Thomas Girke

Botany and Plant Sciences
University of California, Riverside

Date: Friday, December 2, 2011
Location: EBU2 Room 205/206
Time: 12:10am

High-Throughput Biology Approaches for Profiling Cellular Processes

Abstract:

Many novel genome-wide screening approaches have become important research tools in biology. These include next generation sequencing, high-throughput drug/knockout screens, as well as highly parallelized hybridization techniques. My lab works on the development of tools to analyze and model the complex data generated by these techniques in order to predict molecular functions of genes and study the dynamics of biological processes in model and production organisms. In this seminar I will discuss

the opportunities and challenges we are facing in utilizing these modern large scale data sets for discovery oriented research.

RELATED PUBLICATIONS:

Bao E, Jiang T, Kaloshian I, Girke T (2011) SEED: Efficient Clustering of Next Generation Sequences. Bioinformatics: 27, 2502-2509

Backman T, Cao Y, Girke T (2011) ChemMine Tools: an online service for analyzing and clustering small molecules. Nucleic Acids Research: 39, W486-491

Horan K, Shelton CR, Girke T (2010) Predicting conserved protein motifs with Sub-HMMs. BMC Bioinformatics: 11, 205.

Cao Y, Jiang T, Girke T (2010) Accelerated Similarity Searching and Clustering of Large Compound Sets by Geometric Embedding and Locality Sensitive Hashing. Bioinformatics: 26, 953-959.

Horan K, Jang C, Bailey-Serres J, Mittler R, Shelton C, Harper JF, Zhu JK, Cushman JJ, Gollery M, Girke T (2008) Annotating Genes of Known and Unknown Function by Large-Scale Co-Expression Analysis. Plant Physiol: 147, 41-57.