*. The coloring method determines how the color for each atom in the representation (view) is determined. These different methods use the colors assigned to the names in the categories listed above, and use those names to color the atoms. Molecular drawing methods which also draw the bonds between atoms will always color each half of the bond separately, using the color of the nearest atom for each half. Table 5.3 lists the different coloring methods available. The description for each method explains the source of the information used to determine the color.

5.2.3 Coloring by color categories

The default method is to color by the atom name. The way it works is that there is a color category called 'Name' which contains a list of all the atom names (e.g., CA, N, O5', and H) that have been

Method	Description
Name	Atom name, using the Name category
Type	Atom type, using the Type category
ResName	Residue name, using the Resname category
ResType	Residue type, using the Restype category
ResID	Residue identifier, using the resid mod 16 for the color
SegName	Segment name, using the Segname category
Molecule	Molecule all one color, using the Molecule category
Structure	Helix, sheet, and coils are colored differently
Chain	The one-character chain identifier, using the Chain category
ColorID	Use a user-specified color index (from 0 to 15)
Beta	Color scale based on beta value of the PDB file
Occupancy	Color scale based on the occupancy field of the PDB file
Mass	Color scale based on the atomic mass
Charge	Color scale based on the atomic charge
Pos	Color scale based on the distance of each atom to the center of the molecule. This is an interesting way to view globular systems.
Index	Color scale is based on the atom index. Due to the way the PDB file is organized, this actually looks nice.
Backbone	Backbone atoms green, everything else is blue

Table 5.3: Molecular coloring methods.

loaded into VMD. Each name is assigned one of the 16 main colors (e.g., cyan, blue, red, and white). When the drawing representation needs a color for a specific atom, it looks in the appropriate color category and finds that CA is colored cyan, N is blue, and so on.

Most of the coloring methods are based on color categories, so coloring by 'ResName' colors each residue name differently, 'SegName' colors each segment differently, and so on. The mapping between a given item in a color category and a color can be changed using the Color form [§4.4.11]. This allows users to make atoms with the name CA be black and the residue CYS be yellow. Some attention was given to making the colors reasonable, so that oxygens are red, nitrogens blue, sulphur and cysteines yellow, etc.

5.2.4 Color scale

Several of the coloring methods, including 'Beta', 'Charge', and 'Occupancy', describe a range of floating point values rather than a set of names. These are colored via the *color scale*, which is a list of 1024 smoothly changing colors. There are many color gradations available. All of them consist of transformations of three colors. For instance, "RGB" colors the smallest value red, values near the middle of the scale are green, and the largest values are blue. Colors in-between are linear mixes of the two colors. The list of available gradations is given below.

The minimum of the range of values is linearly scaled and shifted to start at 0 and end at 1. Assume the color scale is RGB. For a given value of x in the scale range [0..1], the RGB value is found first from a linear scaling based on the midpoint. If x = 0, R is 1 (for maximum red). This continues linearly until x = midpoint, at which point, R is 0 and stays 0. The green component is 0 at both x = 0 and x = 1 and is 1 at the midpoint. Linear scaling occurs in between. The blue

Method	Description
RGB	small=red, middle=green, large=blue
BGR	small=blue, middle=green, large=red
RWB	small=red, middle=white, large=blue
BWR	small=blue, middle=white, large=red
RWG	small=red, middle=white, large=green
GWR	small=green, middle=white, large=red
GWB	small=green, middle=white, large=blue
BWG	small=blue, middle=white, large=green
BlkW	small=black, large=white
WBlk	small=white, large=black

Table 5.4: Available Color Scale Gradations.

component is 0 for x <= midpoint, and 1 for x = 1.

An additional term, "min", is added to each of the component terms before they are merged. This shifts the final colors more towards white or black. Min can take on values from -1 to 1.

There is only one color scale used at a time so it is impossible to display objects colored by multiple different color scales.

5.2.5 Materials

VMD allows users to apply a materials property to the molecular models they create. The material determines such things as how transparent an object is, or how shiny, or how large the specular reflections are. Making objects semi-transparent is a potentially powerful means of viewing multiple layers of the molecule simultaneously. Imagine a protein on the surface of, and extending part way into, a membrane. One way to visualize the extent of the penetration is to represent the lipids as 'Bonds' and make them transparent. That will show the membrane without completely obstructing the view of the protein.

VMD maintains a database of materials which can be applied to any representation in the system, much like the database for colors. There are two default materials, "Opaque" and "Transparent", which cannot be modified. Each material is defined by five settings, as follows: material is

- Opacity: a number (0.0 to 1.0) describing the transparency; 1 is solid, 0 is transparent. By default, transparent objects are drawn with Opacity set to .3
- Ambient: a value describing how strongly the material reflects ambient light. Ambient light provides a uniform illumination of objects with a background lighting of the object color.
- Diffuse: Diffuse reflections are independent of the viewing direction, but depend on the direction of the light source with respect to the surface of the displayed object.
- Specular: a number describing the intensity of specular reflections. Produces highlights, the higher the value, the smaller and the brighter the highlight.
- Shininess: a number describing how large is the angle of the specular reflections. The smaller the number the wider the angle and the more shiny objects appear. Default corresponds to a Phong exponent of 40.

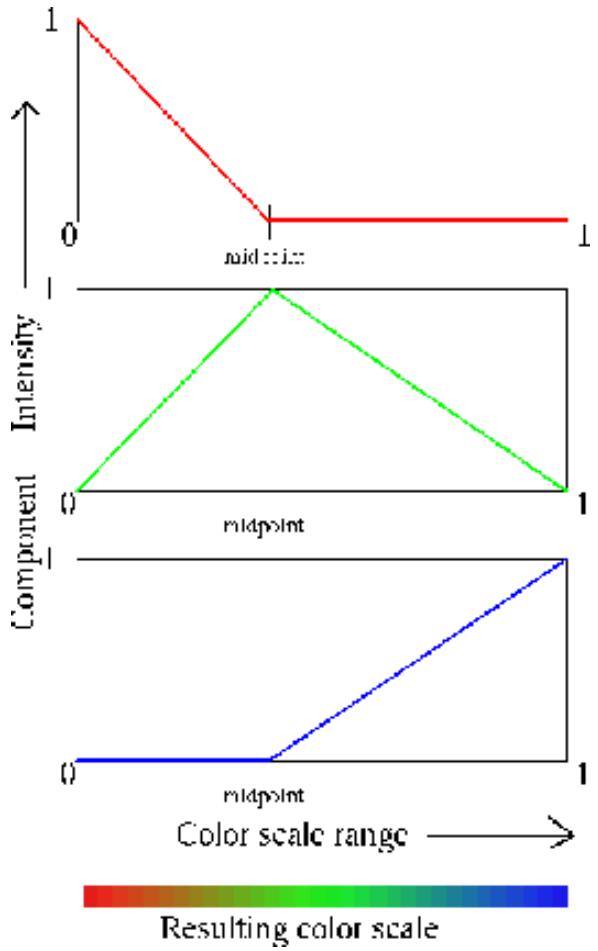

Figure 5.1: RGB color scale: the three plots shows the contributions of each color, and the resulting colors are on the bottom.

For details regarding these material properties, consult an elementary graphics book such as Foley & Van Dam (Computer Graphics).

5.3 Selection Methods

VMD has a rather powerful atom selection language available. It is based around the assumption that every atom has a set of associated with it values which can be accessed through keywords. These values could be boolean (is this a protein atom?), numeric (as in the atom index or atomic mass), or string (the atom name). The values can even be referenced via a Tcl array.

To start off, here are some examples of valid selection commands in VMD. Following these will be a more in depth description of how selections work.

```
name CA
resid 35
name CA and resname ALA
```

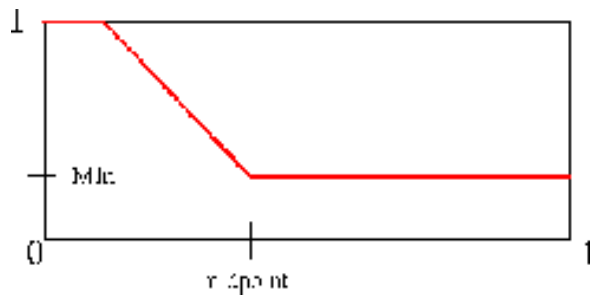

Figure 5.2: The shift to the red component of the RGB scale caused by the value of "min".

```
backbone
not protein
protein (backbone or name H)
name 'A 1'
name 'A *'
name "C.*"
mass < 5
numbonds = 2
abs(charge) > 1
x < 6 and x > 3
sqr(x-5)+sqr(y+4)+sqr(z) > sqr(5)
within 5 of name FE
exwithin 3 of protein
protein within 5 of nucleic
same resname as (protein within 5 of nucleic)
protein sequence "C..C"
name eq $atomname
protein and @myselection
```

There are two types of selection modes. The first is a keyword followed by a list of either values or a range of values. For example,

```
name CA
```

selects all atoms with the name CA (which could be a C_α or a calcium);

```
resname ALA PHE ASP
```

selects all atoms in either alanine, phenylalanine, or asparagine;

```
index 5
```

selects the 6th atom (in the internal VMD numbering scheme).

VMD can also do range selections, similar to X-PLOR's ':' notation:

```
mass 5 to 11.5
```

selects atoms with mass between 5 and 11.5 inclusive,

```
resname ALA to CYS TYR
```

selects atoms in alanine, arginine, asparagine, aspartic acid, cystine, and also tyrosine.

The keyword selection works by checking each term on the list following the keyword. The term is either a single word (eg, `name CA`) or a range (eg `resid 35 to 90`).

The method for determining the range checking is determined from the keyword data type; numeric comparisons are different than string comparisons. The comparison should work as expected so that "8" is between "1" and "11" in a numeric context but not in a string one. This may lead to some peculiar problems. Some keywords, such as `segname`, can take on string values but can also be used by some people as a number field. Suppose someone labeled the `segname` field with the numbers 1 through 12 on the assumption that they are numbers. That person would be rather confused to find that `segname 1 to 11` only returns two segments. Also, strings will be converted (via `atof()`) to a number so if the string isn't a number, it will be given the value of 0. It is possible to force a search to be done in either a string or numeric context using the relational operator discussed in §5.3.6

Selections can be combined with the boolean operators `and` and `or`, collected inside of parenthesis, and modified by `not`, as in

```
(name CA or name CB) and mass 12 to 17
```

which selects all atoms name CA or CB and have masses between 12 and 17 amu (this could be used to distinguish a C-alpha from a calcium). VMD has operator precedence similar to C so leaving the parentheis out of the previous expression, as in:

```
name CA or name CB and mass 12 to 17
```

actually selects all atoms named CA or those that are named CB and have the appropriate mass.

5.3.1 Definition of Keywords and Functions

The keywords available for selecting atoms in VMD are listed in tables 5.5 and 5.6 at the end of this chapter. If a keyword definition is followed by *bool*, it is either on or off. If followed by *str* it takes a value in the string context. If followed by *num* it takes a value in the number context.

Table 5.7 lists the built-in functions which may be used in atom selection expressions with keywords which take on a numeric value.

5.3.2 Boolean Keywords

Some selections take no values. For example, `backbone` selects the backbone atoms of the protein and nucleic acids and `protein` selects protein atoms. Giving options to these selections is an error. The selections can be used in the same way as other selections, as in:

```
protein and backbone
nucleic or protein
```

In addition, if neither `and` nor `or` are located after a boolean keyword, then an implicit `and` is inserted, so that the following are valid:

```
protein name CA         (same as: protein and name CA)
nucleic backbone
```

5.3.3 Short Circuiting

The boolean logic in VMD does *short circuit* evaluation on an element-wise basis. For instance, given one atom, if `X` is true then `X or Y` will be true regradless of the value of `Y`, so there is no need to evaluate it. Similarly, if `X` is false, then `X and Y` will also be false, so `Y` again need not be evaluated.

Knowing how short circuit selections work can speed up several types of selections. Consider a system with a large number of waters and a protein. The expression `protein and segname < 10` is faster than `segname < 10 and protein` since in the first selection only the atoms which are proteins have the `segname` converted to a number, while in the second selection, all the segment names are converted.

The `within` selection has its own form of short circuiting. The command can be interpreted as "find the atoms of A which are withing a given distance from B," and if A isn't given, search all the atoms. The search done in VMD takes a time roughly proportional to the number of atoms in A multiplied by the number of atoms in B, so reducing the number of atoms in A (i.e., by not testing every atoms) make the search faster.

Using the system with a lot of water and a protein, compare the selection

`protein within 5 of resid 1`

to `(within 5 of resid 1) and protein`.

The first is very fast as it does a distance search between all the protein atoms and all the atoms in resid 1. However, the second selection searches through all the atoms for those which are within 5 Å of resid and then finds which of those are protein atoms.

5.3.4 Quoting with Single Quotes

VMD allows two types of quoting mechanisms, single and double quotes. Single quotes are used to include spaces and other non-alphanumeric characters. Believe it or not, there are some residue names with a space in them, so they can be referenced as, for example,

```
resname 'A 1'
```

More importantly, ribose atoms can be given names like `C5'` or `C5*` (depending on the age of the PDB record). The lexer in VMD has been modified so that `C5'`, `O"`, and `N''` can be used without quotes, but it cannot handle an unquoted asterisk (`*` conflicts with multiplication and the parser is not able to resolve the difference). Some examples are:

```
name 'O5*'
segname 'A *'
name O5'
```

Quotes may also be used to get around a reserved selection word, like `x`. The selection command `segname x` will give an error because `x` is another keyword. Instead, use `segname 'x'`. There is an escape mechanism for including single quotes inside a single quoted string which uses a backslash ('\') before the single quote. This allows unusual names like `C '` to be quoted as `'C \''`.

```
segname x      <---- error; conflicts with the 'x' keyword
segname 'x'
name 'O5\''
```

Also, double quotes (discussed in the next section) can be used, as in `"C '"` or `"C \*"`.

5.3.5 Double Quotes and Regular Expressions

Double quotes around a string are used to specify a regular expression search (compatible with Perl 5.005, using the Perl-compatible regular expressions library written by Philip Hazel). Regular expressions are a very powerful concept but rather hard to explain from scratch. If you don't know how to use them, you might have some luck with the unix man pages for `ed`, `egrep`, `vi`, or `regex`. If not, ask someone, or get any one of a number of books including the O'Reilly and Associates Sed and Awk book. The following should given an idea of how they work.

Regular expressions allows selection of all atoms with a name starting with `C` as:

```
name "C.*"
```

or segment names containing a number as

```
segname ".*[0-9]+.*"
```

As expected, multiple terms can still be provided on the list of matching keywords, as in

```
resname "A.*" GLY ".*T"
```

to select residues starting with an `A`, the glycine residues, and residues ending with a `T`. Kind of silly, but it is just to demonstrate. As with a string, a regular expression in a numeric context gets converted to an integer, which will always be zero.

In brief, a regular selection allows matching to multiple possibilities, instead of just one character. Table 5.8 shows some of the methods that can be used.

So there are many ways to do some selections. For example, choosing atoms with a name of either CA or CB can be done in the following ways:

```
name CA CB
name "CA|CB"
name "C[AB]"
name "C(A|B)"
```

Several caveats for those who already understand regular expressions. VMD automatically prepends "`^(`" and appends "`)$`" to the selection string. This makes the selection `O` match only `O` and not `OG` or `PRO`. On the other hand, putting `^` and `$` into the command won't really affect anything, selections that match on a substring must be preceded and followed by ".*", as in `.*O.*`, and some illegal selections could be accepted as correct, but strange, as in `C)|(O` , which gets converted to `^(C)|(O)$` and matches anything starting with a C or ending with an O.

A regular expression is similar to wildcard matching in X-PLOR. Table 5.9 is a list of conversions from X-PLOR style wildcards to the matching regular expression.

5.3.6 Comparison selections

Comparisons can be used in VMD to do atom selections like `mass < 5`, which selects atoms with mass less than 5 amu, and `name eq CA`, which is another way of choosing the CA atoms. The underlying idea for the comparison selection is also based on the concept that every atom has a property as specified by a keyword. When the keyword is given in the expression, the array (or vector) of the corresponding values is constructed, and the size of the array is the same as the number of atoms in the molecule. (If a single number or string is given instead of a keyword, the array consists of copies of that given value.) The operations, like addition, multiplication, string matching, and comparison, are then applied element-wise along the array. This type of selection is similar to the vector statement in X-PLOR.

Take the example `mass < 5` when applied on water, which has an oxygen of mass 15.9994 and two hydrogens of mass 1.008. VMD sees the keyword **mass** and constructs the array [15.9994, 1.008, 1.008], then sees the "5" and makes the array [5, 5, 5]. It then compares each term of the array and returns with the boolean array [False, True, True] (since 15.9994 is not less than 5, but 1.008 is). This final boolean array is then used to determine which atoms are selected; in this case, the hydrogens.

More complicated comparison selections can be constructed, either from arithmetic operations or by using some of the standard math functions (the functions are listed in Table 5.7). Probably the most often used function will be `sqr`, which squares each element of the array. Thus, the command to select all atoms within 5 Å of a point (x,y,z) = (3,4,-5) in space is:

```
sqr(x-3)+sqr(y-4)+sqr(z+5) <= sqr(5)
```

5.3.7 Comparison Operators

There are two types of comparison operators — numeric and string — which allow the user to specify the appropriate comparison function. Suppose the segment name, which takes on a string value, contains the names '11', and '8'. VMD cannot figure out if '8' should be less than '11' (in the numeric sense) or greater than '11' (in the lexographical sense). Instead of trying to resolve this problem through some sort of internal heuristics, VMD leaves it up to the user so that `8 < 11` but `11 lt 8`. (Perl users should recognize this solution.)

The numeric comparisons are the standard ones: `<`, `<=`, `=` or `==`, `>=`, `>`, and `!=`. The corresponding string comparisons are: `lt`, `le`, `eq`, `ge`, `gt`, and `ne`. As in perl there is a "match" operator, `=~`, so that

```
'CA' =~ "C.*"
segname =~ "VP[1-4]" (matches VP1, VP2, VP3, and VP4, present in some
                      virus structures)
```

are valid. No distinction is made between single and double quotes.

5.3.8 Other selections

sequence

VMD supports selection based on the one-letter amino acid sequence with the `sequence` selection keyword. This allows selections of the form

```
sequence APD
sequence "C..C"       (might be used to pick out zinc fingers)
sequence AATCGGAT
```

Unlike the other string selection commands which take one of three types of strings, all the strings for `sequence` are taken as regular expressions (though strings with non-alphanumerics must still be quoted to get past the input parser). The method works by taking each of the protein and nucleic acid fragments (pfrag and nfrag) in turn and constructing the one-letter amino acid sequence. If a regular expression matches any of the sequence, the atoms in the matching residues are selected. Multiple matches are allowed, though they cannot overlap. As is usual with regular expressions, the largest possible match is made, so take care with expressions like `C.*C`.

`within` and `same`

Two useful types of selection mechanisms available in VMDare: `within <number> of <selection>` and `same <keyword> as <selection>`. The first selects all atoms within the specified distance (in Å) from a selection, including the selection itself. Therefore, the command:

```
within 5 of name FE
```

selects all atoms within 5 Å of atoms named FE. One common use for this command is to limit the region of atoms shown on the screen. Another is to find atoms that may be involved in interactions. For instance:

```
protein within 5 of nucleic
```

finds the protein atoms that are nearby nucleic acids. Some selections may be sped up by short circuiting [§5.3.3].

A related atom selection construct is `exwithin`, short for 'exclusive within'. The atom selection `(within 3 of protein) and not protein` is equivalent to `exwithin 3 of protein`.

The `same <keyword> as <selection>` finds all the atoms which have the same 'keyword' as the atoms in the selection. This can be used for selections like

```
same fragment as resid 35
```

which finds all the atoms attached to residue id 35. Any keyword can be used, so selections like

```
same resname as (protein within 5 of nucleic)
```

are fine, although weird. The perhaps the most useful keyword for this command is `residue`, so you can say `same residue as ...`.

Finding contact residues

Suppose you want to view the atoms in "A" which are in contact with "B". Use the `within <distance> of <selection>` selection command. For purposes of demonstration, let A be protein, B be nucleic, and define contact as an atom in A which is within 2 Å of an atom in B. Then the selection command is

```
protein within 2 of nucleic
```

If you want to see all the residues of A which have at least one atom in contact with B, use

```
same residue as (protein within 2 of nucleic)
```

Keyword	Arg	Description
all	*bool*	everything
none	*bool*	nothing
name	*str*	atom name
type	*str*	atom type
index	*num*	the atom number, starting at 0
chain	`str`	the one-character chain identifier
residue	*num*	a set of connected atoms with the same residue number
protein	*bool*	a residue with atoms named `C, N, CA,` and `O`
nucleic	*bool*	a residue with atoms named `P, O1P, O2P` and either `O3', C3', C4', C5', O5'` or `O3*, C3*, C4*, C5*, O5*`. This definition assumes that the base is phosphorylated, an assumption which will be corrected in the future.
backbone	*bool*	the `C`, `N`, `CA`, and `O` atoms of a protein and the equivalent atoms in a nucleic acid.
sidechain	*bool*	non-backbone atoms and bonds
water, waters	*bool*	all atoms with the resname `H2O, HHO, OHH, HOH, OH2, SOL, WAT, TIP, TIP2, TIP3` or `TIP4`
fragment	*num*	a set of connected residues
pfrag	*num*	a set of connected protein residues
nfrag	*num*	a set of connected nucleic residues
sequence	*str*	a sequence given by one letter names
numbonds	*num*	number of bonds
resname	*str*	residue name
resid	*num*	residue id
segname	*str*	segment name
x, y, z	*float*	x, y, or z coordinates
radius	*float*	atomic radius
mass	*float*	atomic mass
charge	*float*	atomic charge
beta	*float*	temperature factor
occupancy	*float*	occupancy
at	*bool*	residues named `ADA A THY T`
acidic	*bool*	residues named `ASP GLU`
acyclic	*bool*	"protein and not cyclic"
aliphatic	*bool*	residues named `ALA GLY ILE LEU VAL`
alpha	*bool*	atom's residue is an alpha helix
amino	*bool*	a residue with atoms named `C, N, CA`, and `O`
aromatic	*bool*	residues named `HIS PHE TRP TYR`
basic	*bool*	residues named `ARG HIS LYS`
bonded	*bool*	atoms for which numbonds¿0
buried	*bool*	residues named `ALA LEU VAL ILE PHE CYS MET TRP`
cg	*bool*	residues named `CYT C GUA G`
charged	*bool*	"basic or acidic"
cyclic	*bool*	residues named `HIS PHE PRO TRP TYR`

Table 5.5: Atom selection keywords.

Keyword	Arg	Description
hetero	*bool*	"not (protein or nucleic)"
hydrogen	*bool*	name "[0-9]?H.*"
large	*bool*	"protein and not (small or medium)"
medium	*bool*	residues named `VAL THR ASP ASN PRO CYS ASX PCA HYP`
neutral	*bool*	residues named `VAL PHE GLN TYR HIS CYS MET TRP ASX GLX PCA HYP`
polar	*bool*	"protein and not hydrophobic"
purine	*bool*	residues named `ADE A GUA G`
pyrimidine	*bool*	residues named `CYT C THY T URI U`
small	*bool*	residues named `ALA GLY SER`
surface	*bool*	"protein and not buried"
helix	*bool*	atom's residue is an alpha helix
helix_3_10	*bool*	atom's residue is an alpha helix
extended_beta	*bool*	atom's residue is a beta sheet
bridge_beta	*bool*	atom's residue is a beta sheet
rasmol	*Rasmol string*	translates Rasmol selection syntax to VMD
alpha_helix	*bool*	atom's residue is an alpha helix
pi_helix	*bool*	atom's residue is a pi helix
helix	*bool*	atom's residue is an alpha or pi helix
sheet	*bool*	atom's residue is a beta sheet ???
turn	*bool*	atom's residue is in a turn conformation
coil	*bool*	atom's residue is in a coil conformation
structure	*str*	single letter name for the secondary structure
phi, psi	*float*	backbone conformational angles
within	*str*	selects all atoms within a specified distance of a selection (i.e `within 5 of name FE`).
exwithin	*str*	'exclusive within'; equivalent to `(within 3 of X) and not X`.
same	*str*	selects all atoms which have the same keyword as the atoms in a given selection (i.e. `same segname as resid 35`)
ufx, ufy, ufz	*num*	force to apply in the x, y, or z coordinates

Table 5.6: Atom selection keywords (continued).

Function	Description
sqr(x)	square of x
sqrt(x)	square root of x
abs(x)	absolute value of x
floor(x)	largest integer not greater than x
ceil(x)	smallest integer not greater than x
sin(x)	sine of x
cos(x)	cosine of x
tan(x)	tangent of x
atan(x)	arctangent of x
asin(x)	arcsin of x
acos(x)	arccos of x
sinh(x)	hyperbolic sine of x
cosh(x)	hyperbolic cosine of x
tanh(x)	hyperbolic tangent of x
exp(x)	"e to the power x"
log(x)	natural log of x
log10(x)	log base 10 of x

Table 5.7: Atom selection functions.

Symbol	Example	Definition
.	`. , A.C`	match any character
[]	`[ABCabc] , [A-Ca-c]`	match any char in the list
[~]	`[~Z] , [~XYZ] , [^x-z]`	match all except the chars in the list
^	`^C , ^A.*`	next token must be the first part of string
$	`[CO]G$`	prev token must be the last part of string
*	`C* , [ab]*`	match 0 or more copies of prev char or regular expression token
+	`C+ , [ab]+`	match 1 or more copies of the prev token
\\\|	`C|O`	match either the 1st token or the 2nd
\(\)	`\(CA\)+`	combines multiple tokens into one

Table 5.8: Regular expression methods.

X-PLOR Wildcard	Description	Regular Expression
*	matches any string	.*
%	matches a single character	.
+	matches any digit	[0-9]
#	matches any number	[0-9]+

Table 5.9: Regular expression conversions.

Chapter 6

Rendering to Raster Image Files

One of the most common tasks performed by users of VMD is producing images which can be loaded into other programs or used in printed documents, posters, slides, and transparencies. The Render form provides a simple mechanism for generating image files from snapshots of the VMD graphics window and through the use of external rendering and ray tracing programs.

6.1 Screen Capture Using Snapshot

The simplest way to produce raster image files in VMD is to use the "Snapshot" feature. The snapshot feature captures the contents of the VMD graphics window, and saves them to a raster image file. On Unix systems, the captured image is written to a 24-bit color SGI "RGB" file. On Windows systems, the captured image is written to a 24-bit color Windows Bitmap, or "BMP" file.

To use the `snapshot` feature, simply open the Render form [§4.4.13[and choose the `snapshot` option. VMD will automatically capture the contents of the graphics window, and attempt to save the resulting image to the requested filename given in the Render form..

After a little practice with this feature, you may find that it is important not to have other windows or cursors in front of the VMD graphics display when doing this type of capture, since the resulting images may include obscuring windows or cursors. This is a platform-dependent behavior, so you will need to determine if your system does this or not.

6.2 Higher Quality Rendering

Sometimes images produced by screen capture aren't good enough; you may want a very large, high quality picture, or a picture with shadows, reflections, or high quality rendering of transparent surfaces. While VMD generally produces nice looking images in its graphics window, it was designed to generate its images very rapidly to maximize interactivity, which precludes the use of photorealistic rendering techniques that would slow down the operation of whole program. Instead of producing high quality images directly, VMD writes scene description files which can be used as input to several popular scanline rendering and ray tracing programs. Tables 6.1 and 6.2 list the currently supported output formats, and where appropriate rendering software may be obtained.

Making the raster image is a two step process. First you must make a scene description file suitable for the chosen rendering program, and then execute the program using the new file as input to produce the raster image output. The problem is that each of the external rendering programs support different output file formats, which may need to be converted to something more

Name	Description	Default Render Command
Raster3D[1]	Fast raster file generator	`render < %s -sgi %s.rgb; ipaste %s.rgb`
PostScript	Direct PostScript Output	`ghostview %s &`
Renderman	Renderman RIB Format	`rgl` - Can be rendered with BMRT, PRMan, Maya, etc
STL	Stereolithography Format	`true` - Renders Triangles Only
VRML-1	Virtual Reality Markup Language	`true` - view this with VRML viewers like webspace

[1]See `http://www.bmsc.washington.edu/raster3d/` for more info.

Table 6.1: Miscellaneous Rendering Options

Name	Description	Default Render Command
Tachyon[1]	Very fast multiprocessor ray tracer	`tachyon -mediumshade %s -o %s.tga`
POV3[2]	POV-Ray 3.x ray tracer	`povray +H500 +W400 -I%s -O%s.tga +D +X +A +FT`
Rayshade[3]	Rayshade ray tracer	`rayshade < %s > %s.rle`
Radiance[4]	Radiosity ray tracer	`oconv %s > %s.oct; rview -pe 100 -vp -3.5 0 0 -vd 1 0 0 %s.oct`
ART[5]	VORT ray tracer	`render < %s -sgi %s.rgb; ipaste %s.rgb`

[1]See `http://www.megapixel.com/` for more info.
[2]See `http://www.povray.org/` for more info.
[3]See `http://www-graphics.stanford.edu/ cek/rayshade/rayshade.html` for more info.
[4]See `http://radsite.lbl.gov/radiance/HOME.html` for Radiance
[5]Available from ftp://gondwana.ecr.mu.oz.au/pub along with the rest of VORT package
[6]See `http://vrml.sgi.com/intro.html` `http://vrml.sgi.com/intro.html`

Table 6.2: Supported ray tracing formats.

appropriate for you. It is impossible to predict what that might be, so we'll describe how to convert the different file types to RGB and let you use the tools listed in Table 6.1 to get what you need. Tachyon and Raster3D can produce SGI RGB files, so you don't need to do anything but specify this output format. POV-Ray produces Targa files, which can be converted on SGI machines with the program `/usr/sbin/fromtarga`. Rayshade creates RLE image files, which can be converted on SGI machines with `/usr/sbin/fromutah`. Radiance generates an .oct file, which can be converted with the `rview` and `rpict` commands in the Radiance distribution.

The free program `display` from ImageMagick – see
`http://www.wizards.dupont.com/cristy/ImageMagick.html` –
should be able to read and convert between all of these formats.

We suggest using either Tachyon or Raster3D as they are generally the fastest programs. Both programs are easy to understand, and are fast even when rendering very complex molecules.

The generated scene files are plain text so they are very easy to modify. This is most often done to create a larger raster file, though some have other global options which you may wish to change. For instance, by default the Raster3D file turns shadows on. We suggest you consult the

relevant renderer's documentation to determine what can be modified in the file.

To actually render the current image into an output file, first set up the graphics in VMD just as you wish the output to appear. Then, either use the Render form [§ 4.4.13], or the following text command, to create the input file and start the rendering program going:

render ***method filename*** [***render command***]

method is one of the names listed in the first column of table 6.1, and *filename* is the name of the file which will contain the resulting image processing program script. Any text following this will be used as a command to be run to process the file. If `%s` appear in the command string, they will be replaced with the name of the script file.

6.3 Known Problems

When VMD creates the output file it will try to match the current view and screen size. For the most part it does a good a job but there can be some problems. The colors in the final raster image can sometimes look different from what is seen in the VMD graphics window. This is because the external rendering programs use different shading equations and algorithms from what VMD uses.

The eye view can be slightly different between the VMD graphics window and externally rendered raster images. This occurs because the Screen Height and Screen Width (see §4.4.10) values are not propagated to the output file, so the programs have slightly different transformation matrices. We have added an extra scaling factor, determined by trial and error, which reduces this effect for the default screen sizes, but the factor is only valid if the parameters are not changed.

The lights are supposed to be positioned in the output file as they are on the screen but not all formats support the number and type of lights available in VMD.

We have primarily tested the Tachyon and Raster3D output and have less experience with the other programs. The only problem we have found with Raster3D is if there are too many objects to render (this could easily occur when using 'Tube' or 'Ribbon' on large molecules), it will not render anything. (Raster3D documentation mentions an "object limit"—Raster3D can be recompiled with a new limit.)

6.4 One Step Printing

A frequently asked question is "How can I quickly get a printout of the VMD Display?" There are several one step solutions to this problem

- Choose the `snapshot` option and type `convert %s eps:%s.ps; lpr %s.ps` in the render command box. This assumes that you have the ImageMagick tools available in your PATH setting.
- As an example of how to directly print a Raster3D file, choose the Raster3D option in the Render form and type `render < %s -sgi %s.rgb; convert %s.rgb eps:%s.ps; lpr %s.ps` in the render command box.
- Choose the PostScript output option in the Render form and type `lpr %s` in the render command box.

6.5 Making a Movie

It is possible to make movies with VMD, though the interface is not well developed. This section is not written for the casual user!

The following Tcl script uses the mpeg encoder available from ftp.cs.berkeley.edu, the image converter `toppm`, and successive Raster3D runs (though it is possible to do screen grabs as well) to make a movie of a spinning molecule. The script rotates the system 35 times by 10 degrees each time. For each orientation, it saves the image as a Raster3D input file, runs Raster3D on it to get an RGB raster image, then converts the RGB file to a ppm graphics file for use by the mpeg encoder. Once all the files are made, the mpeg is created. The temporary files are saved in `./images` and the full process could take up a lot of disk space, depending on the size of the VMD graphics window. This script does not automatically delete the files or the directory.

The encoder input file is given after the Tcl script.

VMD script to make a movie of a rotating system

```
for { set i 0 } { $i < 360 } { set i [ expr $i + 1 ] } {
  render Raster3D out.r3d
  catch { exec render < out.r3d -sgi out.rgb }
# get the right format for the number (only works up to 99)
  if { $i < 1 } {
    set nm "00"
  } elseif { $i < 10 } {
    set nm "0$i"
  } else {
    set nm $i
  }
# convert from RGB to PPM
  catch { exec toppm out.rgb $nm.ppm }
# delete the RGB file
  catch { exec rm out.r3d out.rgb }
# and rotate by 10 degrees
  rot y by 10
}
# now make the mpeg
catch { exec mpeg_encode-1.3.sgi.bin mpeg.input }
```

The mpeg encoder script follows, but be careful as we guessed at most of the values.

```
PATTERN I
OUTPUT spin.mpg
INPUT_DIR .
INPUT
*.ppm [00-89]
END_INPUT
BASE_FILE_FORMAT PPM
INPUT_CONVERT cat *
GOP_SIZE 4
SLICES_PER_FRAME 2
```

```
PIXEL FULL
RANGE 5
PSEARCH_ALG LOGARITHMIC
BSEARCH_ALG SIMPLE
IQSCALE 1
PQSCALE 1
BQSCALE 1
REFERENCE_FRAME DECODED
```

You would use this by first loading a molecule, changing to the directory you wish to use to store the image files, and entering the command

```
play <Tcl script filename>
```

It does work. Honest.

Chapter 7

Viewing Modes

There are many different viewing modes available. These show the scene in orthographic or perspective views, and in several mono- and stereo- graphic displays. The stereo mode can be changed using the `stereo` entry in the Display form or the text command `display stereo` *`mode`*.

7.1 Perspective/Orthographic views

In the perspective view (the default), objects which are far away are smaller than those nearby. In the orthographic view, all objects appear at the same scale. Since some prefer one over the other, both options are available. Perspective viewpoints give more information about depth and are often easier to view because you use perspective views in real life. Orthographic viewpoints make it much easier to compare two parts of the molecule, as there is no question about how the viewpoint may affect the perception of distance.

7.2 Monoscopic Modes

When you normally look at objects, your two eyes see slightly different images (because they are located at different viewpoints). Your brain puts the images together to generate a stereoscopic viewpoint. When generating a single image for the computer display, the default calculations (mode Stereo Off) assume there is one eye centered between where two eyes would be. Sometimes, as when generating ray tracing input files, the left and right eye views need to be generated independently. Choosing mode Left produces the left eye viewpoint, while Right produces the right eye viewpoint.

7.3 Stereoscopic Modes

Molecules may be rendered in stereo, which can greatly enhance the appearance and visual content of the displayed systems. There are several stereo formats available:

1. Side-by-side cross-eyed stereo;
2. Side-by-side wall-eyed stereo;
3. Anaglyph stereo (requires stereo-capable monitor, quad-buffered stereo video board, and red-blue horror-movie-style stereo glasses).

4. CrystalEyes stereo (requires stereo-capable monitor, quad-buffered stereo video board, stereo sync emitters and special stereo glasses equipped with liquid crystal or polarized lenses).

7.3.1 Side-By-Side and Cross-Eyed Stereo

Side-by-side stereo means that the normal display is divided into two halves, a left view and a right view, each occupying one-half of the original display area. Each view displays the current molecules from a slightly different perspective, corresponding to the left and right eye of the viewer. The images are separated, however, so to actually see a 3D object you must direct your eyes until the two images are on top of each other, and then focus on the resulting image until you can see it as three-dimensional.

There are two ways of placing the images. In wall-eyed stereo, the left eye's image is located on the left side of the display, and the right eye's image is on the right. This is the standard method for displaying stereo images in publications as it works well when the display (in this case, the piece of paper) is close to the eyes. It is called wall-eyed because your eyes are directed the same way they would be if looking at a distant wall. In VMD, this method is referred to as "SideBySide" stereo.

In cross-eyed stereo, the left eye's image is located on the right side of the display, and the right eye's image is on the left, and hence the name cross-eyed. This is mostly used for distant displays (such as overhead projections) as it is much easier to cross eyes at that range than use the wall-eyed method – you are already looking at the wall. In VMD, this method is referred to as "CrossEyes" stereo.

7.3.2 Anaglyph Stereo

Anaglyph stereo refers to the use of colors to separate the left and right eye views from each other. The user must wear glasses with colored lenses, such as the red-blue glasses one finds at some sci-fi and horror movie showings. The computer hardware requirements for Anaglyph stereo are currently the same as for CrystalEyes stereo except that no LCD shutter glasses and emitters are not required. The red-blue glasses take the place of the LCD shutter glasses used for the CrystalEyes stereo modes. Anaglyph stereo has one major disadvantage when compared with CrystalEyes stereo, which is that its color rendition is obviously severely constrained. This is just a fact of life with Anaglyph stereo, and it is up to the user to use color schemes for their molecules that still look visually pleasing when displayed in Anaglyph stereo mode.

7.3.3 CrystalEyes Stereo

CrystalEyes stereo refers to a special hardware option available on Silicon Graphics workstations that allows one to view three-dimensional objects through the use of a special display monitor mode and special stereo viewing glasses. Stereographics Corp. is one such supplier of these glasses. This mode also requires special infrared emitters to synchronize the stereo glasses with the display monitor.

There are presently two types of CrystalEyes stereo modes available on SGI machines; which one is used depends on the available graphics hardware (see the man page `stereo(7)`). Follow the outline below for the relevant graphics option:

Stereo in a window (aka new-style stereo): Available on workstations equipped with quad-buffered stereo graphics subsystems only (such as SGI InfiniteReality, Sun Expert3D, HP FX-10) this mode provides separate left and right eye frame buffers. It allows the user to have a window display in stereo, and the other windows appear as normal. Using this mode, however, sometimes requires the monitor to be in a lower-resolution display mode since it requires twice as much video memory over a normal non-stereo display. The monitor must be set in a stereo-capable mode before starting VMD. On SGI systems, one must use either the **setmon** or **xscreen** utilities to configure the display mode. On Sun systems this is done using the **fbconfig** utility. HP systems use the **sam** utility for display configuration. Windows machines use the **Display Properties** tab to control video board display mode settings.

Once set in the proper display mode, start VMD as normal, and select 'CrystalEyes stereo' from the Display form. The image should switch to two images nearly superimposed, but slightly offset.

7.3.4 Problems with stereo on some SGI machines

SGI machines running versions 5.X or early versions of 6.X of IRIX may require patches for their OS in order to run crystal eyes stereo.

7.3.5 Stereo Parameters

A stereo image is generated by drawing two images from two different perspectives, one from the left eye and one from the right. The images are made by finding the view that would be seen by someone located inside the scene. The method uses two parameters to find the view; the *eye separation* and the *focal length*. The first defines the distance between the eyes and gives the parallax effect. Setting the separation to 0 will result in a flat 2D image, while setting it too large will give most people a headache.

The graphics model used by VMD assumes the eyes looking in front of the viewer and focusing at the same point the focal length away. If the focal length is 0, the viewer's eyes are crossed and looking at each other. A larger focal length will often help in creating a viewable image.

The two parameters can be changed with the text commands `display focallength` and `display eyesep`, or using the Display form [§4.4.10].

In general, try to make the eye separation as large as possible without giving the viewer a migrane, and try to vary the focal length to cut down on double images. It may often help to translate the molecule forward or backward and also adjust the scaling, since there is typically an optimum position for a molecule for a given set of stereo parameters.

7.4 Making Stereo Raster Images

As discussed in Chapter §6, VMD can create output files of the current scene in the format needed for input by various image processing packages. These formats do not always natively support the ability to draw stereo images. In principle, it is possible to write the scene to the file twice with the appropriate transformations applied to make the view correct for each eye, but then the shadows would be incorrect.

Instead, we suggest making one image of the current scene, then shift the molecules to the left (or right) to make the other image. (Note that neither the stage nor the axes will move, so they will not be in stereo.) The text commands for this are something like:

```
render Raster3D left.r3d
trans by -.1 0 0
render Raster3D right.r3d
```

The two files must then be rendered to produce the rgb file. As it turns out, this method makes it easy to produce stereo images of ordinary Raster3D files. Since VMD can read the Raster3D format, all you have to do is read the file and then execute the commands listed above. The text commands for generating left or right views also have equivalents in the GUI under the `Stereo` option of the Display form.

Chapter 8

Tcl Text Interface

The Tcl text interface provides complete access to all the VMD commands. Anything that can be done from the menus can be done with VMD text commands.

8.1 Using text commands

Text commands can be entered into VMD in several ways:

- Commands can by entered by typing them at the VMD prompt in the text console window. This window normally contains the prompt `vmd >` . When other text (e.g., from a mouse pick) is displayed to the screen, it will scroll the screen up so the prompt is not at the last line of the screen. To make it reappear, press enter. When entering multi-line commands, an alternate prompt appears, `?` , and will not disappear until the command is finished. Sometimes it is waiting for a close to a double quote, open brace, or open bracket, while at other times it is waiting for a line that doesn't end in a backslash.

- Since you may not want to retype all the data in every time, there are two ways to read the data in from a text file. One is the `play` command. This reads a line from the file, executes it, then updates the screen and checks for any changes in the mouse or forms input, so that VMD stays interactive during execution of the script. The second way is the Tcl command `source`. This reads the whole file before allowing the mouse and forms to respond to new input. This is often more efficient when your script contains many lines.

- On Unix/Linux platforms, if the file `.vmdrc` (see section §13.4.3) exists in your home directory, it is played at VMD startup. If you don't have a `.vmdrc` file, VMD uses a default script in the VMD installation directory. Similarly, at startup the `-e` command line flag can be used to specify an input file to be played after reading the `.vmdrc` file.

  A good use of the `.vmdrc file` is to specify which VMD menus you would like to have open when you start VMD and where they should be placed; see section §8.3.16) for information on usage.

8.2 Tcl/Tk

The standard distribution is compiled with Tcl, which add a complete scripting language including variables, loops, and conditionals along with a standard method for communicating with other

programs via standard TCP/IP sockets. Versions 1.2 and later also include the Tk toolkit,w for creating menus with buttons bound to one's favorite actions.

Tcl (short for Tool Command Language, developed by John Ousterhout) is an embeddable and extensible scripting language. In other words, Tcl sits inside VMD as a language interpreter where it can execute its standard language commands or the various VMD specific extensions.

VMD uses Tcl and Tk version 8.0.4. We refer you to `http://www.scriptics.com/` for more information about Tcl.

8.3 Tcl Text Commands

First Word	Description
animate	Play/Pause/Rewind a molecular trajectory.
atomselect	Create atom selection objects for analysis.
axes	Position a set of XYZ axes on the screen.
color	Change the color assigned to molecules, or edit the colormap.
colorinfo	(Tcl) Obtain color properties for various objects
display	Change various aspects of the graphical display window.
echo	Turn on/off echoing of text commands to the console.
exit, quit	Quit VMD.
help	Display an on-line help file with an HTML viewer.
imd	Control the connection to a remote simulation.
logfile	Turn on/off logging a VMD session to a log file.
label	Turn on/off labels for atoms, bonds, angles, or dihedral angles.
light	Control the light sources used to illuminate graphical objects.
material	Create new material definitions and modify their settings.
menu	Control or query the on-screen GUI menu forms.
molecule or mol	Load, modify, or delete a molecule in VMD.
mouse	Change the current state (mode) of the mouse.
play	Start executing text commands from a specified file.
render	Output the currently displayed image (scene) to a file.
rock	Rotate the current scene continually at a specified rate.
rotate	Rotate the current scene around a given axis by a certain angle.
scale	Scale the current scene up or down.
stage	Position a checkerboard stage on the screen.
tool	Initialize and control external spatial tracking devices.
translate	Translate the objects in the current scene.
user	Add new keyboard commands.
vmdinfo	(Tcl) Get information about this version of VMD
wait	Wait a number of seconds before reading another command. Animation continues.
sleep	Sleep a number of seconds before reading another command. Animation is frozen.

Table 8.1: Summary of core text commands in VMD.

All Tcl commands in VMD are composed of one or more words or phrases separated by white space, and terminated by a newline. In Tcl, a "phrase" is text surrounded by double quotes or by a matching set of open and close braces. The first word of each command indicates the general

purpose for the command, and the following words specify the exact type of command to execute. Table 8.1 summarizes the text commands in VMD by listing the first words, and describing the general purpose for commands starting with those words.

The commands described in the following sections are listed by name, and followed by a list of the available arguments. If an argument is optional, it is enclosed in `[]`s. If only one of a list of arguments is needed, the list is enclosed in `<>`s and the items are separated by `|`. Words in italics indicate a string or value to be specified by the user.

8.3.1 animate

These commands control the animation of a molecular trajectory and are used to read and write animation frames to/from a file or Play/Pause/Rewind a molecular trajectory.

- **dup** [**frame** *number*] *molId*: Duplicate the given frame (default "now") of molecule *molId* and add the new frame to this molecule.
- **forward**: Play animation forward.
- **for**: Same as forward.
- **reverse**: Play animation backward.
- **rev**: Same as reverse.
- **pause**: Pause animation.
- **prev**: Go to previous frame.
- **next**: Go to next frame.
- **skip** *n*: Set stride to n+1 frames.
- **delete all**: Delete all frames from memory.
- **speed** *n*: Set animation speed to *n*.
- **style once**: Set to play animation once.
- **style loop**: Set to loop through animation continuously.
- **style rock**: Set to play animation forward and back continuously.
- **styles**: Return a list of the available styles.
- **goto start**: Go to first frame.
- **goto end**: Go to last frame.
- **goto** *n*: Go to frame *n*.
- **read** *file type filename* [**beg** *nb*] [**end** *ne*] [**skip** *ns*] [*molecule_number*]: Read data for *molecule_number* from *filename*, beginning with frame *nb*, ending with frame *ne*, with a stride of ns+1.

- **write** *file type filename* [**beg** *nb*] [**end** *ne*] [**skip** *ns*] [*molecule_number*]: Write data from *molecule_number* to *filename*, beginning with frame *nb*, ending with frame *ne*, with a stride of *ns*+1.
- **delete** [**beg** *nb*] [**end** *ne*] [**skip** *ns*] [*molecule_number*]: Delete data for *molecule_number*, beginning with frame *nb*, ending with frame *ne*, with a stride of *ns*+1.
- **readdel** *filename* [**beg** *nb*] [**end** *ne*] [**skip** *ns*] [*molecule_number*]: Read data for *molecule_number* from *filename*, beginning with frame *nb*, ending with frame *ne*, with a stride of *ns*+1, overwriting existing data.

8.3.2 atomselect

Atom selection is the primary method to access information about the atoms in a molecule. It works in two steps. The first step is to create a selection given the selection text, molecule id, and optional frame number. This is done by a function called `atomselect`, which returns the name of the new atom selection. the second step is to use the created selection to access the information about the atoms in the selections.

- **list**: Return a list of all undeleted atom selections.
- **keywords**: Return a list of all recognized keywords in an atom selection text.
- *molecule_id selection_text* [**frame** *frame_number*] Creates a new atom selection and returns its name. The returned name can be used as a Tcl proc in order to access the atom selection. The "selection text" is the same as the selection language used in the Graphics form [§ 4.4.6] and described in Chapter §5.3. It is used to pick a given subset of the atom. The text cannot be changed once a selection is made. Some of the terms in the selection depend on data that change during a trajectory (so far only the keywords 'x', 'y', and 'z' can change over time). For these, the optional 'frame value' is used to determine which specific frame to use. The frame number can be a non-negative integer, the word "now" (the current frame), the word "first" (for frame 0) and "last" (for the last frame).

  Some examples are:

  ```
  vmd> atomselect top "name CA"
  atomselect0
  vmd> atomselect 3 "resid 25" frame last
  atomselect1
  vmd> atomselect top "within 5 of resname LYR" frame 23
  atomselect2
  ```

  The newly created atom selection is a Tcl proc, which takes the following options:

  - **num**: Return the number of atoms in the selection.
  - **list**: Return a list of the atom indices in the selection (BTW, this is the same as "get index").
  - **text**: Return the text used to create this selection.

- **molid**: Returns the molecule id used to create this selection.
- **frame**: Returns the animation frame associated with this selection. The result will be either `now`, `last`, or an integer corresponding to the frame. When the frame is `now`, the atom selection will use atomic coordinates from the current frame for its associated molecule. If the frame is `last`, the atom selection will always use coordinates from the last frame. If the frame is a specific integer, the selection will always use coordinates from that frame, even if the current animation frame changes. Note that if a nonexistent frame is specified, the atomic coordinates will all be taken to be 0.
- **frame** *frame*: Set the frame for the selection. *frame* should be either `now`, `last`, or an integer.
- **delete**: Delete this object (removes the function).
- **global**: Moves the object into the global namespace. Atom selections created within a Tcl proc that are not made global are deleted when the proc exits.
- **uplevel** *level*: Moves the object to a new level in the namespace stack. Works the same as the Tcl function `uplevel`.
- **get** *attribute_list*: Given a list of attributes, returns a list containing the list of attribute values. See Tables 5.5 and 5.6 for the recognized attribute keywords.
- **set** *attribute_list values_lists*: Set the attributes in the attribute list with the values gven in the values lists. For each attribute there must be a list of values; each value list must contain either one element, or an element for each atom in the selection.
- **getbonds**: returns a list of bondlists; each bondlist contains the id's of the atoms bonded to the corresponding atom in the selection.
- **setbonds**: Set the bonds for the atoms in the selection; the second argument should be a list of bondlists, one bondlist for each selected atom.
- **move** *4x4 matrix*: Applies the given transformation matrix to the coordinates of each atom in the selection.
- **moveby** *offset*: move all the atoms by a given offset.
- **lmoveby** *offset_list*: move each atom by an offset given in the list.
- **moveto** *position*: move all the atoms to a given location.
- **lmoveto** *position_list*: move each atom to a point given by the appropriate list element.
- **writepdb** [*filename*]: write the selected atoms to a pdb file. If no filename is given, the text of the file is returned as a string.

See Section §12.2 for more on using atom selections for fun and profit.

8.3.3 axes

The axes (orthogonal vectors pointing along the x, y, and z directions) can be placed in any of 5 locations on the screen, or turned off.

- **locations**: Return a list of possible locations.
- **location**: Get the current location.

- **location < off | origin | lowerleft | lowerright | upperleft | upperright >**: Position axes.

Also, though this may seem like a likely command for changing the color of the axes, this function can only be performed from the Colors form or by the `color` command (see below). Future implementations of VMD may change this.

8.3.4 color

Change the color assigned to molecules, or edit the color scale. All color values are in the range 0 ... 1. Please see the section on coloring [§ 5.2] for a full description of the various options.

- *category name color*: Set color of object specified by *category* and *name* to *color*.
- **scale method** < *scale_name* >: Set type of scale to use for coloring objects by values. They are:
  - RGB – Red to green to blue.
  - BGR – Blue to green to red.
  - RWB – Red to white to blue.
  - BWR – Blue to white to red.
  - RWG – Red to white to green.
  - GWR – Green to white to red.
  - GWB – Green to white to blue.
  - BWG – Blue to white to green.
  - BlkW – Black to white.
  - WBlk – White to black.
- **scale midpoint** x: Set midpoint of color scale to x, in the range 0 ... 1.
- **scale min** x: Set minimum of color scale to x, in the range 0 ... 1.
- **scale max** x: Set maximum of color scale to x, in the range 0 ... 1.
- **change rgb** *color*: Reset rgb of *color* to default value.
- **change rgb** *color r g b*: Set rgb of *color* to *r g b*.

See also Chapter § 11 on how to change color of a user-defined graphics object.

8.3.5 colorinfo

(Tcl) This command provides access to the color definitions. For information on the color properties see the chapter on Coloring [§5.2].

- **colorinfo categories**: returns a list of available categories
- **colorinfo category** *category*: returns a list of names for the given category

- **colorinfo num**: returns the number of base solid colors (17)
- **colorinfo max**: returns the total number of colors available (49)
- **colorinfo colors**: returns a list of the named solid colors
- **colorinfo [index | rgb] < name | value >** : returns the index or rgb of the given name or color id.
- **colorinfo scale < method | methods | midpoint | min | max >**: returns the information about the color scales

Examples:

```
# find out what color corresponds to which id:
set i 0
foreach color [colorinfo colors] {
  puts "$i $color"
  incr i
}


# also get a list of RGB values
set i 0
foreach color [colorinfo colors] {
  lassign [colorinfo rgb $color] r g b
  puts "$i $color   \{$r $g $b\}"
  incr i
}
```

8.3.6 display

Change various aspects of the graphical display window. For information about the options, see the section describing the Display form [§4.4.10].

- **update**: Force the display update. Makes sense if the display update is off. This does not necessarily take care of resizing the display window or using the Forms GUI while the display update is turned off.
- **update on**: Turn display update on.
- **update off**: Turn display update off. By default VMD does the display updates constantly. Sometimes it is beneficial to turn the turn the display updates off. This prevents VMD from redrawing the scene as a response to every change, thus saving time while doing changes of representations. See the VMD script library for examples of use.
- **update status**: Return the display update status (on or off).

- **update ui**: Similar to `display update`, but also forces updates of the GUI forms. The Forms interface is subject to the following behavior: if the display update is set to `off` and actions (such as, e.g., iconify/deiconify) have been performed to the Forms, the Form windows do not get updated by just `display update` command, whereas `display update ui` forces both updates to happen. Tk does not seem to have this problem, so this option will become obsolete after switching to Tk graphics user interface.
- **reshape**: Reshape the display. If the display update is turned off, and the display window has been resized command `display update` updates the display, but does not necessarily respond to the resizing of the window.
- **resetview**: Reset the view.
- **eyesep** *value*: Set the eye separation to *value*.
- **focallength** *value*: Set the focal length to *value*.
- **height** *value*: Set the screen height to *value*.
- **distance** *value*: Set the screen distance to *value*.
- **antialias < on | off >**: Turn antialiasing on or off.
- **depthcue < on | off >**: Turn depth cueing on or off.
- **depthsort < on | off >**: Turn depth sorting on or off (useful in transparent mode)
- **detail < full | flat | lines | points | none >**
- **altdetail < full | flat | lines | points | none >**
- **stereo** *mode*: Set the stereo mode to *mode*.
- **nearclip < set | add >** *value*: Add or set near clipping plane position to it value.
- **farclip < set | add >** *value*: Add or set far clipping plane position to *value*.
- **get < eyesep | focallength | height | distance | antialias | depthcue | stereo | projection | detail | altdetail | nearclip | farclip >**: Return information about the given option.
- **get < stereomodes | projections | details >**: Return a list of the availalble values for the given options. (See section § 4.4.10 and chapter § 7 for more information.)

8.3.7 echo

Turn on/off echoing of text commands to the console. When this is turned on, text commands read from a file or from the VMD prompt are echoed to the screen before they are executed. Do not confuse this with the standard Unix `echo` command.

- **< on | off >**: Turn echoing on or off.

8.3.8 exit

Quit VMD.

- **confirm**: Use a form to verify with the user before quitting.
- **[now]**: Quit without asking.

8.3.9 help

Display the on-line help file with an HTML viewer. See Chapter § 13 for information on how to change the default viewer (which is Netscape).

- [*subject*]: Jump to help corresponding to *subject*.

Presently, "subject" can be any one of the following words, which launches the associated URL. To guarantee that the help system will work correctly, you will probably want to start up your web browser before choosing one of these options. After you do this, VMD will properly direct the browser to the pages mentioned below.

Source	Associated URL
faq	http://www.ks.uiuc.edu/Research/vmd/allversions/vmd_faq.html
raster3d	http://www.bmsc.washington.edu/raster3d
stride	http://www.embl-heidelberg.de/stride/stride_info.html
mdscope	http://www.ks.uiuc.edu/Research/mdscope/
homepage	http://www.ks.uiuc.edu/Research/vmd/
quickhelp	http://www.ks.uiuc.edu/Research/vmd/vmd_help.html
babel	http://www.eyesopen.com/babel.html
radiance	http://radsite.lbl.gov/radiance/HOME.html
maillist	http://www.ks.uiuc.edu/Research/vmd/mailing_list/
namd	http://www.ks.uiuc.edu/Research/namd/
vrml	http://www.vrml.org/
rayshade	http://www-graphics.stanford.edu/~cek/rayshade/rayshade.html
povray	http://www.povray.org/
tcl	http://www.scriptics.com/
software	http://www.ks.uiuc.edu/Research/vmd/allversions/related_programs.html
userguide	http://www.ks.uiuc.edu/Research/vmd/vmd-1.3/ug/ug.html

Table 8.2: On-line Help Sources

8.3.10 imd

Controls the connection to a remote simulation.

- **connect** *host port*: connect to an MD simulation running on the machine named *host* and listening on port *port*. This command will fail if a previously-established connection has not yet been disconnected.

- **detach**: Disconnect from the simulation; the simulation will continue to run.
- **kill**: Disconnect from the simulation and also cause it to halt.
- **pause**: Pause the remote simulation.
- **transfer** *rate*: Set the rate at which new coordinates are sent by the remote simulation to VMD to the specified value.
- **keep** *rate*: Set the keep rate, i.e. the frequency at which VMD saves simulation frames, to the specified value.

8.3.11 label

Turn on or off labels for the four categories: atoms, bonds, angles, or dihedral angles. Once a label is created (given the list of associated atoms) it can be turned on or off until it is deleted. Also, the value of the label over the trajectory can be saved to a file and viewed with an external program such as `xmgr`. In the following, *category* implies one of [Atoms—Bonds—Angles—Dihedrals].

- **list**: Return a list of available categories.
- **list** *category*: List all labels in the given category.
- **add** *category molID1/atomID1* [*molID2/atomID2*...]: Add a label involving the atom(s) *atomID* of the molecule *molID* to the given category.
- **show** *category* < **all** | *label_number* >: Turn on labels in the given category.
- **hide** *category* < **all** | *label_number* >: Turn off labels in the given category.
- **delete** *category* < **all** |*label_number*>: Delete labels in the given category.
- **graph** *category label_number* [*command*]: Show a graph of a label from the given category. The data will be written to a temporary file, and the specified command will be run to graph the data. %s in the *command* string will be replaced by the temporary filename.

8.3.12 light

There are four light sources, numbered 0 to 3, which are used to illuminate graphical objects. They are point sources located at infinity, so setting their positions places them along a ray from the origin through the given point.

- **num**: Return the number of lights available.
- *light_number* **on**: Turn a light on.
- *light_number* **off**: Turn a light off.
- *light_number* **status**: Return the pair on/off highlight/unhighlight

- *light_number* **rot < x | y | z >** *angle*: Rotate a light (at infinity) *angle* degrees about a given axis.
- *light _numer* **pos**: Return current position.
- *light _numer* **pos default**: Return default position.
- *light _numer* **pos { x y z}**: Set light position.

8.3.13 logfile

Turn on/off logging a VMD session to a log file. This will create a log file with commands for all the actions taken during the session. The log file may be played back later by using the 'play' command or the Tcl 'source' command. The only actions recorded are those which change the state of the VMD display, so straight Tcl commands are not saved. All of the core VMD commands will write to the log.

- *filename*: Turn on logging to *filename*.
- **off**: Turn off logging.

To write log information to the file 'off', use the file name './off'. To have log information appear on the text console, use `logfile /dev/tty`.

8.3.14 material

This set of commands is used to create new material definitions and modify existing ones.

- **list**: Return a list of the available materials
- **settings** *name*: Return a list of the five material settings for the material of the given name. These settings take on floating point values between 0 and 1. The values are returned in the following order: ambient, specular, diffuse, shininess, opacity. If the specified material has not been defined, nothing is returned.
- **add** *name*: create a new material with the given name. The new material will start with the settings for "Opaque". If the name already exists, no new material is created.
- **rename** *oldname newname*: rename the given material. The command will fail if the name is already used.
- **change** *property name value*: Change a material property of the material named *name* to the value *value*. *property* must be one of the following:
  - ambient
  - specular
  - diffuse
  - shininess
  - opacity
- **delete** *name*: Delete the given material.

8.3.15 measure

The meaure command supplies several algorithms for analyzing molecular structures. In the following options, *selection* refers to an atom selection, as returned by the `atomselect` command described in section 8.3.2. The optional *weight* must be either `none`, an atom selection keyword such as `mass`, or a list of values, one for each atom in the selection, to be used as weights. If *weight* is missing or is `none`, then all weights are taken to be 1. When an atom selection keyword is used, the weights are taken from *selection1*.

- **center** *selection* [**weight** *weight*]: Returns the geometric center of atoms in *selection* using the given `weight`.
- **minmax** *selection*: Returns two vectors, the first containing the minimum x, y, and z coordinates of all atoms in *selection*, and the second containing the corresponding maxima.
- **rmsd** *selection1 selection2* [**weight** *weight*]: Returns the root mean square distance between corresponding atoms in the two selections, weighted by the given *weight*. *selection1* and *selection2* must contain the same number of atoms (the selections may be from different molecules that have different numbers of atoms).
- **fit** *selection1 selection2* [**weight** *weight*]: Returns a 4x4 transformation matrix which, when applied to the atoms in *selection1*, minimizes the weighted RMSD between *selection1* and *selection2*.
- **inverse** *matrix*: Returns the inverse of the given 4x4 matrix.

See section [§12.4.2] for more on RMSD alignment.

8.3.16 menu

The menu forms of the GUI Control or query the on-screen GUI menu forms.

- **list**: Return a list of the available menus
- *menu_name* **on**: Turn a menu on.
- *menu_name* **off**: Turn a menu off.
- *menu_name* **status**: Return `on` if on, `off` if off.
- *menu_name* **loc**: Return the x y location.
- *menu_name* **move** x y: Move a menu to the given (x, y) location

where *menu_name* is one of the following:

- main
- mol
- animate
- edit

- graphics
- labels
- render
- display
- color
- simulation
- tracker

8.3.17 mol

Load, modify, or delete a molecule in VMD. In the following, *molecule_number* is a string describing which molecules are to be affected by the command. It is one of the following: `all`, `top`, `active`, `inactive`, `displayed`, `on`, `off`, `fixed`, `free`, or one of the unique integer ID codes assigned to the molecules when they are loaded (starting with 0). The codes (molIDs) are not reused after a molecule is deleted, so if you, for example, have three molecules loaded (numbered 0, 1, 2), delete molecule with molID equal to 0, and then load another molecule, the new molecule will have molID 3. Thus, the list of available molecule IDs becomes (1 2 3). The index of the molecule on this list is, among many other things, accessible through the `molinfo` command [§8.3.19]. In the above case, for example, molecule that was loaded the last has molID equal to 3, however, it is the third on the list of molecules, so it has the index equal to 2 (since we start countin from 0).

The molecule representations (views) are assigned integer number (starting with 0 for each molecule), which appear in the list on the Graphics form [§4.4.6]. The representations can be added, deleted or changed with the `mol` command. See also sections on `molinfo` command [§ 8.3.19] for more ways of retrieving information about the representations. See Chapter § 11 for information on how to use `mol` command to load user-defined graphics.

- **< new | load >** *structure_file_type structure_file* [*coordinate_file_type coordinate_file*] : Load a new molecule from *filename(s)* using the given *format*.
- **urlload <file type> <URL>**: Load a molecule from a given URL address
- **pdbload <four letter accession id>**: ftp molecule from PDB. **This command is deprecated; please use the following command instead: mol load webpdb <four letter accession id>**
- **list**: Print a one-line status summary for each molecule.
- **list** *molecule_number*: Print a one-line status summary for each molecule matching the *molecule_number*. If only one molecule matches the *molecule_number*, also print the representation status for this molecule, i.e., number of representations as well as the representation number, coloring method , representation style and the selection string for each of the representations.
- **color** *coloring_method*: Change the default atom coloring method setting.

- **representation** *rep_style*: Change the default rendering method setting.
- **selection** *select_method*: Change the default atom selection setting.
- **modcolor** *rep_number molecule_number coloring_method*: Change the current coloring method for the given representation in the specified molecule.
- **modmaterial** *rep_number molecule_number material_name*: Change the current material for the given representation in the specified molecule.
- **modstyle** *rep_number molecule_number rep_style*: Change the current rendering method (style) for the given representation in the specified molecule.
- **modselect** *rep_number molecule_number select_method*: Change the current selection for the given representation in the specified molecule.
- **addrep** *molecule_number*: Using the current default settings for the atom selection, coloring, and rendering methods, add a new representation to the specified molecule.
- **delrep** *rep_number molecule_number*: Deletes the given representation from the specified molecule.
- **modrep** *rep_number molecule_number*: Using the current default settings for the atom selection, coloring, and rendering methods, changes the given representation to the current defaults.
- **delete** *molecule_number*: Delete molecule(s).
- **active** *molecule_number*: Make molecule(s) active.
- **inactive** *molecule_number*: Make molecule(s) inactive.
- **on** *molecule_number*: Turn molecule(s) on (make drawn).
- **off** *molecule_number* : Turn molecule(s) off (hide).
- **fix** *molecule_number*: Fix molecule(s).
- **free** *molecule_number*: Unfix molecule(s).
- **top** *molecule_number*: Set the top molecule.
- **cancel** *molecule_number*: Cancel loading trajectories.
- **ssrecalc** *molecule_number*: Recalculate secondary structure based on the current set of coordinates.

8.3.18 molecule

Same as mol.

8.3.19 molinfo

The `molinfo` command is used to get information about a molecule (or loaded file) including the number of loaded atoms, the filename, the graphics selections, and the viewing matrices. It can also be used to return information about the list of loaded molecules.

Each molecule has a unique id, which is assigned to it when it is first loaded. These start at zero and increase by 1 for each new molecule. When a molecule is deleted, the number is not used again. There is one unique molecule, called the top molecule top molecule [§4.4.3], which is used to determine some parameters, such as the center of view, the data in the animation form, etc.

- **list**: Returns a list of all current molecule id's.
- **num**: Returns the number of loaded molecules.
- **top**: Returns the id of the top molecule.
- **index** *n*: Returns the id of the *n*'th molecule.
- *molecule_id* **get** {*list of keywords*}
- *molecule_id* **set** {*list of keywords*} {*list of values*} Access and, in some cases, modify information about a given molecule. The list of recognized keywords is given in Table 8.3.

```
Examples:
vmd > molinfo top get numatoms
Info) 568
vmd > molinfo 0 get {source filename}
Info) File /home/dalke/pdb/pti.pdb
```

8.3.20 mouse

Change the current state (mode) of the mouse.

- **mode 0**: Set mouse mode to rotation.
- **mode 1**: Set mouse mode to translation.
- **mode 2**: Set mouse mode to scaling.
- **mode 3** *N*: Set mouse mode to rotate light *N*.
- **mode 4** *N*: Set mouse mode to picking mode *N*, where *N* is one of the following:
  - 0: query item
  - 1: pick center
  - 2: pick atom
  - 3: pick bond
  - 4: pick angle
  - 5: pick dihedral

  - 6: move atom
  - 7: move residue
  - 8: move fragment
  - 9: move molecule
  - 10: force on atom
  - 11: force on residue
  - 12: force on fragment

8.3.21 play

Start executing text commands from a specified file, instead of from the console. When the end of the file is reached, VMD will resume reading commands from the previous source. This command may be nested, so commands being read from one file can include commands to read other files.

- *filename*: Execute commands from *filename*.

8.3.22 quit

Same as exit.

8.3.23 render

Output the currently displayed image (scene) to a file.

- **list**: List the available rendering methods.
- *method filename*: Render the global scene to *filename* using *method* and execute the default command, where *method* can be one of the following:
  - Raster3D
  - Tachyon
  - snapshot
  - POV3
  - POV
  - RayShade
  - Radiance
  - ART
  - PostScript
  - STL
  - VRML-1
  - Token

- *method filename command*: Render the global scene to *filename*, then execute '*command*'. Any %s in '*command*' are replaced by the filename (up to 5).
- *options method*: Get the default command string.
- *options method command*: Set new default command.
- *default method*: Get the original default command.

8.3.24 rock

Rotate the current scene continually at a specified rate.

- **off**: Stops rocking.
- **< x | y | z > by** *step*: Rock around the given axis at a rate of *step* degrees per redraw.
- **< x | y | z > by** *step n*: Rock around the given axis at a rate of *step* degrees per redraw for *n* steps, reverse, and repeat.

8.3.25 rotate

Rotate the current scene around a given axis by a certain angle. This does not change atom coordinates.

- **stop**: Stop all rotation, same as rock off.
- **< x | y | z > by** *angle*: Rotate around the given axis *angle* degrees.
- **< x | y | z > to** *angle*: Rotate the given axis to the absolute position *angle*.
- **< x | y | z > < by | to >** *angle step*: Rotate at a rate of *step* degrees per redraw.

8.3.26 scale

Scale the current scene up or down. This does not change atom coordinates.

- **by** *f*: Multiply scene scaling factor by *f*.
- **to** *f*: Set scene scaling factor to *f*.

8.3.27 stage

Position a checkerboard stage on the screen.

- **location < off | origin | bottom | top | left | right | behind >**: Set the location.
- **location**: Get the current location.
- **locations**: Get a list of possible locations.
- **panels** *n*: Set number of panels in stage, up to 30.
- **panels**: Get the number of panels in use

8.3.28 tool

Initialize and control the tools that are controlled by external tracking devices.

- **create**: Create a new tool
- **change** *type* `[` *toolid* `]`: Change the type of a tool.
- **scale** *scale* `[` *toolid* `]`: Change the scale of the coordinates reported by a tool.
- **scaleforce** *scale* `[` *toolid* `]`: Increase or decrease the force on a force-feedback device.
- **rot** `[` **left** `|` **right** `]` A_{00} $A_{01} \ldots A_{33}$ `[` *toolid* `]`: Multiply a tool's orientation matrix on the left or right by a matrix A.
- **offset** x y z `[` *toolid* `]`: Add a vector to a tool's position.
- **delete** `[` *toolid* `]`: Remove a tool.
- **info** `[` *toolid* `]`: Get info about a tool.
- **rep** *molid repid*: Choose only a single representation for tugging or SMD.
- **adddevice** *name* `[` *toolid* `]` : Add a device to a tool, using a name found in the sensor configuration file.
- **removedevice** *name* `[` *toolid* `]` : Remove a device from a tool, using a name found in the sensor configuration file.

8.3.29 translate

Translate the objects in the current scene. This does not change the atom coordinates.

- **by** x y z: Translate by vector (x, y, z) in screen units (note, that this does not change the atom coordinates).
- **to** x y z: Translate to the absolute position (x, y, z) in screen units.

8.3.30 user

Add user-customized commands.

- **add key** *key command*: Assign the given text command to the hot key *key*. When *key* is pressed while the mouse is in the display window, the specified command will be executed.
- **print keys** : Print out the current definition of the hot keys.

See section § 4.1.3 for examples of the use of the `user` command.

8.3.31 vmdinfo

(Tcl) Returns information about this version of VMD.

- **version**: Returns the version number;
- **versionmsg**: Full information about this version;
- **authors**: List of authors;
- **arch**: architecture type (in case you couldn't tell);
- **options**: options used to compile VMD;
- **www**: VMD home page;
- **wwwhelp**: VMD help page.

This function is available without Tcl and the information is displayed to the screen.

8.3.32 wait

Specify a number of seconds to wait before reading another command. Animation *continues* during this time. The wait command will not behave as expected if called within a complex Tcl proc or loop structures. The wait command doesn't actually run until the next complete Tcl code block due to the way VMD processes its commands.

- *time*: wait *time* seconds.

8.3.33 sleep

Specify a number of seconds to sleep before reading another command. Animation *stops* during this time.

- *time*: sleep *time* seconds.

8.4 Tcl callbacks

When certain events occur, VMD notifies the Tcl interpreter by setting certain Tcl variables to new values. You can use this feature to customize VMD, for instance, by causing new graphics to appear when the user picks an atom, or recalculating secondary structure on the fly.

To make these new feature happen at the right time, you need to write a script that takes a certain set of arguments, and register this script with the variable you are interested. Registering scripts is done with the built-in Tcl command `trace`; see `http://dev.scriptics.com/man/tcl8.0/TclCmd/trace.htm` for documentation on how to use this command. The idea is that after you register your callback, when VMD changes the value of the variable, your script will immediately be called with the new value of the variable as arguments. Table 8.4 summarizes the callback variables available in VMD.

In the VMD script library at `http://www.ks.uiuc.edu/Research/vmd/script_library/`, you can find a number of scripts that take advantage of Tcl variable tracing. Below, we give a very simple example.

The following procedure takes the picked atom and finds the molecular weight of residue it is on.

```
proc mol_weight {} {
      # use the picked atom's index and molecule id
      global vmd_pick_atom vmd_pick_mol
      set sel [atomselect $vmd_pick_mol "same residue as index $vmd_pick_atom"]
      set mass 0
      foreach m [$sel get mass] {
            set mass [expr $mass + $m]
      }
      # get residue name and id
      set atom [atomselect $vmd_pick_mol "index $vmd_pick_atom"]
      lassign [$atom get {resname resid}] resname resid
      # print the result
      puts "Mass of $resname $resid = $mass"
}
```

Once an atom has been picked, run the command `mol_weight` to get output like:

```
Mass of ALA 7 : 67.047
```

Since VMD sets the vmd_pick_atom and vmd_pick_mol variables, they can be traced.

```
proc mol_weight_trace_fctn {args} {
      mol_weight
}
```

(This function is needed because the functions registered with trace take three arguments, but "mol_weight" only takes one.)

The trace function is registered as:

```
trace variable vmd_pick_atom w mol_weight_trace_fctn
```

And now the residue masses will be printed automatically when an atom is picked. To turn this off,

```
trace vdelete vmd_pick_atom w mol_weight_trace_fctn
```

Keyword	Aliases	Arg	Set	Description
id		*int*	N	molecular id
index		*int*	N	index on the molecule list
numatoms		*int*	N	number of atoms
source		*str*	N	one of File, Graphics, Remote, or Sigma
name		*str*	N	the name of the molecule (usually the name of the file)
filename		*str*	N	full filename (if two files, the topology file)
filetype		*str*	N	corresponding file type (PSF, PDB, XYZ, ...)
filename2		*str*	N	full filename of coordinate file (if two files)
filetype2		*str*	N	corresponding file type (DCD, PDB, XTC, ...)
active		*bool*	Y	is/make the molecule active
drawn	displayed	*bool*	Y	is/make the molecule drawn
fixed		*bool*	Y	is/make the molecule fixed
top		*bool*	Y	is/make the molecule top
center		*vector*	Y	get/set the coordinate used as the center
center_matrix		*matrix*	Y	get/set the centering matrix
rotate_matrix		*matrix*	Y	get/set the rotation matrix
scale_matrix		*matrix*	Y	get/set the scaling matrix
global_matrix		*matrix*	Y	get/set the global (rotation/scaling) matrix
view_matrix		*matrix*	N	get/set the overall viewing matrix
numreps		*int*	N	the number of representations
selection *i*		*string*	N	the string for the i'th selection
rep *i*		*string*	N	the string for the i'th representation
color *i*	colour	*string*	N	the string for the i'th coloring method
numframes		*int*	N	number of animation frames
frame		*int*	Y	current frame number
bond		*float*	N	the bond energy (for the current frame)
angle		*float*	N	the angle energy
dihedral		*float*	N	the dihedral energy
improper		*float*	N	the improper energy
vdw		*float*	N	the van der Waal energy
electrostatic	elec	*float*	N	the electrostatic energy
hbond		*float*	N	the hydrogen bond energy
kinetic		*float*	N	the total kinetic energy
potential		*float*	N	the total potential energy
energy		*float*	N	the total energy
temperature	temp	*float*	N	the overall temperature

Table 8.3: `molinfo` keywords

Table 8.4: Description of Tcl callback variables in VMD.

When called	Name	New value
The molecule with id `molid` changed animtion frames	`vmd_frame(molid)`	new animation frame
New molecule created with id `molid`	`vmd_initialize_structure(molid)`	1
Molecule with id `molid` deleted	`vmd_initialize_structure(molid)`	0
Bond, angle or dihedral label added	`vmd_pick_value`	Value of geometry label
Atom picked	`vmd_pick_mol`	id of picked molecule
Atom picked	`vmd_pick_atom`	id of picked atom
Atom picked	`vmd_pick_shift_state`	1 if shift key down during pick, 0 otherwise
Coordinate file loaded	`vmd_trajectory_read(molid)`	Name of coordinate file
IMD coordinate set received	`vmd_timestep(molid)`	frame containing new coordinates
Any VMD command executed	`vmd_logfile`	Tcl text equivalent of command

Chapter 9

Python Text Interface

VMD 1.6 contains an embedded, fully-functional Python interpreter. The interpreter acts just like the Python command line: you can import your own modules and run them from with the text console of VMD. In addition, VMD provides a number of modules for loading molecules and controlling their display.

indexPython!version VMD currently uses Python version 2.0.

9.1 Using the Python interpreter within VMD

When you start VMD, the VMD text console uses the Tcl command interpreter to process what you type. In order to use the Python interpreter, you have to tell VMD to switch to 'Python mode'. To do this, simply type 'gopython' in the console window. If VMD prints an error message reporting that the Python interpreter is not available, your version of VMD was not compiled with Python support; contact the VMD developers for help. If all goes well, you should see Python command prompt '>>> ' in the console window. To switch back to the Tcl interpreter, press Ctrl-D as though you were exiting Python. Switching back and forth between Python and Tcl does not destroy any of your work; all variables and modules will still be defined until you exit VMD.

Typing 'gopython <filename>', where <filename> is the name of a file containing Python code will cause VMD to switch to Python mode, process the file, then switch back to Tcl. In this way, you can embed Python functions inside your Tcl scripts!

You can also type 'gopython -command "*your code here*" to run an arbitrary line of python code.

9.2 Atom selections in Python

VMD provides an atom selection class for use in the Python interpreter. Instances of this class correspond to a set of atom indicies in a particular molecule for a particular coordinate set. Once an atom selection is made, you can query the properties of the selected atoms, such as their names, residue ids, or coordinates. In a similar fashion, you can set the values of these properties. You can also perform logical operations on atom selections, including finding the intersection or union of two atom selections or finding the inverse of the set. Finally, you can perform tuple operations on the atom selection object to query the indices of the atoms in the selection.

Below we summarize the methods available from the AtomSel module.

- `AtomSel(selection = 'all', molid = 0, frame = 0)`: Creates a new atom selection object.

  >>> sel = AtomSel('name CA', 1) # Selects the alpha carbons of molecule 1

- `select(selection)`: Change the selected atoms.

  >>> sel.select('resid 5')

- `frame(value = -1)`: Set/get the coordinate frame for the selection. Nonpositive values will return the current value of the frame without changing it.

  >>> sel.frame(5)

  >>> sel.frame()

  5

- `get(attr1, attr2, ...)`: Takes any number of string arguments, which should correspond to a valid atom property such as "name", "x", or "water". Returns a list of the value of the property for each atom in the selection. For boolean properties such as "water", the returned value will be 1 if true and 0 if false.

  >>> x, y, z = sel.get('x', 'y', 'z')

- `set(attr, val)`: Set the atom property corresponding to *attr* using the values in *val*. The number of elements in *val* should be either 1 or the number in the atom selection.

  >>> len(sel)

  12

  >>> sel.set('beta',3)

  >>> sel.set('beta',(1,2,3,4,5,6,7,8,9,10,11,12))

- `sel1 & sel2`: Create a new atom selection using the atoms found in both *sel1* and *sel2*.

- `sel1 | sel2`: Create a new atom selection using the atoms found in either *sel1* or *sel2*.

- `-sel`: Create a new atom selection using the atoms not found in *sel*.

- `len(sel)`: Returns the number of atoms in the selection.

- `sel[0], sel[0:3]`: Index and slice operations return the corresponding atoms in the selection.

9.2.1 An atom selection example

In the first example, we load the molecule alanin.pdb, and create an atom selection consisting of the alpha carbons. Note that AtomSel is the nae of the class which generates atom selection instances. We show the string representation of the object by entering its name and pressing return; this shows the text used in the selection.

Next we demenstrate how atom selections act like tuples: we can get their length using the built-in len() command,and return a copy of the selected atoms in a tuple by using the slice operator [:].

Finally, we demonstrate the get and set operations. The get() operation takes any number of string arguments; for each argument, it returns a Python list of values corresponding to that string. The set() operation allows only one property to be changed at a time. However, you can pass in either a single value, which will be applied to all atoms in the selection, or a tuple or list of the same size as the atom selection, in which case values in the list will be assigned to the corresponding atom in the selection. We take advantage of this behavior in the following example by first saving the current value of beta for the selection, then setting the value of beta to 5 for all selected atoms, and finally resetting the original values using the results of the get().

```
>>> from molecule import *
>>> from AtomSel import AtomSel
>>> load('alanin.pdb')

>>> CA = AtomSel('name CA')
>>> CA
name CA
>>> len(CA)
12
>>> CA[:]
(0, 5, 11, 17, 23, 29, 35, 41, 47, 53, 59, 65)
>>> resname, resid = CA.get('resname', 'resid')
>>> resname
['ACE', 'ALA', 'ALA', 'ALA', 'ALA', 'ALA', 'ALA', 'ALA', 'ALA', 'ALA', 'ALA', 'C
BX']
>>> resid
[1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12]
>>> x,y,z=CA.get('x','y','z')
>>> x
[-2.1840000152587891, 1.4500000476837158, 1.9809999465942383, 0.54100000858306885,
2.8090000152587891, 5.9079999923706055, 5.0440001487731934, 4.5659999847412109,
7.9340000152587891, 9.7329998016357422, 8.1689996719360352, 9.2229995727539062]
>>> y
[0.5910000205039978, 0.0, 3.6429998874664307, 4.8410000801086426, 2.5559999942779541,
3.7860000133514404, 7.4190001487731934, 6.7989997863769531, 5.0819997787475586,
7.9559998512268066, 10.515999794006348, 8.5710000991821289]
>>> z
[0.9100000262260437, 0.0, -0.9089999794960022, 2.3880000114440918, 4.3920001983642578,
2.5859999656677246, 3.244999885559082, 6.9559998512268066, 7.2639999389648438,
5.5669999122619629, 7.8870000839233398, 11.013999938964844]

>>> beta = CA.get('beta')
>>> CA.set('beta',5)
>>> CA.set('beta',beta)
>>>
```

9.2.2 Changing the selection and the frame

When molecule in VMD contains multiple coordinate sets (frames), atom selections must know which frame they are referring to, especially when you make distance-based atom selections or request time-varying properties like the x, y, or z coordinates. By default, atom selections in Python use frame 0, i.e. the first coordinate set. You can specify the frame either when you create the atom selection, or by using the frame() method. Passing no arguments to frame() returns the current value of the frame.

```
>>> load('psf','alanin.psf','dcd','alanin.dcd')

>>> resid5 = AtomSel('resid 5', frame=50)
>>> resid5.frame()
50
>>> resid5.frame(22)
>>> resid5.frame()
22
```

In a similar way, you can change the selected atoms of an atom selection object using the select() operation. Continuing with the previous example:

```
>>> resid5
resid 5
>>> resid5.select('resid 7')
>>> resid5
resid 7
>>>
```

9.2.3 Combining atom selections

Once you've created one or more atom selections, you can combine them to create new ones.

```
>>> CA = AtomSel('name CA')
>>> resid5 = AtomSel('resid 5')
>>> CA
name CA
>>> resid5
resid 5
>>> ANDsel = CA & resid5
>>> ORsel = CA | resid5
>>> NOTsel = -CA
>>> ANDsel
(name CA) and (resid 5)
>>> ORsel
(name CA) or (resid 5)
>>> NOTsel
not (name CA)
>>>
```

When the combined atom selections are from different molecules or have different frame numbers, the molecule and frame from the first atom selection are used.

9.3 Python callbacks

Some of your Python scripts may wish to be informed when various events in VMD occur. The mechanism for expressing this interest is to register a callback function with a special module supplied by VMD. When the event of interest occurs, all registered will functions will be called; VMD will pass the functions information specific to the event. The set of callbacks events is listed in Table 9.3.

Table 9.1: Description of callbacks available to scripts running in the embedded Python interpreter.

Name	When called	Function argument
display_update	Screen redraw	none
frame	Molecule changes coordinate frame	(molid, frame)
help	User pushes help button on main form	(name of topic)
initialize_structure	Molecule created or deleted	(molid, 1 or 0)
pick_atom	Atom picked in graphics window	(molid, atomid, key_shift_state (1 if shift key do
pick_value	Bond, angle, or dihedral label created	(value)
timestep	New IMD coordinate frame received	(molid, frame)
trajectory	Completion of coordinate file read/write	(molid, filename)

All callback functions must take two arguments. The first argument will be an object given at the time the function is registered; VMD makes no use of this object, it simply saves it and passes it to the callback when the callback function is called. The second argument to the callback function will be a tuple containing 0 or more elements, depending on the type of callback. The type of information for each callback is listed in the third column of Table 9.3.

Callbacks are registered/deregistered using the add_callback/del_callback methods of the VMD-Callback module. The syntax for these methods is:

```
def add_callback(name, func, userdata = None):

def del_callback(name, func, userdata = None):
```

`name` should be one of the callback names in Table 9.3. `func` is the function object. `userdata` is any object; if no object is supplied, None will be passed as the first argument to the callback function. To unregister a callback, use the same name, func, and userdata as were used when the callback was registered. The same function may be registered multiple times with different userdata objects.

9.3.1 Using Tkinter menus in VMD

The object-oriented interface to Tk known as Tkinter is included with the embedded Python interpreter. You can create Tkinter GUI's in the usual way; VMD will take care of updating your GUI windows for you, so there is no need to call the mainloop method of the Tk module. This method should not be called when the Tkinter GUI is running inside of VMD, because it will interfere with VMD's own event loop.

9.4 Controlling VMD from Python

Commands for controlling VMD from Python are organized into modules which roughly correspond to Tcl commands. Importing all the commands in a module is not recommended as some of the functions (e.g., listall()) overlap. All commands are listed below, with the name of the module given by the section heading.

9.4.1 animate

Python operations available from the *animate* module, used to control which coordinate frames are displayed.

- `forward()`:
- `reverse()`: `forward()` and `reverse()` causes VMD to start animating frames automatically in order of increasing or decreasing frame number, respectively.
- `once()`:
- `rock()`:
- `loop()`: `once()`, `rock()`, and `loop()` control how frames are cycled when VMD is animating a series of frames. `once()` causes VMD to stop when it reaches the first or last frame. `rock()` causes VMD to reverse direction each time it gets to the beginning or end. `loop()` causes VMD to continue from the beginning when reaches the last frame, or from the last frame if it gets to the beginning.
- `style()`: Returns either `'Once'`, `'Rock'`, or `'Loop'`, corresponding to the animation mode VMD is currently in.
- `goto(frame)`: Set the animation to the given frame, and pause the animation.
- `prev()`: Step to the next-lowest frame, then pause.
- `next()`: Step to the next-highest frame, then pause.
- `pause()`: Stop animating frames.
- `speed(value)`: Get/set the relative rate at which VMD animates frames. `value` should lie between 0 and 1. If a value less than 0 is given, then the speed will not be changed. The new value of the speed is always returned.
- `skip(value)`: Get/set the number of frames to skip when animating. A value of 1 means every frame is shown; 2 means every other frame is shown; etc. If `value` is 0 or less, no change is made. The new value of the speed is always returned.
- `is_active(molid)`: Returns whether the molecule with the given id is active; that is; whether it responds to animation or not.
- `activate(molid, trueorfalse)`: Make the molecule with the given id active or not.

9.4.2 axes

Python operations available from the *axes* module, used to change where the axes are displayed in the graphics window.

- `OFF, ORIGIN, LOWERLEFT, LOWERRIGHT, UPPERLEFT, UPPERRIGHT`: String constants defined in the *axes* module for setting the location of the axes.
- `get_location()`: Returns a string object corresonding the current location of the axes.
- `set_location(location)`: Set the location of the axes, using one of constants defined in the module.

9.4.3 color

Python operations available from the *color* module, used to change the color definitions, color maps, or edit the color scale. All rgb and color scale values should be in the range 0 to 1.

- `categories()`: Returns a list of available color categories.
- `get_colormap(name)`: Returns a dictionary of name/color pairs for the given color category.
- `set_colormap(name, dict)`: Change the color definitions for the colors in the given color category. The keys in `dict` must come from the keys listed by `get_colormap` for that color category, though not all keys need be listed. The values must be legal color names.
- `get_colors()`: Returns a dictionary whose keys are all the legal color names and whose corresponding values are the RGB values of the color, represented as a 3-tuple.
- `set_colors(dict)`: Changes RGB values for colors in VMD. Keys must be chosen from the keys returned by `get_colors()`. Values must be 3-tuples of floats.
- `scale_method()`: Returns the current color scale method.
- `scale_methods()`: Returns a list of all available color scale methods.
- `scale_midpoint()`: Returns the current color scale midpoint.
- `scale_min()`: Returns the current color scale minimum.
- `scale_max()`: Returns the current color scale maximum.
- `set_scale(method, midpoint, min, max)`: Change the color scale method, midpoint, minimum, or maximum. All properties may be set using keyword arguments.

9.4.4 display

Python operations available from the *display* module, used to control the VMD camera as well as screen updates.

- `update()`: Force a display update, without checking the VMD FLTK menus

- `update_ui()`: Update the display as well as any other user interfaces.
- `update_on()`: Tell VMD to regularly update the display and the FLTK menus
- `update_off()`: Tell VMD not to regularly update the display. The display will be updated only when display.update() is called.
- `stereomodes()`: Returns a list of the available stereo modes.
- `PROJ_PERSP, PROJ_ORTHO`: String constants defined in the `display` module for setting the `projection` keyword in the `set` method.
- `DETAIL_NONE, DETAIL_POINTS, DETAIL_WIRE, DETAIL_FLAT, DETAIL_FULL`: String constants defined in the `display module` for setting the `detail` and `altdetail` methods in the `set` method.
- `set(**keywordlist)`:
- `get(key)`: set() and get() control various display properties. The following keywords accept/return floating-point values: `eyesep, focallength, height, distance, nearclip, farclip`. The following keywords accept boolean values for on or off, respectively: `antialias, depthcue, depthsort, culling`. `detail` and `altdetail` should be one of the DETAIL constants defined in this module. `stereo` should be one of the values returned by `stereomodes()`. `projection` should be one of the PROJ constants defined in this module.

9.4.5 graphics

Python operations available from the *graphics* module, used to create custom 3-D objects from graphics primitives. The first argument to all operations is the id of a Graphics molecule. Graphics molecules are created using the `load()` command in the *molecule* module: `load('graphics', 'test')` creates a Graphics molecule named 'test'. For vertices and normals, a tuple with three float items is required.

- `triangle(id, v1, v2, v3)`: Draw a triangle with the given vertices.
- `trinorm(id, v1, v2, v3, n1, n2, n3)`: Draw a triangle with the given vertices and vertex normals.
- `cylinder(id, v1, v2, radius=1.0, resolution=6, filled=0)`: Draw a cylinder with endpoints specified by the given points. Radius, resolution, and filled (whether the ends should be capped or not) may be optionally specified with keyword arguments.
- `point(id, v)`: Draw a point at the given coordinates.
- `line(id, v1, v2, style='solid', width=1)`: Draw a line between the given vertices. Optionally, the line style may be specified as either 'solid' or 'dashed', and width may be any positive integer.
- `materials(id, onoff)`: Turns materials on/off for subsequent graphics primitives. Primitives lying earlier in the stack are not affected. `onoff` should be either 0 (off) or 1 (on).

- `material(id, name)`: Sets the material for all graphics primitives in this molecule. `name` should be one of the material names returned by `material.listall()`.
- `color(id, color)`: Set the color for subsequent graphics primitives. `color` may be (1) a tuple containing three floats specifying the RGB value, (2) an integer corresponding to a color index, or (3) a string corresponding to a color name.
- `cone(id, v1, v2, radius=1.0, resolution=6)`: Draw a cone with base at `v1` and point at `v2`. radius and resolution may optionally be specified with keyword arguments.
- `sphere(id, center=(0.0, 0.0, 0.0), radius=1.0, resolution=6)`: Draw a sphere. The sphere center, radius, and resolution may optionally be specied with keyword arguments.
- `text(id, pos, text, size=1.0)`: Draw text at the given position (specified by a tuple of three floats, using the string `text`. Size may optionally be specified using keyword arguments.
- `delete(id, index)`: Deletes the graphics primitive with the given index. Alternatively, if the string 'all' is passed as the index, all graphics primitives will be deleted.
- `replace(id, index)`: Deletes the graphics primitive with the given index. The next graphics primitive added will go in the newly vacated position. Subsequent graphics primitives will resume at the end of the list.
- `info(ind, index)`: Returns a string describing the graphics primitive with the given index. If the index is invalid, an IndexError exception is raised.
- `listall(ind)`: Returns the indices of the valid graphics primitives in a list.

9.4.6 imd

Python operations available from the *imd* module, used to display and interact with a molecule in a molecular dynamics simulation.

- `connect(host, port)`: Connect to a simulation running on host `host` and listening for incoming connections on port `port`.
- `pause()`: If connected, cause the simulation to pause.
- `detach()`: If connected, detach from the simulation. The simulation will continue to run, but no more frames will be received until a connection is re-established.
- `kill()`: If connected, terminate the simulation. The connection will also be abolished.
- `transfer(rate)`: Set/get how often the remote simulation sends coordinate frames to VMD. If *rate* is omitted or is negative, no action is taken and the current value is returned. A value of 1 corresponds to every frame being sent; a value of 2 corresponds to every other frame, etc.
- `keep(rate)`: Set/get how often received coordinates frames are kept by VMD as part of an animation. If *rate* is omitted or is negative, no action is taken and the current value is returned. A value of 0 means no frames are saved. A value of 1 corresponds to every frame being saved; a value of 2 corresponds to every other frame, etc.

9.4.7 label

Python operations available from the *label* module, used to create, show/hide, and delete labels for atoms, bonds, angles, or dihedrals.

- `ATOM, BOND, ANGLE, DIHEDRAL`: Label types defined by the label module, for use as the first argument to the add, listall, show, hide, and delete methods.
- `add(type, molids, atomids)`: Create a label of the given type. `molids` and `atomids` must be tuples containing 1, 2, 3, or 4 integers for ATOM, BOND, ANGLE, or DIHEDRAL labels, respectively.
- `listall(type)`: Returns a list of labels of the given type. The elements of the list are python dictionary objects, with the following keys: `molid`, `atomid`, `value`, `on`. The values for `molid` and `atomid` are tuples containing the molecule id and atom id for the label. `value` is the numerical value of the geometry label, or zero for ATOM labels. `on` is 1 if the label is shown, and 0 if the label is hidden.
- `show(type, label)`: Turn the given label on. `label` must be a dictionary containing `molid` and `atomid` keys whose values are tuples. If the tuples match the molecule ids and atom ids of the atoms in an existing label, the label will be turned on.
- `hide(type, label)`: Turn the given label off. `label` must be a dictionary containing `molid` and `atomid` keys whose values are tuples. If the tuples match the molecule ids and atom ids of the atoms in an existing label, the label will be turned off.
- `delete(type, label)`: Delete the given label. `label` must be a dictionary containing `molid` and `atomid` keys whose values are tuples. If the tuples match the molecule ids and atom ids of the atoms in an existing label, the label will be deleted.
- `getvalues(type, label)`: Returns a list of values of the given label for each coordinate frame in the label. If the atoms in the label belong to different molecules, only the coordinates of the first molecule will be cycled. If the labels don't have values (like atom labels), None is returned.

9.4.8 material

Python operations available from the *material* module, used to create and modify material properties of molecular representations.

- `listall()`: Returns a Python list of the names of all available materials.
- `settings(name)`: Returns a Python dictionary of the material settings for material with the given `name`.
- `add(name)`: Create a new material with the given name.
- `rename(oldname, newname)`: Rename the material with the given name. The new name must not yet be used.
- `change(name, ambient, specular, diffuse, shininess, opacity)`: Change one or more of the material settings for the material with the given name. Keyword arguments may be used to specify each property.

9.4.9 molecule

Python operations available from the *molecule* module, used to load molecules and change their representations.

- `num()`: Returns the number of loaded molecules.
- `listall()`: Returns the molid's of the all the loaded molecules.
- `structure_type(molid)`: Returns the struture file type for the given molecule.
- `structure_file(molid)`: Returns the struture file for the given molecule.
- `coor_type(molid)`: Returns the coordinate file type for the given molecule.
- `coor_file(molid)`: Returns the coordinate file for the given molecule.
- `load(structure, sfname, coor, cfname)`: Load a molecule with structure type *structure* and filename *sfname*. Additionally, a separate coordinate file may be provided, of type *coor* and name *cfname*.

  >>> load('pdb','alanin.'pdb')

  >>> load('psf','alanin.psf','dcd','alanin.dcd')
- `cancel(molid)`: Cancel loading of coordinates file for the given molecule.
- `delete(molid)`: Delete the specified molecule.
- `read(molid, type, filename, beg = -1, end = -1, skip = -1)`:
- `write(molid, type, filename, beg = -1, end = -1, skip = -1)`: Read/write a coordinate file to/from the specified molecule. Optional arguments `beg`, `end`, and `skip` may be specified with keywords; the default is to load/save all coordinate frames.
- `delframe(molid, beg=-1, end=-1, skip=-1)`: Delete frames from the specified molecule. Optional arguments `beg`, `end`, and `skip` may be specified with keywords; the default is to delete all coordinate frames.
- `dupframe(molid, frame)`: Copy the coordinates from the given frame and append them as a new frame.
- `numframes(molid)`: Return the number of coordinate frames in the specified molecule.
- `get_frame(molid)`: Return the current coordinate frame for the specified molecule.
- `set_frame(molid, frame)`: Set the current coordinate frames in the specified molecule.
- `numatoms(molid)`: Returns the number of atoms in the specified molecule.
- `ssrecalc(molid)`: Recalculate the secondary structure for the given molecule, using the current set of coordinates.
- `get_top(molid)`:
- `set_top(molid)`: Get/set the molid of the top molecule.

9.4.10 molrep

Python operations available from the *molrep* module, used to add and modify representation of molecules.

- `num(molid)`: Returns the number of representations in the given molecule.
- `addrep(molid)`: Add a representation to the specified molecule.
- `delrep(molid, rep)`: Delete the specified rep from the given molecule.
- `modrep(molid, rep, style, sel, color, material)`: Modify the style, atom selection, color, and/or material for the specified molecule and representation. Any combination of the last four arguments may be specified, using positional or keyword arguments.

  >>> modrep(0,0,color='name') # Color the first rep of molecule 0 by name.

  >>> modrep(0,2, selection='name CA', material='Transparent') # For the third representation of molecule 0, change the atom selection to "name CA" and the material to "Transparent"
- `get_style(molid, rep)`:
- `get_selection(molid, rep)`:
- `get_color(molid, rep)`:
- `get_material(molid, rep)`: Returns the representation style, selection, color, or material, respectively, for the given representation of the given molecule.

9.4.11 render

Python operations available from the *render* module, used to export the scene to a file that can be read by external rendering programs.

- `listall()`: Return a Python list of the names of all supported rendering methods. One of these should be the first argument to the `render()` operation below.
- `render(method, filename)`: Using the the given rendering method, export the current scene to the file `filename`. `method` should be one of the values returned by `listall()`.

9.4.12 trans

Python operations available from the *trans* module, used to change the view of the rendered scene.

- `rotate(axis, angle)`: Rotate the scene about the specified axis by the given angle. `axis` should be 'x', 'y', or 'z'; `angle` is measured in degrees.
- `translate(x, y, z)`: Translate the scene by the given x, y, and z values.
- `scale(factor)`: Scale (zoom) the scene by the given factor.
- `resetview(molid)`: Sets the center, scale, rotation for all molecules so that the viewpoint is centered on the molecule with the given id.

- `get_center(molid)`:
- `set_center(molid, vector)`: Get/set the coordinates of the center of the given molecule as a Python list.
- `get_scale(molid)`:
- `set_scale(molid,scale)`: Get/set the scale factor used to display the given molecule.
- `get_rotation(molid)`:
- `set_rotation(molid, matrix)`: Get/set the rotation matrix for the given molecule as a 16-element Python list in row-major order.
- `get_trans(molid)`:
- `set_trans(molid, vector)`: Get/set the global translation applied to the given molecule as a Python list.
- `is_fixed(molid)`: Returns whether the molecule with the given id is fixed; that is, whether it is affected by translation, rotation, or scaling. Fixed molecules may still be animated (see `is_active` in the *animate* section).
- `fix(molid, trueorfalse)`: Make the molecule with the given id fixed or not.
- `is_shown(molid)`: Returns whether the molecule with the given id is shown or not.
- `show(molid, trueorfalse)`: Make the molecule with the given id shown or not.

Chapter 10

Vectors and Matrices

Tcl does not handle mathematical expressions very well. It is slow at evaluating expressions, and provides no facility for handling vectors or matrices. Since the latter two are needed for structure analysis, we have added routines to manipulate them.

A vector in VMD is a list of numbers. All of the vector routines but one will work with vectors of any length; `veccross` will only use vectors of three numbers. A matrix is a 4x4 collection of numbers stored as a list of 4 vectors of 4 numbers, in row-major form.

Following are descriptions and examples of all the commands. For more examples of vectors, though without much documentation, the script used to test the vectors implementation is located at `$env(VMDDIR)/scripts/vmd/test-vectors.tcl`.

Since Tcl is slow at math, some of these commands have been reimplemented in C++. (The original definition is in the vmd script distribution, but it is redefined later on inside VMD). At times, the speedup is a factor of 40 or more. These commands are noted by (C++).

10.1 Vectors

- **veczero** – Returns the zero vector, {0 0 0}

  ```
  Example:
  vmd > veczero
  Info) 0 0 0
  ```

- (C++) **vecadd** *v1 v2* [*v3 ... vn*] – Returns the vector sum of all the terms.

  ```
  Examples:
  vmd > vecadd {1 2 3} {4 5 6} {7 8 9} {-11 -11 -11}
  Info) 1 4 7
  vmd > vecadd {0.1 0.2 0.4 0.8} {1 1 2 3} {3 1 4 1}
  Info) 4.1 2.2 6.4 4.8
  vmd > vecadd 4 5
  Info) 9
  ```

- (C++) **vecsub** *v1 v2* – Returns the vector subtraction of the second term from the first

```
Examples:
vmd > vecsub 6 3.2
Info) 2.8
vmd > vecsub {10 9.8 7} {0.1 0 -0.1}
Info) 9.9 9.8 7.1
vmd > vecsub {1 2 3 4 5} {6 7 8 9 10}
Info) -5 -5 -5 -5 -5
```

- (C++) **vecscale** *c v* –
- (C++) **vecscale** *v c* – Returns the vector of the scalar value c applied to each term of v

```
Examples:
vmd > vecscale .2 {1 2 3}
Info) 0.2 0.4 0.6
vmd > vecscale {-5 4 -3 2} -2
Info) 10 -8 6 -4
vmd > vecscale -2 3
Info) -6
```

- **vecdot** *v1 v2* – Returns the scalar dot product of the two vectors

```
Examples:
vmd > vecdot {1 -2 3} {4 5 6}
Info) 12
vmd > vecdot {3 4} {3 4}
Info) 25
vmd > vecdot {1 2 3 4 5} {5 4 3 2 1}
Info) 35
vmd > vecdot 3 -2
Info) -6
```

- **veccross** *v1 v2* – Returns the vector cross product of the two vectors.

```
Examples:
vmd > veccross {1 0 0} {0 1 0}
Info) 0 0 1
vmd > veccross {2 2 2} {-1 0 0}
Info) 0 -2 2
```

- **veclength** *v* – Returns the scalar length of v ($\|v\|$)

```
Examples:
vmd> veclength 5
Info) 5.0
vmd > veclength {5 12}
Info) 13.0
```

```
vmd > veclength {3 4 12}
Info) 13.0
vmd > veclength {1 -2 3 -4}
Info) 5.47723
```

- **veclength2** *v* – Returns the square of the scalar length of v ($\|v\|^2$)

```
Examples:
vmd > veclength2 5
Info) 25
vmd > veclength2 {5 12}
Info) 169
vmd > veclength2 {3 4 12}
Info) 169
vmd > veclength2 {1 -2 3 -4}
Info) 30
```

- **vecnorm** *v* – Returns the vector of length 1 directed along v

```
Examples:
vmd > vecnorm -10
Info) -1.0
vmd > vecnorm {1 1 }
Info) 0.707109 0.707109
vmd > vecnorm {2 -3 1}
Info) 0.534522 -0.801783 0.267261
vmd > vecnorm {2 2 -2 2 -2 -2}
Info) 0.408248 0.408248 -0.408248 0.408248 -0.408248 -0.408248
```

- **vecdist** *v1 v2* – Returns the distance between the two vectors ($\|v_2 - v_1\|$)

```
Examples:
vmd > vecdist -1.5 5.5
Info) 7.0
vmd > vecdist {0 0 0} {3 4 0}
Info) 5.0
vmd > vecdist {0 1 2 3 4 5 6} {-6 -5 -4 -3 -2 -1 0}
Info) 15.8745
```

- **vecinvert** *v* – Returns the additive inverse of v (−v).

```
Examples:
vmd > vecinvert -11.1
Info) 11.1
vmd > vecinvert {3 -4 5}
Info) -3 4 -5
vmd > vecinvert {0 -1 2 -3}
Info) 0 1 -2 3
```

10.2 Matrix routines

Because matrices are rather large when expressed in text form, the following definitions are used for the examples.

- **transidentity** – Returns the identity matrix.

  ```
  Example:
  vmd > transidentity
  Info) {1.0 0.0 0.0 0.0} {0.0 1.0 0.0 0.0} {0.0 0.0 1.0 0.0} {0.0 0.0 0.0 1.0}
  ```

- **transtranspose** *m* – Returns the matrix transpose of the given matrix

  ```
  Example:
  vmd > transtranspose {{0 1 2 3 4} {5 6 7 8} {9 10 11 12} {13 14 15 16}}
  Info) {0 5 9 13} {1 6 10 14} {2 7 11 15} {3 8 12 16}
  ```

- (C++) **transmult** *m1 m2* [*m3 ... mn*] – Returns the matrix multiplication of the given matrices

  ```
  Examples:
  vmd > set mat1 {{1 2 3 4} {-2 3 -4 5} {3 -4 5 -6} {4 5 -6 -7}}
  vmd > set mat2 {{1 0 0 0} {0 0.7071 -0.7071 0} {0 0.7071 0.7071 0} {0 0 0 1}}
  vmd > set mat3 {{0.866025 0 0 0} {0 1 0 0} {-0.5 0 0.866025 0} {0 0 0 1}}
  vmd > transmult $mat1 [transidentity]
  Info) {1.0 2.0 3.0 4.0} {-2.0 3.0 -4.0 5.0} {3.0 -4.0 5.0 -6.0}
     {4.0 5.0 -6.0 -7.0}
  vmd > transmult $mat1 $mat2 $mat3
  Info) {0.512475 3.5355 0.612366 4.0} {0.7428 -0.7071 -4.28656 5.0}
     {-0.58387 0.7071 5.5113 -6.0} {7.35315 -0.7071 -6.73603 -7.0}
  ```

- **transaxis** <**x**|**y**|**z**> *amount* [**deg**|**rad**|**pi**] – Returns the transformation matrix needed to rotate around the specified axis by a given amount. By default, the amount is specified in degrees, though it can also be given in radians or factors of pi.

  ```
  Examples:
  vmd > transaxis x 90
  Info) {1.0 0.0 0.0 0.0} {0.0 -3.67321e-06 -1.0 0.0} {0.0 1.0 -3.67321e-06 0.0}
           {0.0 0.0 0.0 1.0}
  vmd > transaxis y 0.25 pi
  Info) {0.707107 0.0 0.707107 0.0} {0.0 1.0  0.0 0.0}
           {-0.707107 0.0 0.707107 0.0} {0.0 0.0  0.0 1.0}
  vmd > transaxis z 3.1415927 rad
  Info) {-1.0 -2.65359e-06 0.0 0.0} {2.65359e-06 -1.0 0.0 0.0} {0.0 0.0 1.0 0.0}
           {0.0 0.0 0.0 1.0}
  ```

- **transvec** *v* – Returns the transformation matrix needed to bring the x axis along the v vector. This matrix is not unique, since a final rotation is allowed around the vector. The matrix is made from a rotation around y, then one about z.

```
Examples:
vmd > transvec {0 1 0}
Info) {-3.67321e-06 -1.0 0.0 0.0} {1.0 -3.67321e-06 0.0 0.0} {0.0 0.0 1.0 0.0}
         {0.0 0.0 0.0 1.0}
vmd > vectrans [transvec {0 0 2}] {1 0 0}
Info) 0.0 0.0 1.0
```

- **transvecinv** *v* – Returns the transformation needed to bring the vector v to the x axis. This produces the inverse matrix to transvec, and is composed of a rotation about z then one about y.

```
Examples:
vmd > transvecinv {0 -1 0}
Info) {-3.67321e-06 -1.0 0.0 0.0} {1.0 -3.67321e-06 0.0 0.0} {0.0 0.0 1.0 0.0}
    {0.0 0.0 0.0 1.0}
vmd > vectrans [transvecinv {-3 4 -12}] {-3 4 -12}
Info) 13.0 -1.8e-05 5.8e-05
vmd > transmult [transvec {6 -5 7}] [transvecinv {6 -5 7}]
Info) {0.999999 2.29254e-07 -6.262e-09 0.0} {2.29254e-07 0.999999
    -4.52228e-07 0.0} {-6.262e-09 -4.52228e-07 1.0 0.0} {0.0 0.0 0.0 1.0}
```

- (C++) **transoffset** *v* – Returns the transformation matrix needed to translate by the given offset

```
Examples:
vmd > transoffset {1 0 0}
Info) {1.0 0.0 0.0 1} {0.0 1.0 0.0 0} {0.0 0.0 1.0 0} {0.0 0.0 0.0 1.0}
vmd > transoffset {-6 5 -4.3}
Info) {1.0 0.0 0.0 -6} {0.0 1.0 0.0 5} {0.0 0.0 1.0 -4.3} {0.0 0.0 0.0 1.0}
```

- **transabout** *v amount* [**deg|rad|pi**] – Generates the transformation matrix needed to rotate by the given amount counter-clockwise around axis which goes through the origin and along the given vector. As with transvec, the units of the amount of rotation can be degrees, radians, or multiples of pi.

```
Examples:
# this is a rotation about x by 180 degrees
vmd > transabout {1 0 0} 180
Info) {1.0 0.0 0.0 0.0} {0.0 -1.0 -2.65359e-06 0.0} {0.0 2.65359e-06
        -1.0 0.0} {0.0 0.0 0.0 1.0}
# a rotation about z by 90 degrees
# (compare this to "transaxis z 90"
vmd > transabout {0 0 1} 1.5709 rad
Info) {0.999624 -0.027414 0.0 0.0} {0.027414 0.999624 0.0 0.0}
        {0.0 0.0 1.0 0.0} {0.0 0.0 0.0 1.0}
vmd > transabout {1 1 1} 1 pi
Info) {-0.333335 0.666665 0.666669 0.0} {0.666668 -0.333334 0.666666
        0.0} {0.666666 0.66667 -0.333332 0.0} {0.0 0.0 0.0 1.0}
```

- **trans** [**center** {*x y z*}] [**origin** {*x y z*}] [**offset** {*x y z*}] [**axis x** *amount* [**rad|deg|pi**]] [**axis y** *amount* [**rad|deg|pi**]] [**axis z** *amount* [**rad|deg|pi**]] [**x** *amount* [**rad|deg|pi**]] [**y** *amount* [**rad|deg|pi**]] [**z** *amount* [**rad|deg|pi**]] [**axis** {*x y z*} *amount* [**rad|deg|pi**]] [**bond** {*x1 y1 z1*} {*x2 y2 z2*} *amount* [**rad|deg|pi**]] [**angle** {*x1 y1 z1*} {*x2 y2 z2*} {*x3 y3 z3*} *amount* [**rad|deg|pi**]] –

  This command can do almost everything the other ones can do, and then some. It is designed to be the main function used for generating transformation matrices.

Using it correctly calls for understanding how it works internally. There are three matrices: centering, rotation, and offset. The centering matrix determines where the center of rotation is located. By default, this is the origin, but it can be changed to pivot about any point. The rotation matrix defines the rotation about that centering point, and the offset matrix defines the final translation after the rotation.

For example, to rotate around a given point, the transformations would be 1) the centering matrix to bring that point to the origin, 2) the rotation about the center, and 3) the final offset to return the origin back to its original location.

The different options for the `trans` command modify the matrices in various ways.

- **center** {*x y z*} – Sets the centering matrix so that point x y z is brought to the origin
- **offset** {*x y z*} – Sets the offset matrix so that the origin is brought to x y z
- **origin** {*x y z*} – Sets both the centering and offset matrices to x y z
- **axis x** *amount* [**rad|deg|pi**] – Adds a rotation about the x axis by the given amount to the rotation matrix
- **axis y** *amount* [**rad|deg|pi**] – Adds a rotation about the y axis by the given amount to the rotation matrix
- **axis z** *amount* [**rad|deg|pi**] – Adds a rotation about the z axis by the given amount to the rotation matrix
- **axis** {*x y z*} *amount* [**rad|deg|pi**] – Adds a rotation of the given amount about the given vector to the rotation matrix
- **bond** {*x1 y1 z1*} {*x2 y2 z2*} *amount* [**rad|deg|pi**] – Sets the center and offset transformations to the first point, and defines a rotation about the bond axis by the given amount.
- **angle** {*x1 y1 z1*} {*x2 y2 z2*} {*x3 y3 z3*} *amount* [**rad|deg|pi**] – Sets the center and offset transformation to the second point, and defines a rotation about the axis perpendicular to the plane made by the three points (the vector is computed from the cross product of the vector connecting the first two points with that connected the last two).

10.3 Multiplying vectors and matrices

There are two commands to multiply a matrix and a vector, `vectrans` and `coordtrans`. They assume the vector is in column form and premultiply the matrix to the vector. If the vector contains four numbers, the two commands are identical. If the vector has three elements, a fourth is added; a 0 for `vectrans` and a 1 for `coordtrans`. The difference is that vectors are not affected by translations during transformations, while coordinates are.

- (C++) **vectrans** *m v* – Multiple the matrix m with the vector v (length 4); returns a vector
- **coordtrans** *m v* – Multiple the matrix m with the coordinate v (length 3); returns a vector

```
Examples:
vmd > vectrans [transaxis z 90] {1 0 0}
Info) -3.67321e-06 1.0 0.0
vmd > vectrans [transvecinv {-3 4 -12}] {-3 4 -12}
Info) 13.0 -1.8e-05 5.8e-05
```

10.4 Misc. functions and values

Several other terms are added to the vectors package. The first is the variable M_PI, which contains the value of pi.

```
Examples:
vmd > set M_PI
Info) 3.14159265358979323846
vmd > expr 90 * ($M_PI / 180)
Info) 1.5708
```

The functions `trans_from_rot`, `trans_to_rot`, `trans_from_offset`, and `trans_to_offset` are used to get or set a transformation matrix from either a 3x3 rotation matrix or offset vector. As currently designed, these assume there is no scaling in the matrix. The `trans_from_offset` is identical to `transoffset` and is present for completeness.

The last is `find_rotation_value varname`, which takes a variable name and extracts from the beginning of it those terms which describe an amount of rotation. The rest of the data in the variable remains, and the amount of rotation, in radians, is returned. This is used by those functions which need a rotation. The valid values are: a number, followed by one of `rad`, `radian`, or `radians` for a value in radians, the word `pi` to give the rotation in factors of pi, or one of `deg`, `degree`, or `degrees` for a value in degrees. If no units are given, the value is assumed to be in degrees.

Examples:

```
vmd > set a "180 deg north"
Info) 180 deg north
vmd > find_rotation_value a
Info) 3.14159
vmd > set a
Info) north
vmd > set a "1 pi to eat"
Info) 1 pi to eat
vmd > find_rotation_value a
Info) 3.14159
vmd > set a
Info) to eat
vmd > set a 45
Info) 45
```

```
vmd > find_rotation_value a
Info) 0.785398
vmd > expr $M_PI * 3.0 / 2.0
Info) 4.71239
vmd > set a "4.71238 radians"
Info) 4.71238 radians
vmd > find_rotation_value a
Info) 4.71238
```

Chapter 11

User-Defined Graphics

Sometimes you may want to display graphics other than the standard molecular graphics. You may want to draw a box around a molecule, or an arrow between two atoms, or place a text label somewhere in space, or test a new method for visualizing a molecule. Because of the wide range of objects which can be displayed, VMD cannot be pre-programmed to display them all. Instead, it does offer a way to build up a new object from simple graphical items, including: points, lines, cylinders, cones, spheres, triangles (both with and without specified normals), and text. Since these are displayed in the scene just like all other graphics, they can also be saved to the various ray tracing formats.

This chapter describes how to use the text interface to add new graphics to VMD. It is broken up into four parts. The first is an introduction to the basic graphics available, the second is a tutorial which demonstrates many of the ways to use the graphics feature, the third describes how the base `graphics` command works, and the last describes the `draw` extension which can handle larger, more complicated objects.

11.1 Introduction

There are 10 types of basic graphical items built into VMD, which are used with `graphics` and `draw` commands. These are:

- **point** {*x y z*} –

  draws a point at the given position

- **line** {*x1 y1 z1*} {*x2 y2 z2*} [**width** *w*] [**style** <**solid**|**dashed**>] –

  draws either a solid or dashed line of the given width from the first point to the second. By default, this is a solid line of width 1.

- **cylinder** {*x1 y1 z1*} {*x2 y2 z2*} [**radius** *r*] [**resolution** *n*] [**filled** <**yes**|**no**>] –

  draws a cylinder of the given radius (default `r`=1) from the first point to the second. The cylinder is actually drawn as an `n` sided polygon. If the `filled` option is true (default), the ends are capped with flat disks, otherwise the cylinder is hollow.

- **cone** {*basex basey basez*} {*tipz tipy tipz*} [**radius** *r*] [**resolution** *n*] –

draw a cone with the center of the base at the first point and the tip at the second. The radius(default `r`=1) determines the width of the base. As with `cylinder`, the resolution determines the number of polygons used in the approximation.

- **triangle** {*x1 y1 z1*} {*x2 y2 z3*} {*x3 y3 z3*} –

  draws a triangle with endpoints at each of the three vertices

- **trinorm** {*x1 y1 z1*} {*x2 y2 z3*} {*x3 y3 z3*} {*nx1 y1 z1*} {*nx2 ny2 nz3*} {*nx3 ny3 nz3*} –

  draws a triangle with endpoints at each of the first three points. The second group of three values specify the normals for the three points. This is used for making a smooth shading across the triangle.

- **sphere** {*x y z*} [**radius** *r*] [**resolution** *n*] –

  draws a sphere of the given radius (default `r`=1) centered at the vertex. The resolution (default `n`=6) determines how many polygons are used in the approximation of a sphere.

- **text** {*x y z*} "*text string*" –

  displays the text string with the bottom left of the string starting at the given vertex.

- **color** *colorId* –

- **color** *name* –

- **color** *trans_name* – Each of the above geometrical objects are drawn using the current color. Initially, that color is blue, which has the colorid of 0. The `color` command changes the current color, and stays info effect until the next `color` command. Thus, to draw a red cylinder then a red sphere, first use the command `color red` command to change the color, then use the `cylinder` and `sphere` commands.

- **materials** <**on**|**off**> – Material properties are used to make the graphical objects (lines, cylinders, etc.) be affected by the light sources. These make the objects look more realistic, but are slower on machines which don't implement materials in hardware (see chapter § 5.2 and sections on color [§ 8.3.4] and colorinfo [§ 8.3.5] commands for the information on how to turn off material characteristics for all objects in VMD). One surprising effect of material characteristics is that lines are affected. In some lighting situations, the lines can even appear to disappear. Thus, you may want to turn off materials before drawing lines.

- **material** <**name**> – Sets the material to use for the corresponding graphics molecule. `name` must be a valid material name, as displayed in the Materials menu.

11.2 Tutorials and Examples

We'll start with some basic examples. Load VMD and enter:

```
draw cylinder {0 0 0} {5 0 0} radius 0.2
```

VMD will print:

```
Info) Loading new molecule ...
```

because of the way graphics are implemented (don't worry about the details yet) and draw a blue cylinder on the screen.

Now change the color to red and draw two more cylinders:

```
draw color red
draw cylinder {4 1 0} {5 0 0} radius 0.1
draw cylinder {4 -1 0} {5 0 0} radius 0.1
```

You might want to reset the view. Since the original scene had no data, a default size was chosen. Now that there is data, a reset view will center the graphics just as if it was a regular molecule (in fact, the implementation is a molecule with no atoms and only graphics). You now have a simple arrow. Let's make a nicer looking one now. First, remove all the graphics:

```
draw delete all
```

and make a cylinder with a cone on the end

```
draw cylinder {0 0 0} {4 0 0} radius 0.1
draw cone {4 0 0} {5 0 0} radius 0.15
```

Note that the widest part of the cone is at the first point. As long as we're at it, let's add some text to the end of the arrow in green

```
draw color green
draw text {5 0 0} "This way"
```

Cool, eh? Of course, more things are available than a cylinder, cone, and text. How about a sphere?

```
draw sphere {0 0 0} radius 0.3
draw sphere {0 2 0} radius 0.2
```

The color of the spheres is green because that was the previously assigned color. The color doesn't change until explicitly specified with the color option. The default color is blue.

And some lines, first, a dotted line connecting the spheres

```
draw line {0 0 0} {0 2 0} style dashed
```

then a solid one from the second sphere to the end of the arrow

```
draw line {0 2 0} {5 0 0}
```

Now, reset the view and move things around a bit. You may be surprised to see the lines appear and disappear. This is because the lines have a "material property"; which means they are affected by the lights. For some things, this may be useful, but usually if you want to draw lines, you'll need to turn materials off.

```
draw materials off
```

11.2.1 Drawing a graph

Here's an example of how to draw a 2-D graph. First, get rid of the current graphics (since there may be graphics from the previous tutorial):

```
draw delete all
```

Define a function to graph, in this case, a parabola.

```
proc f {x} {
 expr $x * $x
}
```

The following function draws a graph given the function name, the start and end values, and the step size.

```
proc draw_graph {function start end step} {
  # do some error checking
  if {$step < 0} {set step -$step}
  if {$step == 0} {error "draw_graph: cannot have step size of zero"}
  if {$start > $end} {
      set tmp $start
      set start $end
      set end $tmp
  }
  # turn materials off
  draw materials off
  # draw the data in green
  draw color green

  # calculate and save the initial coordinates
  set y0 [$function $start]
  set x0 $start
  set miny $y0
  set maxy $y0

  # go through the coordinates $start+$step to $end, $step at a time
  for {set x1 [expr $start + $step]} {$x1 <= $end} {
                                      set x1 [expr $x1 + $step]} {
      # calculate the function value for this point
      set y1 [$function $x1]
      # and draw a line to connect the previous point to the current one
      draw line "$x0 $y0 0" "$x1 $y1 0"
      # save the min/max values of y, and copy the x1,y1 into x0,y0
      if {$y1 < $miny} {set miny $y1}
      if {$y1 > $maxy} {set maxy $y1}
      set y0 $y1
      set x0 $x1
   }
```

```
    # draw a red box around everything
    draw color red
    draw line "$start $miny 0" "$end   $miny 0"
    draw line "$start $miny 0" "$start $maxy 0"
    draw line "$end   $maxy 0" "$end   $miny 0"
    draw line "$end   $maxy 0" "$start $maxy 0"
    # and put some labels down
    draw text "$end   $miny 0" "x ->"
    draw text "$start $maxy 0" "f(x)"
}
```

Copy these two definitions into VMD's text console (this script is available from the VMD script library at `http://www.ks.uiuc.edu/Research/vmd/script_library/`), then enter

```
draw_graph f -5 4 0.2
```

and reset the view. Presto, a nice little parabola.

11.2.2 Triangles

If you want to draw the surface of a solid object you can build it out of triangles. The graphics interface to VMD supports two types of triangles, simple triangles with just the corners defined, or "trinorms" which have normals defined for each corner.

First, a simple red triangle

```
draw delete all
draw color red
draw triangle {1 0 0} {0 1 0} {0 0 1}
```

Not bad, so let's put some more in

```
draw triangle {1 0 0} {0 1 0} {0 0 -1}
draw triangle {1 0 0} {0 -1 0} {0 0 1}
draw triangle {1 0 0} {0 -1 0} {0 0 -1}
draw triangle {-1 0 0} {0 1 0} {0 0 1}
draw triangle {-1 0 0} {0 1 0} {0 0 -1}
draw triangle {-1 0 0} {0 -1 0} {0 0 1}
draw triangle {-1 0 0} {0 -1 0} {0 0 -1}
```

And you have yourself an octahedron. See how the colors on the faces don't go smoothly from one side to the next? This is because the surface normals for one face are quite different from another, so the lights are reflected differently. The colors can be made smoother by defining the normals for the corners such that the normals of the edges are the same. One caution about defining the vertices and normals: they must be given in counter-clockwise order or the shading will be wrong.

As an example, here's the above octahedron with the normals specified:

```
draw delete all
draw color red
draw trinorm  {1 0 0} {0 1 0} {0 0 1} {1 0 0} {0 1 0} {0 0 1}
```

```
  draw trinorm  {1 0 0} {0 0 -1} {0 1 0} {1 0 0} {0 0 -1} {0 1 0}
  draw trinorm  {1 0 0} {0 0 1} {0 -1 0} {1 0 0} {0 0 1} {0 -1 0}
  draw trinorm  {1 0 0} {0 -1 0} {0 0 -1} {1 0 0} {0 -1 0} {0 0 -1}
  draw trinorm  {-1 0 0} {0 0 1} {0 1 0} {-1 0 0} {0 0 1} {0 1 0}
  draw trinorm  {-1 0 0} {0 1 0} {0 0 -1} {-1 0 0} {0 1 0} {0 0 -1}
  draw trinorm  {-1 0 0} {0 -1 0} {0 0 1} {-1 0 0} {0 -1 0} {0 0 1}
  draw trinorm  {-1 0 0} {0 0 -1} {0 -1 0} {-1 0 0} {0 0 -1} {0 -1 0}
```

11.2.3 Draw a surface plot

The following will plot the surface of a given function from $-5 <= x, y <= 5$. (This is a bit more complicated, so I don't want to include as much error checking for the inputs.)

The graphics here will be the function

```
proc g {x y} {expr sqrt(abs($x*$y))}

proc draw_surface { f } {
  set minx -5
  set maxx 5
  set miny -5
  set maxy 5
  set step 0.5
  # first, get the data (this isn't the most data efficient way of
  # doing things)
  for {set i $minx} {$i <= $maxx} {set i [expr $i + $step]} {
    for {set j $miny} {$j <= $maxy} {set j [expr $j + $step]} {
      set data($i,$j) [$f $i $j]
    }
  }
  # make another pass through to plot it
  for {set i $minx} {$i <= [expr $maxx - $step]} {set i [expr $i + $step]} {
    for {set j $miny} {$j <= [expr $maxy - $step]} {set j [expr $j + $step]} {
      # get the next two corners
      set i2 [expr $i + $step]
      set j2 [expr $j + $step]
      # find the middle
      set imiddle [expr $i + $step/2]
      set jmiddle [expr $j + $step/2]
      set kmiddle [expr ($data($i,$j) + $data($i2,$j) + $data($i2,$j2) \
+ $data($i,$j2)) / 4.0]
      # use a cool coloring scheme (this depends on the graph having a min
      # value of 0 and max of 5, or at least less than about 30)
      draw color [expr 17 + [int [expr  200 * $kmiddle]] % 1024]
      # make 4 triangles
      draw triangle "$i $j $data($i,$j)" "$imiddle $jmiddle $kmiddle" \
                "$i2 $j $data($i2,$j)"
      draw triangle "$i $j $data($i,$j)" "$i $j2 $data($i,$j2)" \
```

```
                "$imiddle $jmiddle $kmiddle"
      draw triangle "$i2 $j2 $data($i2,$j2)" "$i2 $j $data($i2,$j)" \
                 "$imiddle $jmiddle $kmiddle"
      draw triangle "$i2 $j2 $data($i2,$j2)" "$imiddle $jmiddle $kmiddle" \
                "$i $j2 $data($i,$j2)"
    }
  }
}
```

And graph it with the command:

```
draw_surface g
```

Looks like it should be on a quilt, doesn't it?

11.2.4 Drawing a box around a molecule

Here's a quick function to draw a box around a molecule. Delete any graphics you may have loaded and enter this script.

```
proc box_molecule {molid} {
      # get the min and max values for each of the directions
      # (I'm not sure if this is the best way ... )
      set sel [atomselect top all]

      set coords [lsort -real [$sel get x]]
      set minx [lindex $coords 0]
      set maxx [lindex [lsort -real -decreasing $coords] 0]

      set coords [lsort -real [$sel get y]]
      set miny [lindex $coords 0]
      set maxy [lindex [lsort -real -decreasing $coords] 0]

      set coords [lsort -real [$sel get z]]
      set minz [lindex $coords 0]
      set maxz [lindex [lsort -real -decreasing $coords] 0]

      # and draw the lines
      draw materials off
      draw color yellow
      draw line "$minx $miny $minz" "$maxx $miny $minz"
      draw line "$minx $miny $minz" "$minx $maxy $minz"
      draw line "$minx $miny $minz" "$minx $miny $maxz"

      draw line "$maxx $miny $minz" "$maxx $maxy $minz"
      draw line "$maxx $miny $minz" "$maxx $miny $maxz"

      draw line "$minx $maxy $minz" "$maxx $maxy $minz"
      draw line "$minx $maxy $minz" "$minx $maxy $maxz"
```

```
      draw line "$minx $miny $maxz" "$maxx $miny $maxz"
      draw line "$minx $miny $maxz" "$minx $maxy $maxz"

      draw line "$maxx $maxy $maxz" "$maxx $maxy $minz"
      draw line "$maxx $maxy $maxz" "$minx $maxy $maxz"
      draw line "$maxx $maxy $maxz" "$maxx $miny $maxz"
}
```

If you don't already have a molecule loaded, load one, e.g.,
`mol load pdb $env(VMDDIR)/proteins/alanin.pdb`
and make it the `top` molecule. Then execute the command:

```
  box_molecule top
```

(you could also enter the molecule id instead of `top`).

11.2.5 Adding a label

Here's a quick way to add your own label to an atom selection [§5.3]. This function take the selection text and the labels that atom (in the `top` molecule) with the given string. It returns with an error if more anything other than one atom is selected.

```
proc label_atom {selection_string label_string} {
    set sel [atomselect top $selection_string]
    if {[$sel num] != 1} {
        error "label_atom: '$selection_string' must select 1 atom"
    }
    # get the coordinates of the atom
    lassign [$sel get {x y z}] coord
    # and draw the text
    draw text $coord $label_string
}
```

11.2.6 Interface to picking

When an atom is picked with the mouse, the Tcl variable `vmd_pick_mol` gets set to the moleule id of the picked molecule, and `vmd_pick_atom` contains the atom index. The Tcl command `trace` can be used to call a function when those values change.

As an example of what can be done with this, the following statements will put a sphere around each atom when it has been picked with the mouse. To turn it off, execute
`trace vdelete vmd_pick_atom w sphere_pick`.

```
proc sphere_pick {name element op} {
     # get the atom and molecule picked
     global vmd_pick_atom vmd_pick_mol
     # get the coordinates
     set sel [atomselect $vmd_pick_mol "index $vmd_pick_atom"]
     lassign [$sel get {x y z}] coords
```

```
     draw sphere $coords radius 1.0
}
trace variable vmd_pick_atom w sphere_pick
```

11.2.7 Animation

One last example of what can be done with the user-defined graphics. While VMD is not designed for animation, it can be made to animate objects by repeating the cycle of drawing the objects then calling the `display update` command. Here's an example which has several balls swinging (non-physically) at the end of a chain. If you want to stop it before it finishes, use `<Ctrl-C>`, but if you catch it in the wrong place and nothing moves, you'll need to execute the command `display update on` (see section § 8.3.6 for details about display updates.

```
proc swing {} {
    # get rid of everything else (if there is anything)
    if [expr [molinfo top] != -1] { mol off all }
    # create a new graphics molecule to handle just this
    mol load graphics "swing"
    set mol [molinfo top]
    set center {0 0.5 0}
    set radius 0.125
    set offset ".25 0 0"
    set length 1
    set firsttime 1
    display resetview
    axes location off
    stage location off
    for {set i 0} {$i < 1000} {incr i} {
        display update off
        scale by 1.003
        rotate y by 5
        display update on
        set top1 [vecsub $center $offset]
        set top2 $center
        set top3 [vecadd $center $offset]
        # compute the bottom location
        set bot1 [vecsub $top1 "0 $length 0"]
        set bot2 [vecsub $top2 "0 $length 0"]
        set bot3 [vecsub $top3 "0 $length 0"]
        set xdiff [expr sin($i/10.0)]
        set ydiff [expr 1.0 - abs(cos($i/10.0))]

        if [expr $xdiff < 0] {
            set bot1 [vecadd $bot1 "$xdiff $ydiff 0"]
        } else {
            set bot3 [vecadd $bot3 "$xdiff $ydiff 0"]
        }
```

```
        if $firsttime {
    set firsttime 0
            display resetview
   } else {
            graphics $mol delete all
    }
        # draw the three different balls/strings in different colors
        graphics $mol color red
        graphics $mol sphere $bot1 radius $radius
        graphics $mol color green
        graphics $mol sphere $bot2 radius $radius
        graphics $mol color blue
        graphics $mol sphere $bot3 radius $radius
graphics $mol materials off
        graphics $mol color red
graphics $mol line $top1 $bot1
        graphics $mol color green
graphics $mol line $top2 $bot2
        graphics $mol color blue
graphics $mol line $top3 $bot3
display reshape
    }
    display update on
}
```

11.3 Graphics

This section describes technical aspects of how the graphics commands are implemented and used. It should be read by those who want to understand how to build script-level extensions and those who like knowing more about how things work.

The user controlled graphics are implemented as if they are molecules of zero length which contains only a list of graphical objects. (Indeed, internally the class is called "MoleculeGraphics" and is derived from the Molecule class.) Thus, all the normal controls are applicable, and this is why the graphics "molecules" are on the Mol form. This simplifies matters as many of the controls, such as the mouse controls, do not need to be duplicated. However, some of the commands that apply only to molecules then make no sense, such as the graphics form.

Multiple graphics lists can be created. Since they are just specializations of a normal molecule, they are created with the `mol load` command, just like any other molecule. The full command is:

- **mol load graphics** *name*

The name parameter should be a distictive string related to the molecule. For instance, if the purpose of a new graphics list is to read in a graphics file format, the name should be the file name. If it is a method of viewing data from another, loaded molecule, the name should contain the name of the method and the molecule Id of the molecule from which it was derived. VMD reserves the name "graphics" for use with the `draw` command as that command always adds its graphics to the last graphical molecule with that name.

Once the graphics list is loaded and on the list of molecules, it can be distinguished from a normal molecule by using the `molinfo <molID> get source` command, which returns "Graphics" for graphics molecules.

The information pertaining to a given graphics list is accessed via the `graphics` command, which is of the following form:

- **graphics <molecule id> command** [*options ...*]

where the "molecule id" is the id of the graphics molecule on the molecule list. The *command* field can be one of the graphical items listed in section §11.1, or one of the commands `exists`, `delete`, `replace`, `list` or `info`. The `graphics` command returns a value, which depends on the command given.

As graphical primitives are added to the list they are assigned a unique, increasing value. The first object added is assigned 0, the second is assigned 1, etc. The commands which add an item return its value. A list of the available object ids is available with the `list` command. To test if a specific primitive exists, use the `exists` command followed by the object index. This returns a 1 if the index exists, and 0 if it does not. Information can be retrieved about a given item with the `info` command. This takes one option, which is the number of graphical information from which information is desired.

A given primitive is deleted with the `delete` command followed by the index of the object to delete. It does not have a return value. If the parameter is the string `all`, then all the primitives are deleted and the index count reset to 0.

Another deletion method allows one primitive to be replaced by another; suspiciously enough, this is the `replace` command. What it does is delete the given primitive and set things up so the next primitive is put in the same spot on the list and given the same index. This is designed for situations where the graphics are complicated to build, but where the colors might want to be easily changed. The color definition can be replaced without needing to rebuild the full list.

Here are examples of all the above commands:

```
vmd > mol load graphics testing
Info) Loading new molecule ...
vmd > graphics top sphere {0.1 0.2 0.3} radius 0.4
Info) 0
vmd > graphics top cylinder {-1 -1 -1} {2.6 2.5 2.4} resolution 3
Info) 1
vmd > graphics top line {0 0 0} {3 0 0} style dashed
Info) 2
vmd > graphics top delete 1
vmd > graphics top list
Info) 0 2
vmd > graphics top exists 0
Info) 1
vmd > graphics top exists 1
Info) 0
vmd > graphics top info 0
Info) sphere {0.100000 0.200000 0.300000} radius 0.400000 resolution 6
vmd > graphics top replace 0
vmd > graphics top point {3.3 2.2 1.1}
```

```
Info) 0
vmd > graphics top info 0
Info) point {3.300000 2.200000 1.100000}
vmd > graphics top list
Info) 0 2
```

11.4 Draw and Drawing Extensions

The `draw` command is a straight Tcl function which is meant to simplify the interface to the `graphics` command as well as provide a base for extensions to the standard graphics primitives.

The format of the `draw` command is:

- **draw** *command* [*arguments*]

Unlike the `graphics` command, `draw` does not take a molecule index by default. Instead, it searches for the last graphical molecule with the name "graphics" and uses that. (If such a molecule doesn't exist, it is created.) The basic commands are identical to those used by `graphics`. However, if the command doesn't work or doesn't exists, VMD tries to find an extension draw function.

This is done by searching for a function of the form `vmd_draw_$command`. If the function exists, it is called with the first parameter the molecule index and the rest are the arguments from the original `draw` call.

Here's an example which extends the draw command to include an "arrow" primitive.

```
proc vmd_draw_arrow {mol start end} {
    # an arrow is made of a cylinder and a cone
    set middle [vecadd $start [vecscale 0.9 [vecsub $end $start]]]
    graphics $mol cylinder $start $middle radius 0.15
    graphics $mol cone $middle $end radius 0.25
}
```

and here's one which adds the "color" option to the "cylinder primitive. It works because the draw command tries the "graphics" command and fails, because the "color" option doesn't exist. At that point, the extensions are checked.

```
proc vmd_draw_cylinder {mol start end args} {
    if [expr [llength $args] % 2] {
        error "draw: cylinder: incorrect argument list"
    }
    # start the construction of the graphics command
    set opts [list graphics $mol cylinder]
    lappend opts $start $end
    # search for the "color" option
    while {[string compare $args {}]} {
        # get the parameter and value
        set a [lvarpop args]
        set b [lvarpop args]
        # check if it is the color command
        if [string compare $a "color"] {
```

```
            # if it isn't, save the options
    lappend opts $a $b
} else {
            # otherwise, save the color
    set color $b
        }
    }
    # call the graphics commands
    graphics $mol color $color
    eval $opts
}
```

Chapter 12

Molecular Analysis

12.1 Using the molinfo command

This section covers how to extract information about molecules and atoms using the VMD text command molinfo.

Examples:

Two functions, one to save the current view position, the other to restore it. The position of the axis is not changed by these operations.

```
proc save_viewpoint {} {
   global viewpoints
   if [info exists viewpoints] {unset viewpoints}
   # get the current matricies
   foreach mol [molinfo list] {
      set viewpoints($mol) [molinfo $mol get {
center_matrix rotate_matrix scale_matrix global_matrix}]
   }
}
proc restore_viewpoint {} {
   global viewpoints
   foreach mol [molinfo list] {
      puts "Trying $mol"
      if [info exists viewpoints($mol)] {
         molinfo $mol set {center_matrix rotate_matrix scale_matrix
   global_matrix} $viewpoints($mol)
      }
   }
}
```

Cycle through the list of displayed molecules, turning each one on one at a time. At the end, return the display flags to their original state.

```
# save the current display state
foreach mol [molinfo list] {
  set disp($mol) [molinfo $mol get drawn]
}
```

```
# turn everything off
mol off all
# turn each molecule on then off again
foreach mol [molinfo list] {
  if $disp($mol) {
     mol on $mol
     sleep 1
     mol off $mol
  }
}
# turn the original ones back on
foreach mol [molinfo list] {
  if $disp($mol) {mol on $mol }
}
```

The last loop, which turns the originally drawn molecules back on, doesn't turn them on at the same time. That's because some commands (those which use the command queue) redraw the graphics when they are used. This can be disabled with the `display update` (see section § 8.3.6 for more information). Using this, the final loop becomes

```
#turn the original ones back on
display update off
foreach mol [molinfo list] {
  if $disp($mol) {mol on $mol }
}
display update on
```

Alternatively, since the `drawn` option is settable, you could do:

```
foreach mol [molinfo list] {
  if $disp($mol) {molinfo $mol set drawn 1}
}
```

However, that won't set the flag to redraw the scene so you need to force a redraw with `display redraw`.

12.2 Using the `atomselect` command

Atom selection is the primary method to access information about the atoms in a molecule. It works in two steps. The first step is to create a selection given the selection text, molecule id, and optional frame number. This is done by a function called `atomselect`, which returns the name of the new atom selection. the second step is to use the created selection to access the information about the atoms in the selections.

Atom selection is implemented as a Tcl function. The data returned from `atomselect` is the name of the function to use. The name is of the form `atomselect%d` where '%d' is a non-negative number (such as 'atomselect0', atomselect26', ...).

The way to use the function created by the `atomselect` command is to store the name into a variable, then use the variable to get the name when needed.

```
vmd> set sel [atomselect top "water"]
atomselect3
vmd> $sel text
water
```

This is equivalent to saying

```
vmd> atomselect3 text
```

The easiest way of thinking about this is that the `atomselect` command creates an object. To get information from the object you have to send it a command. Thus, in the example above (`atomselect1 num`) the object "atomselect1" was sent the command "num", which asks the object to return the number of atoms in the selection. These derived object functions (the ones with names like atomselect3) take many options, as described in section §8.3.2,

For instance, given the selection

```
vmd> set sel [atomselect top "resid 4"]
atomselect4
```

you can get the atom names for each of the atoms in the selection with

```
vmd> $sel get name
{N} {H} {CA} {CB} {C} {O}
```

(which, remember, is the same as

```
vmd> atomselect4 get name
```

)

Multiple attributes can be requested by submitting a list, so if you want to see which atoms are on the backbone,

```
vmd> $sel get {name backbone}
{N 1} {H 0} {CA 1} {CB 0} {C 1} {O 1}
```

and the atom coordinates with

```
vmd>  $sel get {x y z}
{0.710000 4.211000 1.093000} {-0.026000 3.700000 0.697000} {0.541000
4.841000 2.388000} {-0.809000 4.462000 2.976000} {1.591000 4.371000
3.381000} {2.212000 5.167000 4.085000}
```

It is very important to note that the information returned by one of these commands is a list of lists. Specifically, it is a list of size n where each element is itself a list of size i, where n is the number of atoms in the selection and i is the number of attributes requested.

One quick function you can build with the coordinates is a method to calculate the geometrical center (not quite the center of mass; that's a bit harder). This also uses some of the vector commands discussed in the section about vectors and matrices [§10], but you should be able to figure them out from context.

```
proc geom_center {selection} {
        # set the geometrical center to 0
        set gc [veczero]
        # [$selection get {x y z}] returns a list of {x y z}
        #    values (one per atoms) so get each term one by one
        foreach coord [$selection get {x y z}] {
           # sum up the coordinates
           set gc [vecadd $gc $coord]
        }
        # and scale by the inverse of the number of atoms
        return [vecscale [expr 1.0 /[$selection num]] $gc]
}
```

With that defined you can say (assuming $sel was created with the previous atomselection example)

```
vmd> geom_center $sel
0.703168 4.45868 2.43667
```

I'll go through the example line by line. The function is named `geom_center` and takes one parameter, the name of the selection. The first line sets the variable "gc" to the zero vector, which is 0 0 0. On the second line of code, two things occur. First, the command

```
$selection get {x y z}
```

is executed, and the string is replaced with the result, which is

```
{0.710000 4.211000 1.093000} {-0.026000 3.700000 0.697000} {0.541000
4.841000 2.388000} {-0.809000 4.462000 2.976000} {1.591000 4.371000
3.381000} {2.212000 5.167000 4.085000}
```

This is a list of 6 terms (one for each atom in the selection), and each term is a list of three elements, the x, y, and z coordinate, in that order.

The "foreach" command splits the list into its six terms and goes down the list term by term, setting the variable "coord" to each successive term. Inside the loop, the value of $coord is added to total sum.

The last line returns the geometrical center of the atoms in the selection. Since the geometrical center is defined as the sum of the coordinate vectors divided by the number of elements, and so far I have only calculated the sum of vectors, I need the inverse of the number of elements, which is done with the expression

```
expr 1.0 / [$selection num]
```

The decimal in "1.0" is important since otherwise Tcl does integer division. Finally, this value is used to scale the sum of the coordinate vectors (with vecscale), which returns the new value, which is itself returned as the result of the procedure.

The center of mass function is slightly harder because you have to get the mass as well as the x, y, z values, then break that up into to components. The formula for the center of mass is $\sum m_i x_i / \sum mass_i$

```
proc center_of_mass {selection} {
        # some error checking
        if {[$selection num] <= 0} {
                error "center_of_mass: needs a selection with atoms"
        }
        # set the center of mass to 0
        set com [veczero]
        # set the total mass to 0
        set mass 0
        # [$selection get {x y z}] returns the coordinates {x y z}
        # [$selection get {mass}] returns the masses
        # so the following says "for each pair of {coordinates} and masses,
#  do the computation ..."
        foreach coord [$selection get {x y z}] m [$selection get mass] {
           # sum of the masses
           set mass [expr $mass + $m]
           # sum up the product of mass and coordinate
           set com [vecadd $com [vecscale $m $coord]]
        }
        # and scale by the inverse of the number of atoms
        if {$mass == 0} {
                error "center_of_mass: total mass is zero"
        }
        # The "1.0" can't be "1", since otherwise integer division is done
        return [vecscale [expr 1.0/$mass] $com]
}

vmd> center_of_mass $sel
Info) 0.912778 4.61792 2.78021
```

The opposite of "get" is "set". A few of the keywords (most notably, "x", "y", and "z") can be set to new values. This allows, for instance, atom coordinates to be changed, the occupancy values to be updated, or user forces to be added. Right now the only things that can be changed are the coordinates, the beta and occupancy values and user forces.

```
  set sel [atomselect top "index 5"]
  $sel get {x y z}
{1.450000 0.000000 0.000000}
  $set set {x y z} {{1.6 0 0}}
```

Note that just as the get option returned a list of lists, the set option needs a list of lists, which is why the extra set of curly braces were need. Again, this must be a list of size n containing elements which are a list of size i. The exeception is if n is 1, the list is duplicated enough times so there is one element for each atom.

```
  # get two atoms and set their coordinates
  set sel [atomselect top "index 6 7"]
  $sel set {x y z} { {5 0 0} {7.6 5.4 3.2} }
```

In this case, the atom with index 6 gets its (x, y, z) values set to 5 0 0 and the atom with index 7 has its coordinates changed to 7.6 5.4 3.2.

It is possible to move atoms this way by getting the coordinates, changing them (say by adding some offset) and replacing it. Following is a function which will do just that:

```
proc moveby {sel offset} {
  set newcoords {}
  foreach coord [$sel get {x y z}] {
    lvarpush newcoords [vecadd $coord $offset]
  }
  $sel set $newcoords
}
```

And to use this function (in this case, to apply an offset of (x y z) = (0.1 -2.8 9) to the selection "$movesel"):

```
moveby $movesel {0.1 -2.8 9}
```

However, to simplify matters some options have been added to the selection to deal with movements (these commands are also implemented in C++ and are much faster than the Tcl versions). These functions are `moveby`, `moveto`, and `move`. The first two take a position vector and the last takes a transformation matrix.

The first command, `moveby`, moves each of the atoms in the selection over by the given vector offset.

```
$sel moveby {1 -1 3.4}
```

The second, `moveto`, moves all the atoms in a selection to a given coordinate (it would be strange to use this for a selection of more than one atom, but that's allowed). Example:

```
$sel moveto {-1 1 4.3}
```

The last of those, `move`, applies the given transformation matrix to each of the atom coordinates. This is best used for rotating a set of atoms around a given axis, as in

```
$sel move [trans x by 90]
```

which rotates the selection 90 degrees about the x axis. Of course, any transformation matrix may be used.

A more useful example is the following, which rotates the side chain atoms around the CA-CB bond by 10 degrees.

```
# get the sidechain atoms (CB and onwards)
set sidechain [atomselect top "sidechain residue 22"]
# get the CA coordinates -- could do next two on one line ...
set CA [atomselect top "name CA and residue 22"]
set CAcoord [lindex [$CA get {x y z}] 0]
# and get the CB coordinates
set CB [atomselect top "name CB and residue 22"]
set CBcoord [lindex [$CB get {x y z}] 0]
# apply a transform of 10 degrees about the given bond axis
$sidechain move [trans bond $CAcoord $CBcoord 10 deg]
```

12.3 Analysis scripts

Following are some more examples of routines that could be used for analysing molecules. These are not the best routines to used since many of these are implemented with the `measure` command, which calls a much faster built-in function.

Get the total mass given a selection.

```
proc total_mass {selection} {
  set sum 0
  foreach mass [$selection get mass] {
    set sum [expr $sum + $mass]
  }
  return $sum
}
```

Here's another (slower) way to do the same thing. This works because the mass returned from the selection is a list of lists. Putting it inside the quotes of the eval makes it a sequence of vectors, so the vecadd command will work on it.

```
proc total_mass1 {selection} {
  set mass [$selection get mass]
  eval "vecadd $mass"
}
```

Find the min and max coordinate values of a given molecule in the x, y, and z directions (see also the `measure` command 'minmax'). The function takes the molecule id and returns two vectors; the first contains the min values and the second contains the max.

```
proc minmax {molid} {
  set sel [atomselect $molid all]
  set coords [$sel get {x y z}]
  set coord [lvarpop coords]
  lassign $coord minx miny minz
  lassign $coord maxx maxy maxz
  foreach coord $coords {
    lassign $coord x y z
    if {$x < $minx} {set minx $x} else {if {$x > $maxx} {set maxx $x}}
    if {$y < $miny} {set miny $y} else {if {$y > $maxy} {set maxy $y}}
    if {$z < $minz} {set minz $z} else {if {$z > $maxz} {set maxz $z}}
  }
  return [list [list $minx $miny $minz] [list $maxx $maxy $maxz]]
}
```

Compute the radius of gyration for a selection (see also `measure rgyr`). The square of the radius of gyration is defined as $\sum_i m_i(\vec{r}_i - \vec{r}_c)^2 / \sum_i m_i$. This uses the center_of_mass function defined earlier in this chapter; a faster version would replace that with `measure center`.

```
proc gyr_radius {sel} {
  # make sure this is a proper selection and has atoms
```

```
  if {[$sel num] <= 0} {
    error "gyr_radius: must have at least one atom in selection"
  }
  # gyration is sqrt( sum((r(i) - r(center_of_mass))^2) / N)
  set com [center_of_mass $sel]
  set sum 0
  foreach coord [$sel get {x y z}] {
    set sum [vecadd $sum [veclength2 [vecsub $coord $com]]]
  }
  return [expr sqrt($sum / ([$sel num] + 0.0))]
}
```

Applying this to the alanin.pdb coordinate file

```
vmd > mol load pdb alanin.pdb
vmd > set sel [atomselect top all]
vmd > gyr_radius $sel
Info) 5.45443
```

Compute the rms difference of a selection between two frames of a trajectory. This takes a selection and the values of the two frames to compare.

```
proc frame_rmsd {selection frame1 frame2} {
  set mol [$selection molindex]
  # check the range
  set num [molinfo $mol get numframes]
  if {$frame1 < 0 || $frame1 >= $num || $frame2 < 0 || $frame2 >= $num} {
    error "frame_rmsd: frame number out of range"
  }
  # get the first coordinate set
  set sel1 [atomselect $mol [$selection text] frame $frame1]
  set coords1 [$sel1 get {x y z}]
  # get the second coordinate set
  set sel2 [atomselect $mol [$selection text] frame $frame2]
  set coords2 [$sel2 get {x y z}]
  # and compute the rmsd values
  set rmsd 0
  foreach coord1 $coords1 coord2 $coords2 {
    set rmsd [expr $rmsd + [veclength2 [vecsub $coord2 $coord1]]]
  }
  # divide by the number of atoms and return the result
  return [expr $rmsd / ([$selection num] + 0.0)]
}
```

The following uses the frame_rmsd function to list the rmsd of the molecule over the whole trajectory, as compared to the first frame.

```
vmd > mol load psf alanin.psf dcd alanin.dcd
vmd > set sel [atomselect top all]
```

```
vmd > for {set i 0} {$i < [molinfo top get numframes]} {incr i} {
?   puts [list $i [frame_rmsd $sel $i 0]]
? }
0 0.0
1 0.100078
2 0.291405
3 0.523673
 ....
97 20.0095
98 21.0495
99 21.5747
```

The last example shows how to set the beta field. This is useful because one of the coloring methods is 'Beta', which uses the beta values to color the molecule according to the current color scale. (This can also be done with the occupancy field.) Thus redefining the beta values allows you to color the molecules based on your own definition. One useful example is to color the molecule based on the distance from a specific point (for this case, coloring a poliovirus protomer based on its distance to the center of the virus (0, 0, 0) helps bring out the surface features).

```
proc betacolor_distance {$sel point} {
  set newbeta {}
  # get the coordinates
  foreach coord [$sel get {x y z}] {
   # get the distance and put it in the "newbeta" list
    set dist [veclength2 [vecsub $coord $point]]
    lvarpush newbeta $dist
  }
  # set the beta term
  $sel set beta $newbeta
}
```

And here's one way to use it:

```
# load pdb2plv.ent using anonymous ftp to the PDB
vmd > mol load webpdb 2plv
vmd > set sel [atomselect top all]
vmd > betacolor_distance $sel {0 0 0}
```

Then go to the graphics menu and set the 'Coloring Method' to 'Beta'.

12.4 RMS Fit and Alignment

When one has two similar structures, one often wants to compare them. What's the difference between two X-ray structures? How much did the structure change during a simulation? To answer these questions, you must first figure out how to compare two structures, which usually means that you must find the root mean square deviation (RMSD).

Formally, given N atom positions from structure x and the corresponding N atoms from structure y with a weighting factor $w(i)$, the RMSD is defined as:

$$RMSD\,(N; x, y) = \left[\frac{\sum_{i=1}^{N} w_i \|x_i - y_i\|^2}{N \sum_{i=1}^{N} w_i}\right]^{\frac{1}{2}}$$

Using this equation by itself probably won't give you the answer you are looking for. Imagine two identical structures offset by some distance. The RMSD should be 0, but the offset prevents that from happening. What you really want is the minimum RMSD between two given structures; the best fit. There are many ways to do this, but for VMD we have implemented the method of Kabsch (Acta Cryst. (1978) A34, 827-828 or see file Measure.C in the VMD source code). This algorithm computes the transformation, needed to move one structure onto another in order to minimize the RMSD.

With the mathematical prerequisites behind us, we still need to be able to specify how to choose the atoms to compare. If you want to compare all the atoms in both structures, and they both have the same number of atoms, then the problem is easy – N is everything. This occurs most often in MD simulations when the only thing different between two structures are the coordinates.

But what about homologous sequences? In this case, the number of atoms differ because while the number of residues is the same, the sidechains have different numbers of atoms. The usual solution is to determine the RMSD based solely on the backbone atoms or, in some X-ray structures where only the C_α atoms have been determined, based on the C_α atoms. VMD allows you to fit and align based on any valid atom selection, as long as the atom selection specifies the same number of atoms in each molecule being compared.

12.4.1 Fit and Alignment Menus

To get started with RMS fitting and alignment, type `vmdrmsd` from the command line. Alternatively, you can source the script called rmsd.tcl, which should be located in the scripts/vmd subdirectory of your VMD installation. For example, if VMD is installed in /usr/local/lib/vmd, type the following from the command line: `source /usr/local/lib/vmd/scripts/vmd/rmsd.tcl`. You should now have two new menus, titled RMSD calculator and RMS Alignment (kindly provided by Alexander Balaeff from the Theoretical Biophysics Group). We'll describe the RMSD calculator first.

RMSD Calculator

The RMSD Calculator menu is used to calculate RMS distances between molecules.

The upper left corner of the menu is where you specify which atoms are to be used in the calculation. In the input field, type the atom selection text just as you would in the Graphics form. The checkbox below the input field entitled "Backbone only" restricts whatever atom selection you typed to just the backbone atoms of the selection; in effect, it adds "and backbone" to the atom selection text.

The upper right corner of the menu has a button labeled "RMSD". Its effect depends on which of the two radio buttons, "Top" or "Average", is pressed down. If "Top" is pressed, VMD calculates the RMS distance between the top molecule (which is usually the last molecule loaded) and every other molecule. If "Average" is pressed, VMD first computes the average x, y, z coordinates of the selected atoms in each molecule, then computes the RMS distance of each molecule from that average structure.

Results of the RMS calculations for each molecule are shown in the browser in the bottom half of the menu. Note that this list is not updated until you presse the RMSD button, so the effects of loading/deleting molecules will not be immediately reflected. The "Total RMSD" label at the bottom of the menu shows the average RMSD for all molecules listed.

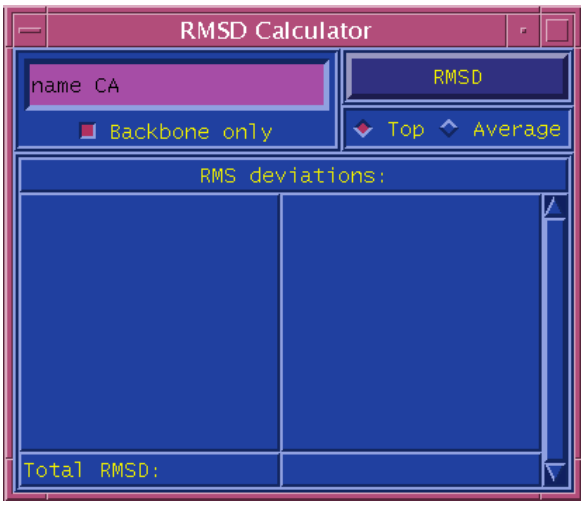

Figure 12.1: RMS Calculation Tk menu

RMS Alignment

Figure 12.2: RMS Alignment Tk menu

The RMS Alignment menu fits molecules based on selected groups of atoms. Whereas the RMSD Calculator finds the RMS distance between molecules without disturbing their coordinates, the RMS Alignment menu actually moves molecules to new positions.

This menu is quite simple: Enter an atom selection in the input field, and press Align to align the molecules based on the atoms in that selection. If you recompute the RMSD between molecules in the RMSD Calculator menu, you will probably find that the values are different; this is because the calculation is made based on the current positions of the atoms.

12.4.2 RMS and scripting

The same actions can be taken on the scripting level. The Text interface also gives you more flexibility through the atom selection mechanism allowing to choose the atoms to fit/compare.

RMSD Computation

There are two atom selections needed to do an RMSD computation, the list of atoms to compare in both molecules. The first atom of the first selection is compared to the first atom of the second selection, fifth to fifth, and so on. The actual order is identical to the order from the input PDB file.

Once the two selections are made, the RMSD calculation is a matter of calling the `measure rmsd` function. Here's an example:

```
        set sel1 [atomselect 0 "backbone"]
        set sel2 [atomselect 1 "backbone"]
        measure rmsd $sel1 $sel2
  Info)  10.403014
```

This prints the RMSD between the backbone atoms of molecule 0 with those of molecule 1. You could also use a weighting factor in these calculations. The best way to understand how to do this is to see another example:

```
        set weighted_rmsd [measure rmsd $sel1 $sel2 weight mass]
  Info)  10.403022
```

In this case, the weight is determined by the mass of each atom. Actually, the term is really one of the standard keywords available to an atom selection. Other ones include index and resid (which would both be rather strange to use) as well as charge, beta and occupancy. These last terms useful if you want to specify your own values for the weighting factors.

Computing the Alignment

The best-fit alignment is done in two steps. The first is to compute the 4×4 matrix transformation that takes one set of coordinates onto the other. This is done with the `measure fit` command. Assuming the same selections as before:

```
        set transformation_matrix [measure fit $sel1 $sel2]
Info) {0.971188 0.00716391 0.238206 -13.2877}
{0.0188176 0.994122 -0.106619 3.25415} {-0.23757 0.108029 0.965345 -2.97617}
{0.0 0.0 0.0 1.0}
```

As with the RMSD calculation, you could also add an optional `weight <keyword>` term on the end.

The next step is to apply the matrix to a set of atoms using the move command. So far you have two coordinate sets. You might think you could do something like `$sel1 move $transformation_matrix` to apply the matrix to all the atoms of that selection. You could, but that's not the right selection.

The thing to recall is that `$sel1` is the selection for the backbone atoms. You really want to move the whole fragment to which it is attached, or even the whole molecule. (This is where the discussion earlier comes into play.) So you need to make a third selection containing all the atoms which are to be moved, and apply the transformation to those atoms.

```
        # molecule 0 is the same molecule used for $sel1
        set move_sel [atomselect 0 "all"]
        $move_sel move $transformation_matrix
```

As a more complicated example, say you want to align all of molecule 1 with molecule 9 using only the backbone atoms of residues 4 to 10 in both systems. Here's how:

```
        # compute the transformation matrix
        set reference_sel  [atomselect 9 "backbone and resid 4 to 10"]
```

```
set comparison_sel [atomselect 1 "backbone and resid 4 to 10"]
set transformation_mat [measure fit $comparison_sel $reference_sel]

# apply it to all of the molecule 1
set move_sel [atomselect 1 "all"]
$move_sel move $transformation_mat
```

A simulation example script

Here's a longer script which you might find useful. The problem is to compute the RMSD between each timestep of the simulation and the first frame. Usually in a simulation there is no initial global velocity, so the center of mass doesn't move, but because of angular rotations and because of numerical imprecisions that slowly build up, the script aligns the molecule before computing its RMSD.

```
# Prints the RMSD of the protein atoms between each timestep
# and the first timestep for the given molecule id (default: top)
proc print_rmsd_through_time {{mol top}} {
        # use frame 0 for the reference
        set reference [atomselect $mol "protein" frame 0]
        # the frame being compared
        set compare [atomselect $mol "protein"]

        set num_steps [molinfo $mol get numframes]
        for {set frame 0} {$frame < $num_steps} {incr frame} {
                # get the correct frame
                $compare frame $frame

                # compute the transformation
                set trans_mat [measure fit $compare $reference]
                # do the alignment
                $compare move $trans_mat
                # compute the RMSD
                set rmsd [measure rmsd $compare $reference]
                # print the RMSD
                puts "RMSD of $frame is $rmsd"
        }
}
```

To use this, load a molecule with an animation (for example, `$VMDDIR/proteins/alanin.DCD` from the VMD distribution). Then run `print_rmsd_through_time`. Example output is shown here:

```
vmd > print_rmsd_through_time
RMSD of 0 is 0.000000
RMSD of 1 is 1.060704
RMSD of 2 is 0.977208
RMSD of 3 is 0.881330
RMSD of 4 is 0.795466
```

```
RMSD of 5 is 0.676938
RMSD of 6 is 0.563725
RMSD of 7 is 0.423108
RMSD of 8 is 0.335384
RMSD of 9 is 0.488800
RMSD of 10 is 0.675662
RMSD of 11 is 0.749352
 [...]
```

12.5 VMD Script Commands for Colors

In order to fine tune color parameters, one typically needs more sophisticated controls than those offered in the GUI. For this reason, VMD provides a number of scripting level commands for color access. These commands will be discussed in detail in chapter §8, but to give you a flavor for their use, here are a couple of examples that you may find useful right away. Most things can be done with `color` [§8.3.4] and `colorinfo` [§8.3.5] commands.

12.5.1 Changing the color scale definitions

Suppose that of the 1024 colors, the first 511 should be red, then 2 whites, and finally 511 blues. You can use the 'color' command to modify the color scale values accordingly. The only sticky point is that you must update the transparent definitions as well or things might look strange.

```
proc tricolor_scale {} {
  set color_start [expr [colorinfo num] * 2]
  display update off
  for {set i 0} {$i < 1024} {incr i} {
    if {$i == 0} {
      set r 1;  set g 0;  set b 0
    }
    if {$i == 511} {
      set r 1;  set g 1;  set b 1
    }
    if {$i == 513} {
      set r 0;  set g 0;  set b 1
    }
    color change rgb [expr $i + $color_start     ] $r $g $b
  }
  display update on
}

tricolor_scale
```

12.5.2 Creating a set of black-and-white color definitions

To map grayscale on the color ids 0-16 (0=black; 16=white):

```
proc make_grayscale {} {
  display update off
  for {set i 0} {$i < 17} {incr i} {
    set val [expr $i / 16.0]
    color change rgb $i $val $val $val
  }
  display update on
}
```

Note that the display updates are switched off for the time of redefinition, so that the screen would not be redrawn every time one color is changed. This way the procedure works faster. The only bad thing about this idea is that black becomes white, and white changes too, so the names of the colors (yellow, orange, etc.) become useless.

12.5.3 Revert all RGB values to defaults

After some of the color definitions have been changed and you want to restore the default definitions, the following procedure might be useful.

```
proc revert_colors {} {
  display update off
  foreach color [colorinfo colors] {
    color change rgb $color
  }
  display update on
}
```

12.5.4 Coloring Trick - Override a Coloring Category

There is currently no user-defined coloring method. This makes it hard to color residues by property "X" if X is not already defined in VMD. It is possible to get around this limitation somewhat by overriding one of the values in the PDB or PSF. For instance, suppose you wanted to color the atoms by the distance of the atom from a given point. One way is to compute the distance and put it in either the occupancy or beta field of the PDB file. Then when the molecule is colored by occupancy it is actually coloring by distance.

You could also override, say, the segment name field or even the residue name. Don't override the atom name unless you are really desperate as VMD uses it to determine which residues are proteins and nucleic acids, and hence which residues can be drawn as a tube or ribbon.

Chapter 13

Customizing VMD Sessions

There are a number of ways to change the behavior of VMD from the default settings, both in how the program starts up and in how the program behaves during a session. This Chapter describes the data files, command-line options, and environment variables which are used to customize a VMD session.

These files control the initial appearance and behavior of VMD at the start, and may be customized to suit each user's particular tastes. Default versions of these files are placed in the VMD installation directory (On Unix this is usually `/usr/local/lib/vmd`, on Windows this defaults to `C:\Program Files\University of Illinois\VMD`). Each user may specify their own versions of some of these files, but unless this is done the commands and values in the default files are used. In this way, an administrator may customize the default behavior of VMD for all users, while giving each user the option to change the default behavior however they choose.

Several configurable parameters may also be set in a number of ways, including use of command-line options or environment variables. The order of precedence of these methods is as follows (highest precedence to lowest):

1. Command-line options.
2. Environment variable settings.
3. Built-in defaults, as specified by compilation configurable parameters. These are used only if no other values are specified by the other methods mentioned in this list. The Installation Guide describes how to change these default values when compiling VMD.

13.1 VMD Windows Command-Line Options

The Windows version of VMD accepts only one command line argument, which is the full pathname of its installation directory. This is done so that when VMD is spawned from the Windows desktop or start menu, it will find its data files and scripts.

13.2 VMD Unix Command-Line Options

When started, the following command-line options may be given to VMD. Note that if a command-line option does not start with a dash (-), and is not part of another option, it is assumed to be a PDB filename. Thus, the command

```
vmd molecule.pdb
```

will start VMD and load a molecule from the file `molecule.pdb`.

- `-h | -?` : Print a summary a command-line options to the console.
- `-e filename` : After initialization, execute the text commands in filename, and then resume normal operation.
- `-psf filename` : Load the specified molecule (in PSF format) at startup. The PSF file only contains the molecular structure; a PDB or DCD file must also be specified when this option is used.
- `-pdb filename` : Load the specified molecule (in PDB format) at startup.
- `-dcd filename` : Load the specified trajectory file (in binary DCD format) at startup. The DCD file only contains atomic coordinates; a PDB or PSF file must also be specified when this option is used.
- `-dispdev < win | text | cave | caveforms | none >` : Specify the type of graphical display to use. The possible display devices include:
  - `win`: a standard graphics display window.
  - `text`: do not provide any graphics display window.
  - `cave`: use the CAVE virtual environment for display, forms are disabled.
  - `caveforms`: use the CAVE virtual environment for display and with forms enabled. This is useful with `-display machine:0` for remote display of the forms when the CAVE uses the local screen.
  - `none`: same as text.

  It is possible to use VMD as a filter to convert coordinate files into rendered images, by using the `-dispdev text` and `-e` options.
- `-dist z` : Specify the distance to the VMD image plane.
- `-height y` : Specify the height of the VMD image plane.
- `-pos x y` : Specify the position for the graphics display window. The position (x,y) is the number of pixels from the lower-left corner of the display to the lower-left corner of the graphics window.
- `-size x y` : Specify the size for the graphics display window, in pixels.
- `-nt` : Do not display the VMD title at startup.
- `-startup filename` : Use filename as the VMD startup command script, instead of the default **.vmdrc** file.
- `-debug [level` : Turn on output of debugging messages, and optionally set the current debug level (1=few messages ... 5=many verbose messages). Note this is only useful if VMD has been compiled with debugging option included.

13.3 Environment Variables

Several environment variables are used by VMD to determine the location of certain files and directories. These variables are accessible to text interface through array `env`. These variables include:

- `DISPLAY` : **(Unix-only)** The X-Windows display that VMD should use for displaying the VMD forms and menus, as well as the graphics window. If this environment variable is not overridden by VMDGDISPLAY all VMD windows will be directed to this display.
- `VMDDIR` : The directory which contains the VMD data files (such as this help file) and architecture-specific executables. By default, this is /usr/local/lib/vmd on Unix systems, and `C:\Program Files\University of Illinois\VMD` on Windows sytems.
- `VMDTMPDIR` : The directory which VMD should use for temporary data files. By default, this is /tmp, or /usr/tmp on Unix systems, and `C:\` on Windows.
- `VMDBABELBIN` : The complete path and filename for the program babel, which is used by VMD to convert molecular structure/coordinates files into PDB files which VMD can actually understand. If this is not set explicitly, the VMD startup script will attempt to find babel in the current path. If Babel cannot be found or is not installed, VMD will not be able to read molecular file formats other than PDB, PSF, and binary DCD files.
- `VMDCAVEMEM` : **(Unix-only)** This overrides the default size of the shared memory arena which is allocated by VMD when the CAVE starts up. The variable must be an integer number of megabytes. Since this is the only shared memory pool allocated, and it is done only once, you must choose a value sufficient to account for the largest scene you intend to render in VMD in that CAVE session. The default value unless otherwise specified is 80 Megabytes. Values of 200MB to 512MB are commonly needed for large molecular systems containing several hundred thousand atoms.
- `VMDGDISPLAY` : **(Unix-only)** The name of an X-Windows display that VMD will use to display the graphics window. This environment variable is only used on Unix systems. Through the use of the the DISPLAY and VMDGDISPLAY envrironment variables, the VMD graphics window can be placed on a separate screen from the forms and menus. This is particularly useful when giving 3-D demonstrations using a projector. The forms and menus can be kept on a different screen from the graphics so that they do not distract the audience.
- `VMDHTMLVIEWER` : The name of the HTML viewer (Netscape, Mosaic, whatever you prefer) that VMD should use to display HTML documents (such as this help file). By default, this is Netscape.
- `VMDIMAGEVIEWER` : The name of the external program to use for displaying VMD snapshots (or other images), in various formats.
- `VMDSCRDIST` : Distance to the VMD image plane.
- `VMDSCRHEIGHT` : Height of the VMD image plane.
- `VMDSCRPOS` : Position of the VMD graphics window (x,y).
- `VMDSCRSIZE` : Size of the VMD graphics window (x,y).

13.4 Startup Files

13.4.1 Core Script Files

In the following, the value of `$VMDDIR` is the vmd installation directory. During the original installation this is the value of `INSTALLLIBDIR`. It can also be found by looking at the first few lines of the vmd startup script (`head ‘which vmd‘`) or by starting VMD and using the command `set env(VMDDIR)`.

As mentioned elsewhere, VMD uses the Tcl interpreter. VMD read Tcl scripts at initialization, which are contained in VMD distribution. The locations of the scripts is determined by the `TCL_LIBRARY` environment variable, which is set in the vmd startup script to `$VMDDIR/scripts/tcl`. In addition, VMD has its own directory of core Tcl routines.

The most important of these is tt $VMDDIR/scripts/vmd/vmdinit.tcl. This file sets up the basic Tcl initialization commands, defines some environment variables, and adds the vmd script directory to the Tcl autoindex path. Most of the other files are referenced through the `auto_path`.

There are a few non-Tcl scripts in this directory. Currently these are perl scripts used for the `urlload` command and `web client` startup (see section § 8.3.17 and section §13.5).

13.4.2 User Script Files

A user-written run-time command file `.vmdrc` can be used. with a list of initial VMD text commands to process. This file may be changed to customize individual user's initial screen appearance and to set the proper display characteristics for displaying in stereo. If it does not exist, default values are used.

13.4.3 `.vmdrc` File

After everything is initialized, VMD reads the *startup* file using the equivalent of the command `play .vmdrc`. This file contains text commands for VMD to execute just as if they had been entered at the VMD text console command prompt. The file can contain any number of commands, including blank lines and comment lines (which begin with the `#` character). If an error is encountered while reading this file, the command in error is skipped and processing of the file continues.

VMD searches for this file in three locations; `./.vmdrc`, `$HOME/.vmdrc` and `$VMDDIR/.vmdrc`. Only the first file found will be read in and processed.

See chapter § 8 for a description of the VMD text commands which may be put in this file. Also, section § 4.1.3 discusses how to put commands into the `.vmdrc` file to customize the behavior of the hot keys.

Here is an example of a startup file:

```
# add personalized keyboard shortcuts
user add key E echo on
user add key e echo off
user add key g display reset
user add key A stage location bottom
user add key m mol list

# position the stage and axes
axes location lowerleft
```

```
stage location off

# position and turn on menus
menu main move 5 196
menu display move 386 90
menu animate move 124 7
menu edit move 125 196
menu graphics move 5 455
menu files move 5 496
menu mol move 5 745

menu main on

# start the scene a-rockin'
rock y by 1
```

13.5 Using VMD as a WWW Client (for chemical/* documents)

Mosaic, Netscape, and possibly other browsers can be configured to use VMD as a helper application for viewing some `chemical/*` documents.

13.5.1 MIME types

When a web browser receives a document from a server it actually gets two pieces of information: the header and the body. The header contains information about the message and body. One of the most important pieces of data, called the *MIME type* specifies what the body of text describes. For instance, a GIF image is given the MIME type of `image/gif`, a JPEG image is `image/jpg`, and postscript is `application/postscript`. A class of types, `chemical/*`, has been created for chemical models so the MIME type for PDB files is `chemical/pdb`, for XYZ is `chemical/xyz`, etc.

Helper Applications

The web browser uses the MIME type to determine how to view the body of the message. Some of the documents are viewed by the browser itself, like `text/html` which describes HTML documents. In other cases, the browser has to start up another application. From here on, we'll describe how Mosaic and Netscape do this. First, it saves the incoming message body to a temporary file. It then scans the global and local *mailcap* files to determine which application is used to view the given MIME type. The application, which must take a file name on the command line, is then executed. When the application exits, the temporary file is deleted.

13.5.2 Setting up your `.mailcap`

The Unix versions of VMD have an extra `-webhelper` command line flag which causes VMD not to be spawned in the background, so that it has time to read temporary files downloaded by the web browser. This command line flag is just slightly simpler to use than the `chemical2vmd` script, as it does not depend on having Perl installed, so may be more appropriate for some cases.

In the VMD installation directory ($VMDDIR/scripts/vmd/) there is a perl script called `chemical2vmd` which will create a VMD command file and execute VMD. Since VMD does not block the calling process, Netscape and other web browsers cannot directly call VMD, as they do not know when to delete the temporary file containing the molecule or other data. The `chemical2vmd` script starts VMD with the -e command line option which runs the saved VMD script or molecule file.

It is also possible to install the previous script in the global `.mailcap` file to make it accessible to everyone. You will have to consult the documentation for your web browser(s) to find out how.

13.5.3 Example sites

Some web sites that send `chemical/pdb` types are the Protein Data Bank at `http://www.rcsb.org/` and "Molecules R US" at `http://www.nih.gov/htbin/pdb`.

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