Project	Faculty	Layman's description
Life and Death: advice for NIH.	Onufriev	Use simple statistical models to understand the relative influence of disease on human life expectancy
Rational drug design – really?	Onufriev	Use web-based tools to estimate likelihood of structural changes upon protein-ligand docking
DNA – the cellular Contortionist	Onufriev	Use database of protein DNA complexes to understand how easy bendable the double helix is and why.
Computational gene silencing	Onufriev	Use computational tools to improve predictions of RNAi effectiveness.
Functional wormholes in proteins	Onufriev	Use available software to identify functional voids in proteins, particularly in the oxygen carrier/storage protein Myoglobin..
Pulling on molecules	Bevan	Use and adapt existing hardware and software to implement interactive molecular dynamics
Comparing protein structures	Bevan	Develop web-based interface to provide tools for comparison of protein structures, particularly active sites
Role of water molecules in docking	Bevan	Survey protein database for water molecules in and around binding sites and compare with prediction methods for water positions

Is drug design done right?

Heavy CS background not required.

- Hypothesis to explore:
  Ionization states (pK) of key ionizable groups at the protein – ligand (drug) interface change drastically upon ligand binding.   This effect must be taken into account for proper drug desin.

  Approach: web-based (mostly).

Computational Gene Silencing

(best for a CS + life science team)

- Hypothesis to test: is computed mRNA secondary structure correlated with the experimental rate of gene silencing?
- Large experimental data base available
- Approach: begin by using web-based tools on small data sets. Then move to larger data sets + downloadable tools.

How flexible is the DNA

(best for CS + life science team)

- Hypothesis to test: DNA flexibility can be described by the old, accepted model.
- Retrieve and analyze a data base of protein-DNA complexes to see how bent the DNA really is. Fit to the standard model. If does not fit, propose corrections.
- Tools: available tools for DNA structure analysis.

Life and Death

(no prerequisites)

- Has nothing to do with structural biology.
- Develop a minimal model of life expectancy based on available vital statistics.
- Tools: simple probabilistic models (Monte-Carlo). Minimal programming skills.
- Question: is NIH spending its money right?

Wormholes in proteins

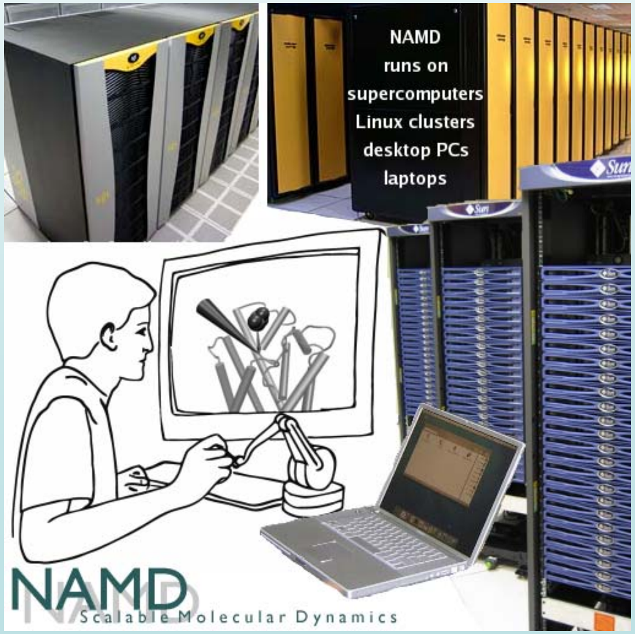
(best for a CS + life science team)

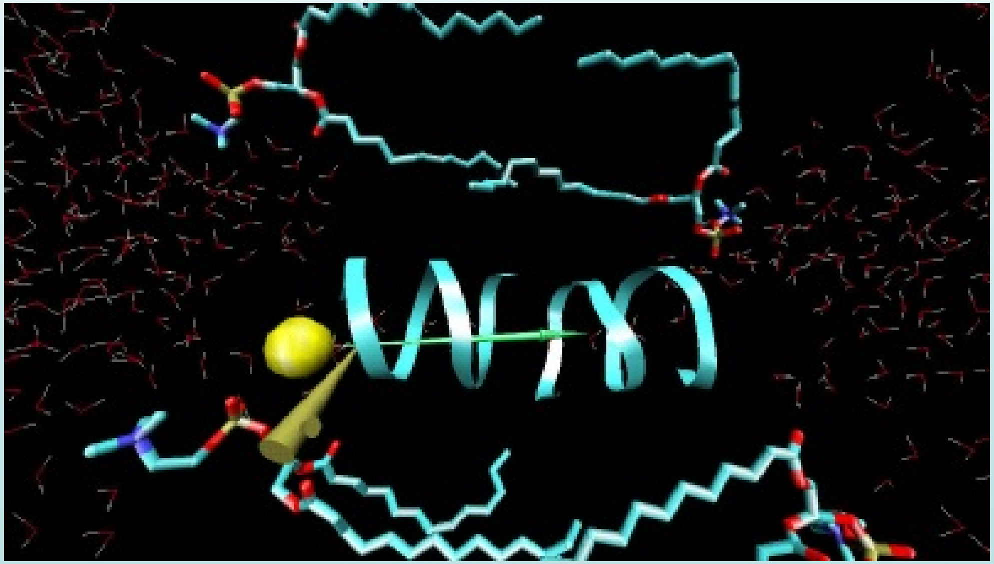
- Are «channels» a ubiquitous phenomenon in proteins?
- Use available computational tools to explore the insides of enzymes and complexes. Start with the analysis of available myoglobin structures.
- Move on to others. Visualization may be important.

Pulling on Molecules

(best for a CS major who also has some life science background or a team in which the life scientist is also reasonably computer savvy so he/she can participate in all stages of the project)

- How do ligands enter/exit binding sites?
- Interactive molecular dynamics
- http://www.ks.uiuc.edu/Research/vmd/imd





Pulling on molecules, cont'd (Interactive MD)

- Integrate haptics with MD
- NAMD running on System X
- Implement IMD at VT
- Tutorials/examples available for IMD
- Hopefully extend to additional example(s)

Analyzing Protein Structures

(best for a CS + life science team)

- What is the information content of 3-D structures of proteins?
- Survey and apply existing methods of structure comparison and analysis
- Devise ways to compare protein structures, especially active site regions
- Use existing tools (many in Perl) to extract information from structure files

Water and Docking

Heavy CS not required, except for last step which may be optional.

- Does the presence of water in a binding site influence molecular docking results?
- How should water molecules be placed in a protein binding site?
- Survey current work in this area
- Apply molecular docking
- Develop methods of placing water molecules in protein structures