Tutorial 5:
Accessing gene expression profiles using BarChart

Overview of BarChart

Why use BarChart:

Displays expression data for a single gene across multiple arrays within the same experiment or across different experiments. It gives the user an overview of the differential expression levels of this gene across different samples.

How to get BarChart:

<1> From Gene List (the most popular usage)
<2> From Tool Panel
<3> From T-test result
<4> From Library windows, such as ChipLib or other Libs
<5> Advanced: launch BarChart from data content tree

Functions associated with BarChart:

<1> Query/sort BarChart table
<2> Grouping bars with color
<3> View standard deviation
<4> Others: apply log2, flip fold, link to Libraries, ScatterPlot, etc.
<5> Advanced: cross multi-experiment comparison

Access BarChart

<1> From gene list

1) Double click a genelist node from database content tree in the top left window.
2) A genelist table will show up.
3) Highlight a record from genelist table, and right-clicking shows a popup menu.
4) Select 'Bar Chart' from the popup menu.
5) A Bar Chart window is displayed with the selected gene's profile across all normalized data set within the specific experiment that this genelist belongs to.

Access BarChart

<2>From TOOL panel
Use it when you know gene id and experiment name
-Double click BarChart node from Tool Panel (the bottom left window)
-A BarChart window is shown.
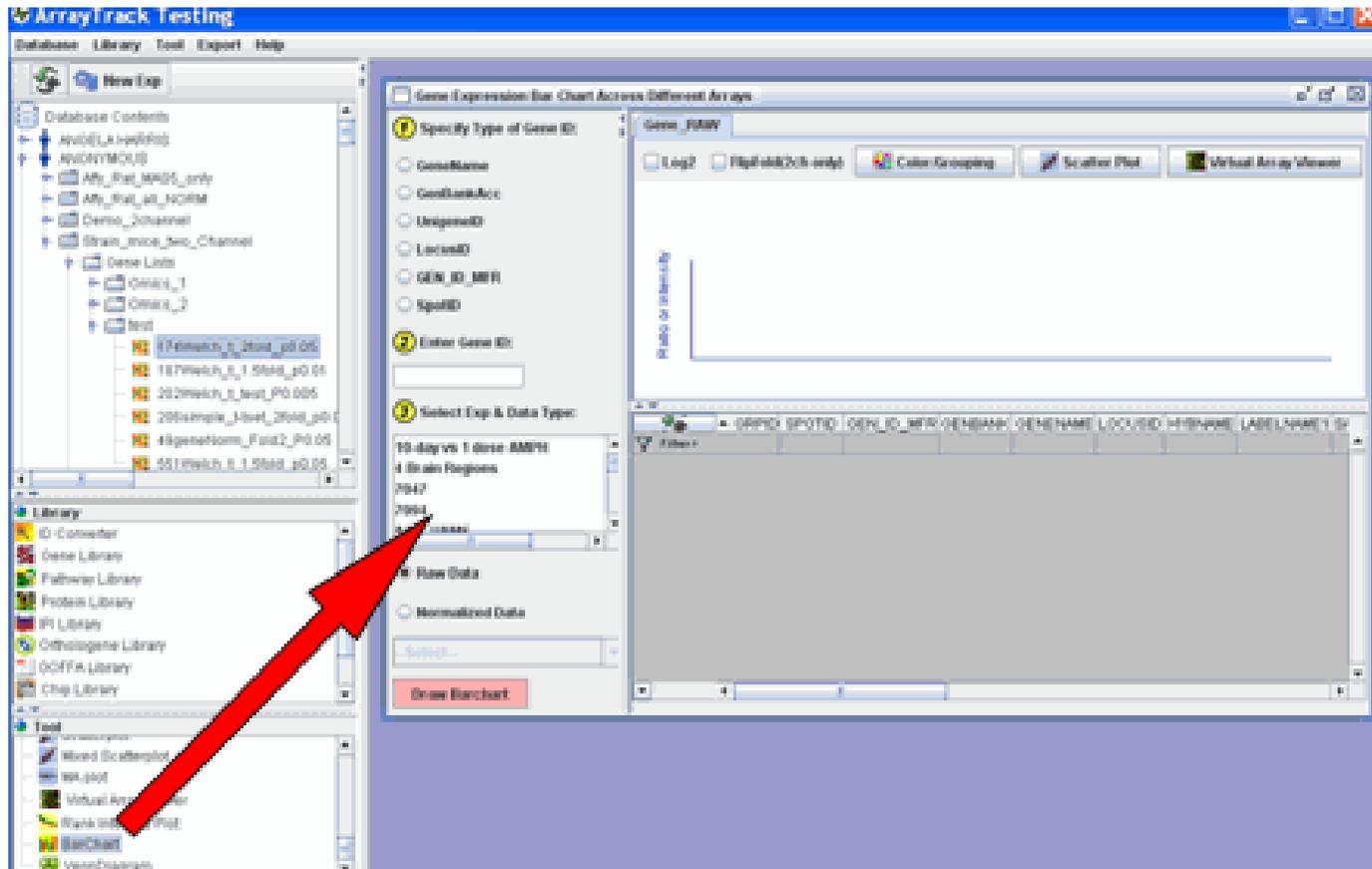
Access BarChart

<2> From Tool panel (cont.)
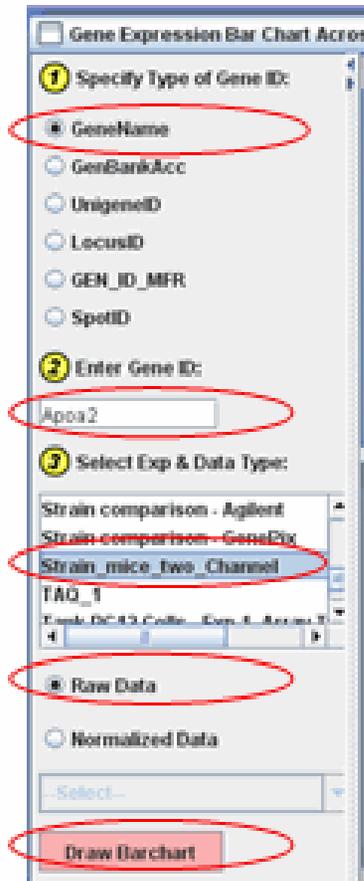
1) Specify gene type

2) Specify gene ID

3) Select experiment name

4) Select data type mod
   - Raw
   - Normalized (select normalization method from drop down list)

5) Click 'Draw Barchart' button
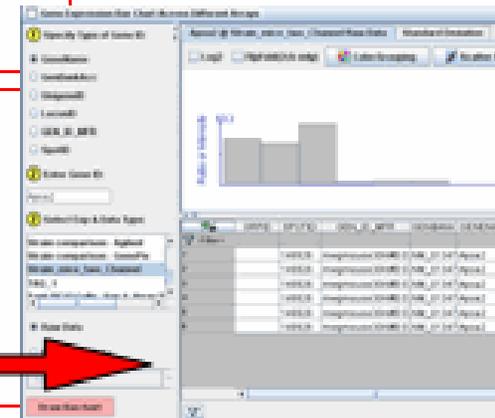
Access BarChart

<3> From T-test Result
Please refer Tutorial 1 for generating T-test result.

Select a gene in the T-test result and choose BarChart from "Selected-Spot" menu.

Access BarChart

<4> From ChipLib and other Libs
- Select gene from library table
- Click "BarChart" button on the top of tool bars

Select the gene from library table, then click BarChart button

Access BarChart

<5> Advanced: From Data Tree
- Select experiment name, then right click to select datasets
- Type in search pattern, matched data will be highlighted in the tree.
- Right click and select "BarChart" to launch.   (continue on next page..)

Access BarChart

4) Specify gene ID and Type, then click "Draw Barchart" button

BarChart Functions – Query/Sort

Query:
1) Type constraint in a particular field on the query row.
2) Click query button.
3) BarChart will be re-drawn based on the search result.

**Sort:** Click header to sort table by columns.

BarChart Functions - Grouping

1) Select group of records from table or highlight bars from bar chart panel
2) Click "Color/Grouping" button and select "Assign Group by Color"
3) Once grouping is done, Click "Color/Grouping" button again and select "Save Group by Color". (the grouping info will be saved for that particular experiment, so when you view other genes within the same experiment, the color of grouping will automatically be applied).

BarChart Functions - Standard Deviation

1) Click "Standard Deviation" tab on the top of barchart panel
   (the standard deviation chart makes more sense after grouping.)

standard deviation chart after grouping.
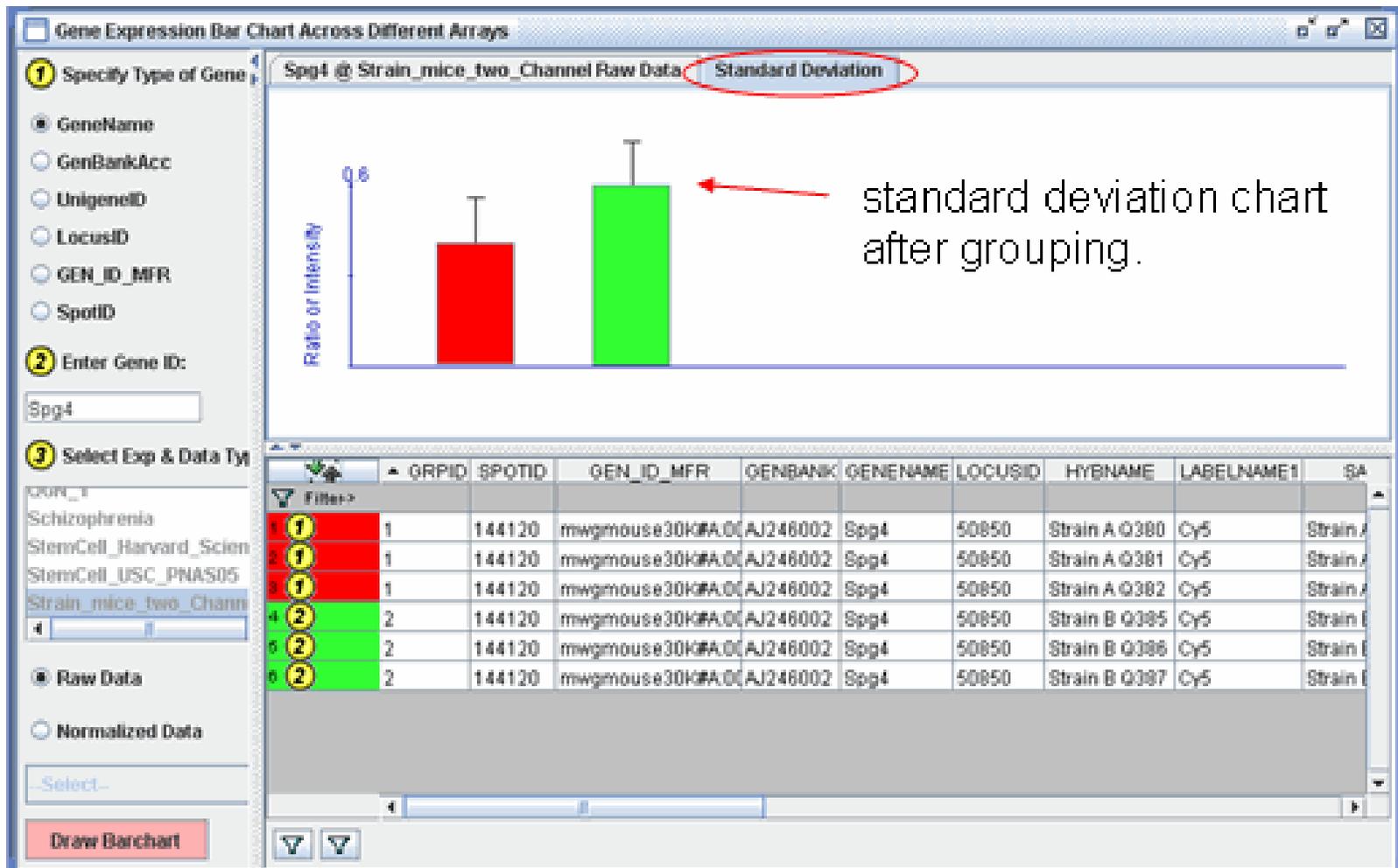
BarChart Functions - Others

1) "Log2" apply to fold for 2 channels data
2) "Flip Fold" applies to 2 channels data.
3) Link to ScatterPlot
4) Link to ChipLibrary

Gene is highlighted

Advanced Function: cross-experiment comparison