

# Cluster Users

## ***Math Department***

### **Beck Group**

*Prof. Matthias Beck is the Principle Investigator*

Andrew VanHerick—Computational Methods of Lattice Point Enumeration

My research concerns computational methods of lattice point enumeration in a polytope minus a union of hyperplanes. Using an implementation of one such method the CCLS cluster has enabled the computation of several previously intractable results, among them compact formulas counting the number 4x4 magic squares with distinct entries, both as a function of line-sum and as a function of maximum allowable entry.

Andrew Bayer—Latin Rectangle Enumeration

I need the clusters processing power to compute the number of 2X3 latin rectangles. I've based the method of computation on a few papers by Matthias Beck and Thomas Zaslavsky. I use Andrew Van Herick's program which has been developed using the theory of Inside-Out polytopes described in those papers. The ehrhart series for 2X3 rectangles has not been computed.

## ***Biology Department***

### **Desjardin Lab**

*Prof. Dennis Desjardin is the Principle Investigator*

Dr. Brian Perry—Characterizing the Evolution and Systematics of Mycenoid Fungi

This research focuses on the evolution and systematics of the Mycenoid fungi (using programs such as PAUP\* and MrBayes). Our goals also include using the phylogeny(s) we generate to infer patterns of ecological and morphological evolution, measure rates of evolution, and investigate the biogeography of these fungi.

### **Smith Lab**

*Prof. Chris Smith is the Principle Investigator*

Jay Kim—Annotating microRNA Secondary Structures in the Fruit Fly Genome

The purpose of this study is to discover, identify, and characterize microRNA secondary structures in *Drosophila melanogaster*. Our approach employs the computational capacity of the CCLS cluster for miRNA prediction and secondary structure homology across model fly species. The goal is to find expression regulation and behavior based on miRNA.

Anthony Manlutac—Identifying Genes for Social Behavior in Native California Ants

This research seeks to develop a comparative genomic annotation for social behavior genes in native California ant species. Our approach uses the CCLS cluster for comparative genome analysis and annotation. In addition to *in silico* analysis, this research intends to verify with *in vivo* RNA interference of behavior genes.

Lala Motlhabi—Purpose and Function of Dicistronic Genes in Fruit Flies

A comparative genomic annotation of Drosophilid dicistronic genes: Dicistronic genes are genes which express two proteins, and are unusual in eukaryotes. This research investigates and annotates ~50 dicistronic genes across 12 closely related drosophila (fly) species, with genomes of sizes that range from ~13.9-23.5 Mb in size. The CCLS cluster provides the computation power and necessary tools for genome comparison and annotation. The goal is to better understand the purpose and function of dicistronic genes in a model eukaryotic organism and across closely related species.

### **Tobias Sayre—Characterizing Common *cis*-acting Elements in Genes**

This research addresses the question, “What are the unknown common *cis*-acting elements in genes?” Previous studies have shown that in WAKL4, a member of the wall associated kinase family (WAK) in *A. thaliana*, expression is induced by minerals including Na<sup>+</sup>, K<sup>+</sup>, Cu<sup>2+</sup>, Ni<sup>2+</sup>, and Zn<sup>2+</sup>. Previous BLASTN analysis on gene promoters in the WAK family in *A. thaliana* and *O. sativa* have identified three highly conserved subregions within these promoters. This study uses multiple sequence alignment analysis and motif finding analysis to further characterize these conserved promoter regions in *O. sativa*.

### **Spicer Lab**

*Prof. Greg Spicer is the Principle Investigator*

### **Jenner Banbury—Characterizing Nasal Mite Taxonomy, Systematics and Cospeciation**

The Spicer lab has been actively studying the taxonomy, systematics and cospeciation of nasal mites for several years. We use direct sequencing of DNA to obtain molecular phylogenies of the nasal mites and then use those phylogenies to compare the evolution rates/patterns with the corresponding bird host phylogenies to look for cospeciation. We use the CCLS cluster to parcel out our large bootstrap jobs, which give approximate confidence values at each node of our phylogeny.

### **Romberg Tiburon Center**

### **Stillman Lab**

*Prof. Jon Stillman is the Principle Investigator*

### **Anu Sharma—Comparative Genomic Approach to Understand Porcelain Crab Physiology**

Current research goals are to use genomic approaches to understand the mechanistic bases of the physiological adaptations porcelain crabs have made as well as to study physiological variation of animal across ecological gradients in nature. To accomplish these goals we have embarked on a significant EST sequencing project as part of the Joint Genome Institute 2006 Community Sequencing Program. We use the CCLS cluster to perform homology searches of unique consensus sequences against databases including GenBank, SwissProt, PFAM, and Gene Ontology. We are also presently working to make these data publicly available at the Porcelain Crab Array Database (PCAD) at <http://array.sfsu.edu>, and they will be uploaded to GenBank. This work was supported by NSF-IOB 0533920 to JHS and the DOE JGI 2006 CSP.

### **Kimmerer Lab**

*Prof. Wim Kimmerer is the Principle Investigator*

### **Dr. Karen Edwards—Individual-based model simulation of SF Estuary delta smelt**

This research is part of a large effort to study and model the delta smelt in San Francisco Estuary. Delta smelt is a threatened species found only in the low salinity waters of the Estuary. Specifically, the presented model is an Individual-based Model (IBM) that is used to follow individual model smelt and focuses on the biological details of delta smelt during all of their life

stages. The IBM allows exploration of population responses to simultaneous variation in multiple environmental factors and management actions. The IBM will simulate the entire life cycle of the delta smelt. Individual fish will be tracked on a daily basis through the processes of growth, development, mortality, reproduction, and movement. One-year and multi-year simulations of the IBM will be performed for model calibration, corroboration, evaluation of hypotheses and management actions, as well as for comparison to the matrix projection models. Primary model prediction variables include annual values of life stage-specific survival rates, annual egg production, number surviving to 20-mm, total population abundance, population growth rate, and snapshots of delta smelt spatial distributions in the estuary.