Seminar Series

geWorkbench, An Open-Source Platform for Integrated Genomics

Part 1: Basics and Gene Expression Analysis
Presenter: Udo Többen, PhD

In the first part of the seminar series we will introduce the basic functionality of the geWorkbench application. This includes a description of the graphic user interface as well as the execution of basic data handling operations. We will demonstrate how to organize the large number of probe sets and arrays comprising a gene expression experiment into groups that can be used to drive subsequent data analysis. We will also discuss data filtering and normalization.

Equipped with a general understanding of geWorkbench’s basic features, we will showcase a number of analytical and visualization components (using the gene expression data set from a research publication):

- Differential Expression Analysis – this component allows for the identification of markers with statistically significant differential expression between two sets of microarrays.
- Hierarchical Clustering - a method to group arrays and/or markers together based on similarity on their expression profiles.
- Gene Ontology Enrichment Analysis - the “GO Terms” component in geWorkbench supports the identification of functional Gene Ontology categories statistically enriched for a list of interesting genes, e.g., such as those derived from differential expression analysis or hierarchical clustering.


Part 1 in this series will introduce key concepts which will be used in subsequent seminars. Attendance is highly recommended for participants who plan to RSVP for Parts 2 or 3.

Monday, April 30, 2012
12:00 - 1:00p
Irving Institute Educational Center Classroom (PH-10-405)
622 West 168 Street, Floor 10, Room 405, NYC 10032

RSVP to Michelle McClave
mm3098@columbia.edu or (212) 305-9425

Lunch will be provided