NanoEngineer-1: An open source multi-scale molecular modeling and simulation front-end for Rosetta (*Potentially*)

Mark Sims
President
Nanorex, Inc.
About Nanorex

- Founded in 2004
- 11 employees in 4 states
- Based in Bloomfield Hills, Michigan
Mission

• To develop open-source computational tools to support the design and development of advanced nanosystems
NanoEngineer-1

- Open source (GPLv2)
- Mac, Windows and Linux
- Written in Python and C
- Qt/PyQt GUI framework
- GROMACS v3.3.3 integrated
- Emphasis on ease of use and 3D interactive modeling
NE1: CAD for Structural DNA Nanotechnology

Renderings by QuteMolX
Nanorex
Double Crossover (DX) Molecule

NanoEngineer-1 Reduced model

Atomistic model
Triple Crossover (TX) Molecule

NanoEngineer-1 Reduced model

Atomistic model

14 nm
Example: 4-Point Star Tile and Lattice

H. Yan, T.H. LaBean, et al.
*DNA-Templated Self-Assembly of Protein Arrays and Highly Conductive Nanowires*
Example: DNA Polyhedra

3-Point Star with “Sticky” Ends
7 unique strands
246 bases

Chengde Moa, et al.
“Hierarchical self-assembly of DNA into symmetric supramolecular polyhedra”
Nature, 452:198-201 (March 2008)
Example: Scaffolded DNA Origami

Paul Rothemund
Folding DNA to create nanoscale shapes and patterns
DNA Origami Folding Process

- Scaffold strand (red)
- Staple stands (blue)
- Self-assembles into target structure
“Smiley face” origami (NE1 reduced model)

Smiley Face
294 staple strands
14,300 bases
First NE1 experiment design: Four hole tile
AFM Image of “Four hole tile” DNA origami

- All strand sequences assigned by NE1 and written to excel file
- All oligonucleotides were purchased from IDT, Inc.
- Synthesis and imaging performed by Paul Rothemund at Caltech
- First attempt worked (April, 2008)
Rosetta Plug-in for NanoEngineer-1

- This is currently a prototype
  - Not available in current release of NanoEngineer-1 (version 1.1.1)
- Demos:
  - Fixed backbone design
  - Rotamer optimization
Step 1: Install Rosetta (Windows version)

- Create C:\Rosetta
- Copy rosetta.exe to C:\Rosetta
- Copy the Rosetta database into C:\Rosetta\rosetta_database
Step 2: Edit C:\Rosetta\paths.txt

Rosetta Input/Output Paths (order essential)
path is first '/', './', or '../' to next whitespace, must end with '/'

INPUT PATHS:
pdb1
pdb2
alternate data files
fragments
structure dssp, ssa (dat, jones)
sequence fasta, dat, jones
constraints
starting structure
data files

OUTPUT PATHS:
movie
pdb path
score
status
user

FRAGMENTS: (use '*****' in place of pdb name and chain)
2
3
aa*****03_05.200_v1_3
9
aa*****09_05.200_v1_3

number of valid fragment files
frag file 1 size
name
frag file 2 size
name
Step 3: Enable Rosetta as a NE1 plug-in

1. Start NanoEngineer-1
2. Select **Edit > Preferences**
3. In the Preferences dialog, select **Plug-ins**
4. Check **Rosetta**
5. Check **Rosetta DB**
6. Click **OK**
File > Fetch > PDB from RCSB
PDB file loaded
Build > Protein
(new command set in development)

Global display style was changed to “Protein” display style.
Edit Protein Display Style
Edit Rotamers
Edit Residues
Simulation > Rosetta
Rosetta Results
(designed sequence inserted into model automatically)
Rosetta Results
(designed sequence inserted into model automatically)
Compare Proteins

Select protein structures to compare.

First structure: 2q1A
Second structure: native_out_0001A
Threshold: 1000 dps

Compare
Hide differences
Free Download

URL: www.nanorex.com
Username: rosettacon2008
Password: rosettacon2008

Tutorials: www.nanoengineer-1.net