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S Y S T E M S



## IPA Data Analysis Comparison

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# Tools for Data Analysis Comparison

- Core, Tox, Metabolomics Analysis Comparison
  - Side-by-side bar-charts and combined data tables
- Compare
  - Allows set comparison (union, unique, common) of entities in data sets, analyses, custom lists, and custom pathways
    - Does not account for directional changes in data sets and analyses, i.e., a gene that is up in one data set and down in another is considered common. Creating filtered data sets to include only up or down regulated genes in conjunction with Compare can be used to determine common directionality.
- Overlay -> Analysis or Data Set Values
  - Gives capability of visualizing expression values of any uploaded on the current pathway
  - Has expression bar-chart option for visualizing changes across all observations for a given gene/protein on a pathway

# Strategies for Multi-comparison

- Review single core analyses first to get a sense of global biological changes
- Choose a reference analysis and compare others to it
  - Use Overlay -> “Analyses, Data sets, and Lists” extensively
- Optional: Use Compare to subset genes not in common or directionality, run core analysis on these genes
  - Use filtered data sets by direction first to use the Compare tool and determine genes differentially up in one analysis and down in another

# IPA Compare Feature

## Set Analysis of Lists



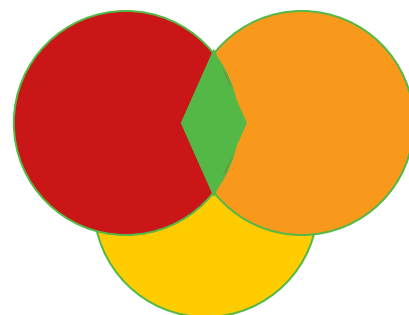
List 1



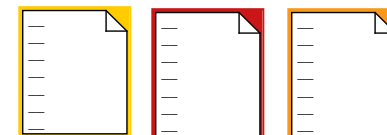
List 2



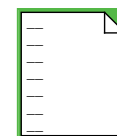
List 3



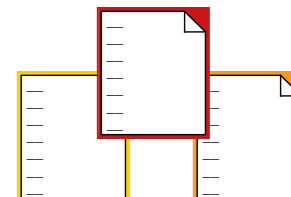
Compare



Unique molecules  
to each List



Common molecules  
Across all Lists



Union of all molecules

# Using the Compare Tool

- Allows set comparison (union, unique, common) of entities in data sets, analyses, custom lists, and custom pathways
  - File -> New -> Compare
  - Select data sets, analyses, gene lists, pathways that you want to compare
  - Designate common, unique, or union of entities
  - To take into account gene expression changes, i.e. to distinguish genes that do not have the same direction as common, create filtered data sets (File -> New -> Create Filtered Data Set) of specific directionality for each gene set, then compare the directional lists
    - For example, compare common “Observation 1 Up Genes” to “Observation 2 Down Genes” to identify genes that are changing in differential expression between observations

# Using the Compare Tool

- Allows you to associate separately uploaded data sets as a multi-observation data set for overlay bar charts
  - Select data sets you wish to make multi-observation
  - Create a Union of the data sets
  - Click “ANNOTATION” button
  - Select all
  - Click “Create Data Set”
  - Name observations and SAVE

# Pathway Comparison

- Run “Core, Tox, Metabolics Comparison Analysis”
- Compare pathway significance column chart
- Interrogate different or similar pathways as desired
  - Note that a pathway can appear significant in two different analyses, but the gene expression may be very different
  - Use of Overlay to overlay expression values from different observations and using the MAP tool is extremely helpful for interpretation expression differences across observations
- Re-sort based on significance in other observations by using the “Customizing Chart” option
- New heatmap view will be available in April 2013

# Downstream Function Analysis Comparison

- Tree Map Chart Comparison
  - Compare tree map charts side-by-side on large monitor and visually compare using mouse and chart highlight feature
- Function Table Comparison
  - Visually compare either combined table from Analysis Comparison or compare as separate tables.
  - Sort table by p-value, positive z-score, negative z-score and compare top scoring upstream regulators to other observations
  - Export to other program
- Visualize Gene Expression Differences
  - Drill in on gene sets of differential process/function
  - Send genes to pathway from one or multiple observations
  - Overlay gene expression



# Upstream Regulator Analysis Comparison

- Visually compare either combined table from Analysis Comparison or compare as separate tables.
  - Sort table by p-value, positive z-score, negative z-score and compare top scoring upstream regulators to other observations
- Export to other program

# Mechanistic Network and Standard Network Comparison

- Because networks are very dependent on input genes list and network “seed” determination, side-by-side comparison is difficult
- Begin with a reference network of interest, one to use as a point of comparison, and determine how other observations compare by overlaying gene expression and using the MAP overlay tool



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