**Research interests/descriptions**

***Postdocs***

**Ryan Cheng**

My research focuses on building quantitative models of the correlated mutations that are observed in large collections of sequence data for a given protein family or families of proteins that have evolved together. I am primarily interested in the sequence-level origin of interaction specificity in the bacterial two-component signaling proteins and the construction of models that can be used to rationally redesign bacterial signal transduction systems. I am also working on problems related to the construction of statistical potentials using genomic data, maximum entropy modeling, and critical phenomena in the sequence-space of naturally occurring proteins.

***Graduate Students***

**Xingcheng**

I am interested in investigating the function of biomolecular system with the tools based on physical science. Especially, I am studying the structural switch of Influenza hemagglutinin (HA) highly relevant to the invasion of flu viruses. By implementing both coarse-grained model, which is based on the well-founded energy landscape theory in the context of protein folding, and the explicit-solvent simulation combined with enhanced sampling algorithms, I am trying to understand the physical mechanism guiding the conformational transition of this delicate molecular machine.

Generally, I am interested in various scientific questions with the application of mathematical and computational tools.

**Bin Huang**

I’m interested to use theoretical models to understand some biology behaviors at different scales. Some examples as follow:

Gene regulatory network involved in cancer metastasis, such as Rac1-RhoA circuit for amoeboid-to-mesenchymal transition

Cell-cell interactions between cancer and immune cells.

Also, I’m exploring some more fundamental and universal properties of gene regulatory network in order to understand the design principles of biological network.

http://bh14.blogs.rice.edu/

***Alumni***

**Ryan L. Hayes**

My thesis research focused on the magnesium dependence of RNA. The  
energy landscape of biological macromolecules such as RNA must be  
smooth and funneled in order for them to fold on biological time  
scales. In such a landscape, native contacts are on average more  
stabilizing than nonnative contacts and guide the search for the  
native state. A structure-based or Gō model includes only native  
contacts and topological constraints and is a useful approximation. In  
addition to being funneled, the energy landscape of RNA is strongly  
dependent on ionic conditions, because positive counterions such as  
magnesium are required to mitigate the electrostatic repulsion by  
negative backbone phosphates. Magnesium binds tightly to RNA because  
it is divalent and small. I developed models that described the  
sensitivity of competing RNA states to magnesium. My present interests  
include functional dynamics and design of proteins and RNA.

rhaye@umich.edu

**Faruck Morcos**

My research is at the interface between biology, computation, mathematics and biophysics. I am interested in the development and application of methods to extract biological information from sequence and genomic data in combination with physical models to study molecular evolutionary landscapes, biomolecular structure and function, macro-complex formation, specificity in biological networks and its applications to understand and fight disease.

Time at CTBP:  2010-2015

morcoslab.org

**Jeffrey Noel**

smog-server.org/noel