

J-Express Basics and Fundamentals

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Computational Biology Unit

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Selections

Groups

Branching

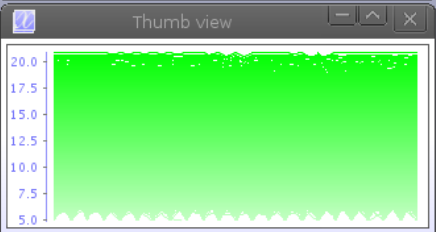
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Project

- AB Rat Brain 160507
 - Quantile normalized intensity data
 - Log(2) Quantile normalized intensity data

Rows 26857
 Columns 23
 Last modified Tue 10 Nov 2009 11:12:35
 Column groups 0
 Row groups 0



Notes and meta data

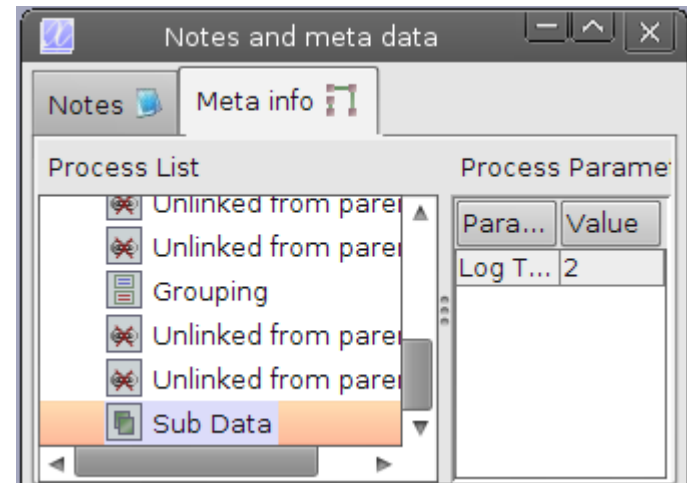
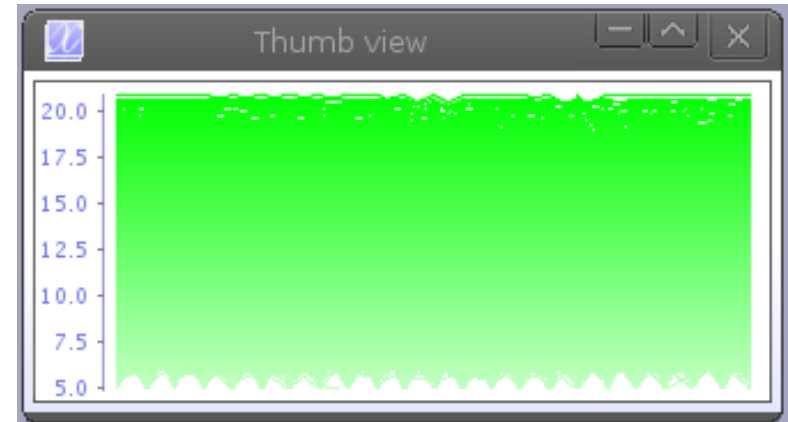
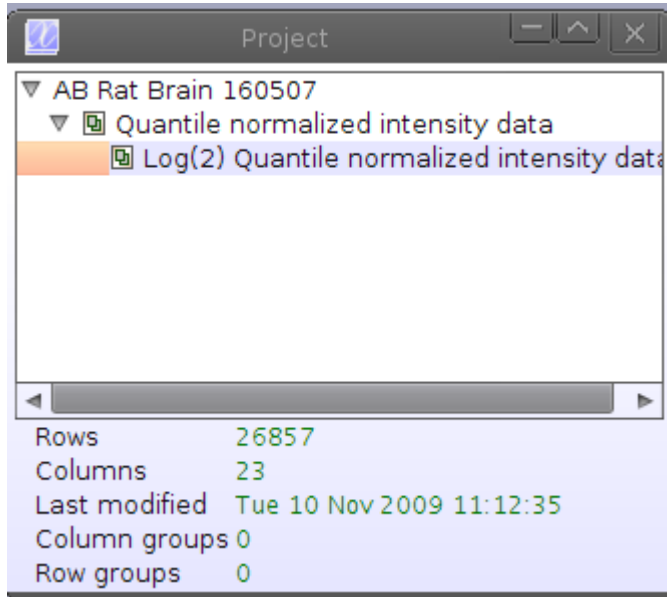
Notes | Meta info

Process List	Process Param
<input checked="" type="checkbox"/> Unlinked from parent	Para... Value
<input checked="" type="checkbox"/> Unlinked from parent	Log T... 2
<input type="checkbox"/> Grouping	
<input checked="" type="checkbox"/> Unlinked from parent	
<input checked="" type="checkbox"/> Unlinked from parent	
<input checked="" type="checkbox"/> Sub Data	

Project Thumb view Notes and met...



Three basic windows



Project Window =
Command Central

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Other windows open on a dataset

The screenshot displays the J-Express 2009 software interface with several windows open on a dataset. The main window shows the 'Properties for Log(2) Quantile normalized intensity data' with a histogram of the 'Intensity Distribution'. The histogram shows a peak around 8 on the x-axis (Histogram Bins) and a y-axis ranging from 0 to 25,000. The 'Info fields and settings' tab shows statistics: Max value 20.9, Min value 4.96, Median 9.57, Mean 10.22, and Replaced Missing Values 0.

Other windows include:

- Project:** Shows the project hierarchy: AB Rat Brain 160507 > Quantile normalized intensity data > Log(2) Quantile normalized intensity data. It also displays metadata: Rows 26867, Columns 23, Last modified Tue 10 Nov 2009 11:12:35, Column groups 0, Row groups 0.
- Thumb view:** A small line graph showing a fluctuating signal.
- Notes and meta data:** A window for notes and meta information, including a process list and parameters (Log Transform... 2).
- Gene Graph - Log(2) Quantile normalized intensity data:** A window showing a gene graph with a main chart and a detailed view of the data points for various brain regions.

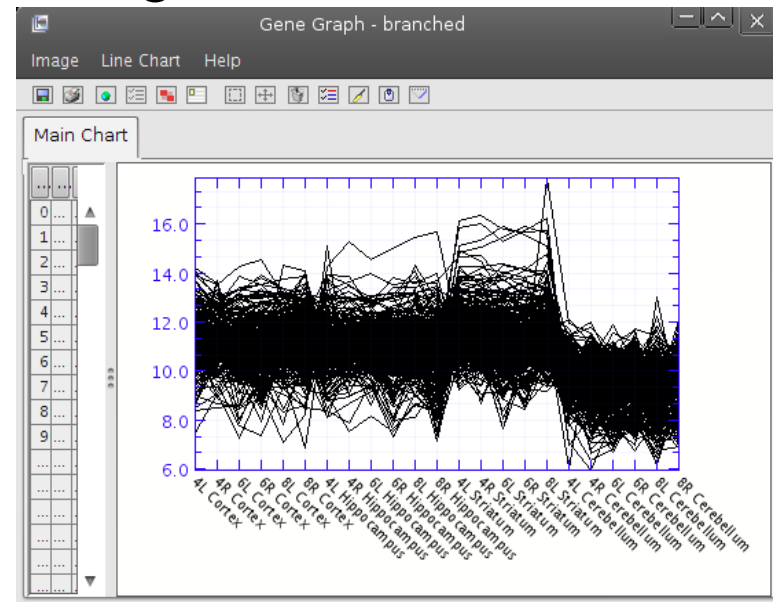
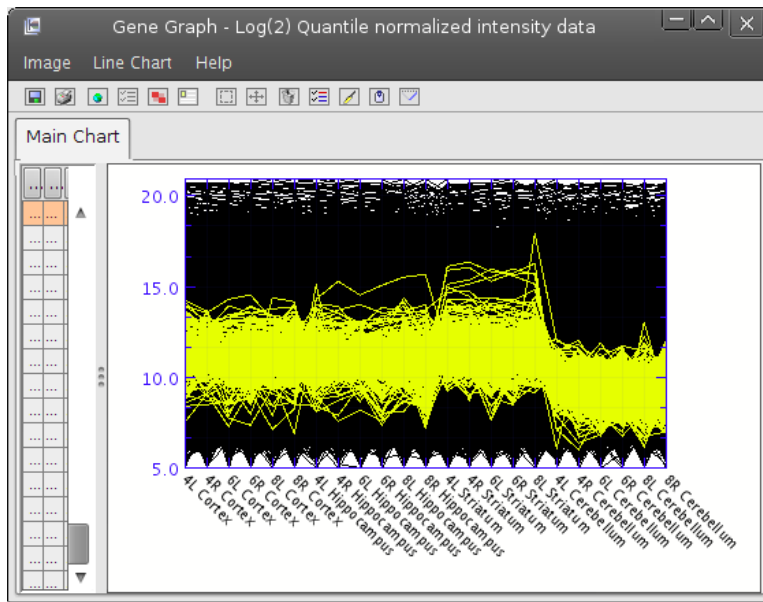
The 'Gene Graph' window shows a main chart with a y-axis from 5.0 to 20.0 and a detailed view of the data points for various brain regions. The detailed view shows a grid of data points for regions like 4L Cortex, 4R Cortex, 8L Cerebellum, 8R Cerebellum, etc. The y-axis represents the intensity value.

Blue arrows point from the 'Log(2) Quantile normalized intensity data' entry in the Project window to the 'Properties for Log(2) Quantile normalized intensity data' window, and from the 'Gene Graph' window to the 'Properties for Log(2) Quantile normalized intensity data' window, illustrating that these windows are linked to the selected data set.

These windows “stick”
to the data set they
were opened on

Interesting relations

- Want to find interesting genes:
 - Need to work interactively with subsets of the data
- Two key mechanisms in J-Express
 - Grouping and Branching

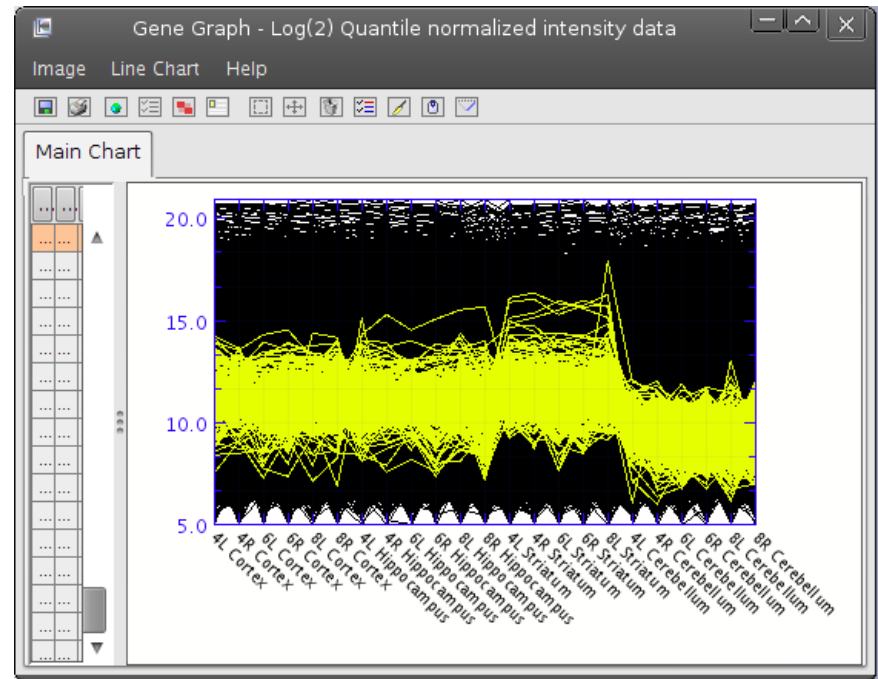


Group example

Project

- AB Rat Brain 160507
 - Quantile normalized intensity data
 - Log(2) Quantile normalized intensity data

Rows 26857
Columns 23
Last modified Fri 16 Apr 2010 12:53:49
Column groups 0
Row groups 1



Groups

Copy Combine Delete View Help

AND/OR/XOR ↑ ↓

Group list and priority

Acti...	Group Name	Color	Count	Style
<input checked="" type="checkbox"/>	Cluster 1	Yellow	385	
<input checked="" type="checkbox"/>	ALL	Black	26857	

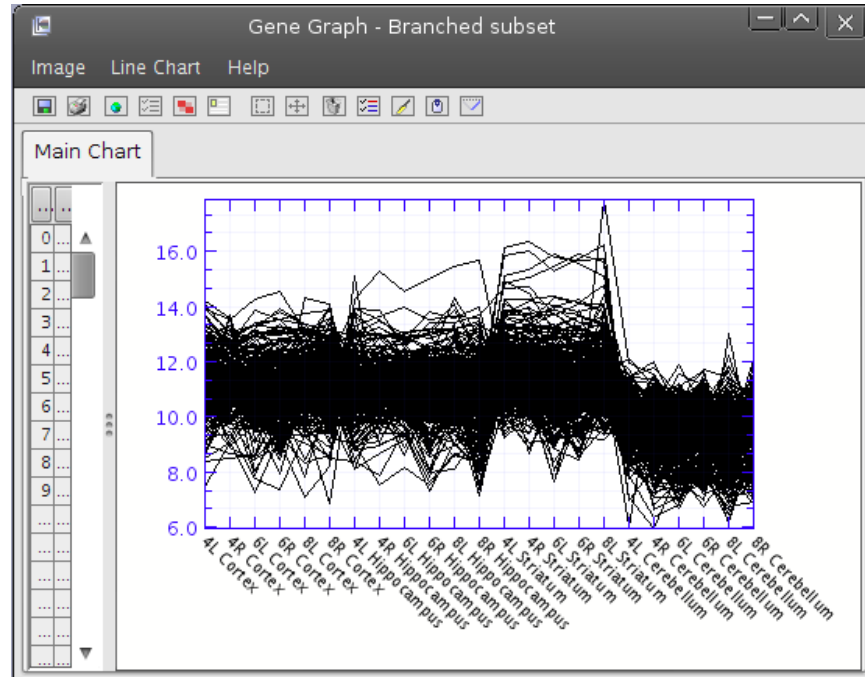
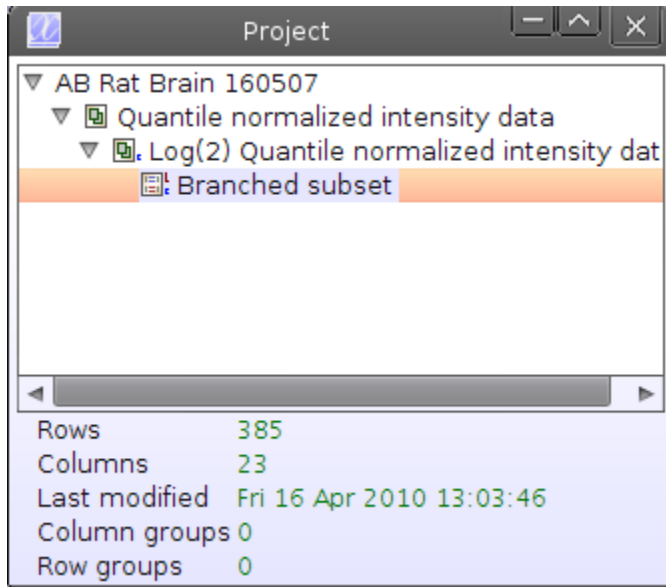
Group Description

Components

Rows Columns

Update all Components

Branching example



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Selections

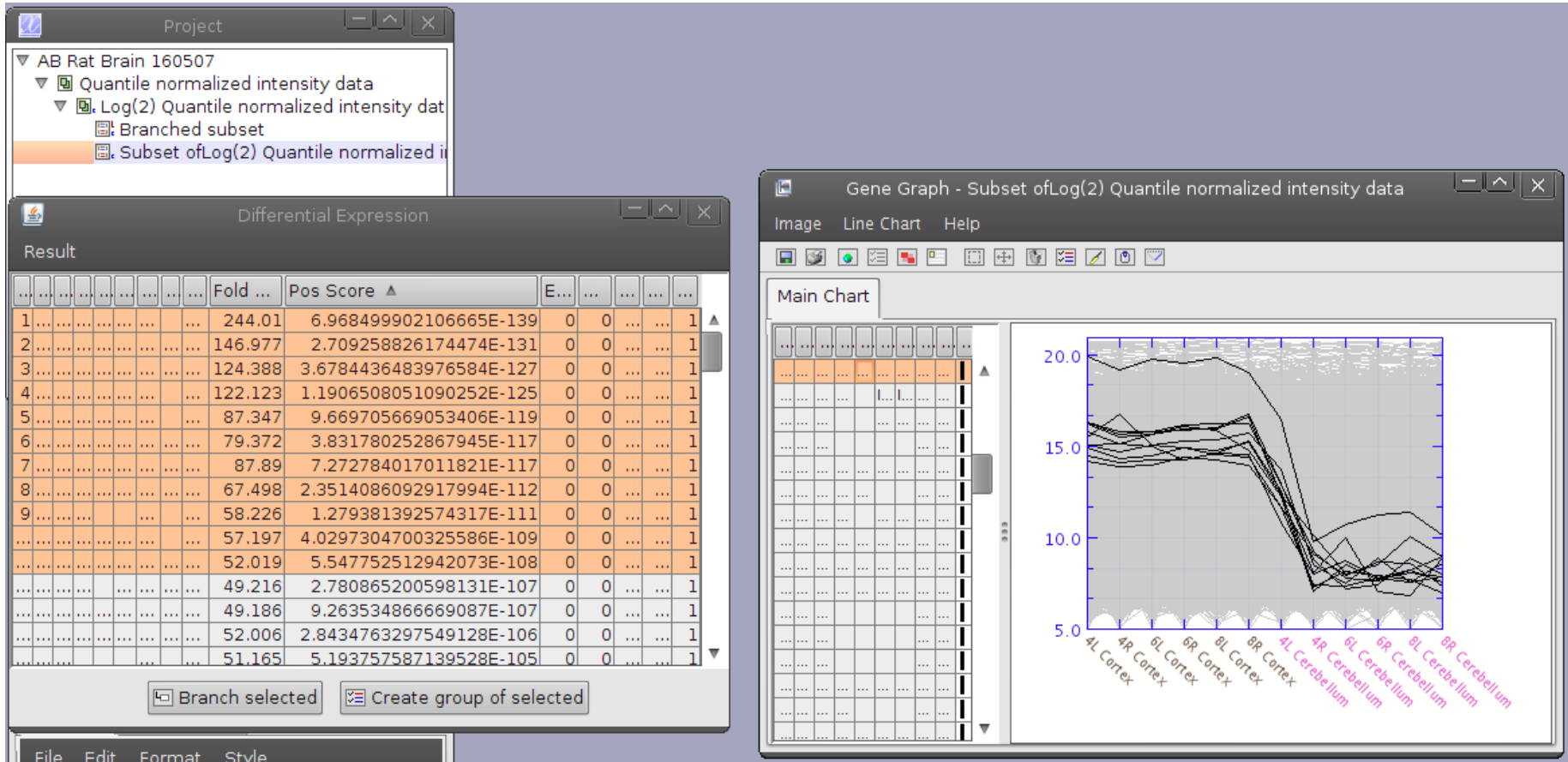
- In many windows you can make a selection of genes (and sometimes samples) interactively
- A selection may serve different purposes:
 - Highlight specific genes in a data set for visualization or similar
 - Prepare for an operation, for instance “Create group” or “Branching”

Making selections

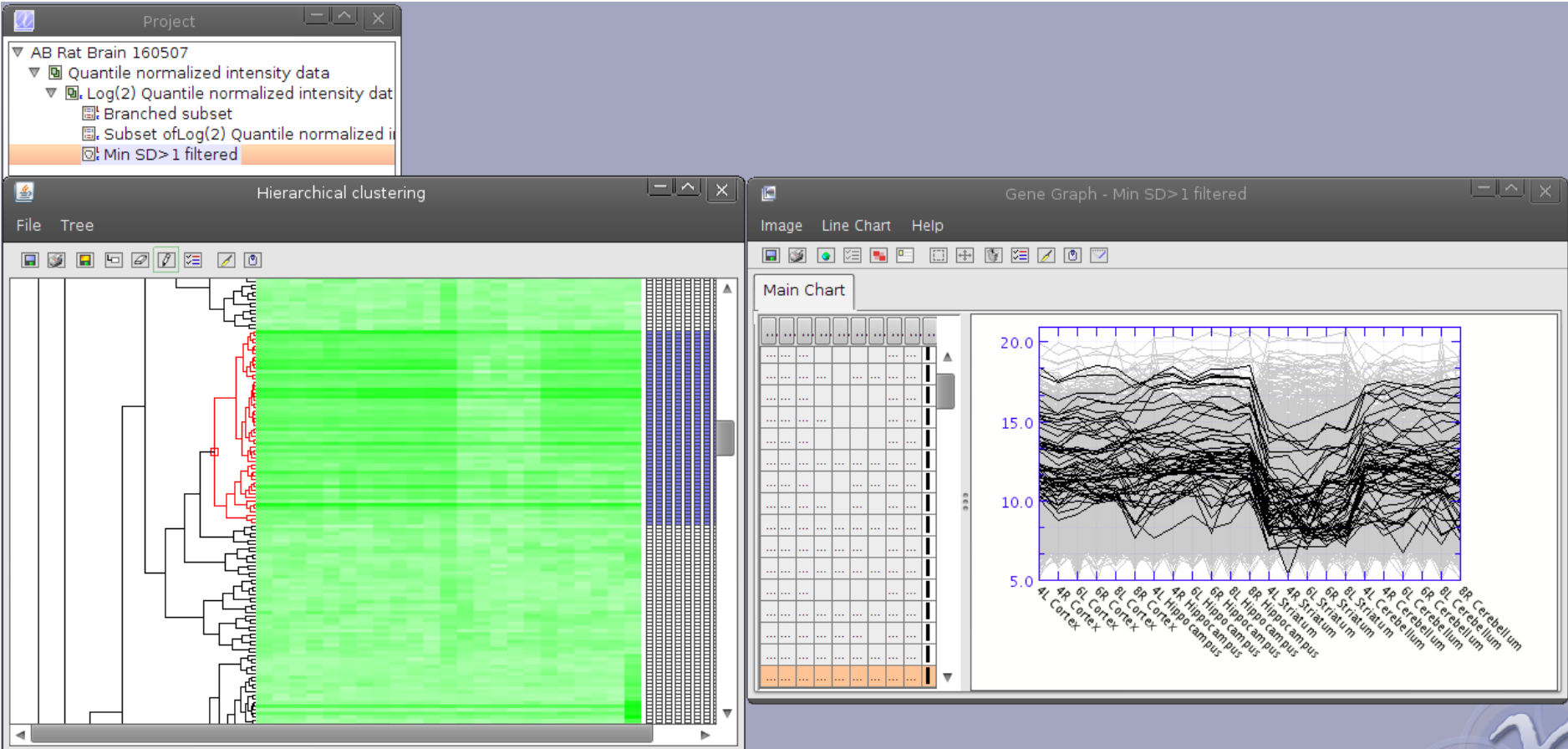
- In lists:
 - Point and click
 - Click and drag (for small sub sets)
 - Click first and Shift + click on last row you want
- Many methods predefine subsets for you that you can select
- In charts: click and drag around objects
- You can easily select all members of groups and branched datasets

1 selection – multiple views

- All views/windows open on the same dataset has the same active selection



1 selection – multiple views (2)

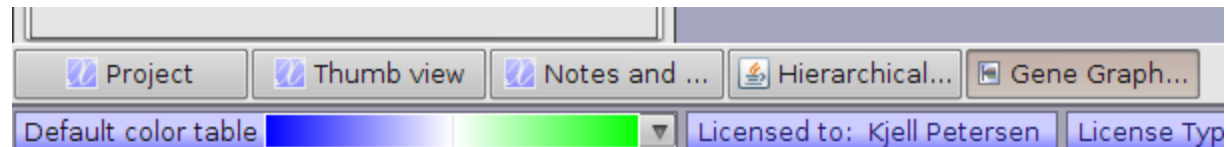
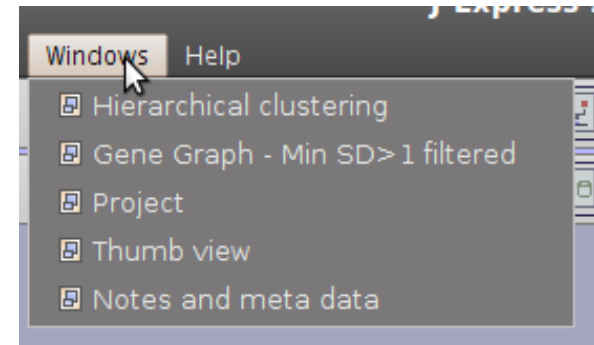


Outline

- Today:
 - Get to know J-Express
 - No statistical analysis
 - Play example analysis: FC viewer
- Tomorrow - some statistics
 - Clustering
 - Differential expression
- Thursday – more statistics
 - Interpreting groups of genes

Tips

- Use titlebar of windows actively – often containing the name of the data set your working on
- Be conscious about which data set is active in the Project window
- Close windows you don't need anymore
- Use the “Windows” menu or
- The Task bar at the bottom to manage your open windows



Course page

1. <http://www.bioinfo.no/training>
2. “read more” on J-Express course in Oslo
3. “Click here to go to Course Home Page” at the bottom of the page