



presents Guest Speaker :

Martin Ester

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*Data Mining Methods for Learning Regulatory
Modules from High-Throughput Data*

The reconstruction of regulatory networks from high-throughput experimental data is one of the major challenges of current bioinformatics research. An important task toward this goal is the discovery of regulatory modules, consisting of a regulatory program, in particular a set of transcription factors, and a corresponding set of co-regulated genes. Genes can have different regulatory programs in different experimental conditions such as tissues and developmental stage, which implies that genes may not be co-regulated in all experimental conditions observed in comprehensive expression data sets. This has motivated the development of subspace clustering (biclustering) methods that find clusters of genes that have similar expression patterns in subsets of the set of all conditions. We present the KiWi algorithm, a novel subspace clustering algorithm that scales much better to large and high-dimensional datasets than existing algorithms. Different high-throughput data such as cDNA microarrays, protein-protein interaction data and ChIP-Seq data reflect only partial information of the biological system from different points of view, and none of them can alone accurately reconstruct a regulatory network. Therefore, integrated approaches incorporating different types of experimental data are required. We propose a new approach to module discovery based on interaction network and expression data, finding dense subnetworks of genes that are co-expressed in large enough subspaces. The talk concludes with the discussion of future research directions.

Introductory Presentation (10 mins):

Olena Morozova, BCGSC (Marra lab)

Thursday, January 10, 2007, 6:00 pm

Gordon and Leslie Diamond Family Theatre,
BC Cancer Research Centre,
675 West 10th Avenue



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