Computational Biology
Department of Computer Science at UMass Amherst
Robotics & Biology Laboratory (RBO) - http://robotics.cs.umass.edu
Computational Biology Laboratory (CBL) - http://cbl.cs.umass.edu

Graduate Studies at UMass

Computer Science
In the RBO and CBL Labs, we are concerned with the problems behind many of the major questions in molecular biology and genetics. As part of our research, we use machine learning, modeling, optimization techniques and principles from Robotics.

The UMass Experience
The University of Massachusetts Amherst is a coeducational, nationally ranked research institution located in a beautiful, New England town surrounded by hills, forests, lakes, and meadows, just a few hours from Boston and New York.

Lab Resources

Haptic Device
We utilize a 6-degree of freedom haptic device to physically interact with our protein models.

Computer Cluster
Our main computation platform is a 176-core computer cluster with dual core 2.4 GHz Xeon processors, each with 8GB of memory.

Protein Folding

Protein Structure Prediction
We use insights from robot motion planning to build algorithms that predict the natural folded conformation of a protein. Our technique exploits information acquired during exploration of the conformational space to direct computational resources toward biologically relevant regions. This dramatically improves the efficiency of search for the protein's native structure.

Microarray Resequencing

Variation Detection
High density oligonucleotide microarrays are used for genome-wide SNP mapping and discovery. We are exploring new approaches for the analysis of variation detection arrays using thermodynamic physical models and by modifying the microarray probe design. Our approaches have led to higher accuracy and call rate. We are applying this technology in studies as diverse as human breast cancer and viral genome resequencing.

Expression Genetics
Regulatory networks describe the relationships among transcription or splicing factors and the DNA regions of the target genes to which they bind. We are combining large data sets of genome-wide polymorphisms with measures of the levels of expression of millions of exons. These associations lead to discoveries of trans and cis-acting DNA variation that regulate expression.

Protein Motion & Docking

Using Insights from Robotics
We model proteins as kinematic robotic chains, and we analyze the motions of these mechanical robots to predict protein motions.

We directly interact with our protein model using a haptic device, and this allows us to quickly predict how forces affect a protein's overall structure.