591V Multiscale Materials Modeling

Computational Lab-1

Outline: Today's class

Outline:

Part A: Simulation tools (nanoHUB etc.)

Example: Deformation of nanowire

Part B: Visualization (VMD)

Examples: visualize the output file, make snapshots and movie.

Objectives:

- Everyone has account on nanoHUB, logged in, reviewed tools
- 2. Basic idea of how to use nanoHUB
- 3. Everyone has VMD downloaded and installed and done some basic tests

PART A: nanoHUB website

Limited code development required

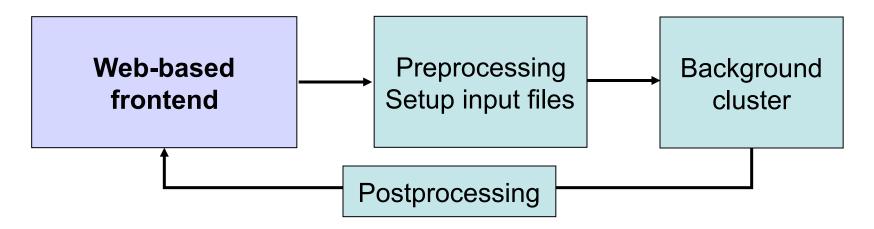
We will use a website-driven simulation framework https://nanohub.org/

Web-enabled high performance computing

- Run complex code through simple web interface
- Submission of jobs to queuing system (background), notification per email when job is done

Benefits

- Avoid coding and complexities of particular codes
- Make complex simulation tools available to broad community

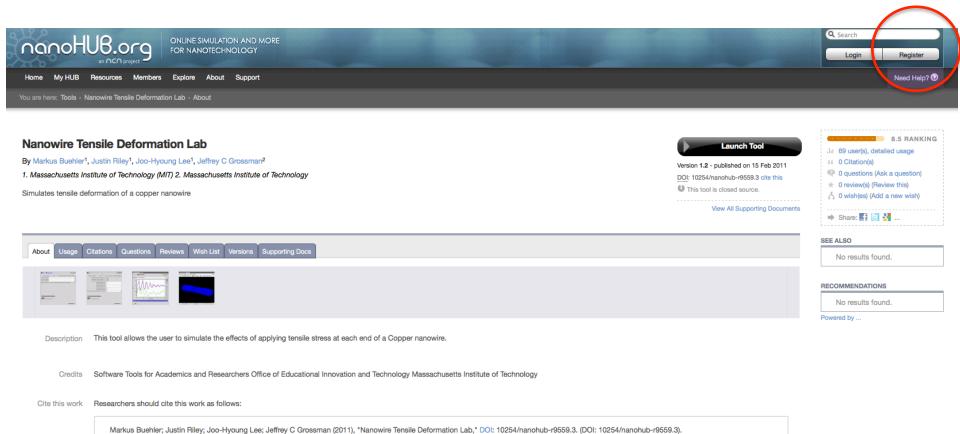


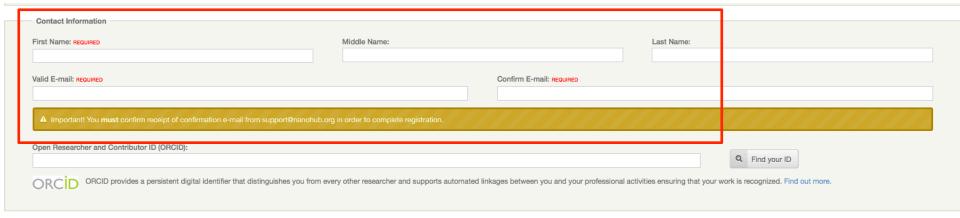
nanoHUB: https://nanohub.org

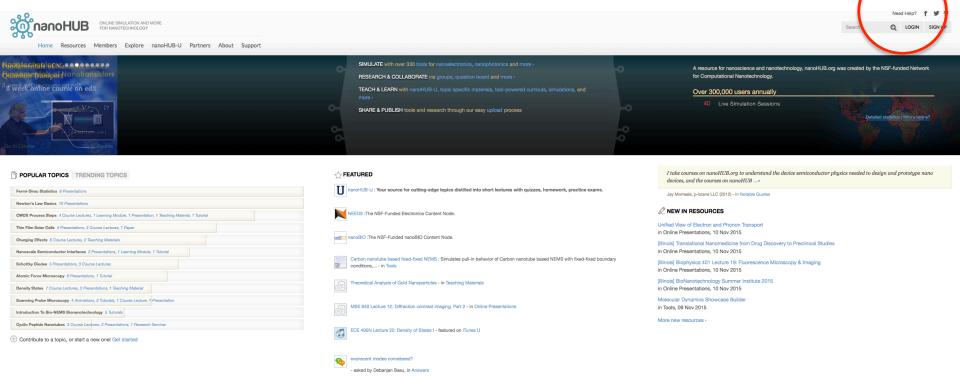
More than 330 tools:

https://nanohub.org/resources/tools

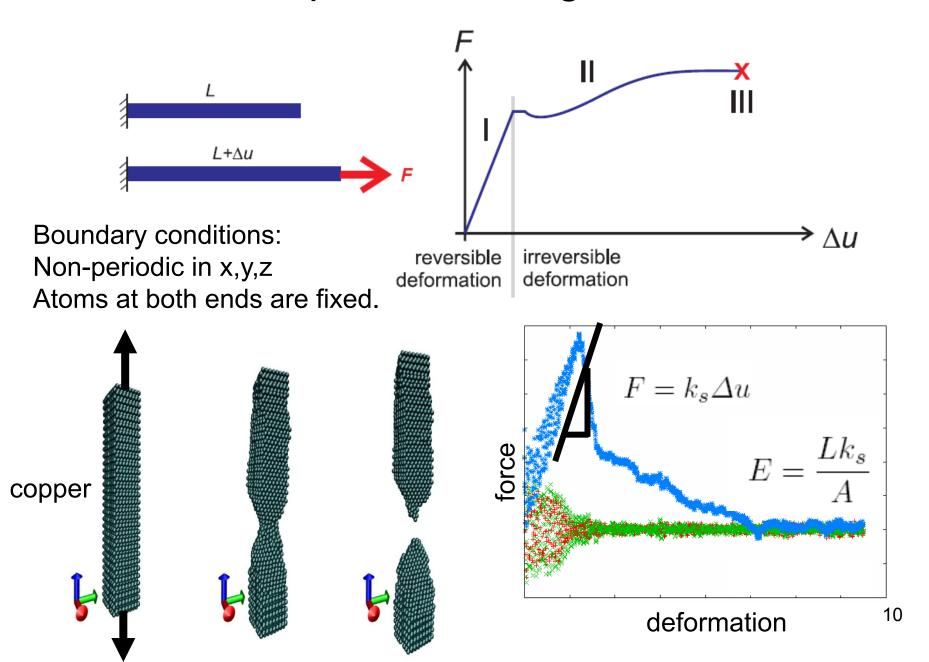
For new accounts

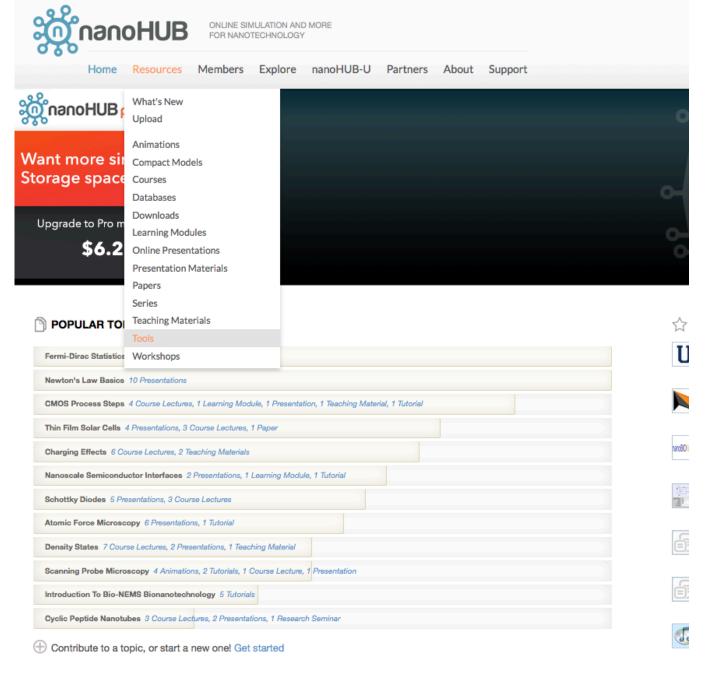




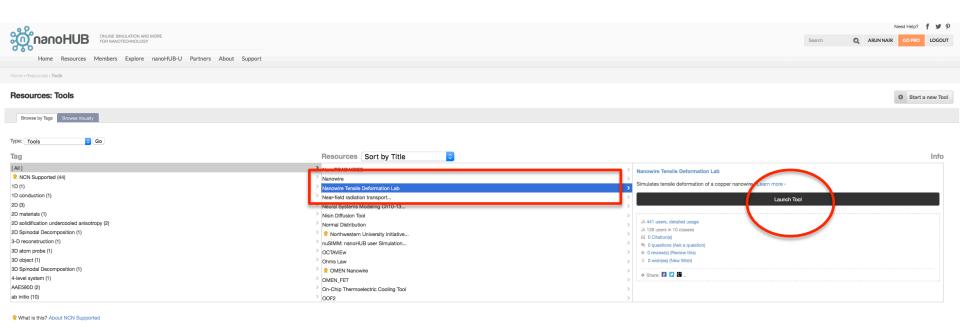


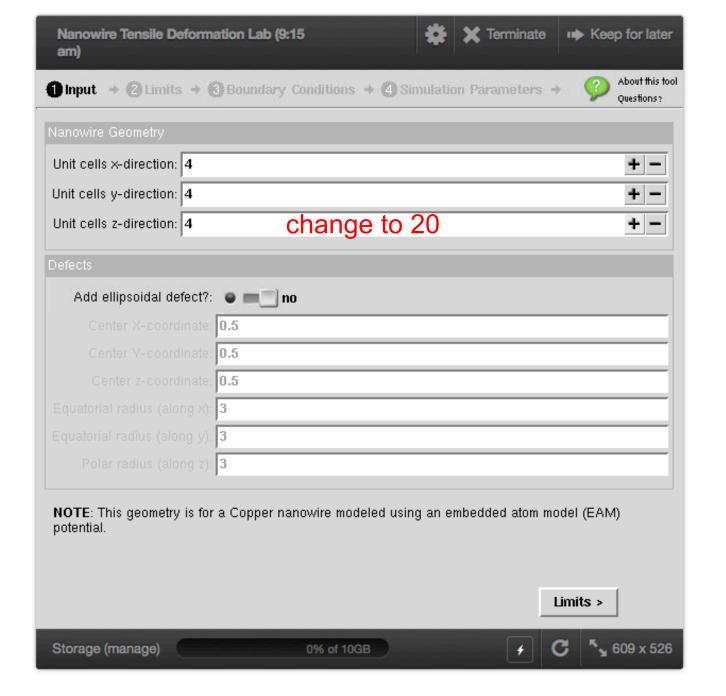
Example: Stretching nanowire

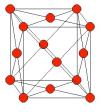




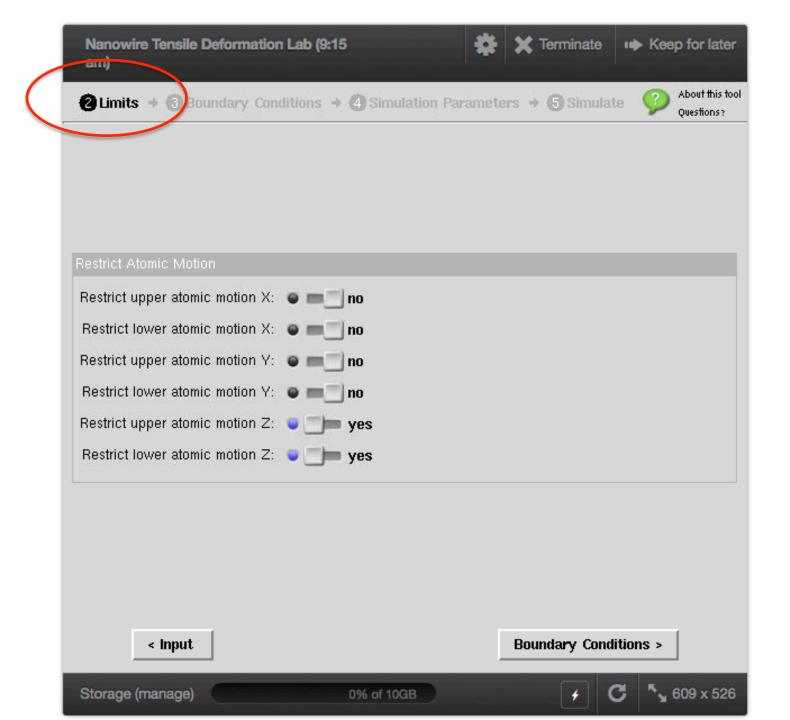
Select Nanowire Tensile Deformation Lab

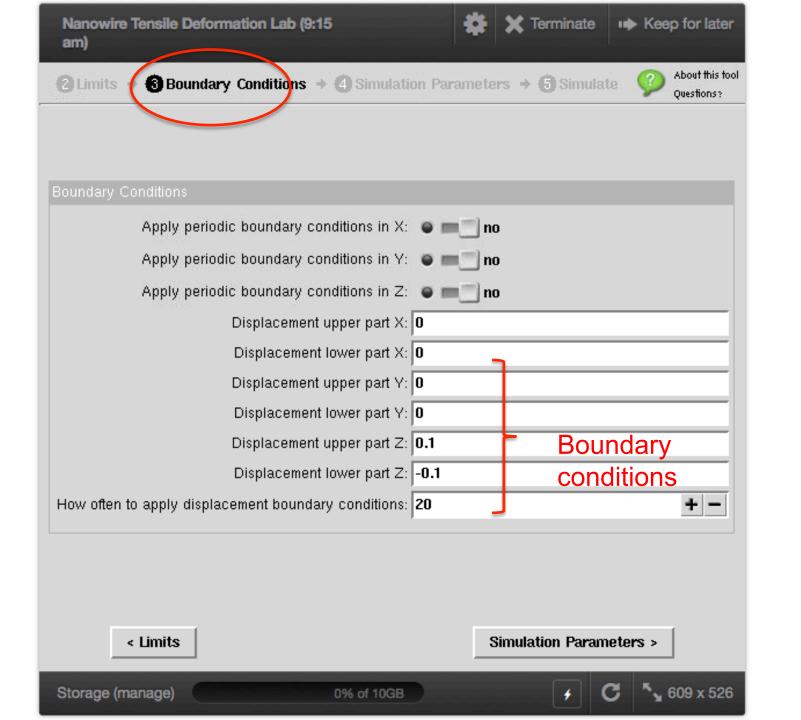


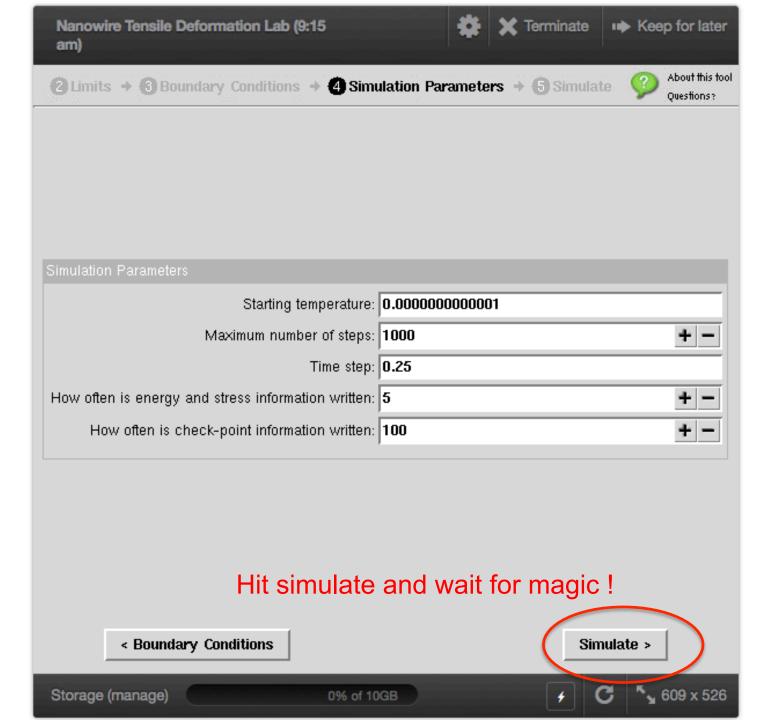


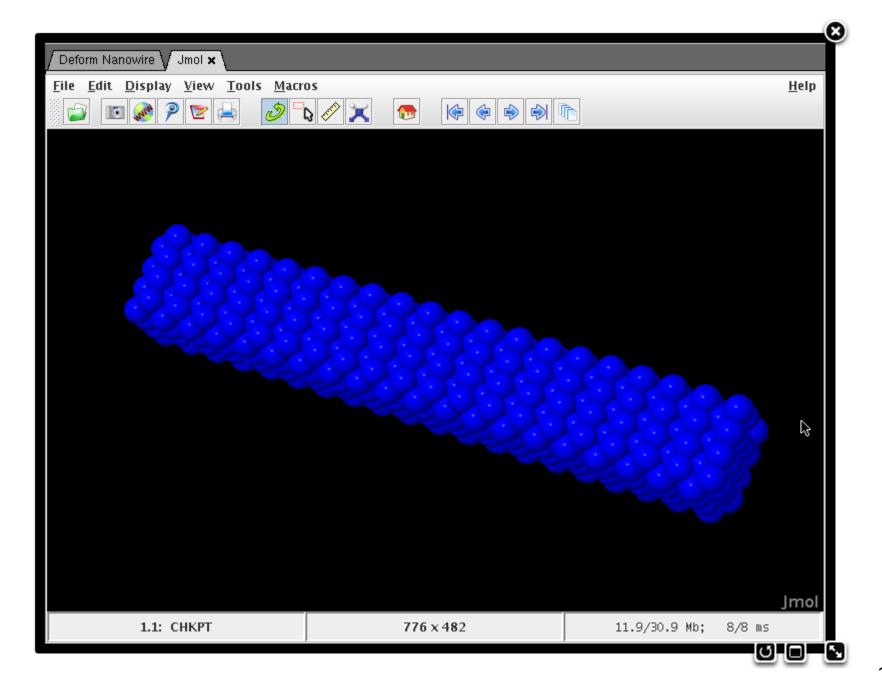


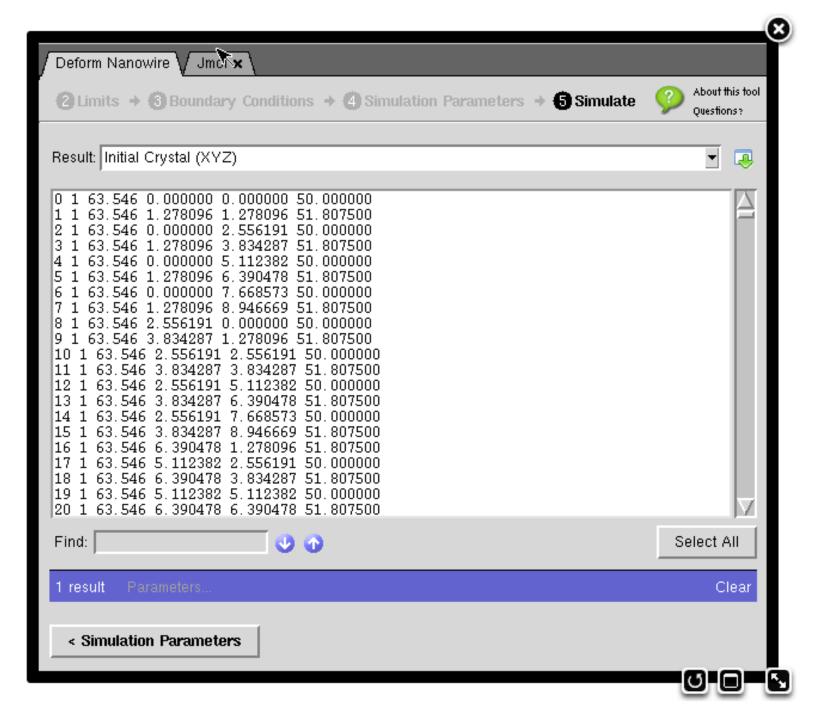
FCC lattice has 4 atoms per unit cell

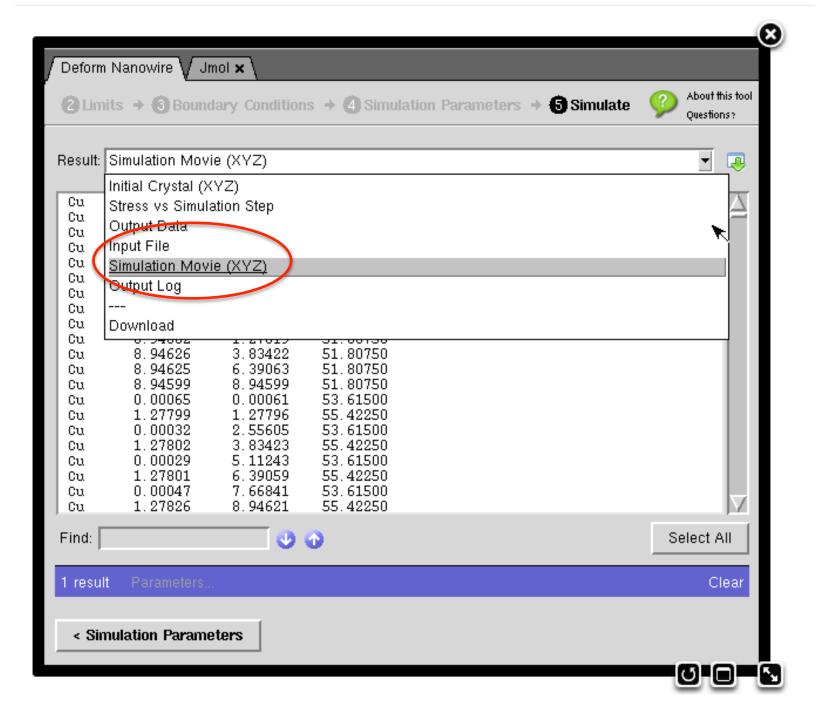








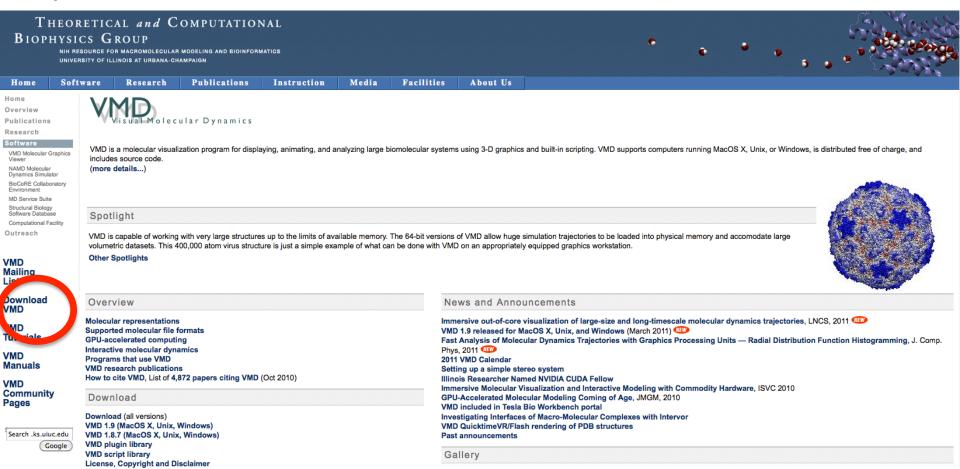




PART B: Visualization

Visualization of results

http://www.ks.uiuc.edu/Research/vmd/



Home

Overview

Publications

Research

Software

- NAMD
- VMD
- GPU Computing
- BioCoRE
- MDFF
 Other
- Outreach

Software Downloads

Download VMD:

VMD is a molecular visualization program for displaying, animating, and analyzing large biomolecular systems using 3-D graphics and built-in scripting.

Selecting an archive below will lead to a user registration and login page. Your download will continue after you have registered or logged in.

Version 1.9.2 (2014-12-29) Platforms:

We recommend that all users upgrade to VMD 1.9.2

- Source Code
- Blue Waters (64-bit Cray XK7) (NCSA Blue Waters (64-bit Cray XK7) MPI, CUDA, OpenGL Pbuffers, TachyonL-OptiX)
- . LINUX_64 OpenGL, CUDA, TachyonL-OptiX (Linux (RHEL 5.5 and later) 64-bit Intel/AMD x86_64 SSE, with CUDA and TachyonL-OptiX)
- LINUX_64 OpenGL, CUDA (Linux (RHEL 4.6 and later) 64-bit Intel/AMD x86_64 w/ SSE, with CUDA)
- . LINUX_64 Text-mode (Linux (RHEL 4.6 and later) 64-bit Intel/AMD x86_64 w/ SSE, Text-mode)
- LINUX OpenGL, CUDA (Linux (RHEL 4.6 and later) Intel/AMD x86 w/ SSE, with CUDA)
- MacOS X OpenGL, CUDA (32-bit Intel x86) (Apple MacOS-X 10.5.x or later with CUDA)
- MacOS X OpenGL (32-bit Intel x86) (Apple MacOS-X (10.4.7 or later) with hardware OpenGL (native bundle))
- SOLARISX86_64 OpenGL (Sun Solaris 10 (64-bit x86) with OpenGL)
- Windows OpenGL, CUDA (Windows XP/Vista/7/8 (32-bit) with OpenGL and CUDA)
- Windows OpenGL (Microsoft Windows XP/Vista/7/8 (32-bit) using OpenGL)

New user registration

THEORETICAL and COMPUTATIONAL BIOPHYSICS GROUP

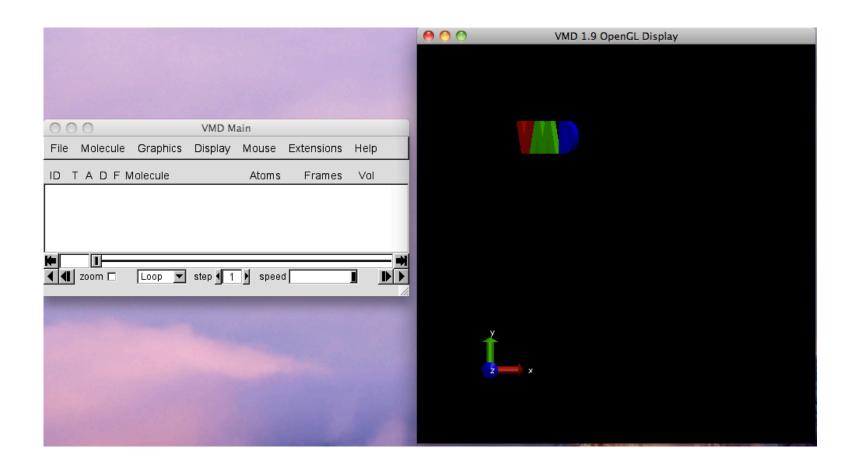
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Funded by a grant from the National Institute of General Medical Sciences of the National Institutes of Health





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To view your output file

