Tutorial 6: GeneList – An important concept in ArrayTrack
Introduction

The Gene List folder contains gene lists that are usually derived from applying certain filtering criteria (e.g. P-value, fold change, etc) on the microarray data. As a common practice, a list of gene is identified by researchers and then carried forward for biological interpretation and/or further analysis.

There are several ways to create a gene list in ArrayTrack:
- Create a gene list through statistical analysis (page 3)
- Create a gene list through volcano plot (page 5)
- Create a gene list through data filtering (page 6)
- Create a gene list through querying chip information (page 7)
- Create a gene list through GOFFA (page 8)
- Create a gene list through pathway (page 10)
- Alternatively, the user can import a list of genes that is created outside of ArrayTrack. (page 12)

ArrayTrack allows the following operations solely based on gene lists:
- Normalization based on a gene list (page 21)
- Statistical analysis (t-test, PCA, HCA) applied on a gene list (page 22)
- Venn diagram drawn on two or three gene lists (page 19)
- Functional analysis on a gene list (page 26)
- Export a set of microarray data with genes that are specified by a gene list (page 28)
- Miscellaneous: delete a gene list (page 17); create a Gene List subfolder (page 15)
Create a gene list through statistical analysis

From data analysis results (e.g. T-test result. See Tutorial 1 for doing T-test).
Create a gene list through statistical analysis - continued

The saved gene list will be displayed under the experiment.

Can be saved into different experiment.
Create gene list through volcano plot
Create a gene list through data filtering

User can set the criteria (like flag, intensity value) to create a gene list, e.g. find out all the genes which intensity is greater than 3.0 in at least 6 out of 12 hybridizations.

Right-click the selected data, choose “Create gene list by data filtering.

The total number of selected hybridizations.
Create a gene list through querying chip information

The user can filter out some genes (e.g. spike-in genes) to get a gene list for further normalization.

This image shows a raw dataset using filtering criteria to only display the genes the user inquired. User can open any raw data to get the following spreadsheet.

Keyword search – ‘AFFX’
Create Gene List through GOFFA

This is the GOFFA table. Click Gene tab, then right-click the gene table, select “Create significant gene list…”
Create Gene List through GOFFA

When the user type in the cutoff p value, the number of genes will change according to the value of P.
Create Significant Gene List through Pathway

Right-click the pathway table, Then select “Create significant Gene list…”
Create Significant Gene List through Pathway

- Type in the cutoff P value
- Name the gene list
- Select the experiment name for the location of the saved gene list
Import/Export a gene list

Right-click the experiment, then choose Gene Lists ⇒ Import
Import/Export a gene list – cont.

Choose the gene list from the local drive and click “Open” button.
Import/Export a gene list – cont.

Assign table columns to the corresponding fields.
Every user can export the gene list in ArrayTrack. To rename, delete, or move the gene list, you have to be the owner of the experiment or you are assigned privilege by the owner.
Import/Export a gene list - continued

Move gene list to a new folder

The gene is moved to new Folder - Temp
Import/Export a gene list - continued

- Rename the gene list
- Delete the gene list
Draw Venn Diagram from gene lists

Select gene lists

Draw Venn Diagram
By different approach

Draw Venn Diagram
By various ID
Draw Venn Diagram from gene lists -continued

More detail about Venn Diagram is explained in Tutorial 3.
By clicking any sections from VennDiagram, the regions will be highlighted. Then right click to choose the options. One option allows display the selected genes in the original data sheet.

Fold change direction option
Only applies to genelists saved in ArrayTrack and fold info available. If gene id is same, but with different fold change direction, then it will be considered as different genes.
Conduct normalization filtered by a gene list

User can do data normalization based on a filtered gene list. Refer tutorial 7 for Normalization methods.
Conduct statistical analysis based on a gene list

Doing T-test based on a filtered gene lists
Refer tutorial 1 for T-test
Conduct statistical analysis based on a gene list - continued

Doing PCA based on a filtered gene lists. Refer Tutorial 4 for PCA
Conduct statistical analysis based on a gene list - continued

Doing Correlation Matrix based on a filtered gene list. Refer Tutorial 10 for Correlation Matrix.
Conduct statistical analysis based on a gene list - continued

Doing HCA based on a filtered gene list
Refer Tutorial 4 for HCA
Biological interpretation using ArrayTrack Pathway, GO and other tools

- Individual gene annotation and analysis
- Pathway analysis
- GO-based functional analysis

Double click
Individual gene annotation and analysis using GeneLib
Export a dataset by specifying the gene list

The user can export data with only selected genes. Refer Tutorial 9 for data export.