Genevestigator – Module I

Overview of Genevestigator
Genevestigator components
Genevestigator Website

- Start link for analysis tool (client java application)
- User registration and/or subscription
- User manual, FAQ
- Teaching modules
- Community pages
- Publications
Database and application server

- Expression measurement data (Affymetrix arrays)
- Experiment and sample information (meta-data)
- Data from mouse, rat, arabidopsis, barley
- Metabolic and regulatory pathways
- User management
- MySQL database
Genevestigator client java application

- Java tool - starts in browser
- Four tool sets
  - Meta-Profile Analysis
  - Biomarker Search
  - Clustering Analysis
  - Pathway Projector
- Focus on the biological context
  (anatomy, development, stimulus, mutation)
Genevestigator client java application

- Minimal requirements:
  - Java 1.4.2 or higher (working in browser)
  - 128 MB RAM

- Recommended:
  - Screen resolution: 1024 x 768 or higher
  - 500 MB RAM or more (for advanced tasks, e.g. you perform a clustering analysis of many genes)
Quality control

- Unprocessed probe intensity
- Affymetrix QC metrics
- RNA degradation plots
- Probe-level analysis (RLE, NUSE)
- Border element analysis
- Array-array correlation plots
Tools & Products

Genevestigator® Classic

(Free for academic users)

Genevestigator® Advanced

(Small fee requested per academic laboratory to support costs of development and curation)
Meta-Profile Analysis

- Goal: study expression in given biological contexts
- Tools:
  - **Selection** (all signal values on screen; magnifying glass)
  - **Northern** (view signal values in a selected subset of arrays)
  - **Anatomy** (expression across anatomy categories)
  - **Development** (expression throughout development)
  - **Stimulus** (expression in response to stimuli or drugs)
  - **Mutation** (expression in response to genetic modifications)
Meta-Profile Analysis - screenshots
Biomarker Search

- Goal: to identify genes that exhibit specific expression

- Tools:
  - Anatomy
  - Development
  - Stimulus
  - Mutation

- Single or multiple target categories possible

- „Supervised biclustering“
Biomarker Search - screenshots

Mouse development: markers for stage 4 or 5 (Theiler: 16 or 21)

Multiple targets or „supervised biclustering“
Clustering Analysis

- Goal: identify groups of genes with similar expression profiles
- Tools:
  - Hierarchical clustering (with leaf ordering)
  - Biclustering (BiMax algorithm)
- Clustering of "raw" gene expression or meta-profiles (generate gene-array or gene-meta-profile matrix)
Clustering Analysis

Hierarchical clustering

Without leaf ordering

With leaf ordering

Biclustering
Pathway Projector

- Goal: study the expression state or response of metabolic and regulatory networks
- Top-down or bottom-up analysis possible
- Nodes = reactions
- Edges = metabolites (met. map) or enzymes (reg. map)
- Automatic layout, but often suboptimal: user can relocate nodes and save view to file
Pathway Projector - screenshot

ABA response
Starch / sucrose
Cold response
Inositol phosphate
ABA biosynthesis
Beta-alanine
Phenylalanine / Tyrosine
Proline
Phenylalanine / Tyrosine

ABA response
Starch / sucrose
Cold response
Inositol phosphate
ABA biosynthesis
Beta-alanine
Phenylalanine / Tyrosine
Proline
Phenylalanine / Tyrosine

Extend
Monoamine / Threonine Metabolism
Deletion
Starch metabolism
Add neighbours

Gibberellin Biosynthesis
Glycerophospholipid Metabolism
Arginine Biosynthesis
Porphyrin / Chlorophyll Metabolism
Pyrimidine Metabolism
Fatty Acid Biosynthesis
Starch metabolism

Gibberellin Biosynthesis
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Pyrimidine Metabolism
Fatty Acid Biosynthesis
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Gibberellin Biosynthesis
Glycerophospholipid Metabolism
Arginine Biosynthesis
Porphyrin / Chlorophyll Metabolism
Pyrimidine Metabolism
Fatty Acid Biosynthesis
Starch metabolism
Saving workspace

- Goal: to allow a user to return to an analysis started previously, or to share your analysis with colleagues

- Workspace is saved to a file (*.gvw) and stores
  - Array selections
  - Gene (probe set) selections
  - State of selections (marked/unmarked checkboxes)
Saving pathway views

- Goal: to allow a user to build reaction networks and store the layout and projected data

- View is saved to a file (*.gvp) and stores:
  - pathways involved
  - positions of nodes
  - data which is being projected (comparison set selections)
Exporting figures

- Goal: to allow users to export high-quality, publish-ready figures
- Result views can be resized and exported as:
  - PNG
  - JPEG
  - EPS (for high resolution)
Summary of this module

- Genevestigator has a website, a client Java application, and several webservers.
- The data is quality-controlled using Bioconductor and R.
- Two products (Classic and Advanced) are based on four tool sets (Meta-Profile Analysis, Biomarker Search, Clustering Analysis, Pathway Projector).
- Saving workspaces and pathway views.
- Exporting figures.
Thank you for your attention!