

Improving Usability of Molecular Dynamics Simulation Software

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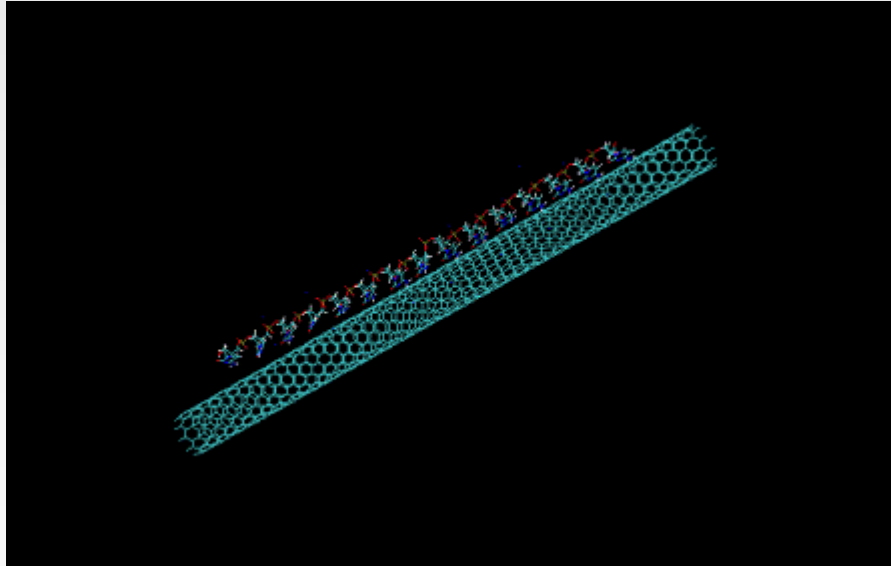
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Molecular Dynamics Simulations

- Molecular Dynamics simulation are the study of the atoms by computer simulations.



Available MD Software

- **GROMACS**

- editconf
- x2top
- make_ndx
- gen_box

- **Tinker**

- nucleic
- xyzpdb

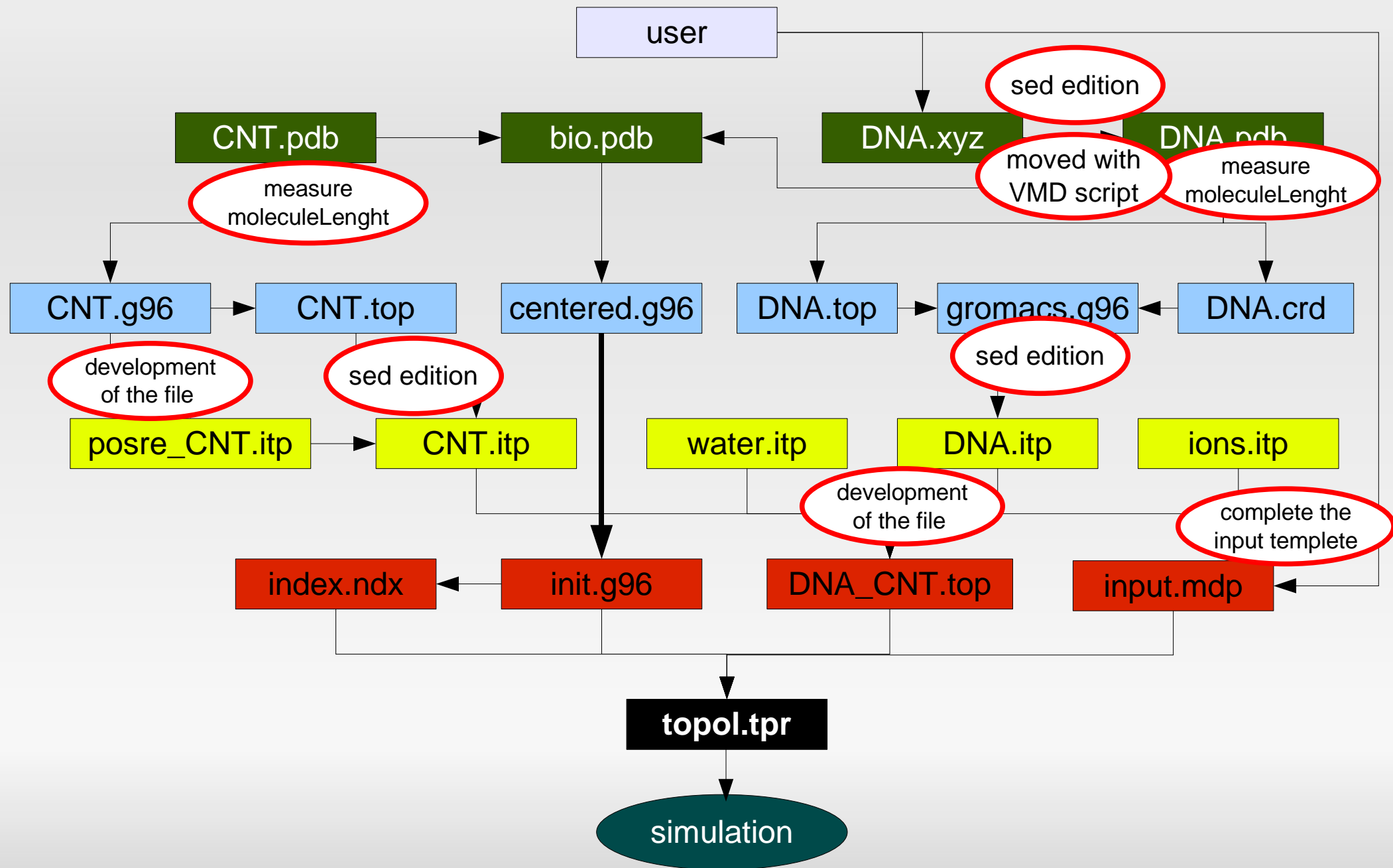
- **NAMD**

- VMD
- psfgen
- solvate
- minmax

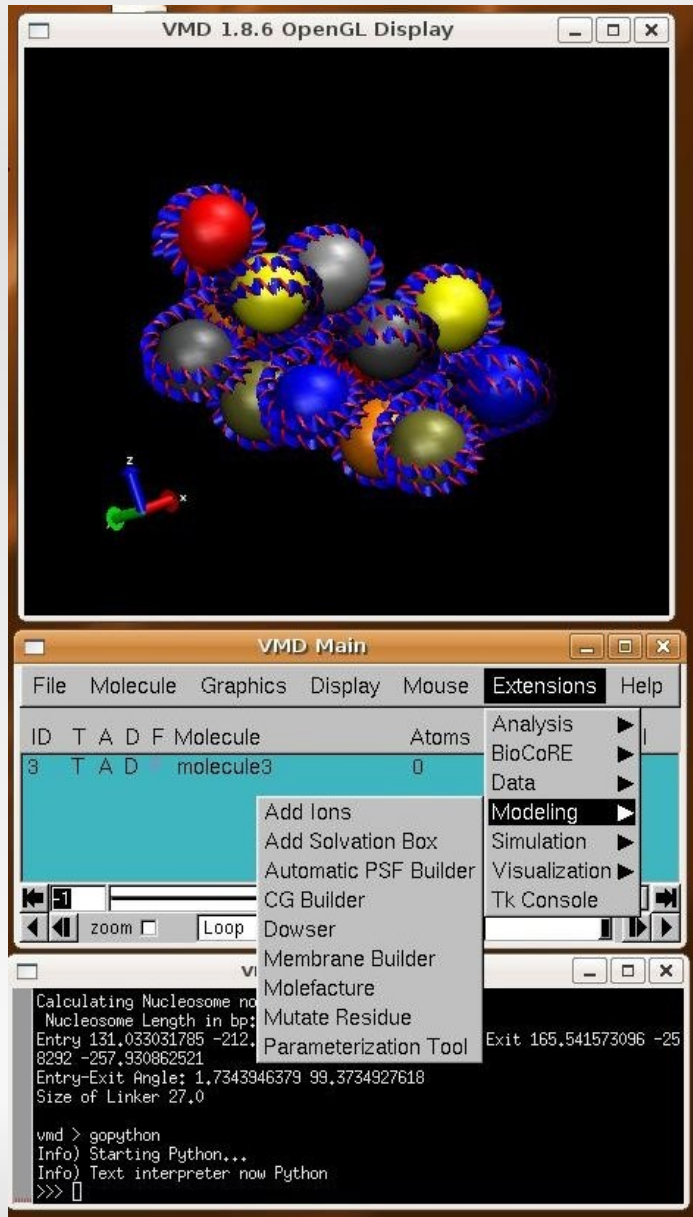
- **Amber**

- xleap
- tleap

Requirements to setup a simulation



Visual Molecular Dynamics (VMD)



- Main purpose is molecule visualization
- Additional functionality added as extensions
- Built-in Python language interpreter with:
 - Tkinter
 - library for interacting with VMD features

VMD Extensions Usability Problems

The image shows a screenshot of the NAMDgui window, which is a graphical user interface for running NAMD simulations. The window has a title bar with the text "NAMDgui" and standard window controls (minimize, maximize, close). Below the title bar is a menu bar with "File", "Edit", and "Help". The main content area is divided into several sections, each with a tab-like header. The "General" section contains a "Working dir" field with the path "/mnt/home_jaguey/mymese" and a "Browse" button, and a "Simulation basename" field. The "Input files" section contains three fields: "PSF file:", "PDB file:", and "XSC file:" (with "XSC" entered), each with a "Browse" button. The "Parameter files" section contains a list box with the path "/usr/local/lib/vmd/plugins/noarch/tcl/readcharmm.par1.0/par_all2" and "Add" and "Delete" buttons. The "Timesteps" section contains three checkboxes: "Minimization" (checked), "Molecular dynamics", and "Continue simulation (get first timestep from XSC file)". To the right of these are input fields for "Number of steps:" (1000 for minimization, 10000 for molecular dynamics) and "First time step:" (0). The "Ensemble" section contains three radio buttons: "NVE" (selected), "NVT", and "NPT". To the right are input fields for "Temperature (Kelvin):" (310) and "Pressure (bar):" (1.01325). There are also checkboxes for "Periodic boundary conditions (read unit cell from XSC file)" and "Particle Mesh Ewald (needs periodic boundary conditions)", with an "Edit" button. The "Mobile/fixed atoms" section contains a "Selection of mobile atoms:" field with "(0/0 atoms)" and a text box containing "all", with a "Show selection" button. At the bottom of the window are two buttons: "Write NAMD config file" and "Run NAMD".

NAMDgui

File Edit Help

General

Working dir: /mnt/home_jaguey/mymese Browse

Simulation basename:

Input files:

PSF file: Browse

PDB file: Browse

XSC file: XSC Browse

Parameter files:

/usr/local/lib/vmd/plugins/noarch/tcl/readcharmm.par1.0/par_all2 Add Delete

Timesteps

☒ Minimization Number of steps: 1000

☐ Molecular dynamics Number of steps: 10000

☐ Continue simulation (get first timestep from XSC file) First time step: 0

Ensemble

☒ NVE Temperature (Kelvin): 310

☐ NVT Pressure (bar): 1.01325

☐ NPT

☐ Periodic boundary conditions (read unit cell from XSC file) Edit

☐ Particle Mesh Ewald (needs periodic boundary conditions)

Mobile/fixed atoms

Selection of mobile atoms: (0/0 atoms)

all Show selection

Write NAMD config file Run NAMD

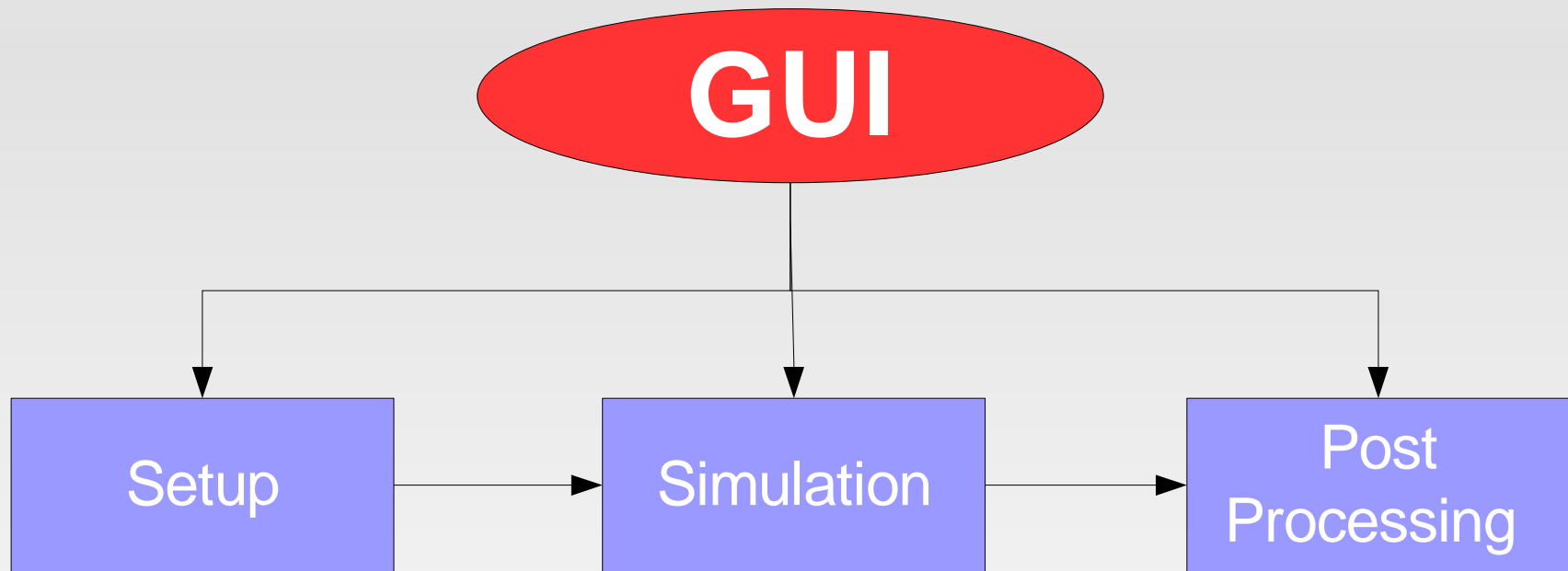
Problem

To develop a Molecular Dynamics Simulation software for Fiber-Polymer Hybrid systems that avoids the actual problems of usability.

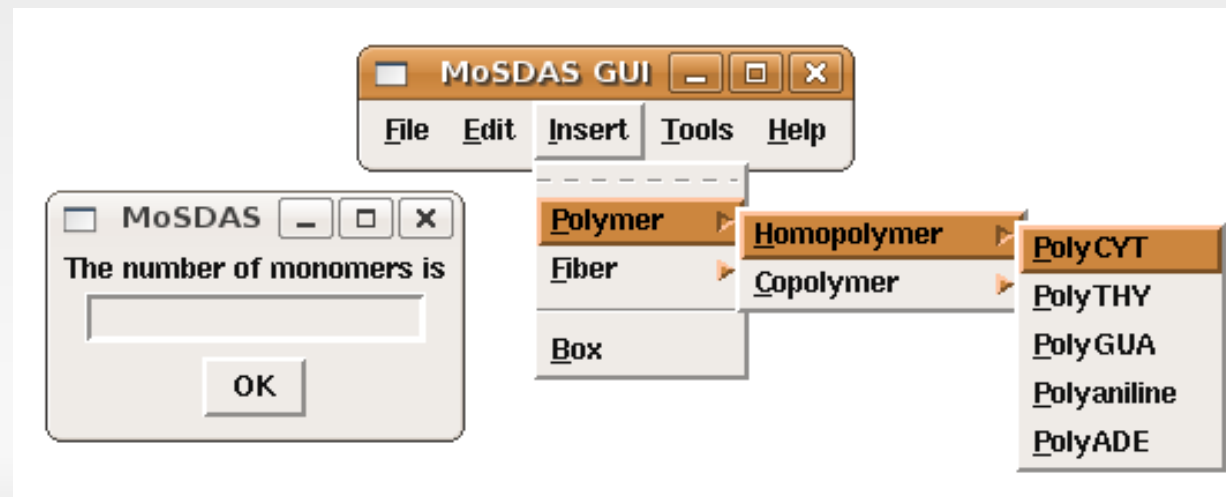
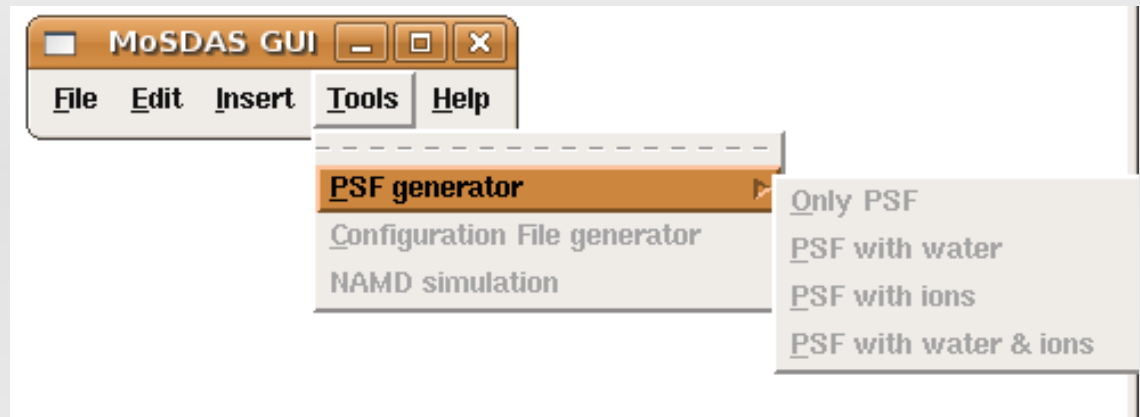
MoSDAS and VMD

- VMD Python Library
- MoSDAS Library
 - by Computational Science Group of UPR-H

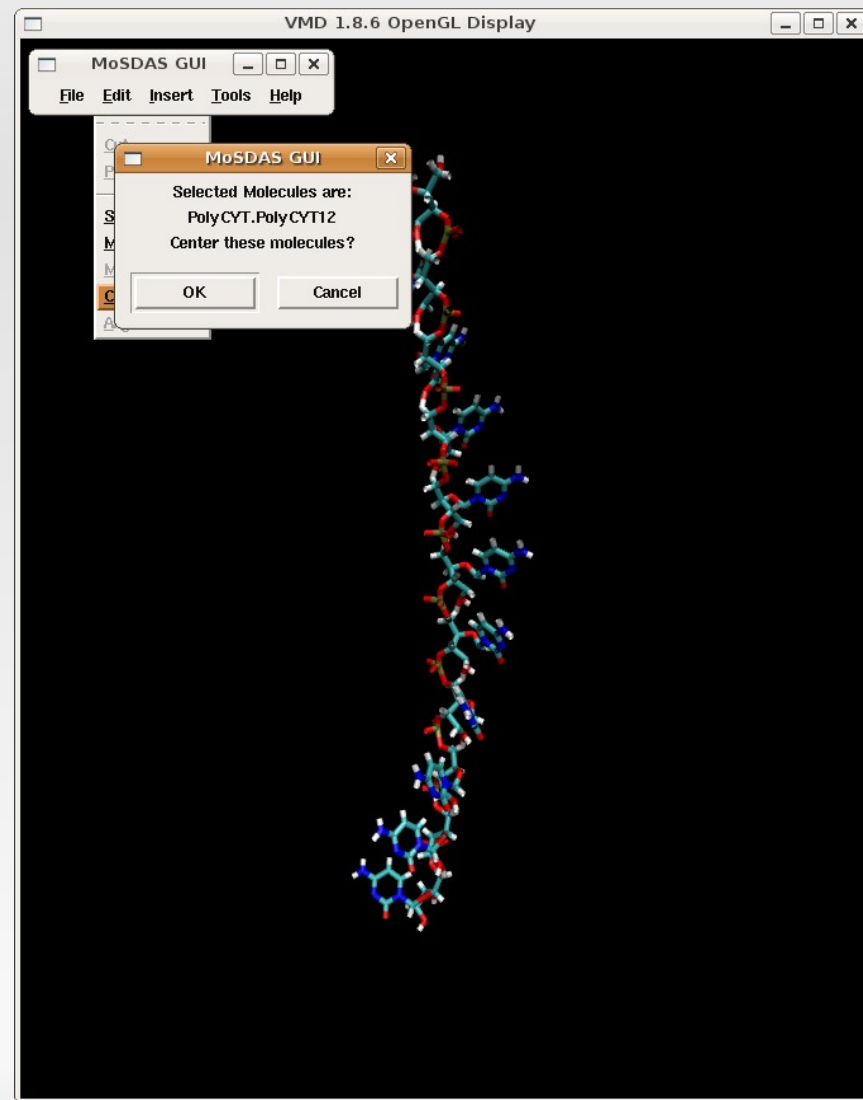
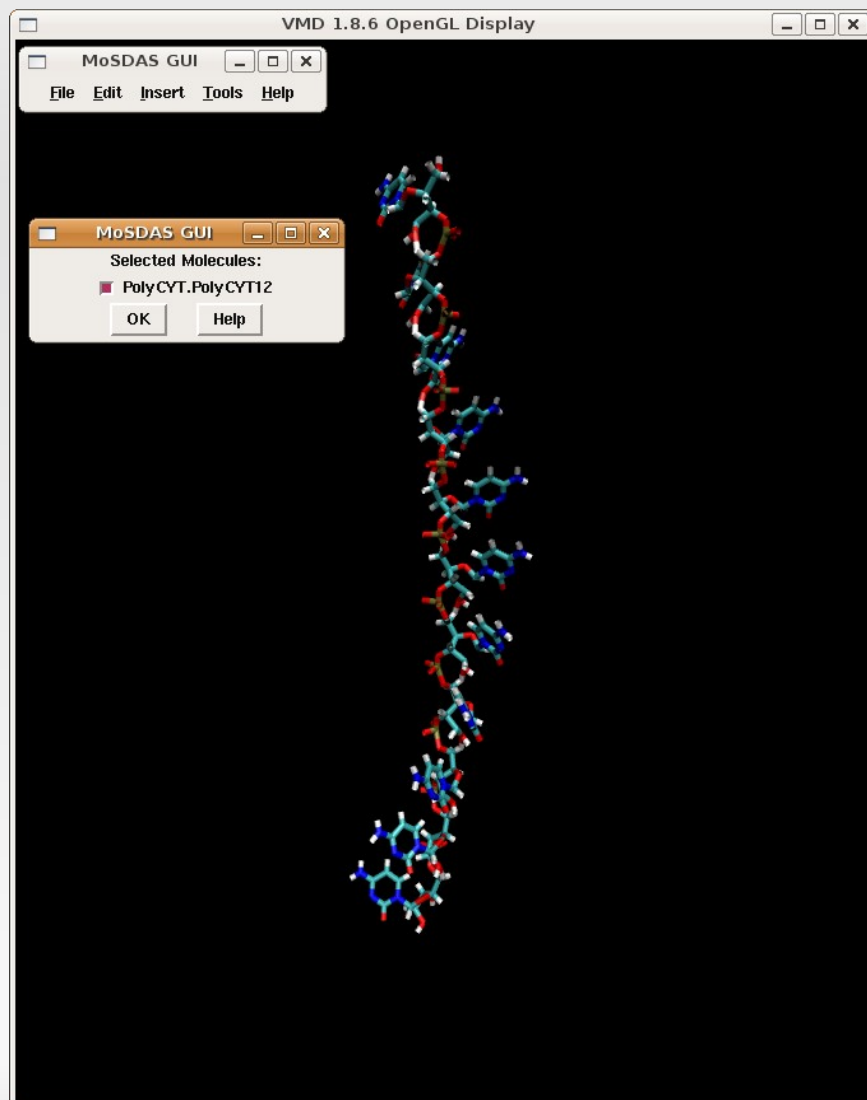
MoSDAS GUI



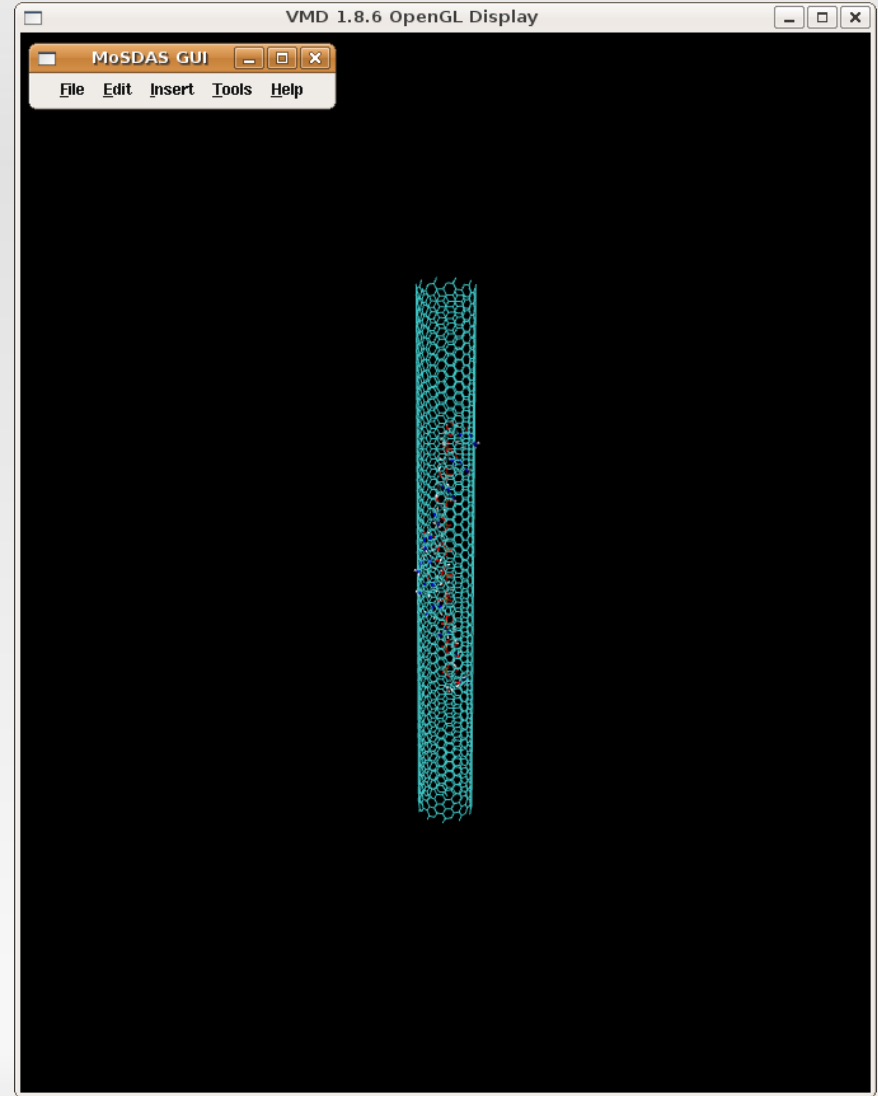
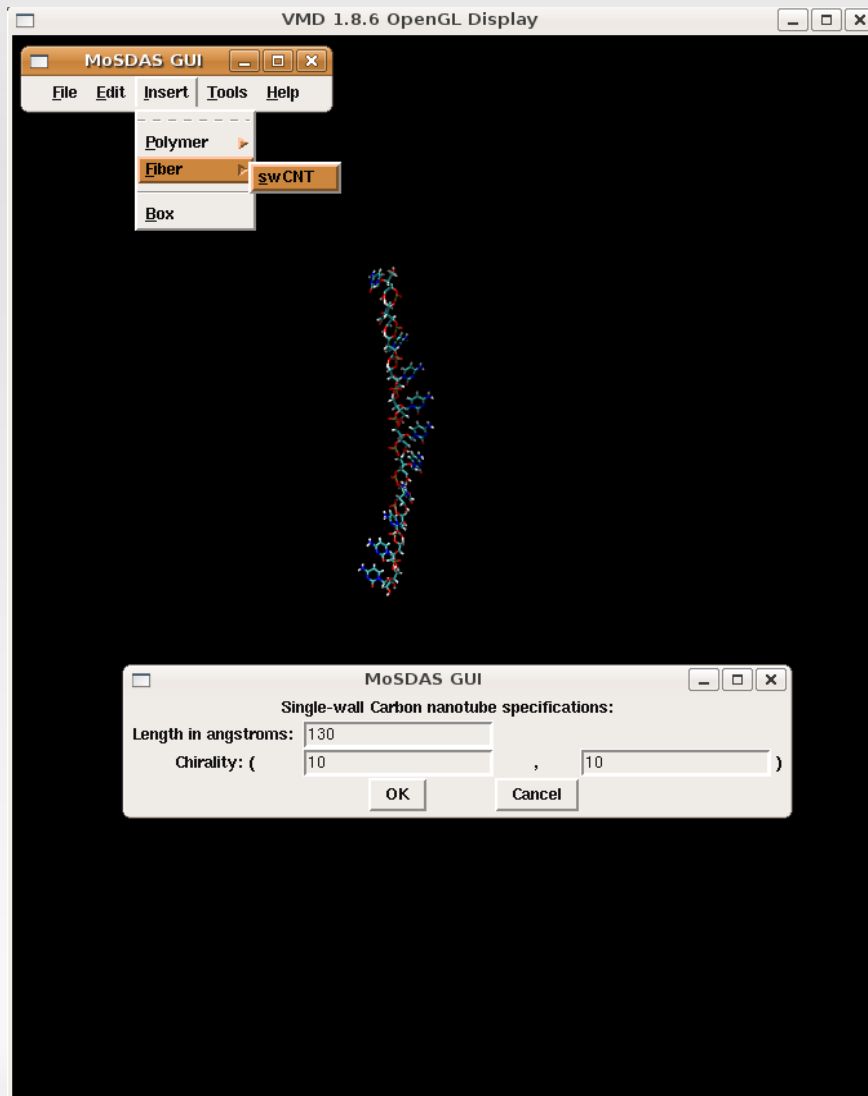
MoSDAS GUI



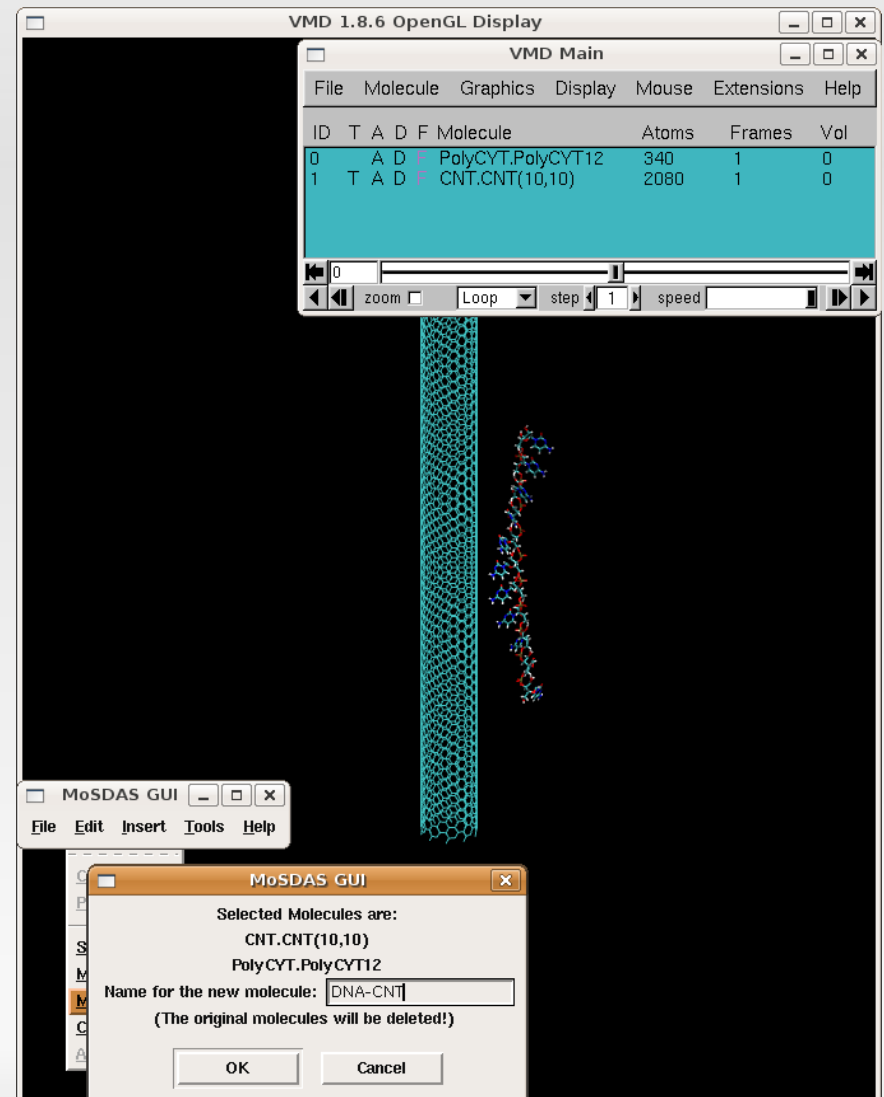
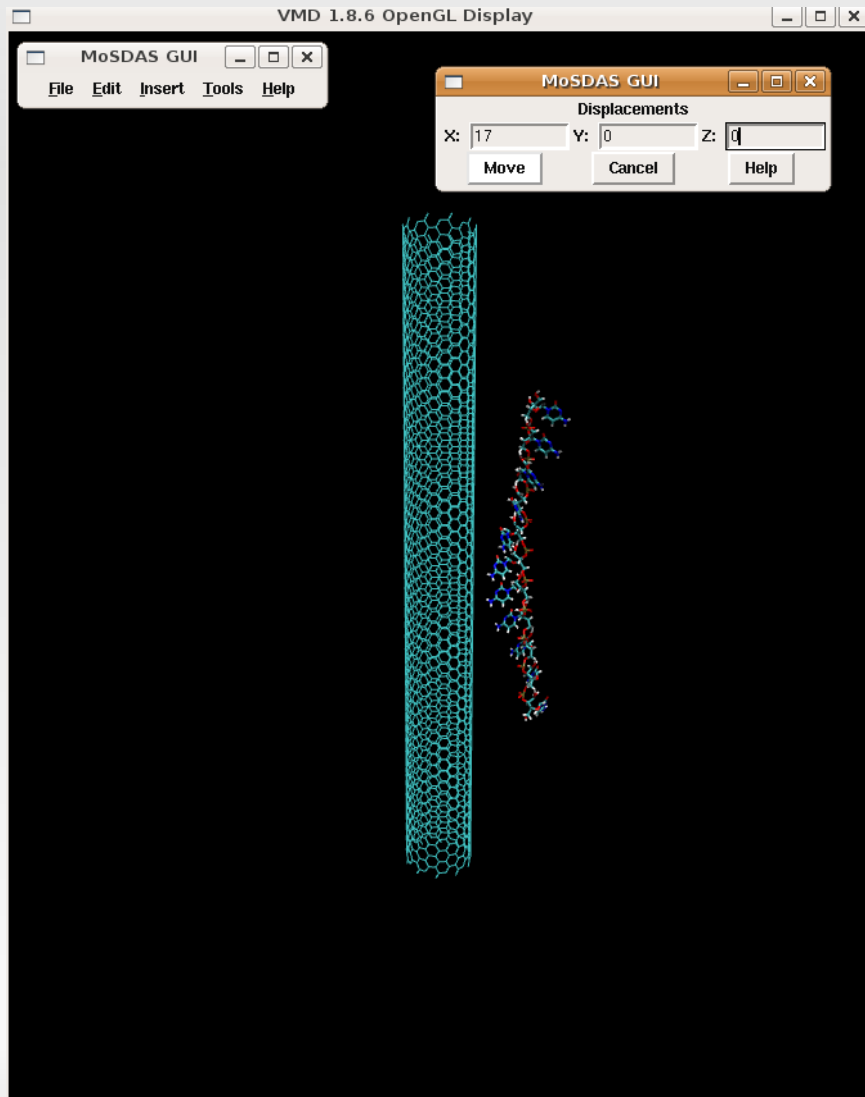
MoSDAS GUI



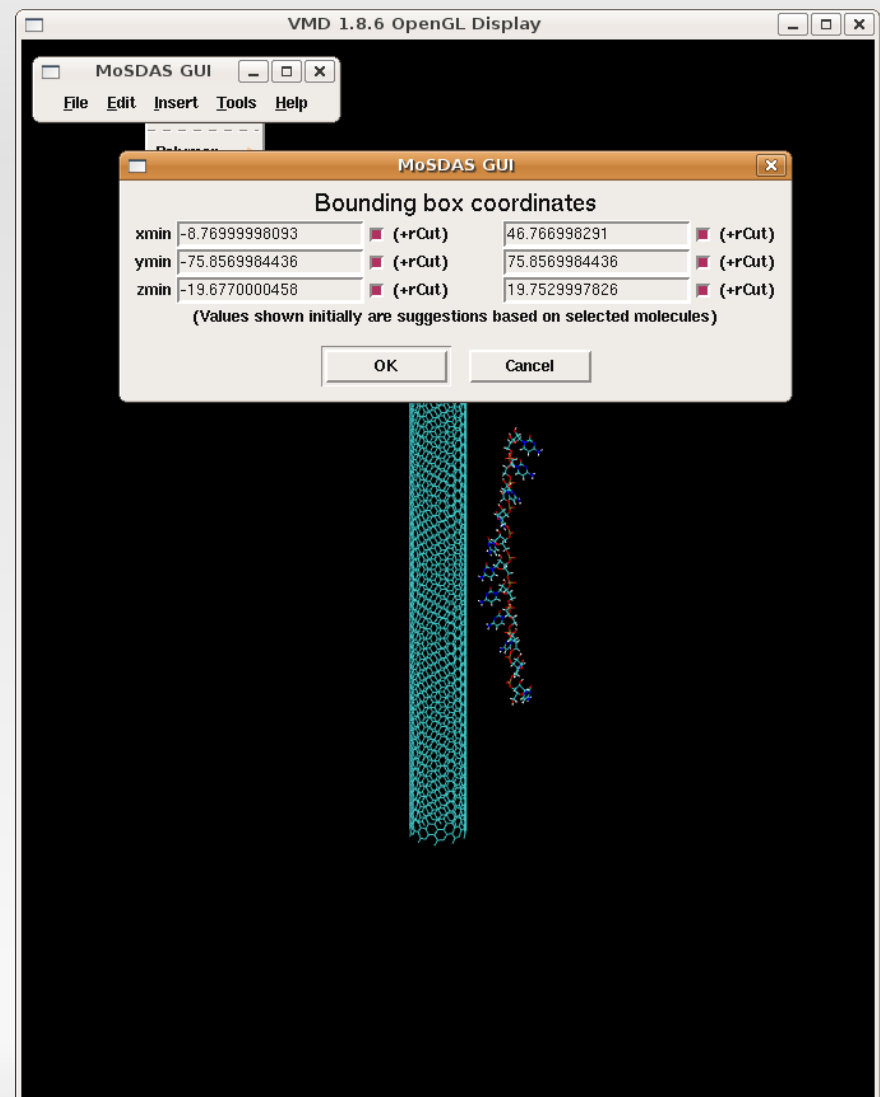
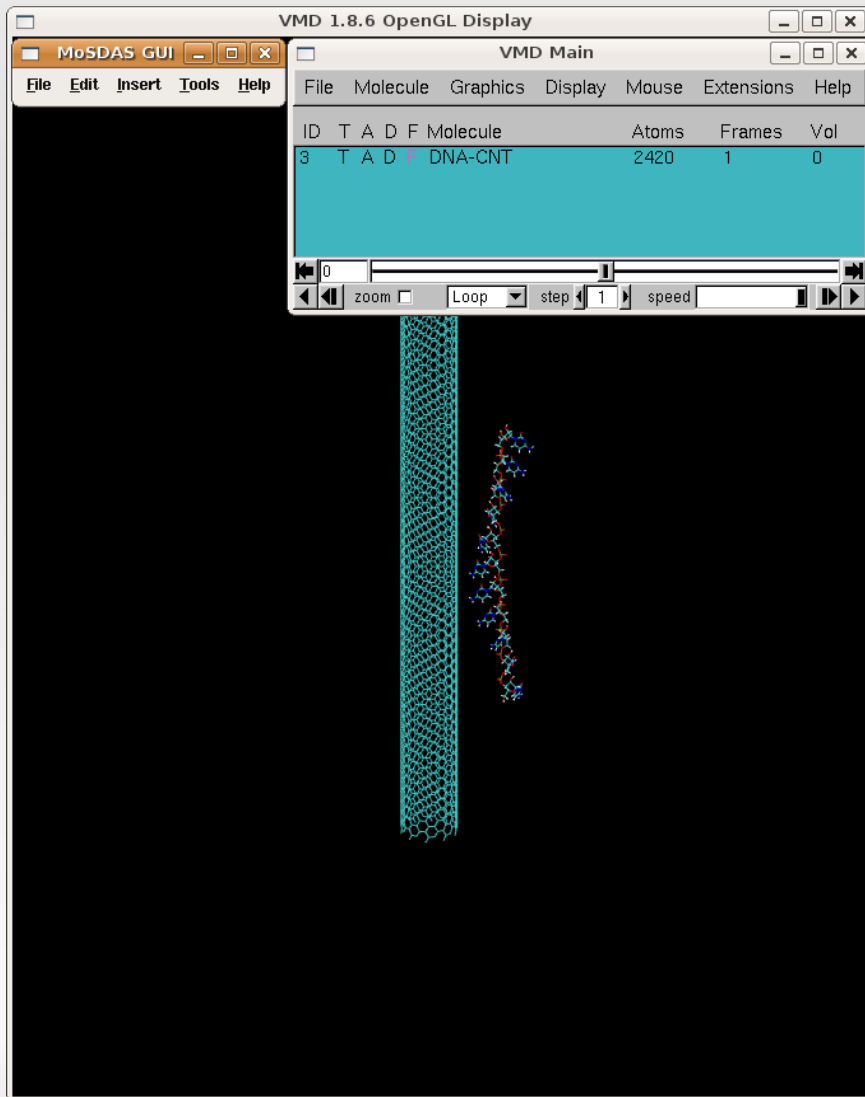
MoSDAS GUI



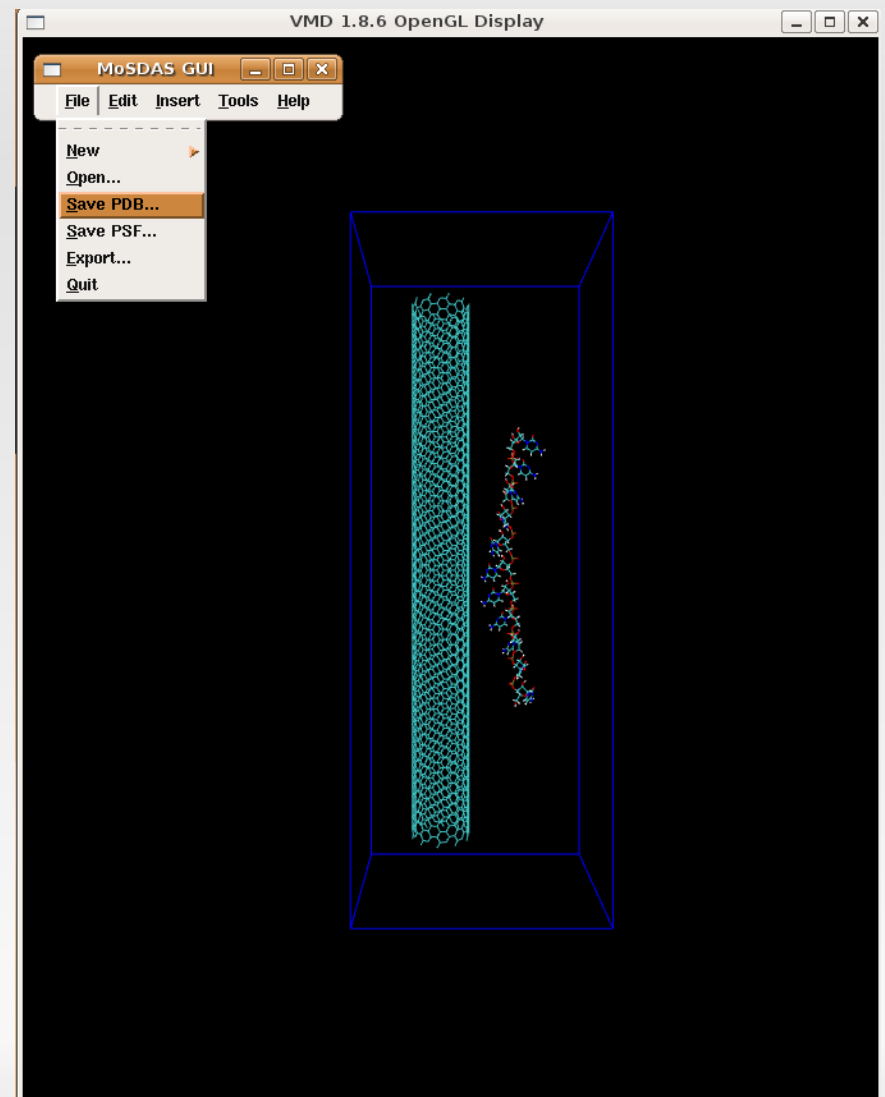
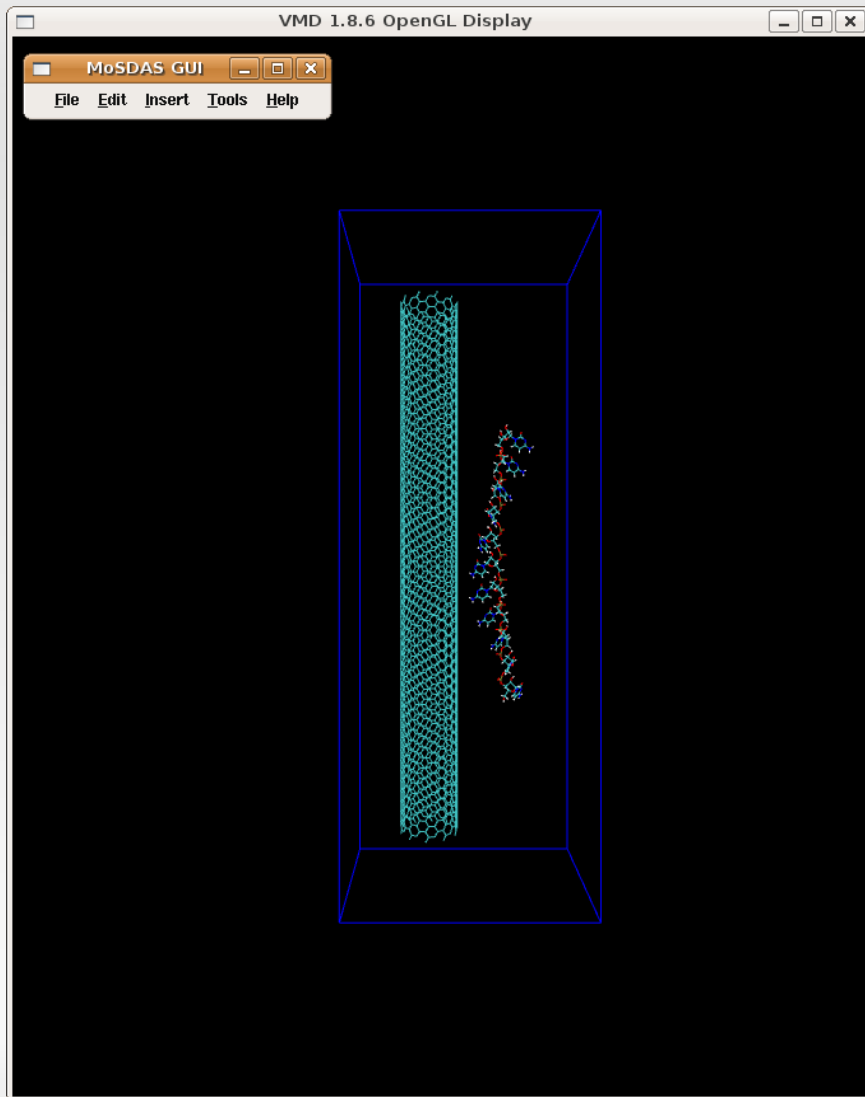
MoSDAS GUI



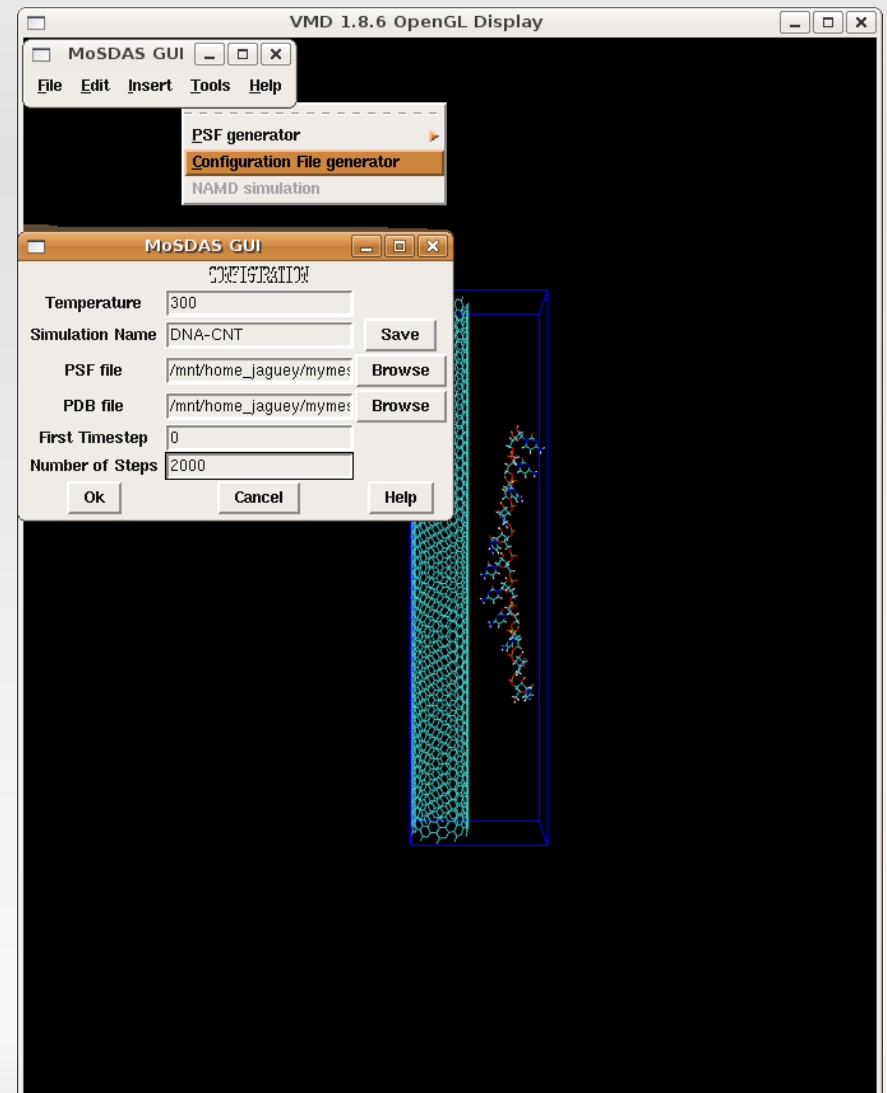
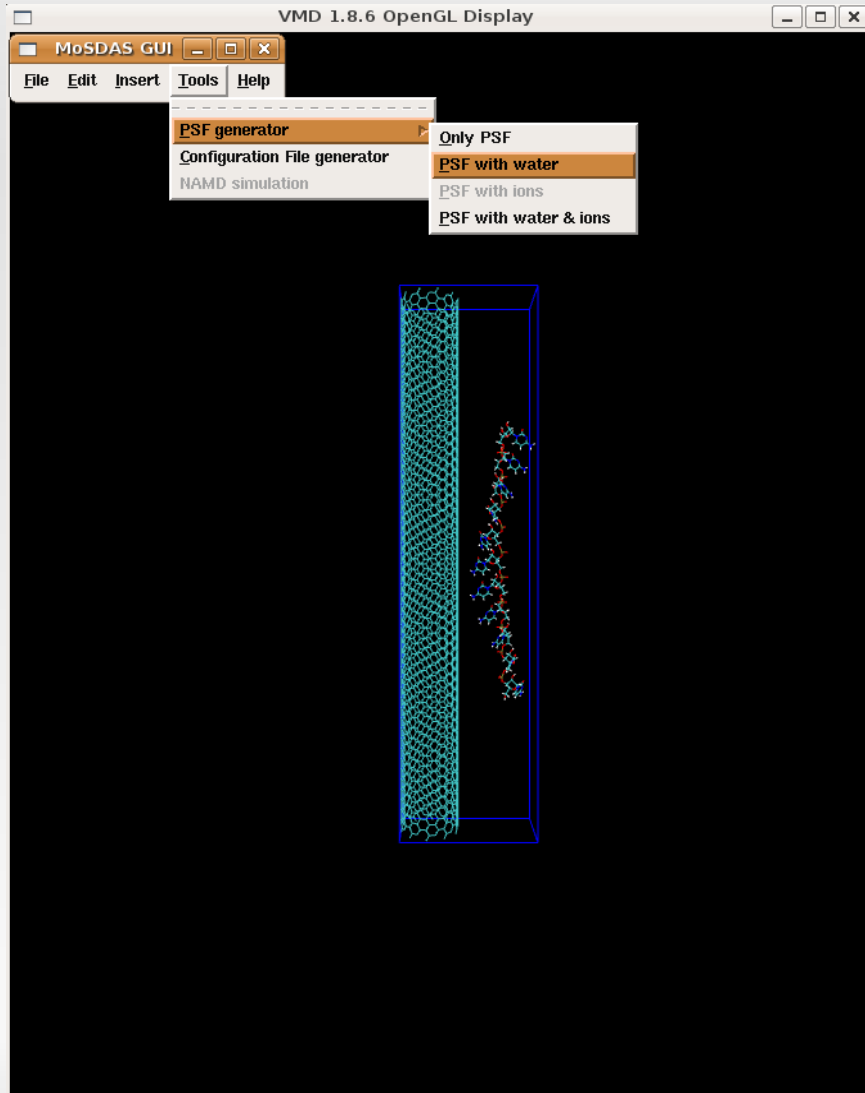
MoSDAS GUI



MoSDAS GUI



MoSDAS GUI



MoSDAS GUI Video



Conclusions

- MoSDAS GUI greatly simplifies the setup of the simulation and avoids the risk of errors in the setup process.
- The time to setup and make all the necessary files to run a MD simulation was reduced from hours to minutes.
- MoSDAS GUI are going to be a good tool to perform MD simulations of CNT-Polymer hybrids.

Acknowledgments

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References

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