



# 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>



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### Graduate Studies at UMass



#### 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.

#### 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.



### Lab Resources



#### Haptic Device

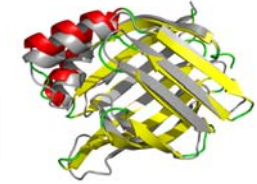
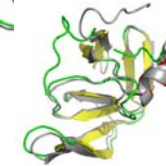
We utilize a 6-degree of freedom haptic device to physically interact with our protein models.



#### 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



Our Predictions : Color  
Native Structures: Gray

#### 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



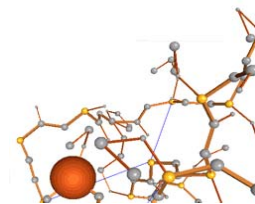
#### Variation Detection

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.

