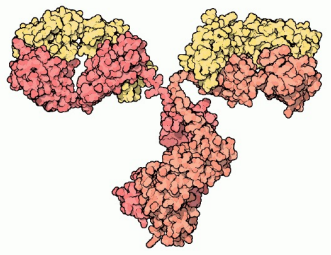
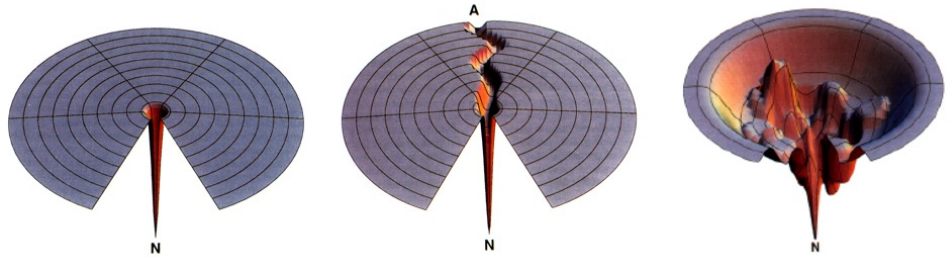


BIOC 670: Structural Bioinformatics

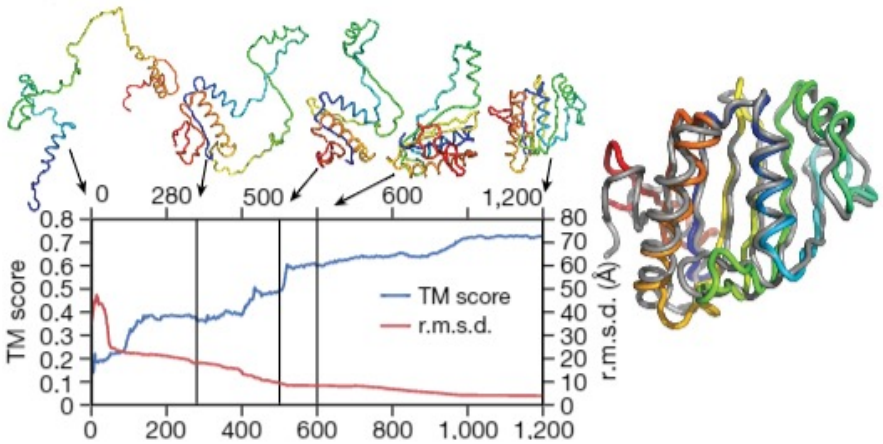
PyRosetta
Interactive Molecular Modeling for Proteins

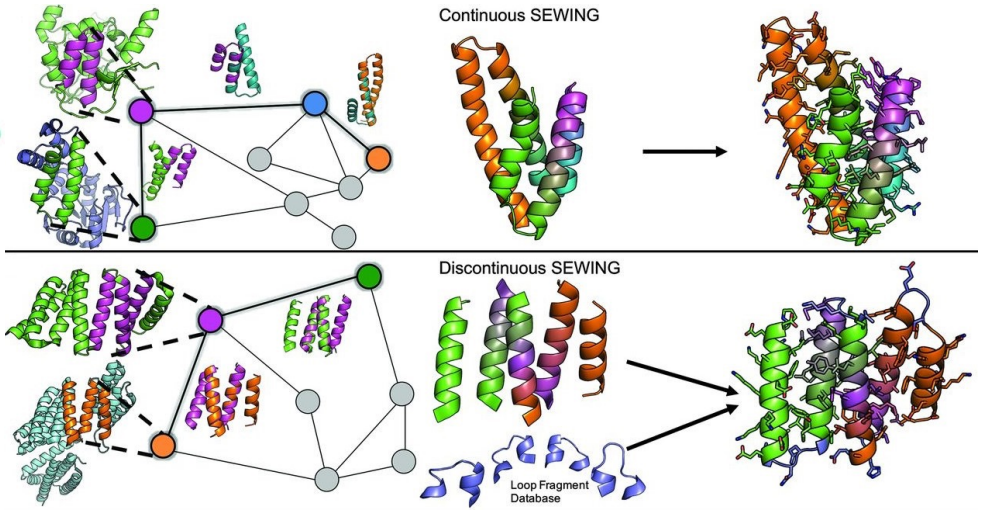
Discover common techniques for protein structure prediction and protein design, and learn to perform these tasks using the program PyRosetta



Topics:

- Protein Structure
- Stability and Folding
- Homology Modeling
- De Novo Structure Prediction
- ML in Structure Prediction
- Protein Design





Instructor: Andrew Leaver-Fay (leaverfa@email.unc.edu)

Assignments will require scripting in Python, so a basic understanding of the language will be beneficial

To register, contact Holly Shepherd (holly_shepherd@med.unc.edu)