



Using MetaCore for Gene Expression Analysis

Leverage GeneGo's best-in-class molecular interaction database that now includes over 700,000 compounds and their targets, GeneGo provides a solution for using "omics" gene lists to generate and prioritize hypotheses with MetaCore.

This course will highlight how to:

- uncover genetic and functional pathways and networks in gene expression data
- assess connectivity and regulatory hubs with interactome analysis
- analyze microRNA function
- generate biomarker discovery workflows
- extract functional relevance from gene lists by enrichment histograms
- use workflows to compare data from different experiments



Date: May 21st, 2010

Time: 10:00 am- 5:00 pm

Instructor:

Dr Eugene Myskhin

Location:

***University of Lausanne
Dorigny Campus
Amhipole Building
Room 204.2***

Hosts: GeneGo Inc &

***Lausanne Genomic
Technologies Facility***