

# VMD & OVITO Visualization of Molecular Dynamics

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**Goal: Publication-quality image of “your” data  
(gallery as final project?)**

<http://www.ks.uiuc.edu/Research/vmd/gallery/>



# Scientific Visualization Tools

- **Atomsviewer: Billion-atom visualizer**

[http://cpc.cs.qub.ac.uk/summaries/ADUM\\_v1\\_0.html](http://cpc.cs.qub.ac.uk/summaries/ADUM_v1_0.html)

- **VMD: Molecular-dynamics data**

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

- **OVITO: Open visualization tool**

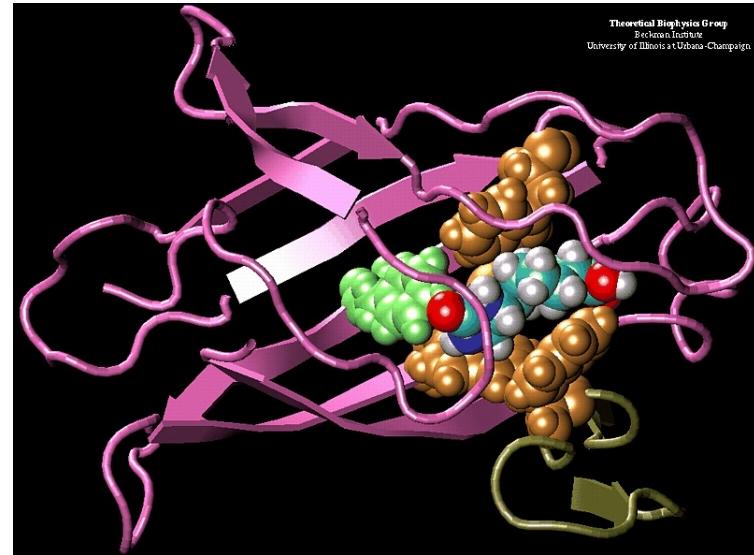
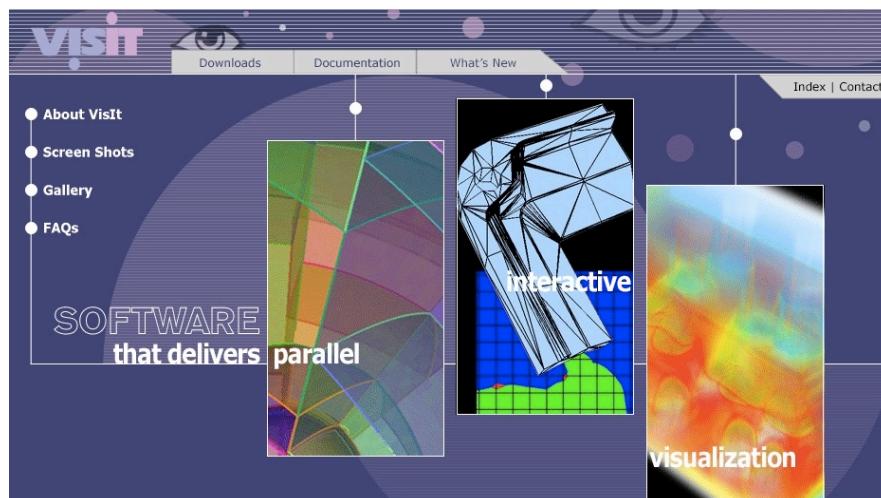
<https://ovito.org>

- **VisIT: General visualization system**

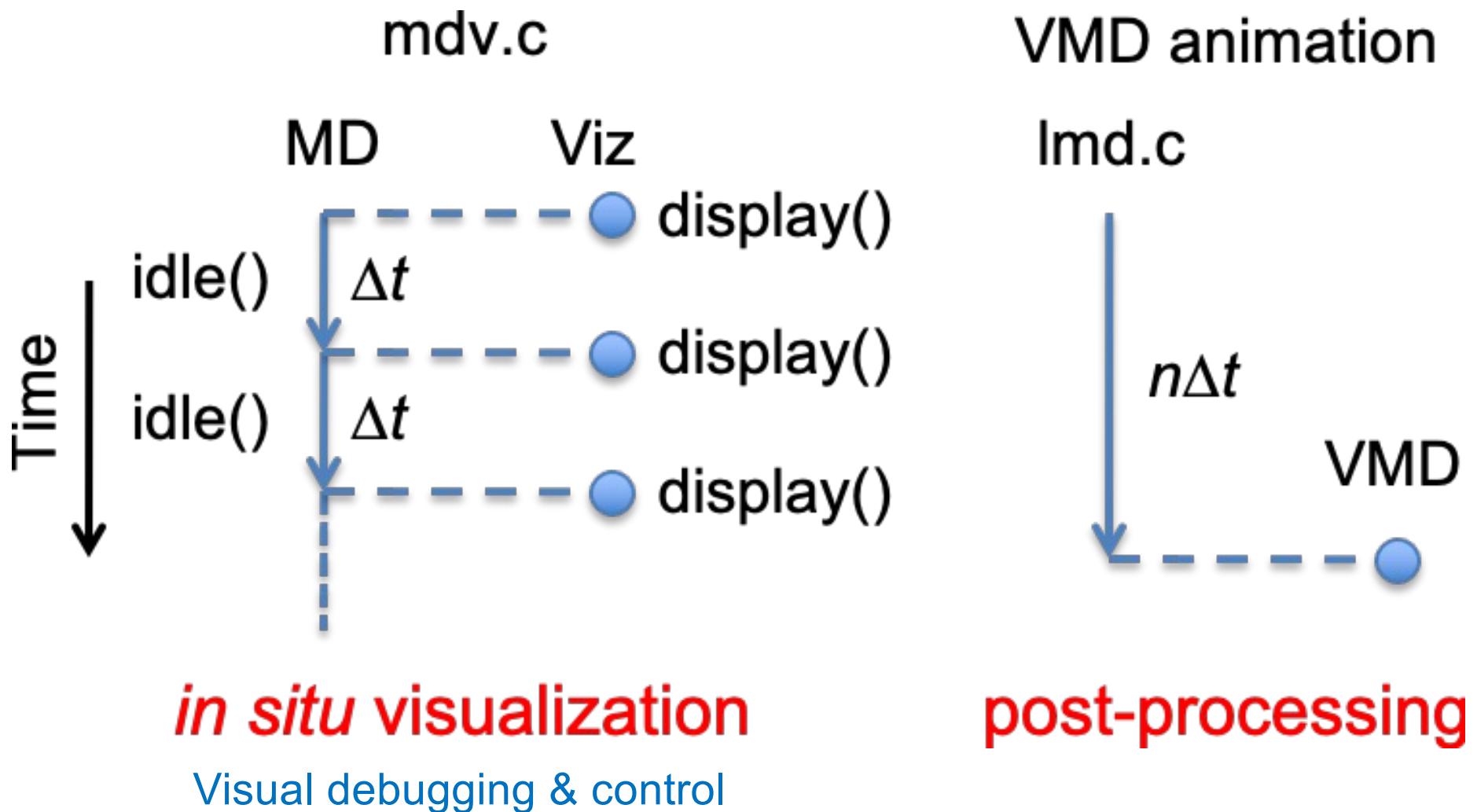
<https://visit.llnl.gov>

- **ParaView: General visualization system**

<http://www.paraview.org>



# *In Situ* vs. Post-processing



***In situ* visualization using common visualization software?**

See [B. Whitlock et al., PGV11](#)

# VMD Software

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- **VMD (Visual Molecular Dynamics): Molecular visualization program developed at the University of Illinois, Urbana-Champaign.**
- **Downloadable for various platforms—Linux, Windows, and Mac.**
- **Install it on your laptop.**

## Version 1.9.4 LATEST ALPHA (2022-04-27) Platforms:

Latest pre-release ALPHA test version

- **Source Code**
- **LINUX\_64 (RHEL 7+) OpenGL, CUDA, OptiX RTX, OSPRay** (Linux (RHEL 7+) 64-bit Intel/AMD x86\_64 SSE/AVX+ with CUDA 10, OptiX6.5 RTX, OSPRay)
- **LINUX\_64 (RHEL 7+) OpenGL, CUDA, OptiX RTX, OSPRay, RTX RTRT** (Linux (RHEL 7+) 64-bit Intel/AMD x86\_64 SSE/AVX+ with CUDA 10, OptiX6.5 RTX, OSPRay, RTX RTRT)
- **MacOS 11.x, ARM64 (64-bit "M1" Macs)** (Apple MacOS-X 11 or later)
- **MacOS 10.15, x86\_64 (64-bit Intel x86\_64)** (Apple MacOS-X 10.15 or later)
- **Windows 64-bit, CUDA, OptiX, OSPRay (64-bit Intel x86\_64)** (Windows 10)

## Version 1.9.3 (2016-11-30) Platforms:

We recommend that all users upgrade to VMD 1.9.3

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

# XYZ File Format

- VMD can read various file formats such as XYZ and PDB (Protein Data Bank).
- **XYZ file format:**  
Repeat the following for as many times as the number of frames (i.e. time steps) you would like to store

line 1: <number of atoms, N>

line 2: comment line

line 3 - N+2: atomic element, atom's x, y & z coordinates  
(space delimited; coordinate in angstrom)

## Example: a methane molecule

```
5
methane molecule (in ångströms)
C      0.000000      0.000000      0.000000
H      0.000000      0.000000      1.089000
H      1.026719      0.000000     -0.363000
H     -0.513360     -0.889165     -0.363000
H     -0.513360      0.889165     -0.363000
```

# Writing an XYZ File from lmd.c

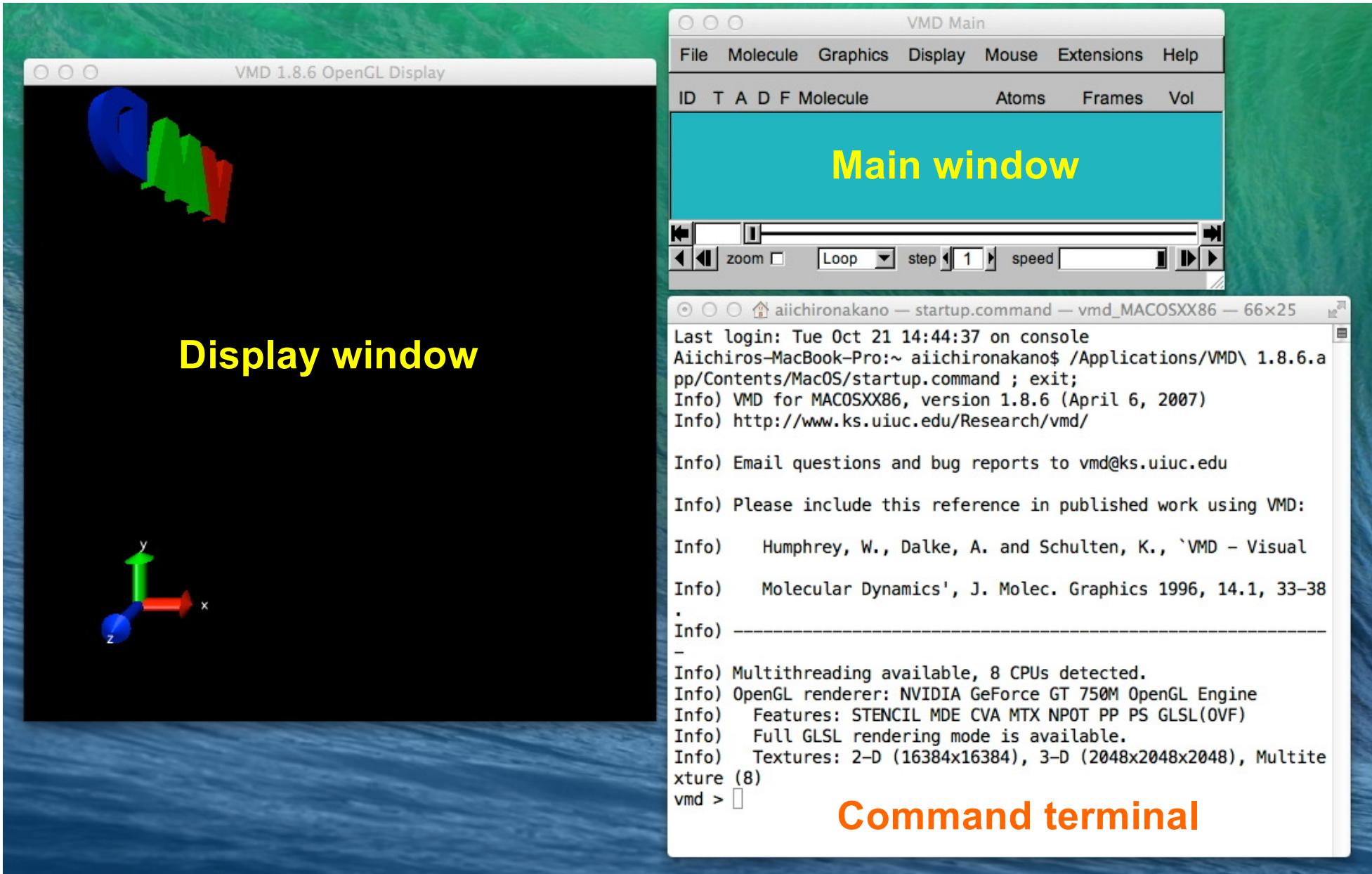
```
#define SIGMA 3.4 // Lennard-Jones length scale in angstrom
FILE *fxyz;
...
int main(int argc, char **argv) () {
    ...
    fxyz = fopen("lmd.xyz", "w");
    ... // Main MD for loop
    fclose(fxyz);
    ...
}
...
void EvalProps() {
    ...
    fprintf(fxyz, "%d\n", nAtom);
    fprintf(fxyz, "Molecular dynamics simulation of argon\n");
    for (n=0; n<nAtom; n++)
        fprintf(fxyz, "Ar %f %f %f\n", r[n][0]*SIGMA, r[n][1]*SIGMA, r[n][2]*SIGMA);
    ...
}
```

- Run the program with the following input parameters in lmd.in

```
3 3 3 // # of crystalline unit cells in the x, y & z directions
0.8 // Density in the Lennard-Jones (LJ) unit
1.0 // Temperature in the LJ unit
0.005 // Time discretization unit in the LJ unit
500 // Total # of time steps
10 // Interval between consecutive dumps to the XYZ file
```

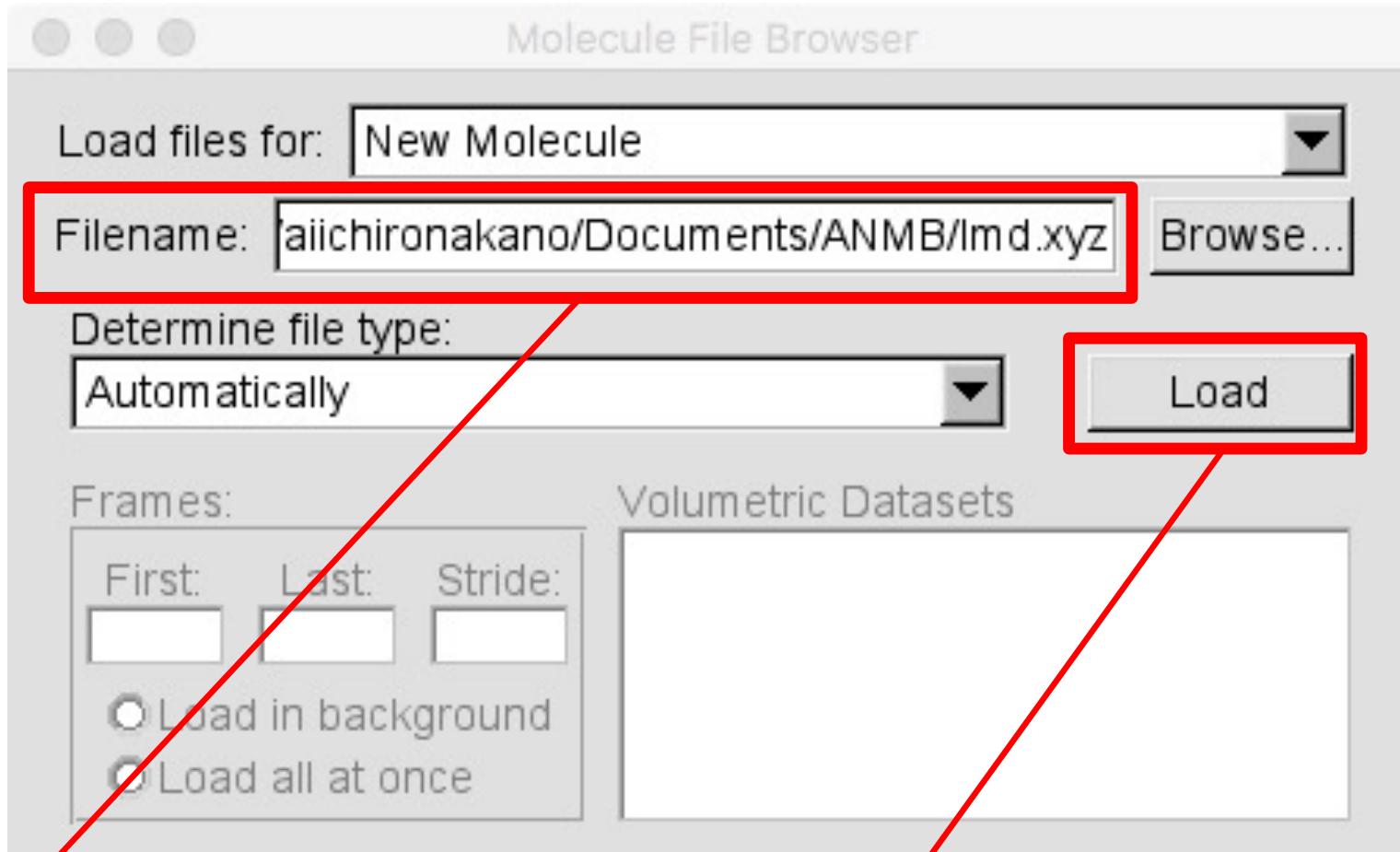
# Start VMD

- It will open 3 windows



# Load the MD-Trajectory XYZ File

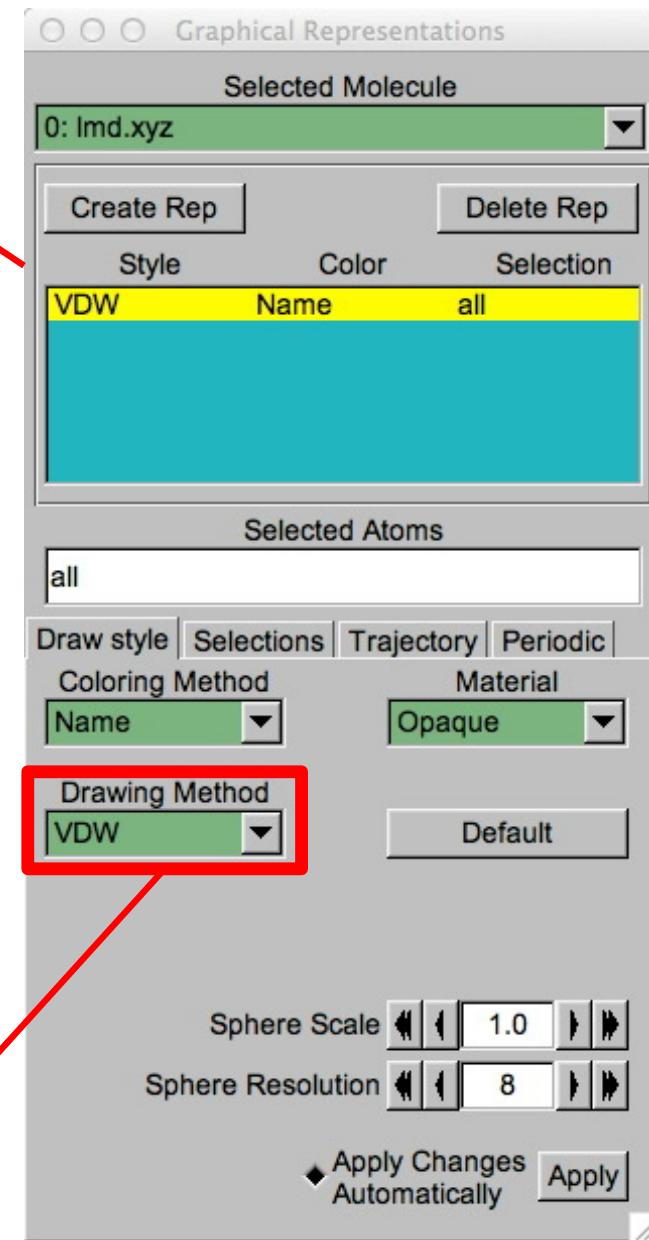
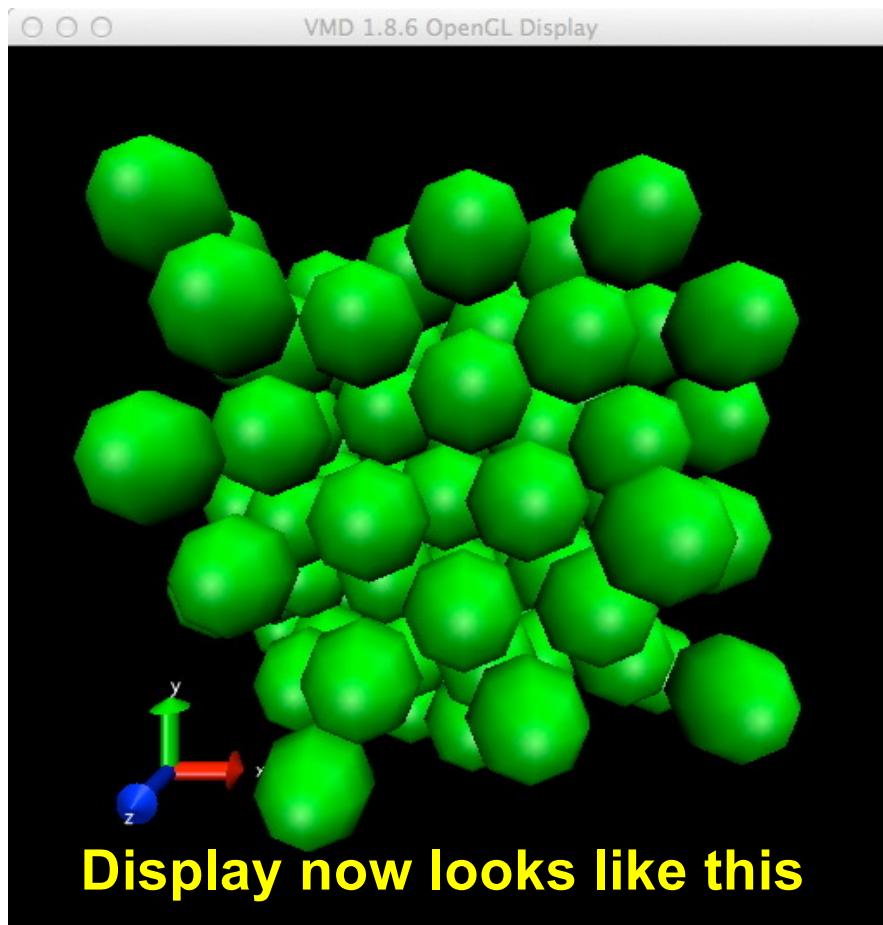
- In the File menu in the VMD main window, select New Molecule; the following new window will open.



- Drag and drop the XYZ file you have created in the Filename field (or press the browse button to locate the file).
- Click the Load button to load the file.

# Choose the Graphic Representation

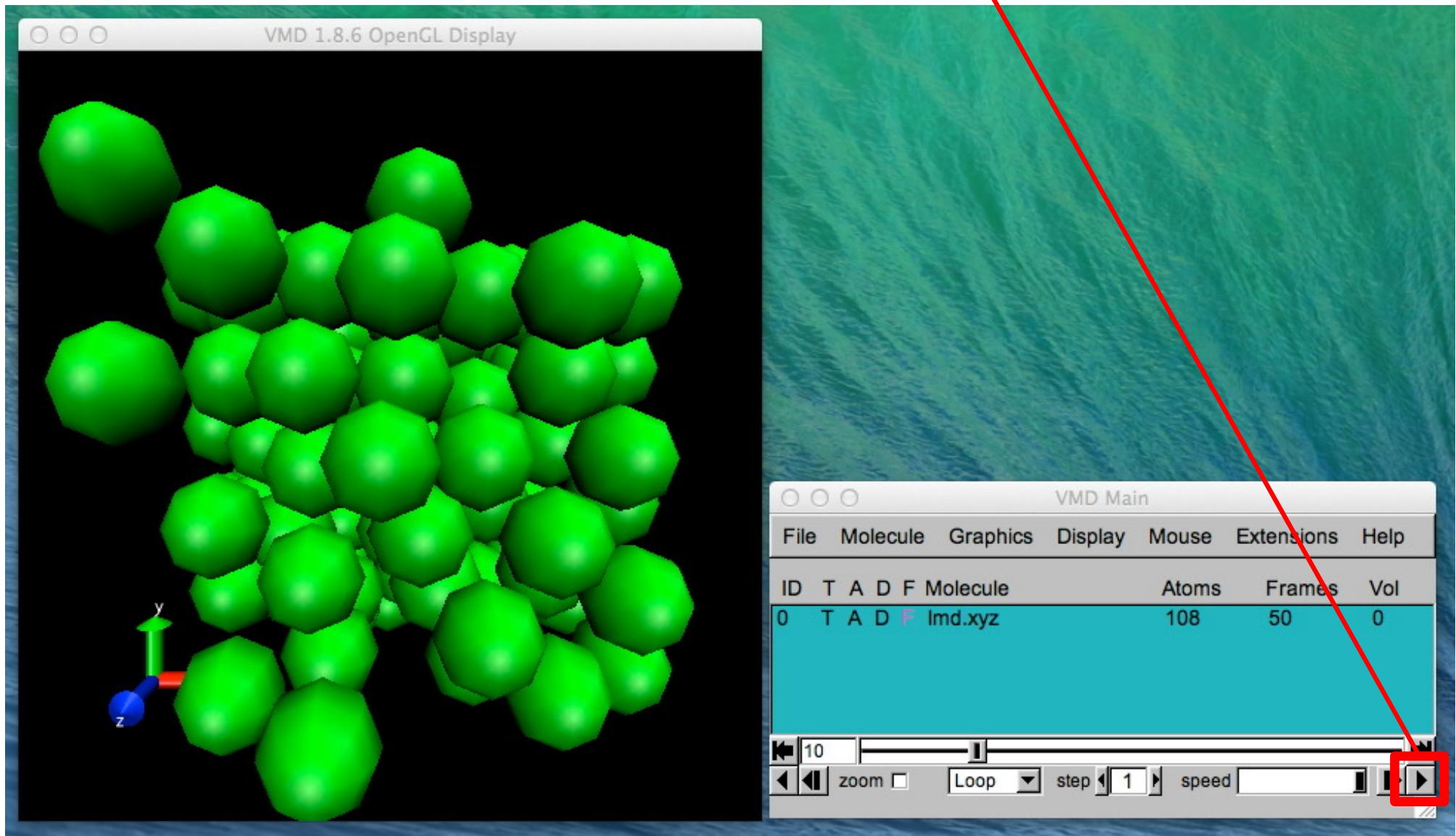
- In the Graphics menu in the VMD main window, select Representations; the following new window will open.



- In the Drawing Method menu, choose the VDW (van der Waals radius) representation.

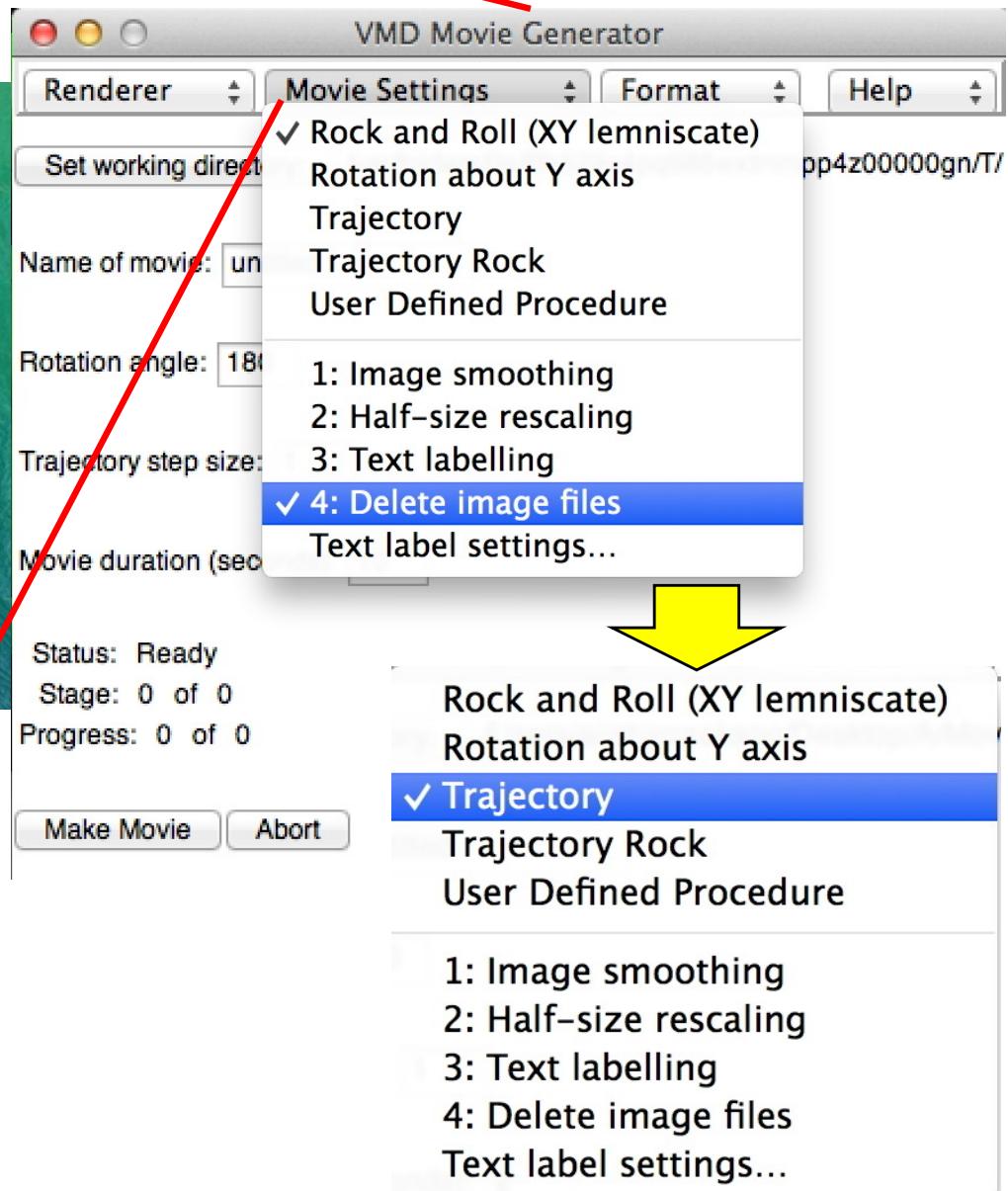
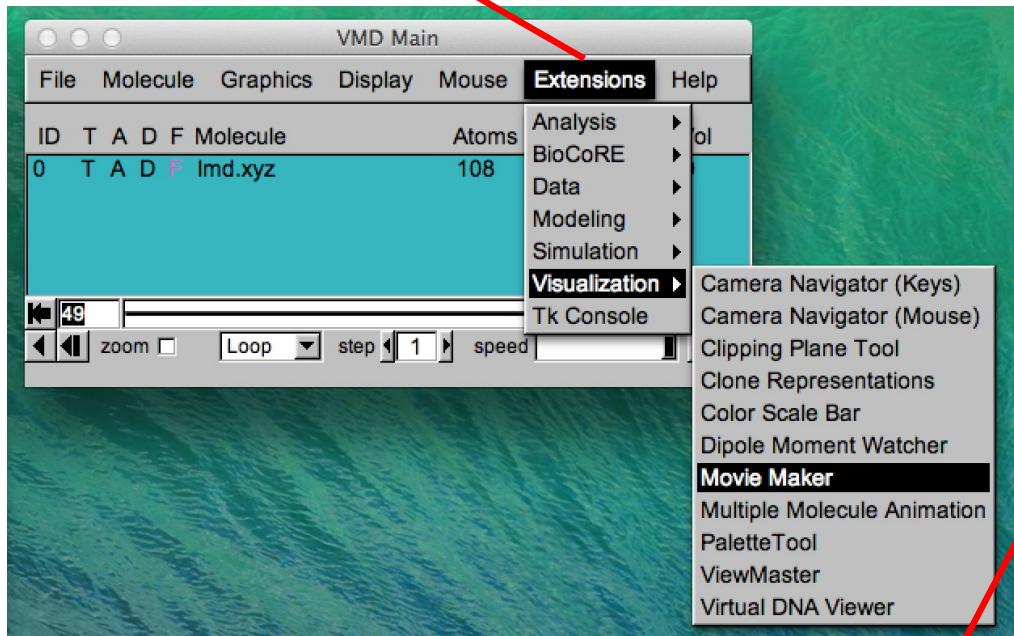
# Animation

- Click the play button in the VMD main window to play the movie.



# Optional: Creating a Movie File (1)

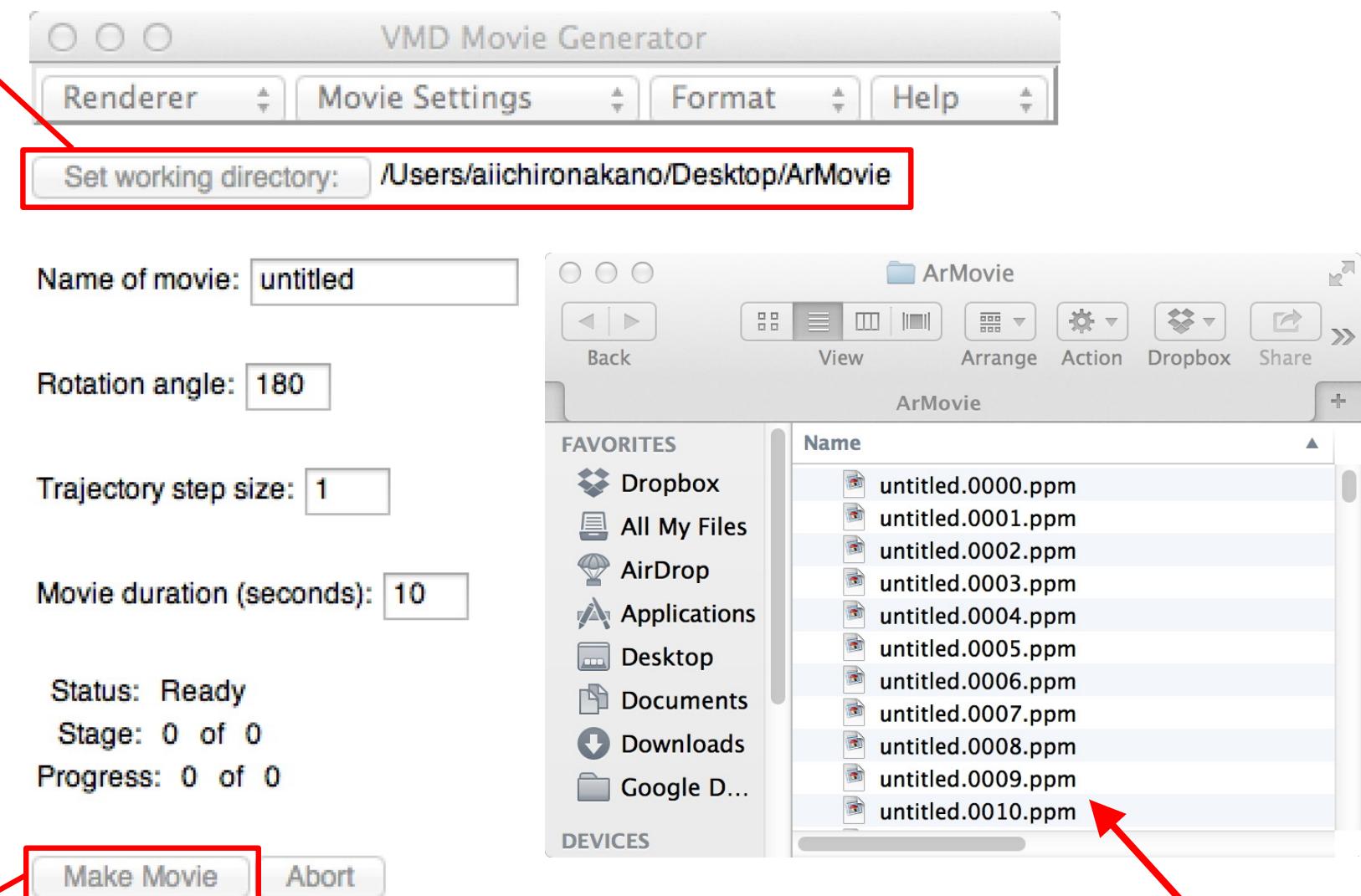
- Choose the Extensions → Visualization → Movie Maker menu; this will open a VMD Movie Generator window.



- Unclick (1) the “Rock and Roll” & (2) “Delete image files” options, while clicking the “Trajectory” option, in the “Movie Settings” menu.

# Optional: Creating a Movie File (2)

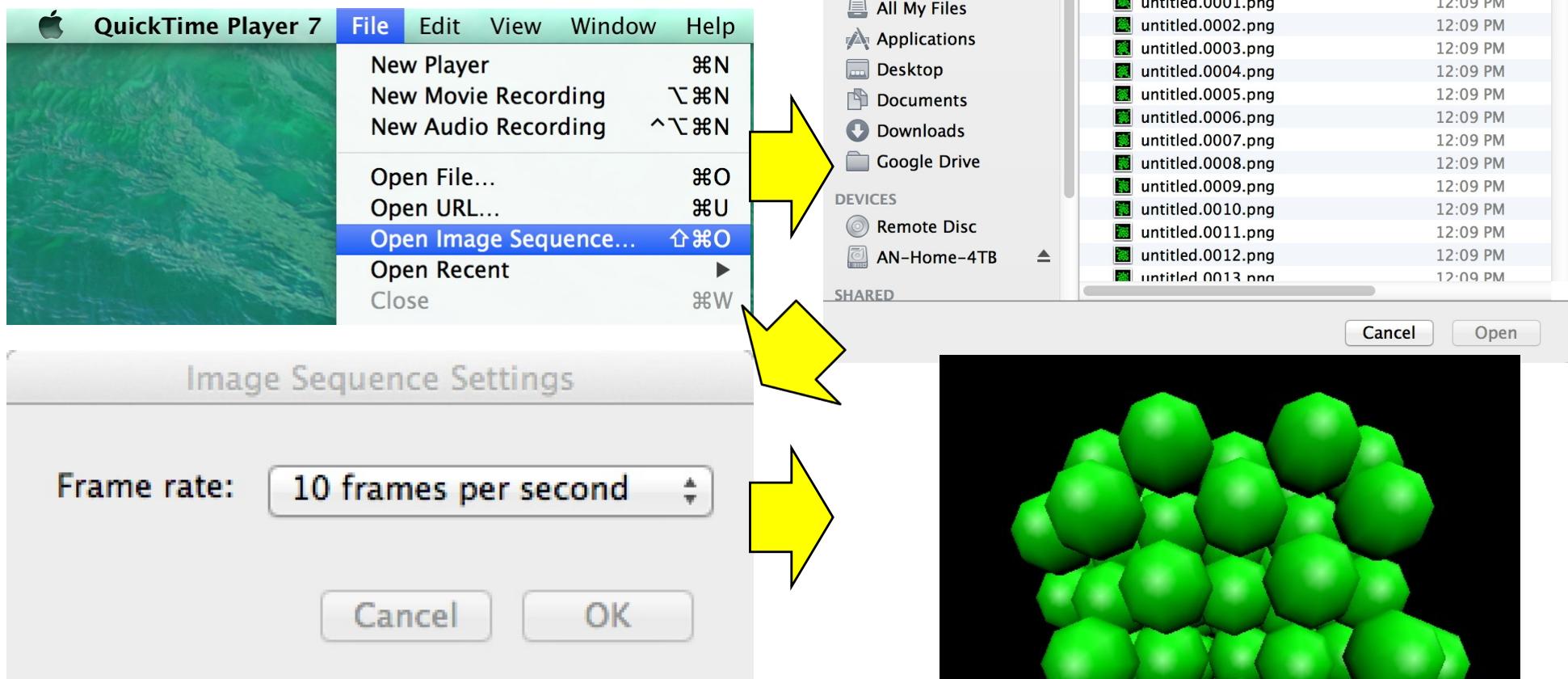
- Choose a directory, in which a sequence of image files will be stored, using the “Set working directory” field.



- Click the “Make Movie” button; you will find image files in the directory.

# Optional: Creating a Movie File (3)

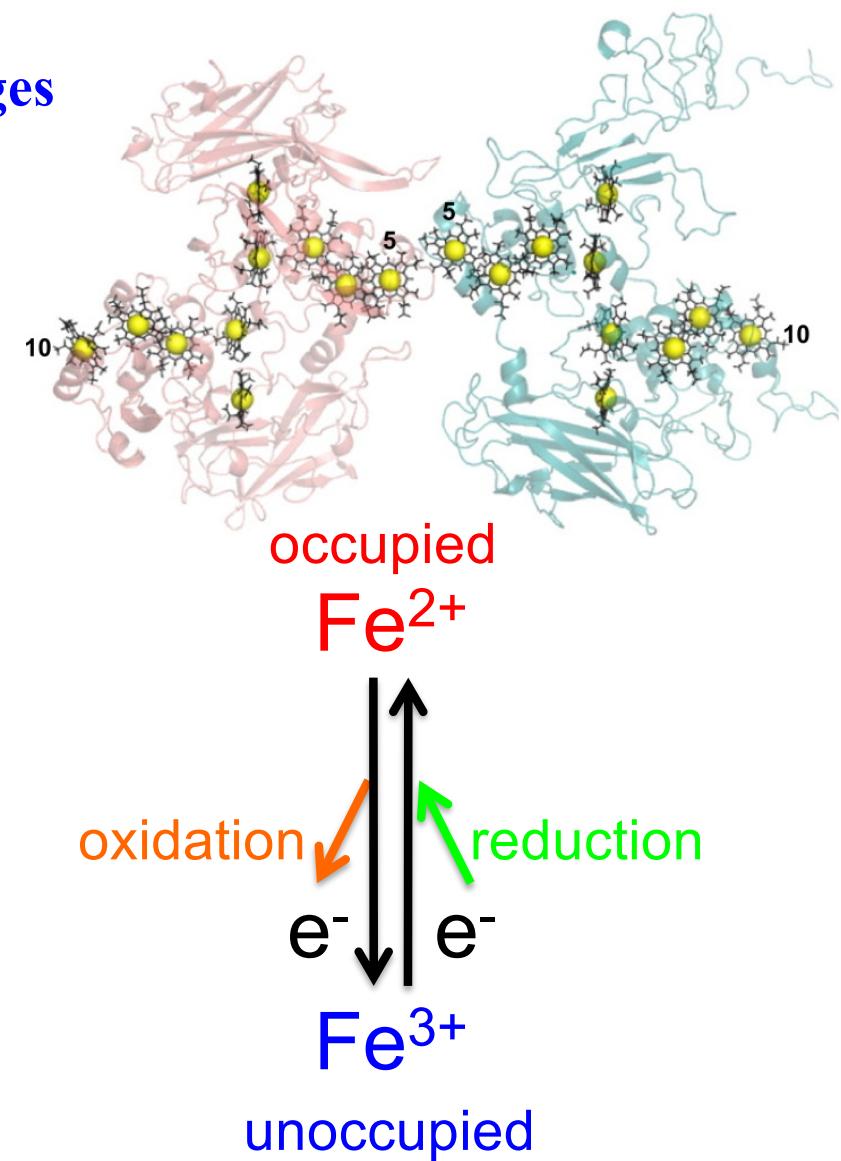
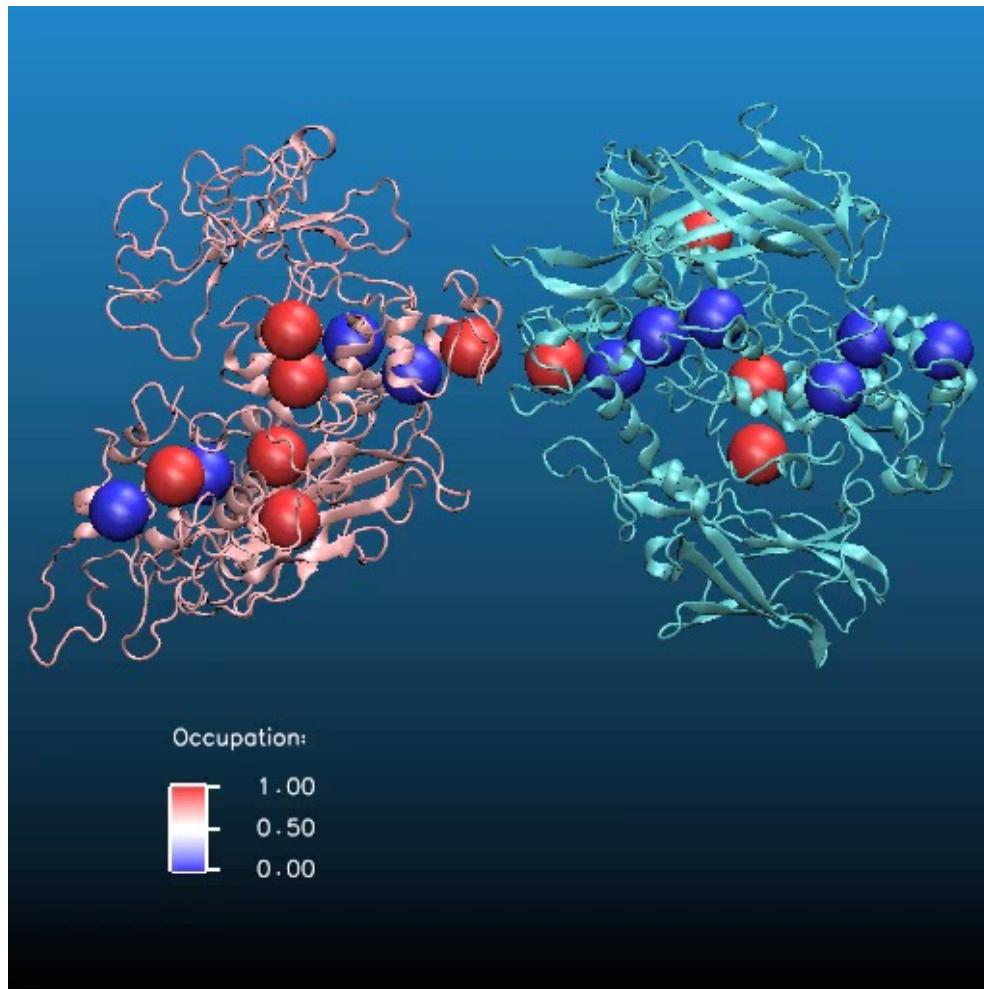
- Use a software such as QuickTime Player to convert the image sequence to a movie file.



- Before this step, we have converted the PPM (portable pixmap) image files created by VMD to PNG (portable network graphics) image files that QuickTime Player can read, using the GraphicsConverter software.

# Dynamic Coloring

- In VMD, USER fields in the TRAJECTORY data category can be animated as color changes according to one of the built-in color scales



# Scripting in VMD

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- VMD allows **Tcl** scripting language for user to control visualization
- Go to File → New Molecule menus → load complex16.pdb—cytochrome (MtrF-OmcA) dimer data—in Filename textbox
  - > Graphics → Representations → choose NewCartoon in Drawing Method
- Extensions → Tk Console → type the following commands in console

```
%cd csci596-as07      Absolute path that contains Tcl script named userb.tcl
%source userb.tcl
```
- It loads FeOcc.pdb—time series of Fe positions & their occupations (0 or 1)
  - > Graphics → Representations (make sure Selected Molecule is FeOcc.pdb)
    - >> Drawing Method → VDW; set sphere scale to be 4.0
    - >> Coloring Method → Trajectory → User → User
  - > Graphics → Colors → Color scale → Method: BWR
- Click play button in VMD main window for animation

# Tcl Script

- In FeOcc.pdb file, “beta” value in the last column is customized to represent electron occupation (0 or 1) for each Fe atom; Tcl script FeOcc.pdb transfers it to “user” field used for VMD coloring

<https://aiichironakano.github.io/cs596/src/viz/userb.tcl>

```
mol new FeOcc.pdb waitfor all
set all [atomselect top all]
set frame 0
set in [open FeOcc.pdb r]
set beta {}
while { [gets $in line] != -1 } {
    switch -- [string range $line 0 3] {
        END {
            $all frame $frame
            $all set user $beta
            set beta {}
            incr frame
        }
        HETA -
        ATOM {
            lappend beta [expr [string range $line 60 65]]
        }
    }
}
```

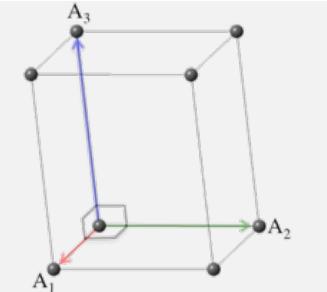
Find more examples: [https://www.ks.uiuc.edu/Research/vmd/script\\_library/](https://www.ks.uiuc.edu/Research/vmd/script_library/)

Publish your Tcl script as VMD plugin: I. Balabin *et al.*, *J. Comput. Chem.* **33**, 906 ('12)

# Gaussian Cube File Format

- **Cube file format:** Describes volumetric data (e.g., electronic wave function or charge density) as well as atom positions

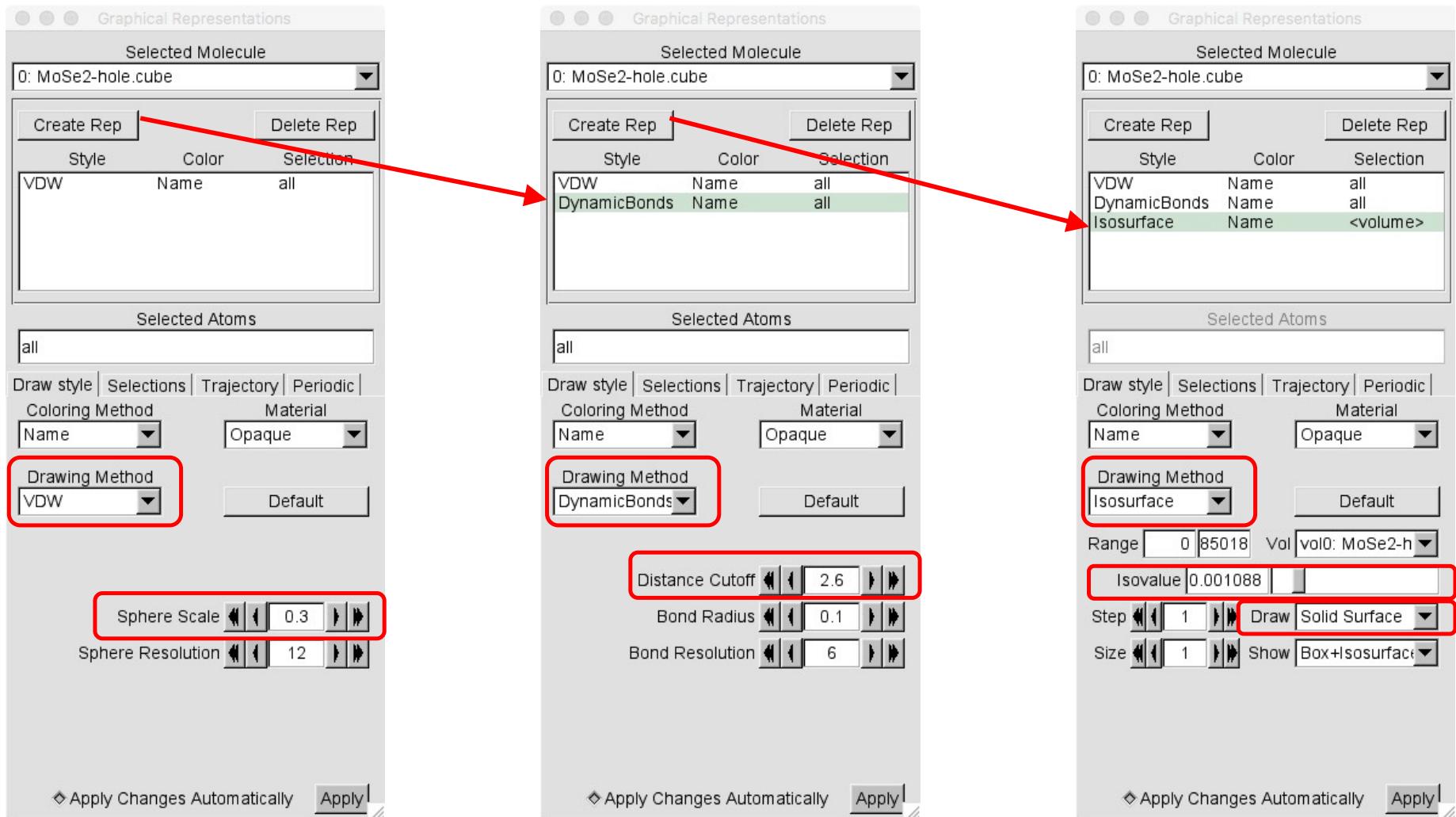
```
<header>
<comment>
 24    0.000000    0.000000    0.000000 // # atoms & origin
 63    0.198958    0.000000    0.000000 // # of voxels 1st axis
 63   -0.099479    0.172302    0.000000 //                      2nd
189    0.000000    0.000000    0.194054 //                      3rd
 42    0.000000   -0.000013    3.618358  4.860106 // atomic #, nuclear charge,
 42    0.000000    6.267168    3.618358  4.860106 // & atomic position vector
...
0.29654E-04  0.25769E-04  0.20454E-04  0.15027E-04  0.98477E-05  0.53243E-05
... // volumetric data (see the code below)
```



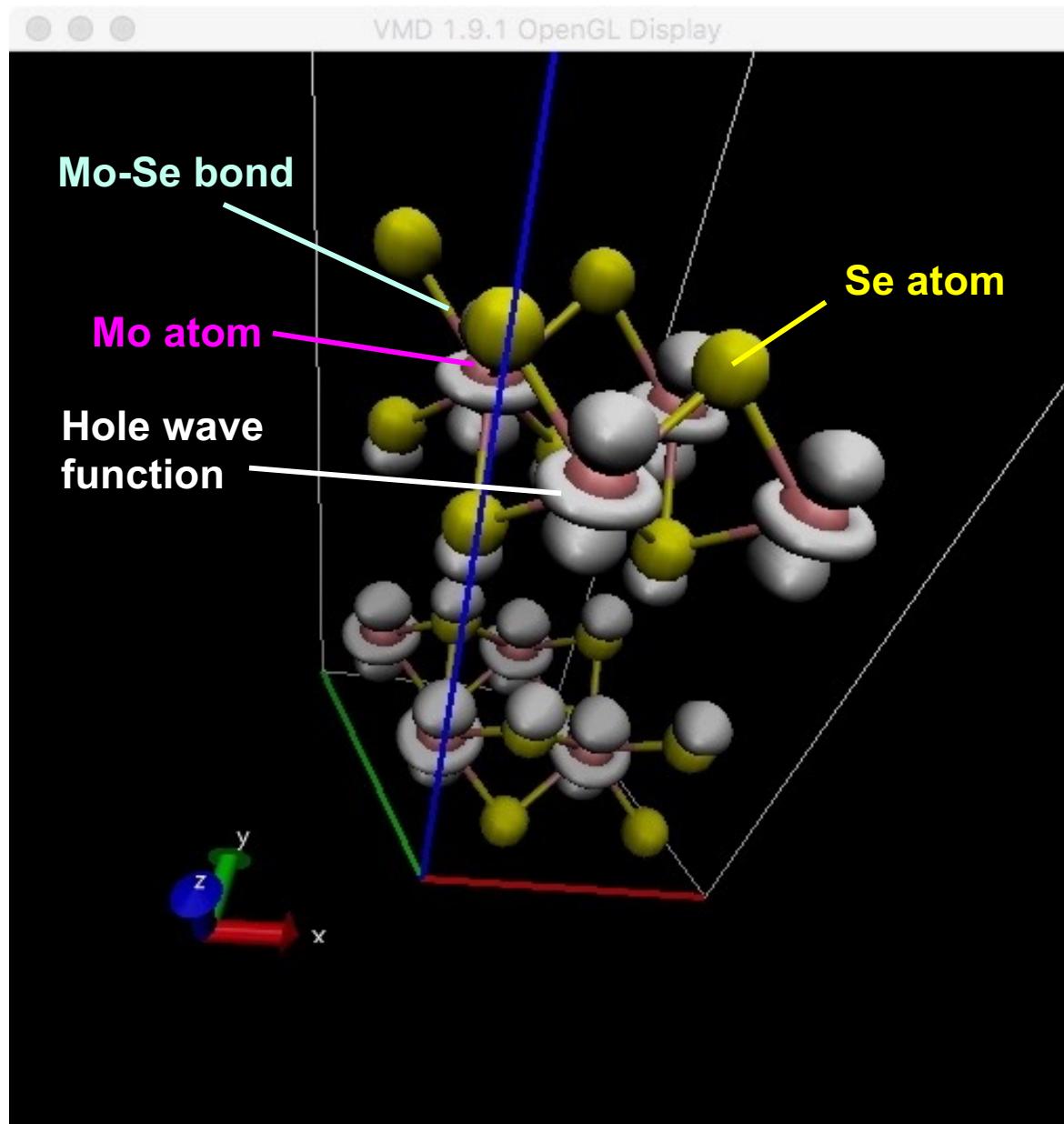
```
for (ix=0;ix<NX;ix++) {
    for (iy=0;iy<NY;iy++) {
        for (iz=0;iz<NZ;iz++) {
            printf("%g ",data[ix][iy][iz]); if (iz % 6 == 5) printf("\n");
        } printf("\n");
    }
}
```

# Isosurface Rendering

- Load a cube file <https://aiichironakano.github.io/cs596/src/viz/MoSe2-hole.cube>
- Draw atoms using VDW representation & bond between atoms using dynamic–bond representation (adjust sphere radius & bond cutoff)
- Draw the volumetric data using isosurface representation (adjust isovalue)

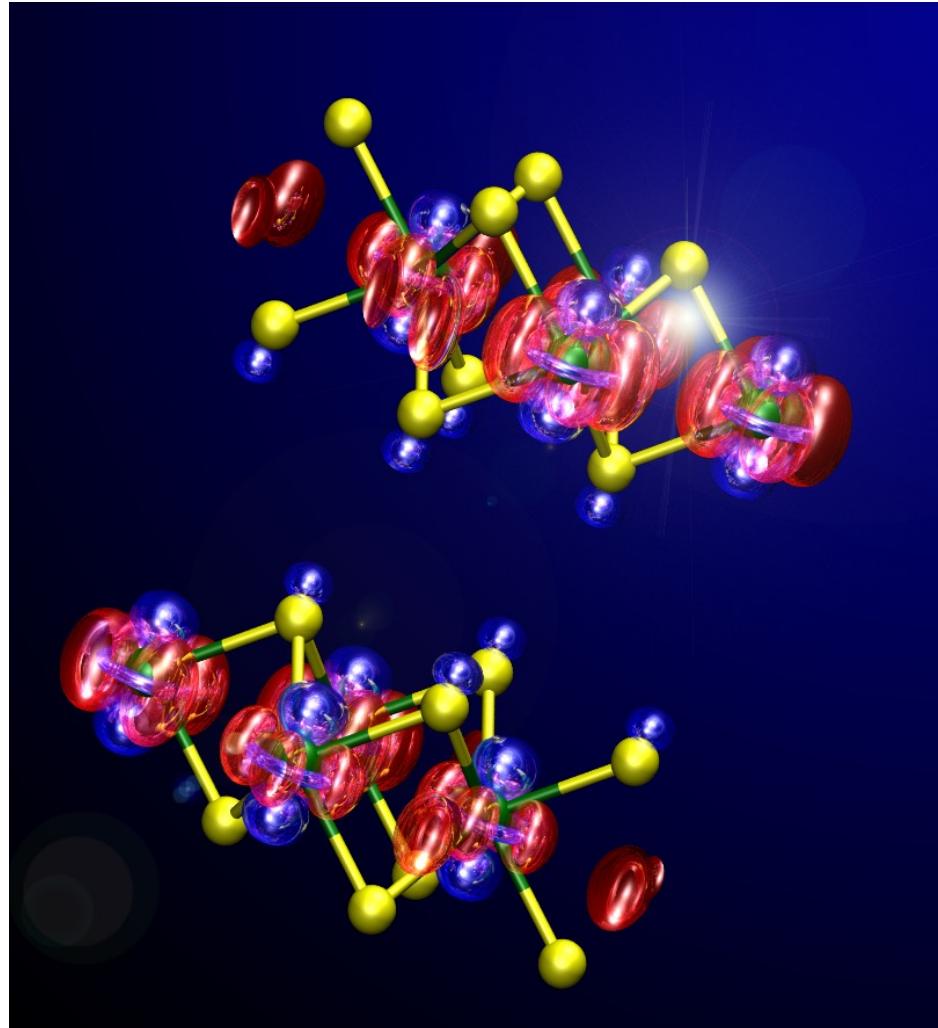


# Isosurface Rendering

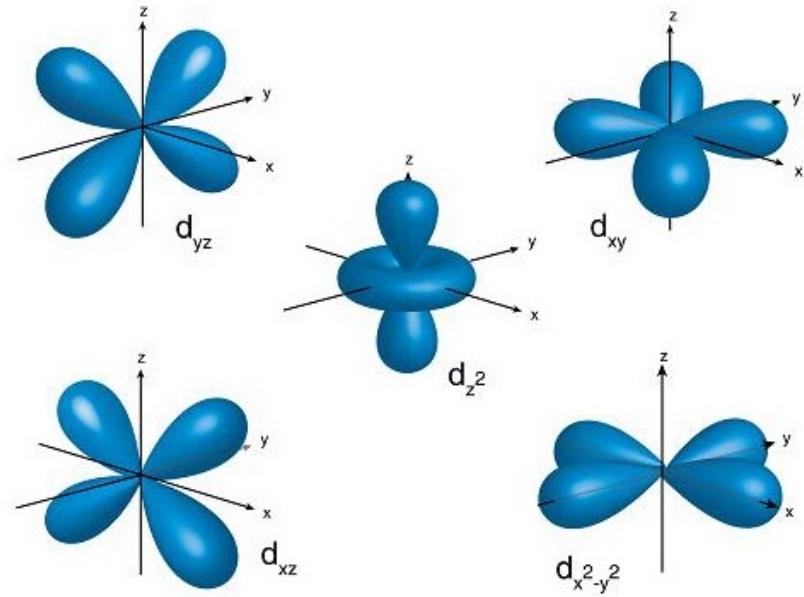


# Wave Functions in MoSe<sub>2</sub> Bilayer

- Highest occupied states (blue) are d<sub>z2</sub>-like
- Lowest unoccupied states (red) are d<sub>xy</sub>-like

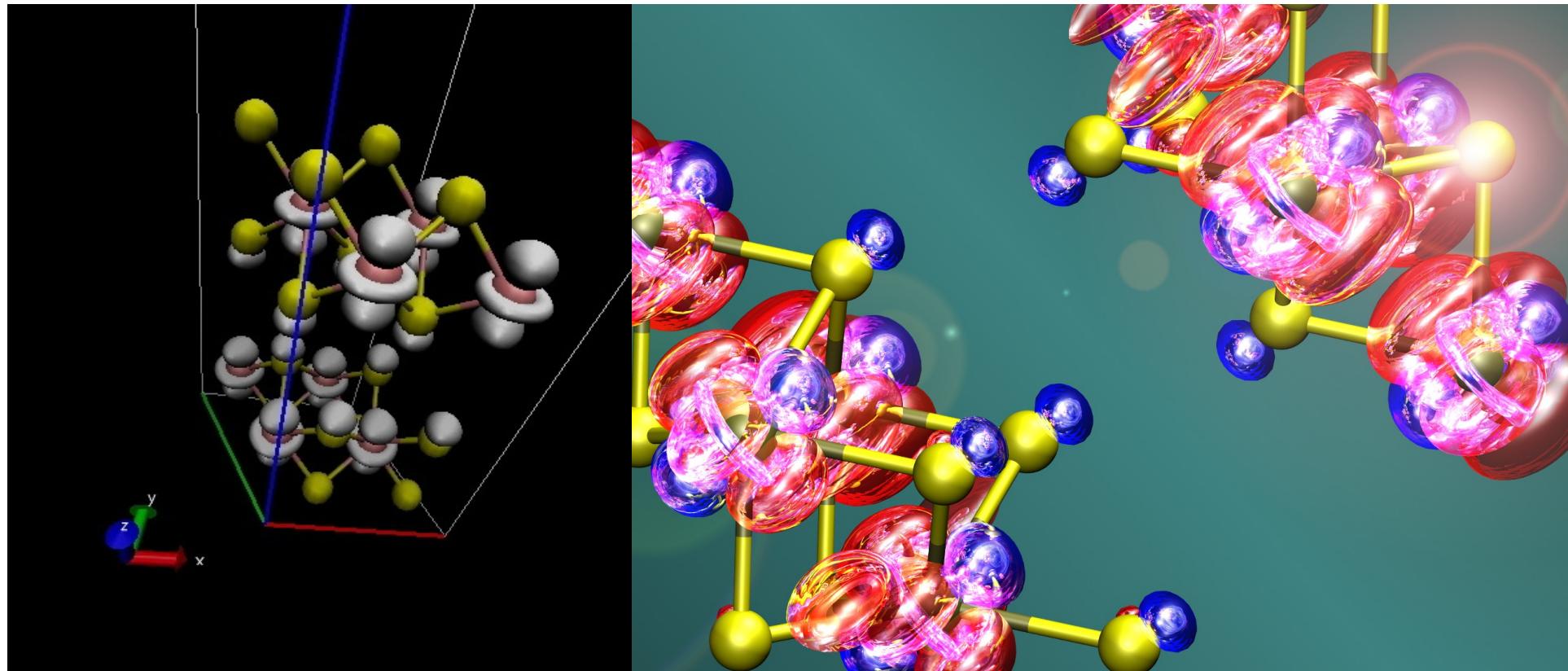


Electron  
Hole



Try a different rendering method:  
File → render → tachyon internal

# Beautify in One Hour?



**Before**

Default VMD rendering

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

**After**

Enhanced with POV-ray ray tracer

<http://www.povray.org>

**Try: File → render → POV-Ray**

M.F. Lin *et al.*, *Nature Commun.* **8**, 1745 ('17)

# OVITO Software

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- **OVITO (Open Visualization Tool): Scientific visualization and analysis software for atomistic & particle simulation data.**

A. Stukowski, “Visualization and analysis of atomistic simulation data with OVITO – the Open Visualization Tool,” *Modelling Simul. Mater. Sci. Eng.* **18**, 015012 ('10)

- **Downloadable for various platforms—Linux, Windows, and Mac.**
- **Install it on your laptop.**

<https://www.ovito.org>

## OVITO Basic

Open-source software – limited feature set

Version 3.9.2 – 31 Aug, 2023

## OVITO Pro

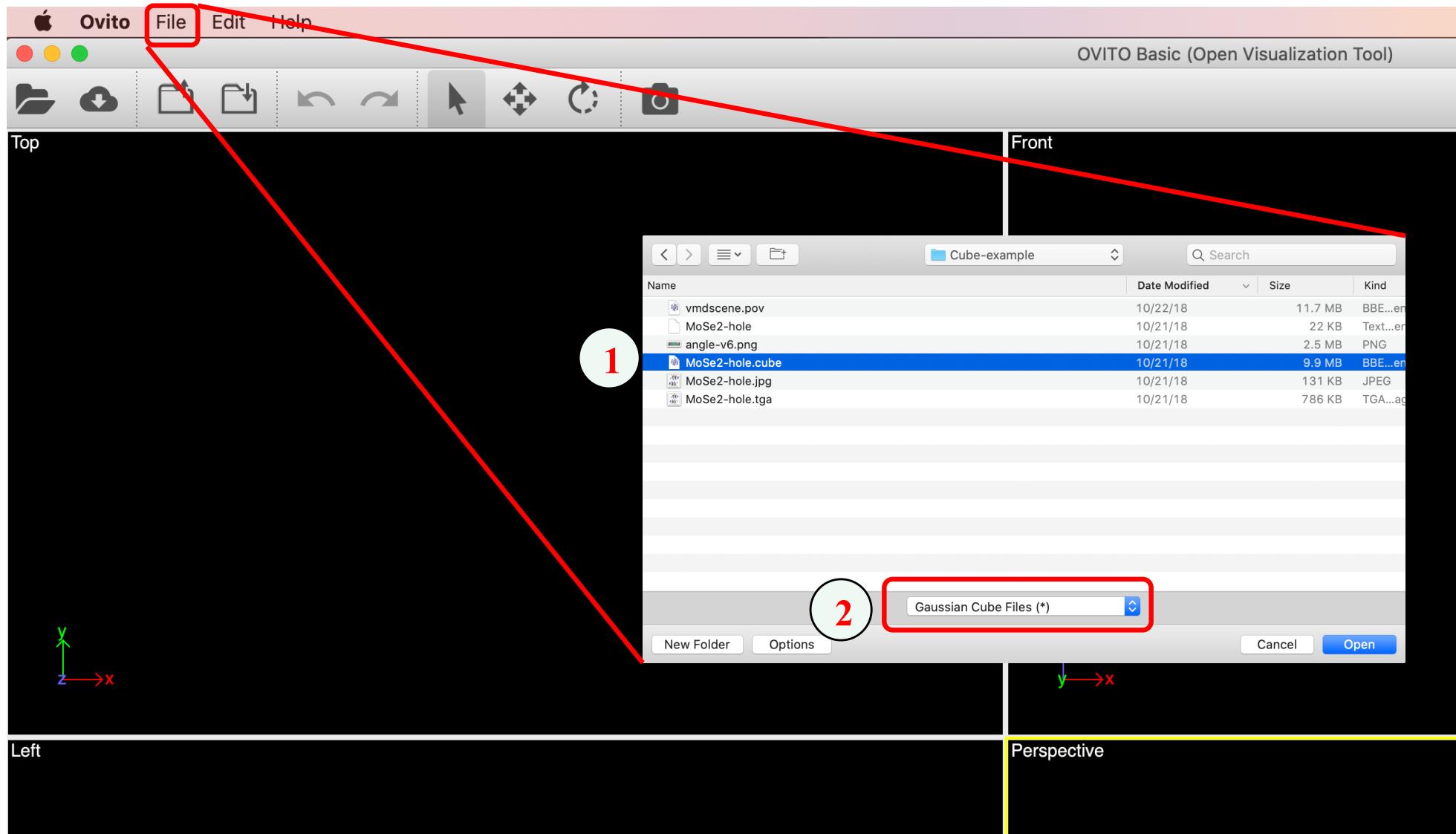
Professional version – full functionality

Version 3.9.2 – 31 Aug, 2023

Unfortunately, the isosurface feature is no longer free!

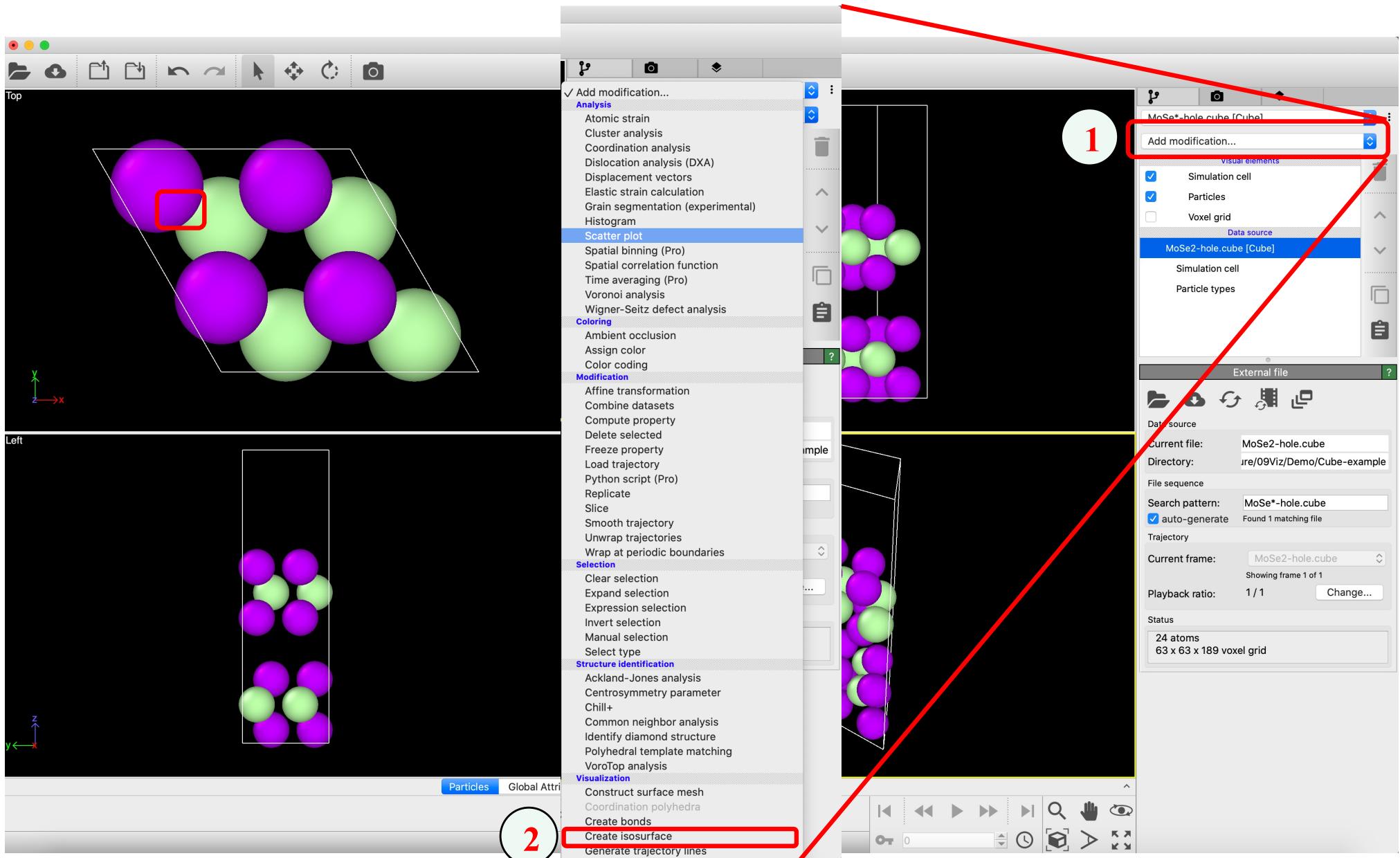
# Isosurface Rendering Using OVITO

- Start OVITO & choose the “file” then “load file” menu
- (1) Load a cube file <https://aiichironakano.github.io/cs596/src/viz/MoSe2-hole.cube>,  
(2) specifying “Gaussian Cube Files” format



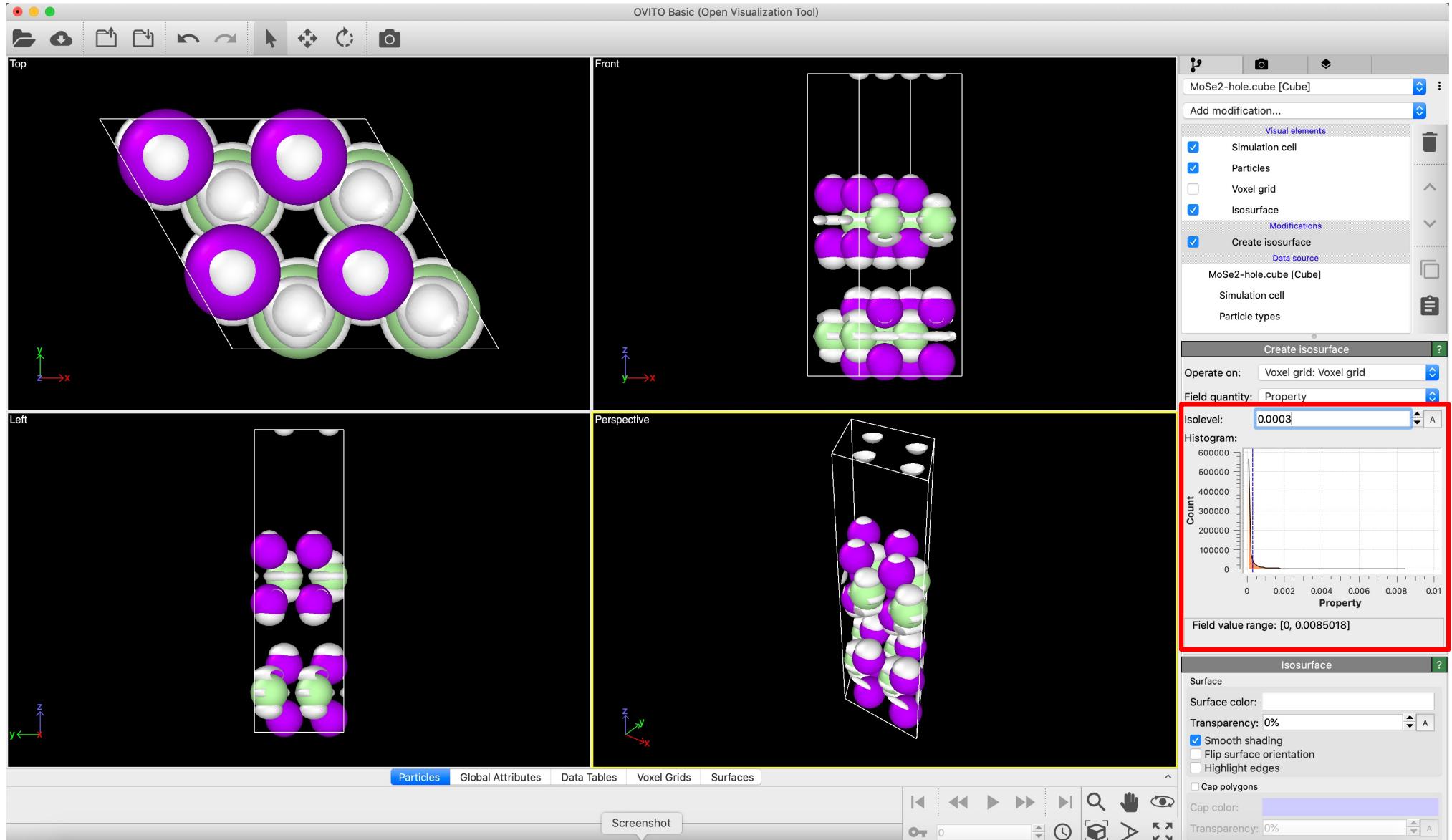
# Isosurface Rendering Using OVITO

- Choose (1) “Add modification” then (2) “Create isosurface” menu

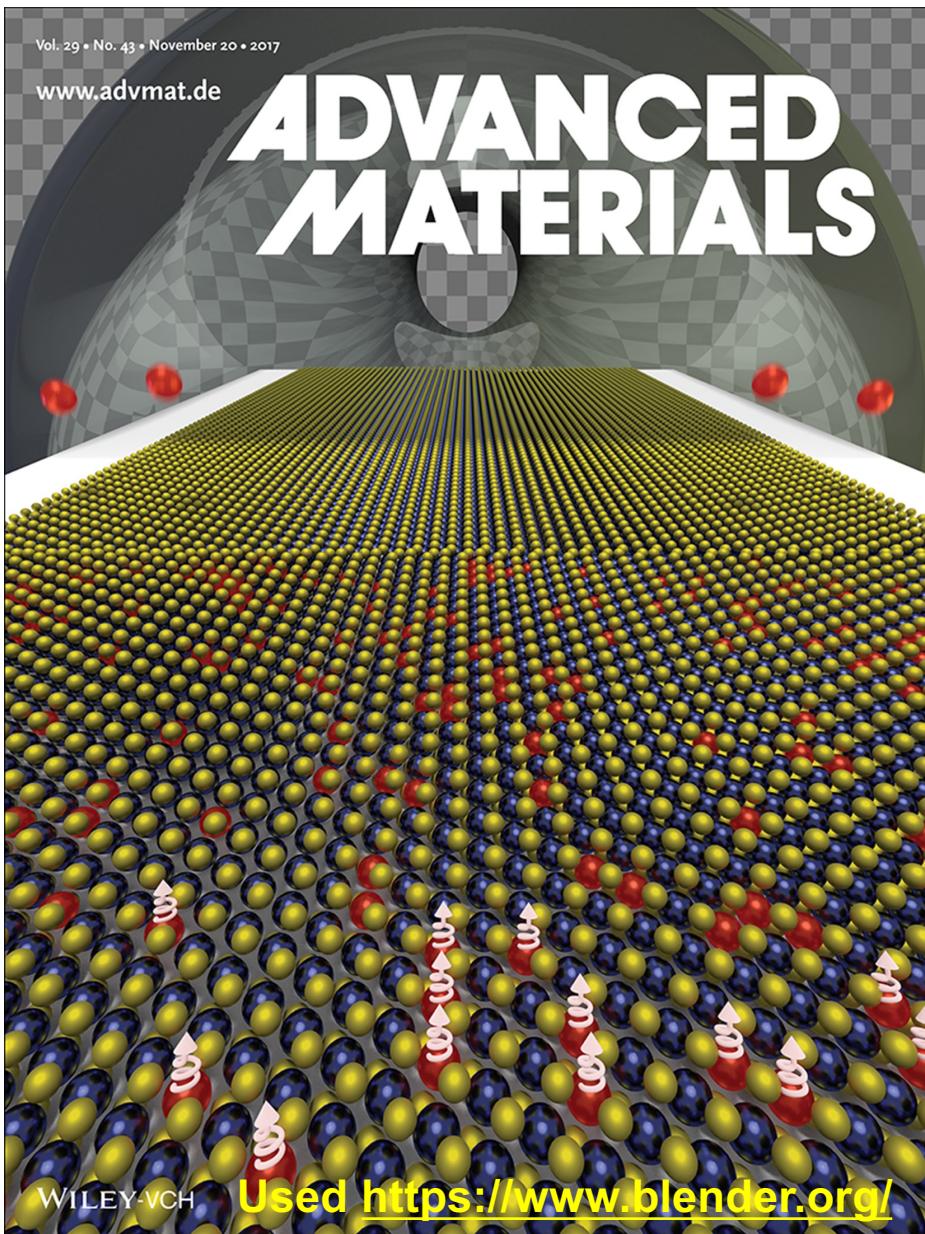


# Isosurface Rendering Using OVITO

- Adjust isolevel to draw a desired isosurface



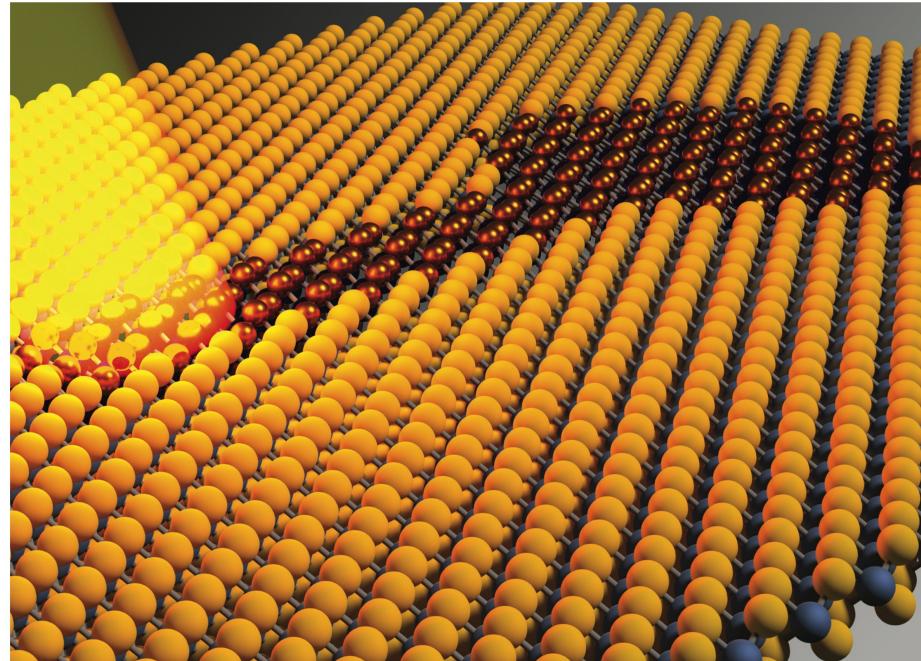
# Make Journal Covers



WILEY-VCH

Used <https://www.blender.org/>

V. Kochat et al., *Adv. Mater.* **29**, 1703754 ('17)

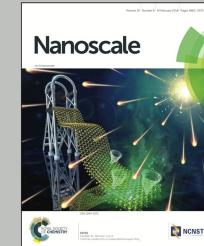


Showcasing research from Collaboratory for Advanced Computing and Simulations (CACS), University of Southern California, Los Angeles, USA.

Semiconductor–metal structural phase transformation in MoTe<sub>2</sub> monolayers by electronic excitation

Optical control of transformations between semiconducting and metallic phases of two-dimensional materials can open the door for phase patterning of heterostructures for 2D electronics and catalysis applications. This work shows how optically-induced changes to the electronic structure and Fermi surface of monolayer semiconductors couple to lattice distortions, resulting in a more facile phase transformation pathway. This work highlights photoexcitation as a viable technique for functionalizing these material systems.

As featured in:



See Aravind Krishnamoorthy et al.,  
*Nanoscale*, 2018, **10**, 2742.

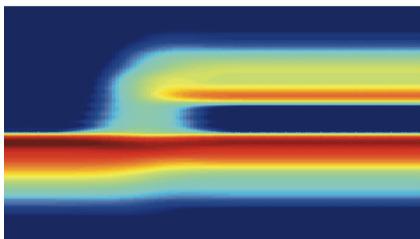
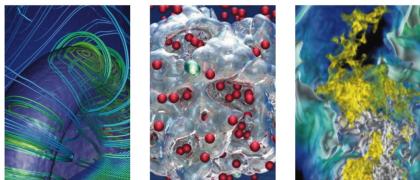
rsc.li/nanoscale

Registered charity number: 207890



A. Krishnamoorthy et al., *Nanoscale* **10**, 2742 ('18)

# BES



NOVEMBER 3-5, 2015

ROCKVILLE, MARYLAND

Or report cover

BASIC ENERGY SCIENCES

## EXASCALE REQUIREMENTS REVIEW

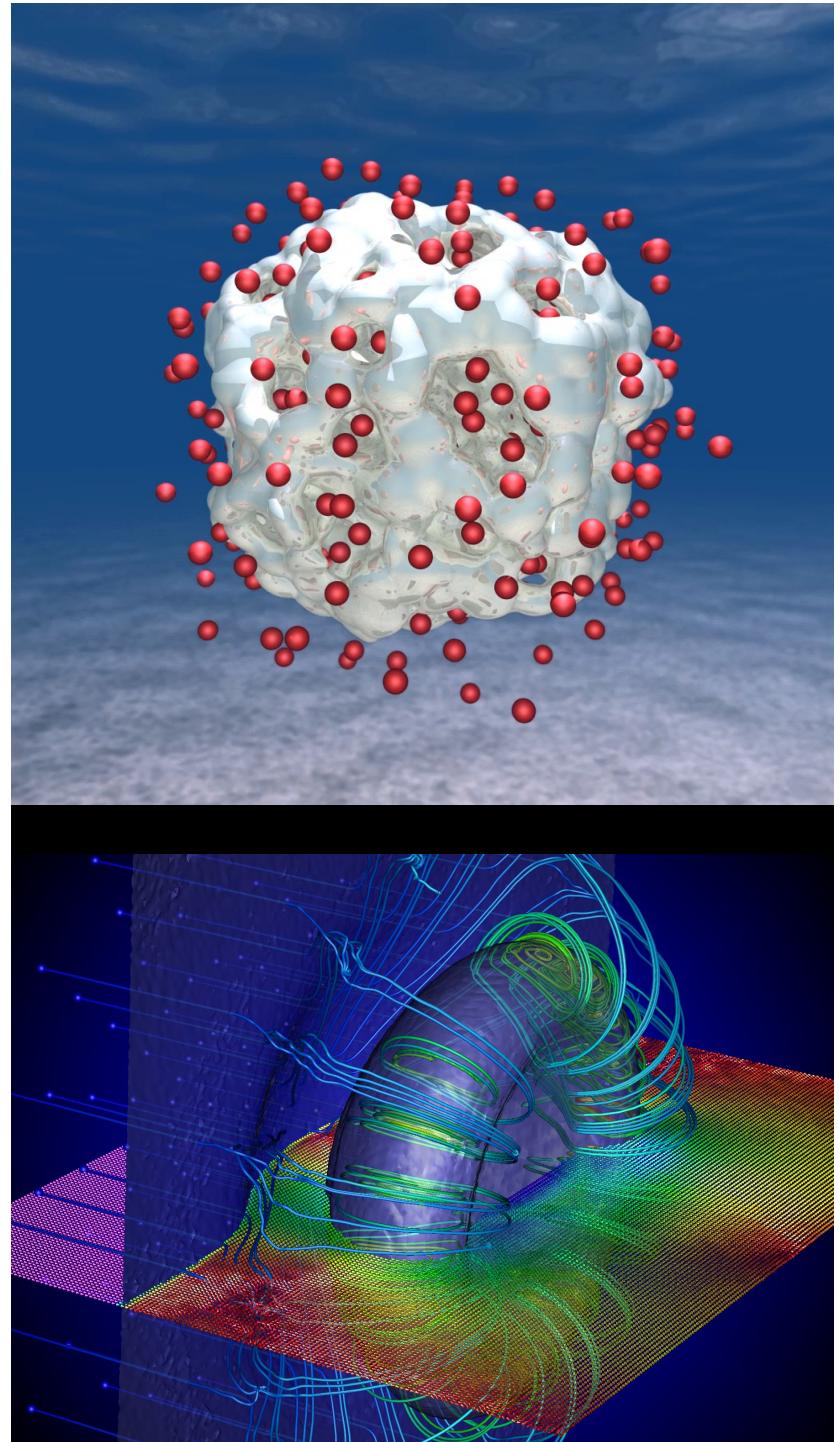
An Office of Science review sponsored jointly by  
Advanced Scientific Computing Research and Basic Energy Sciences

**16,661-atom QMD**

Shimamura *et al.*,  
*Nano Lett.*  
**14**, 4090 ('14)

**$10^9$ -atom RMD**

Shekhar *et al.*,  
*Phys. Rev. Lett.*  
**111**, 184503 ('13)



# Touch of Art



# Where to Go from Here

- Keep refining your visualization skill using the examples in this lecture as a starting point: “Seeing is believing”
- It’s the content that matters: “Summarize your work in 100 milliseconds or less... the importance of the table of contents image,” J. Buriak, *ACS Nano* 5, 7687 ('11); <https://aiichironakano.github.io/cs596/Buriak-ToC-ACSNano11.pdf>
- Appeal to fast thinking by ToC image, convince via slow thinking by abstract; see “Thinking about thinking” by Daniel Kahneman:  
<https://www.edge.org/events/the-edge-master-class-2007-a-short-course-in-thinking-about-thinking>

## Application of First-Principles-Based Artificial Neural Network Potentials to Multiscale-Shock Dynamics Simulations on Solid Materials

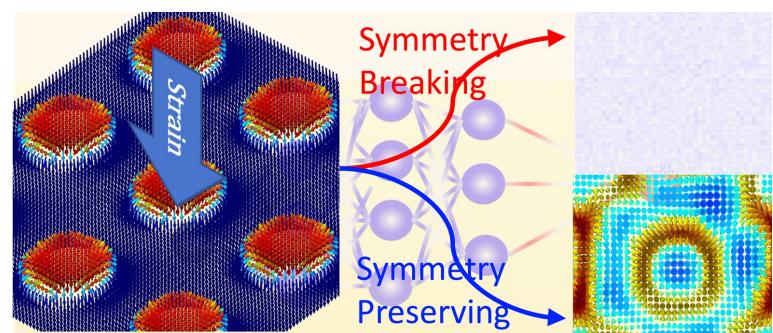
Masaaki Misawa,\* Shogo Fukushima, Akihide Koura, Kohei Shimamura, Fuyuki Shimojo, Subodh Tiwari, Ken-ichi Nomura, Rajiv K. Kalia, Aiichiro Nakano, and Priya Vashishta



Cite This: *J. Phys. Chem. Lett.* 2020, 11, 4536–4541



Read Online



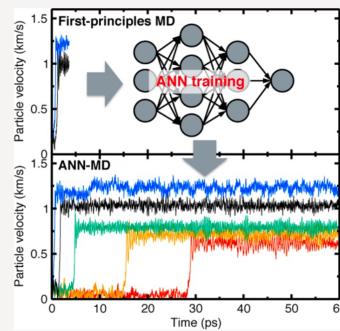
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Supporting Information

**ABSTRACT:** The use of artificial neural network (ANN) potentials trained with first-principles calculations has emerged as a promising approach for molecular dynamics (MD) simulations encompassing large space and time scales while retaining first-principles accuracy. To date, however, the application of ANN-MD has been limited to *near-equilibrium* processes. Here we combine first-principles-trained ANN-MD with multiscale shock theory (MSST) to successfully describe *far-from-equilibrium* shock phenomena. Our ANN-MSST-MD approach describes shock-wave propagation in solids with first-principles accuracy but a 5000 times shorter computing time. Accordingly, ANN-MD-MSST was able to resolve fine, long-time elastic deformation at low shock speed, which was impossible with first-principles MD because of the high computational cost. This work thus lays a foundation of ANN-MD simulation to study a wide range of far-from-equilibrium processes.



**Squishing skyrmions: symmetry-guided dynamic transformation of polar topologies under compression**

T. Linker *et al.*, *J. Phys. Chem. Lett.* 13, 11335 ('22)

# Where to Go from Here

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Assignment package provides enough materials to get started!