



# Version 1.0: functionality summary

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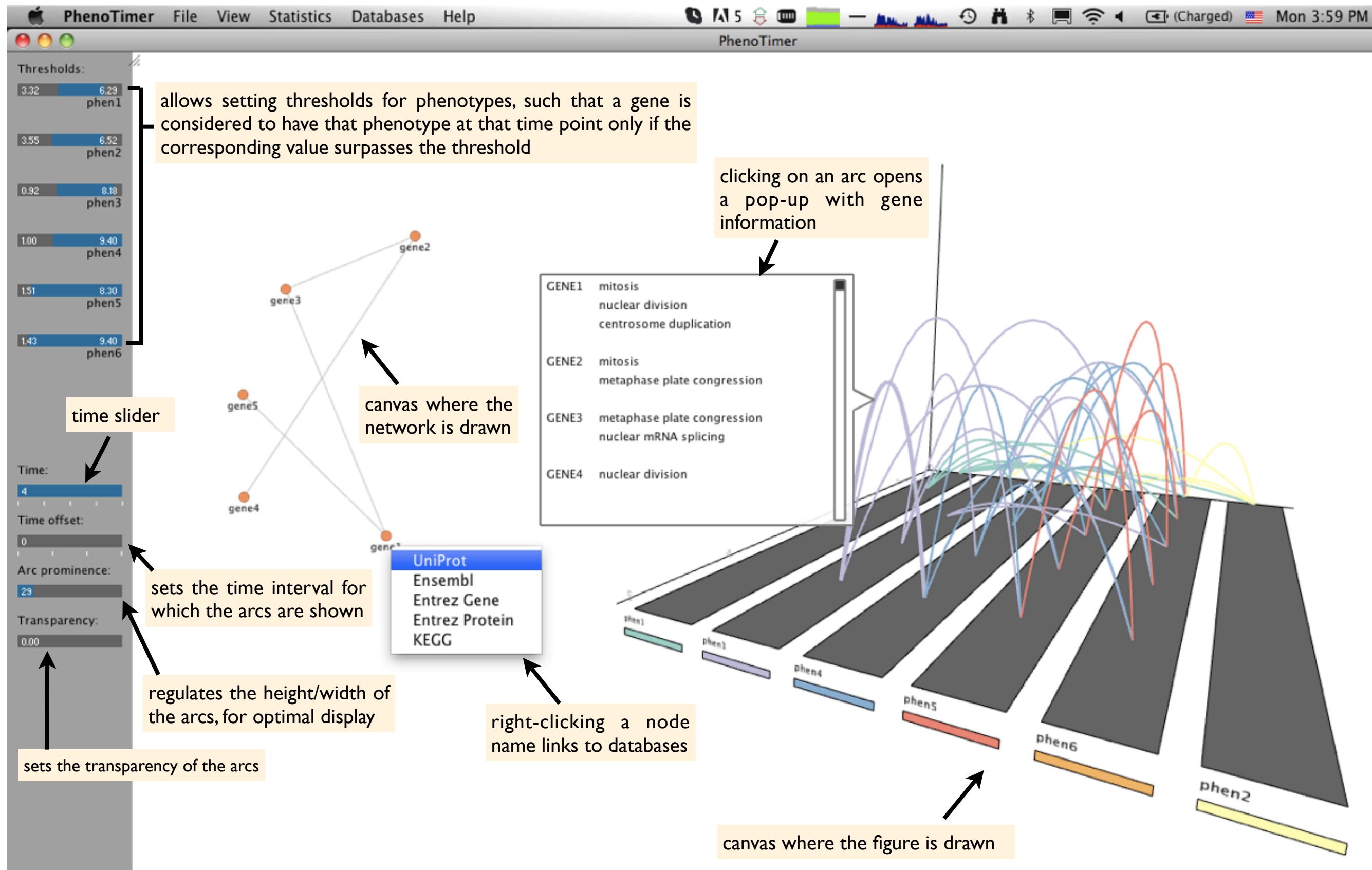


# PhenoTimer

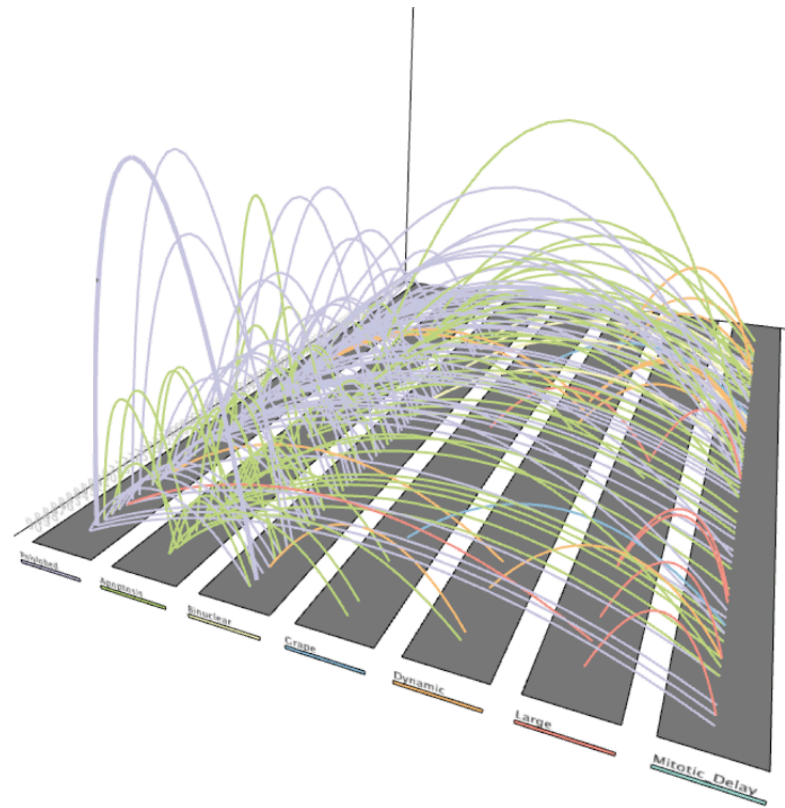
*Connecting time-resolved phenotypes*

The tool enables loading files with gene expression values or other measurements for different phenotypes/pathways, then displays phenotypes that have common genes above threshold levels as arcs. Gene Ontology or other types of networks can be loaded and visualized in parallel, in a time-dependent fashion. Networks of genes that have the same phenotype at a time point can be inferred and displayed. Several view modes are available to the user: 2D/3D arc representations of links between phenotypes, heat maps and line plots of gene-associated values.

# PhenoTimer graphical user interface

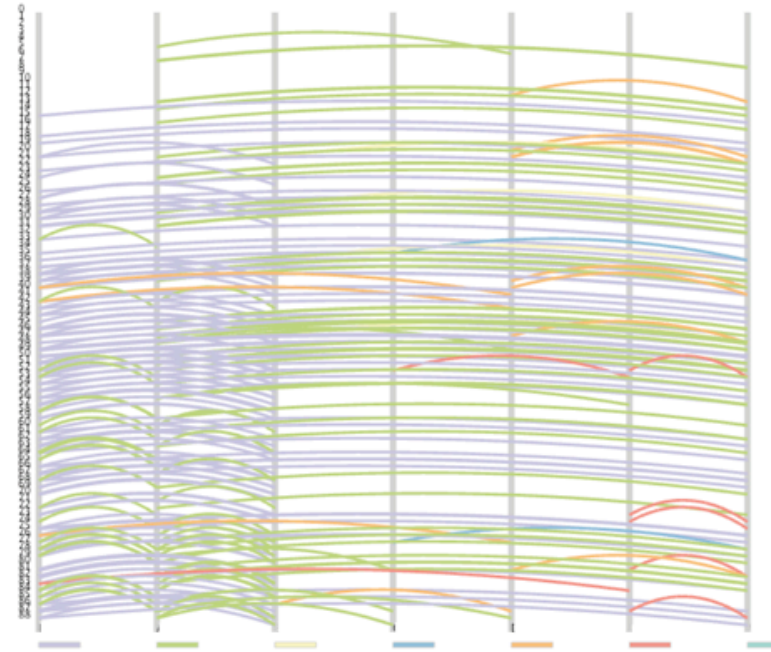


# The view modes

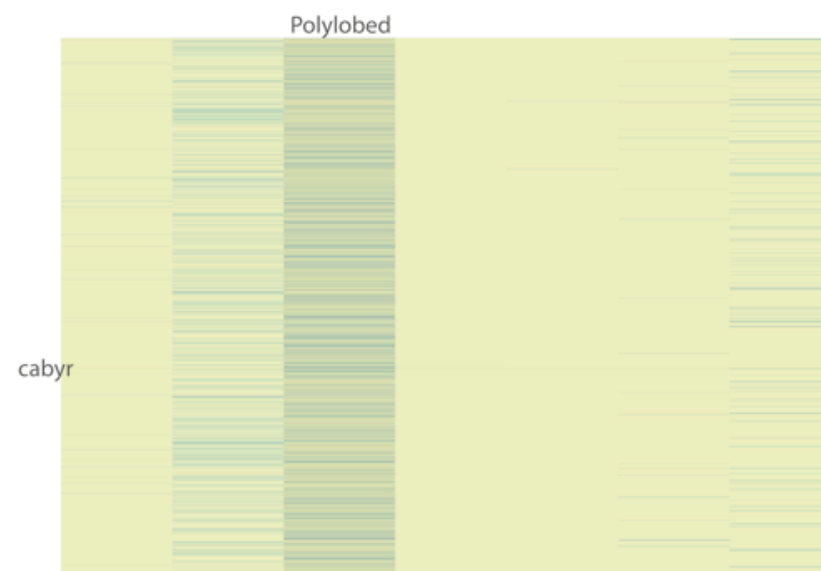
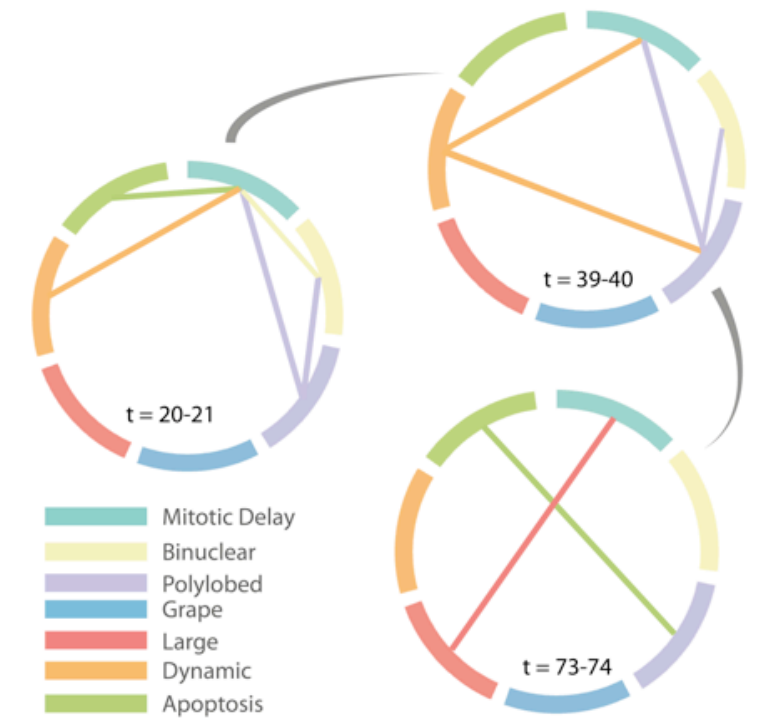


3D arc mode

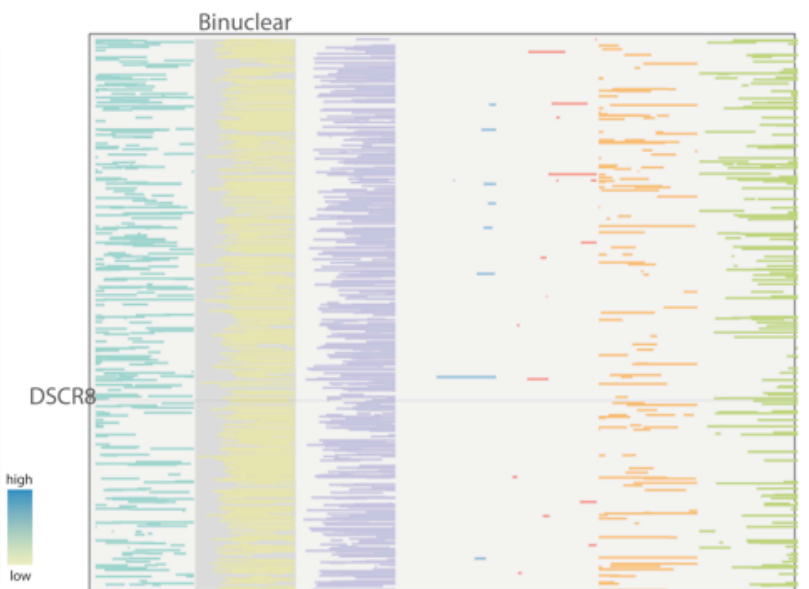
2D arc mode



circular mode

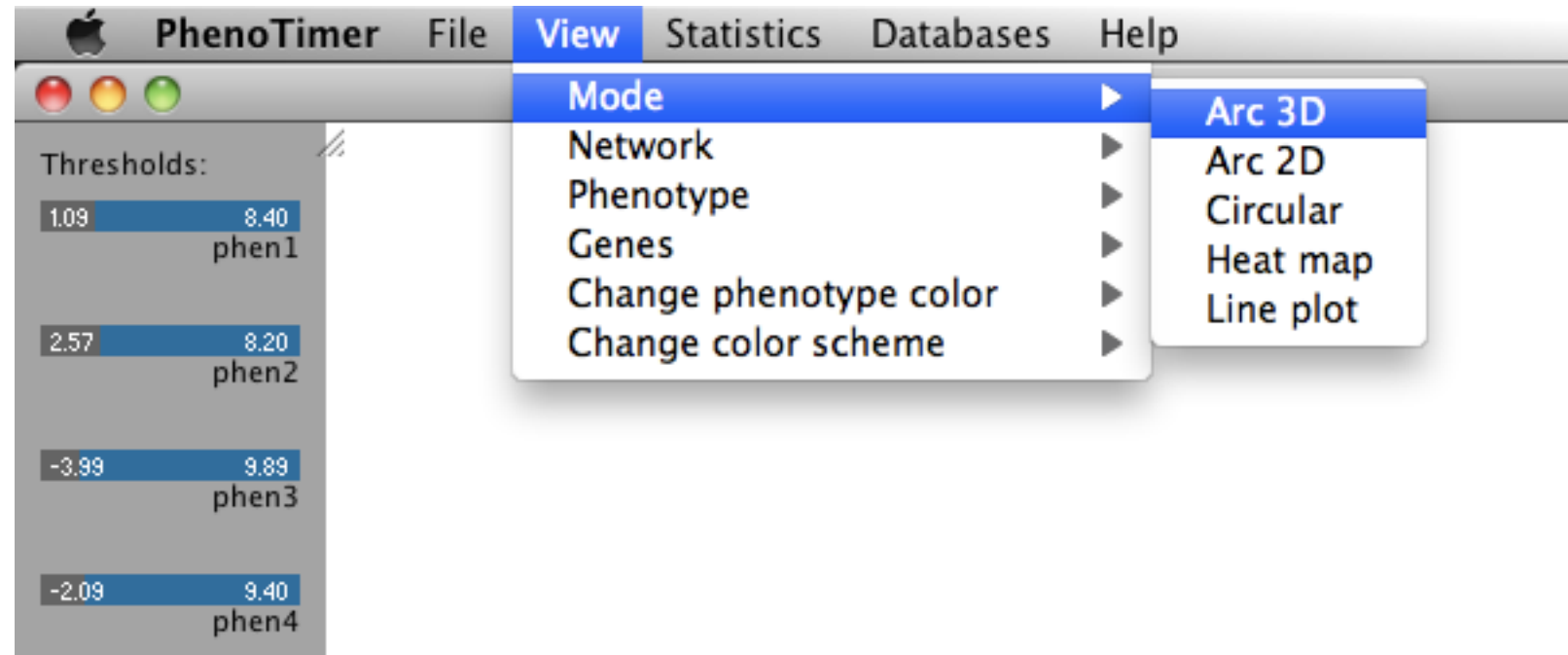


heat map mode

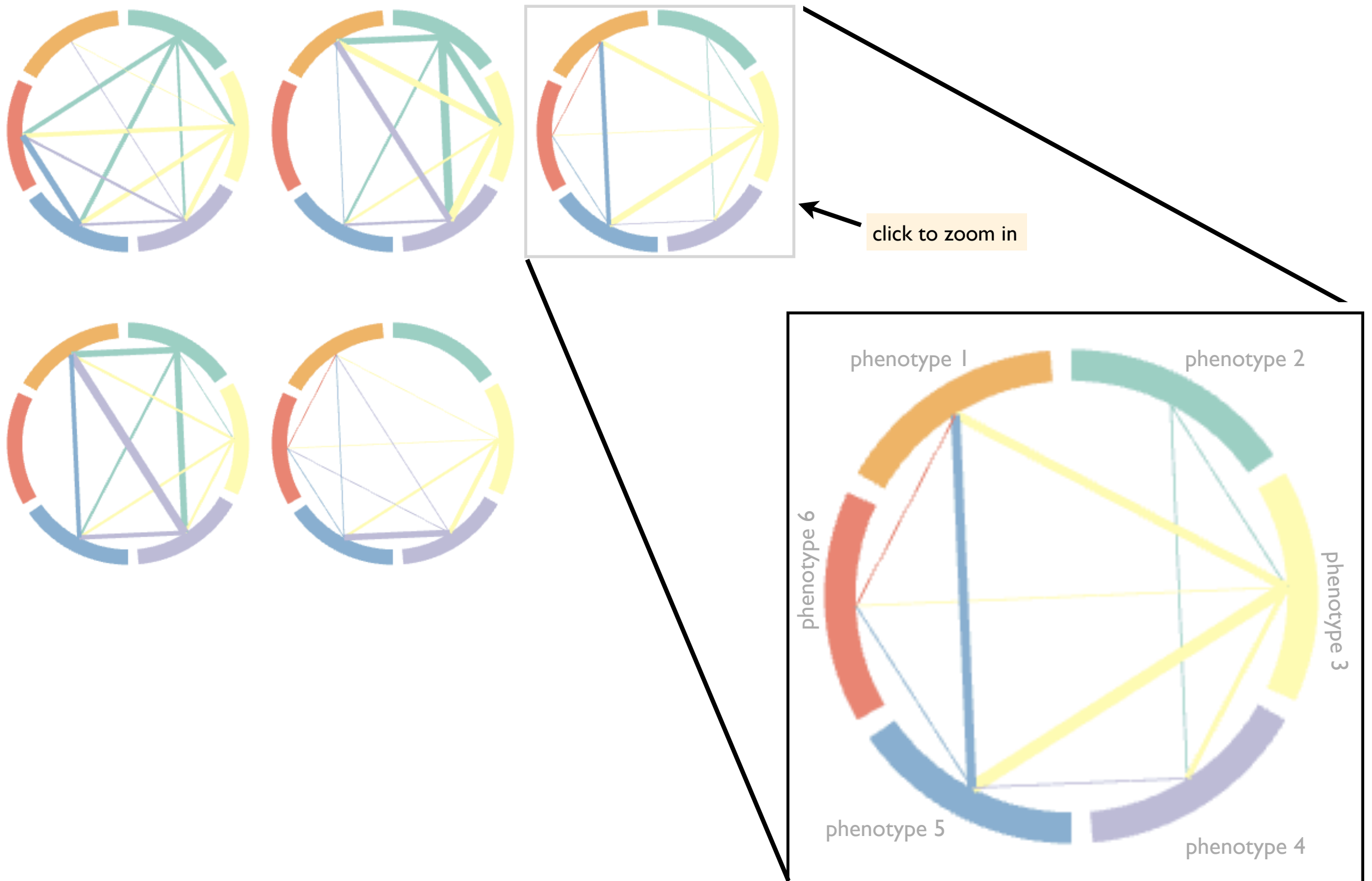


line plot mode

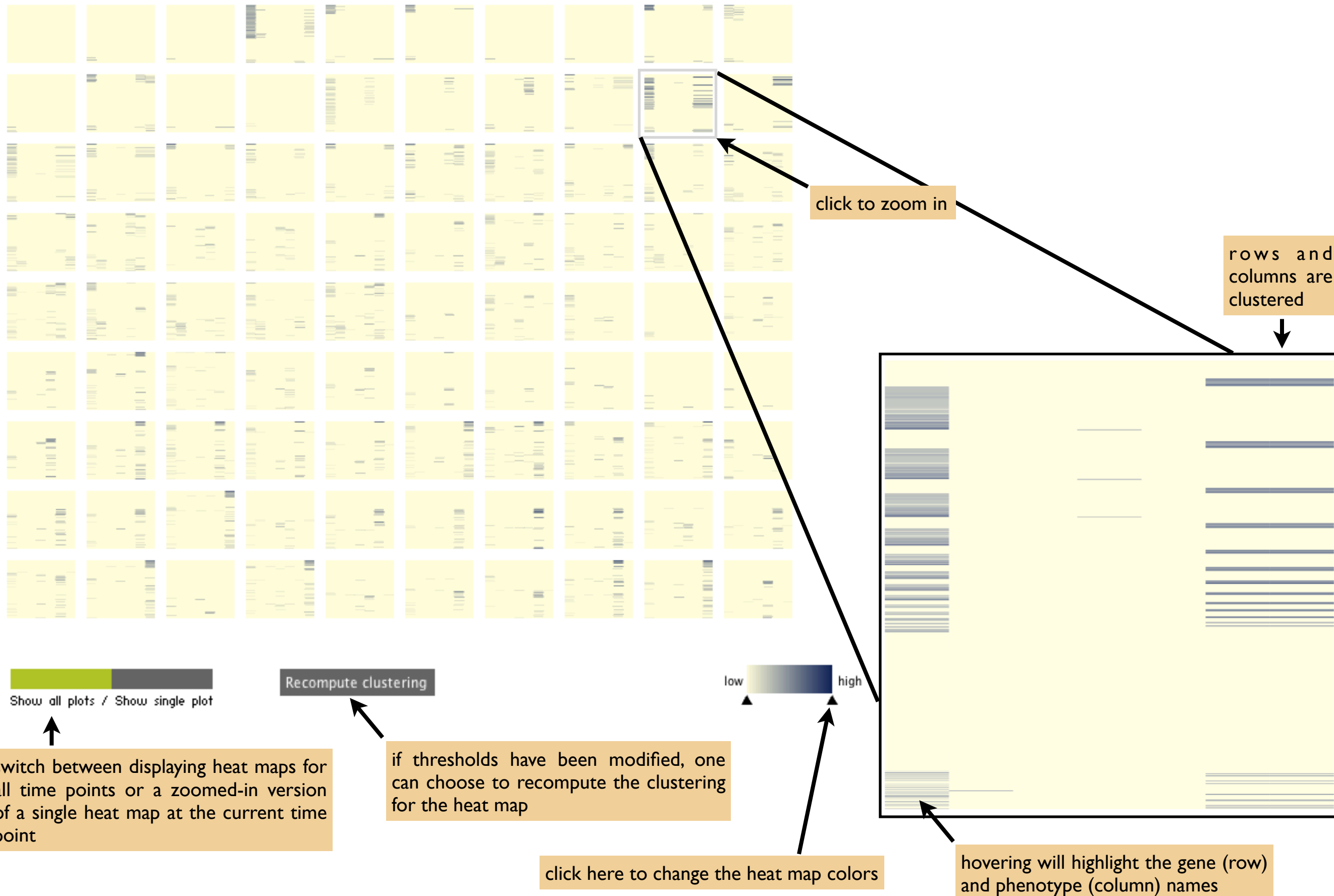
# Switching between view modes



# Circular view mode

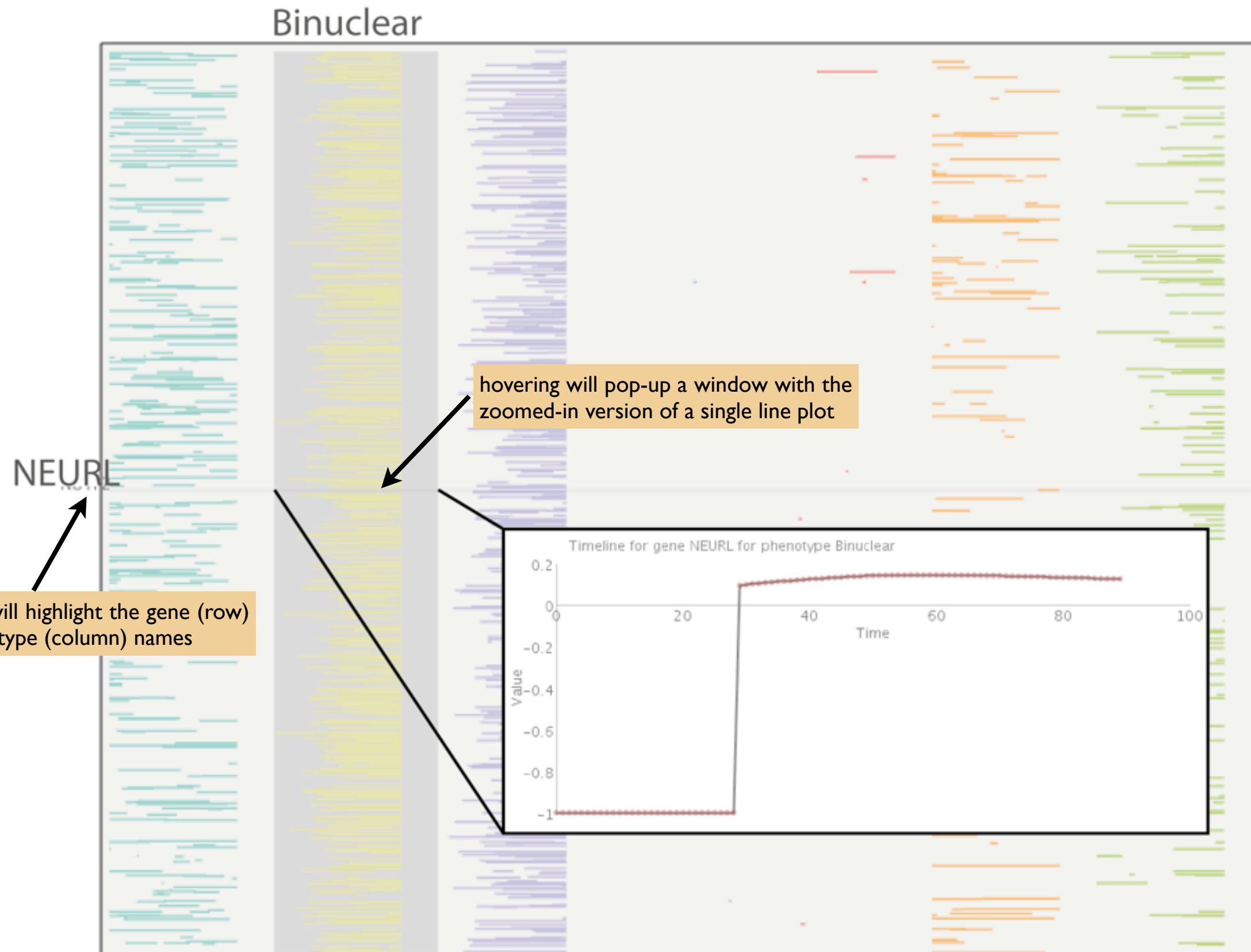


# Heat map mode



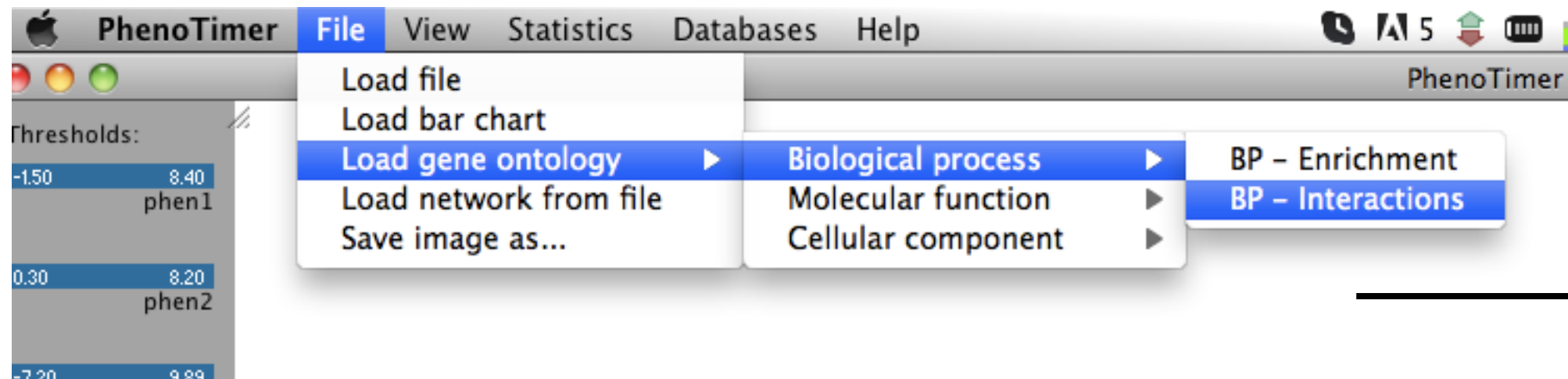


# Line plot mode

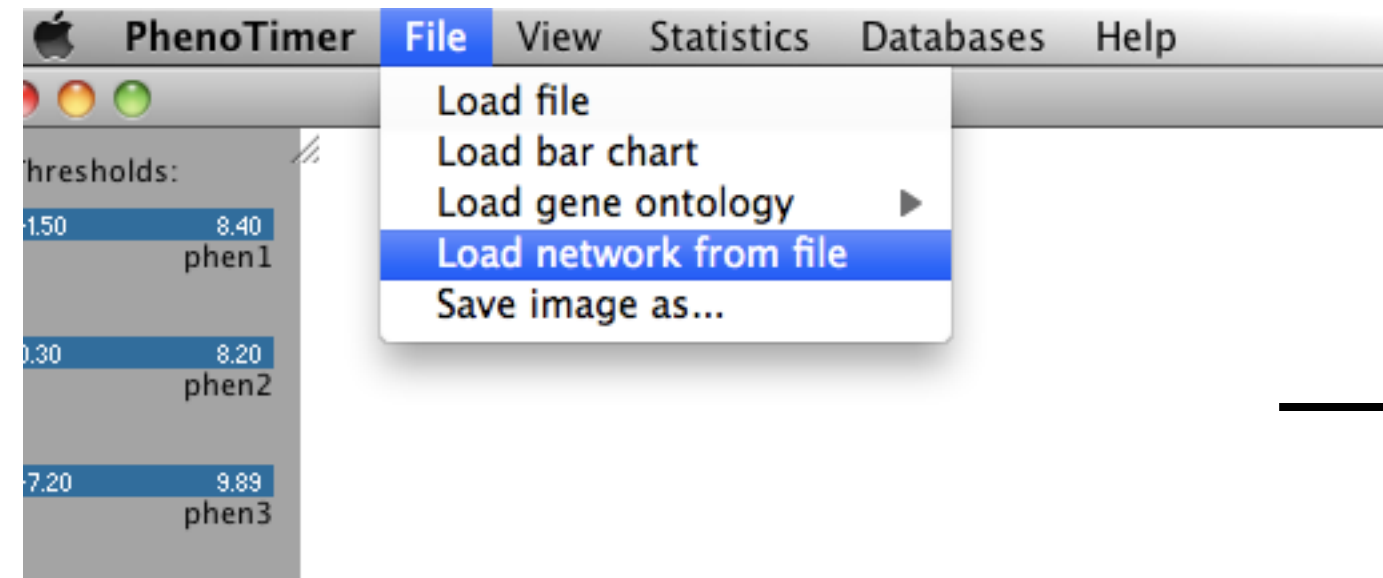




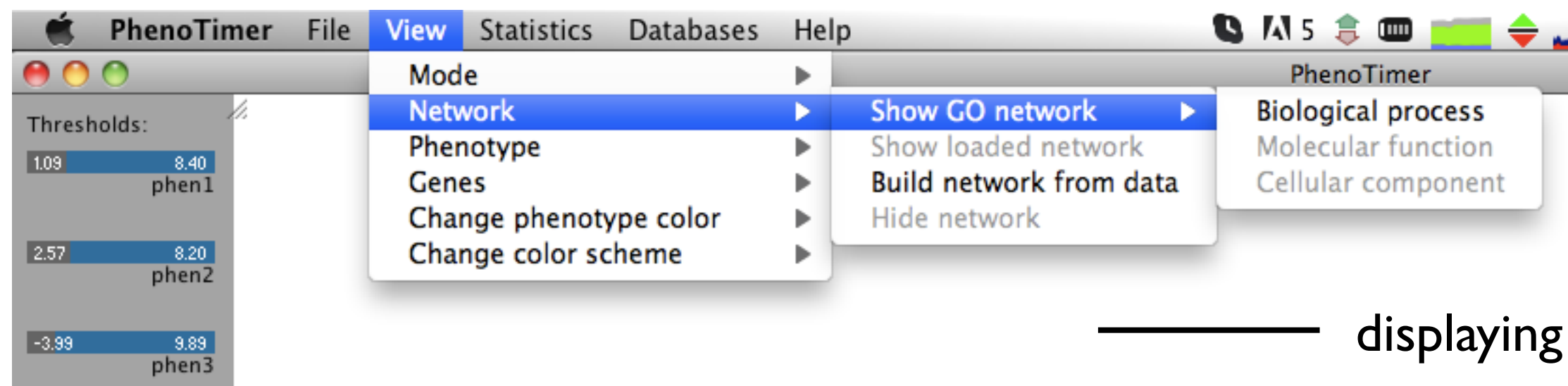
# Loading and displaying networks



GO networks

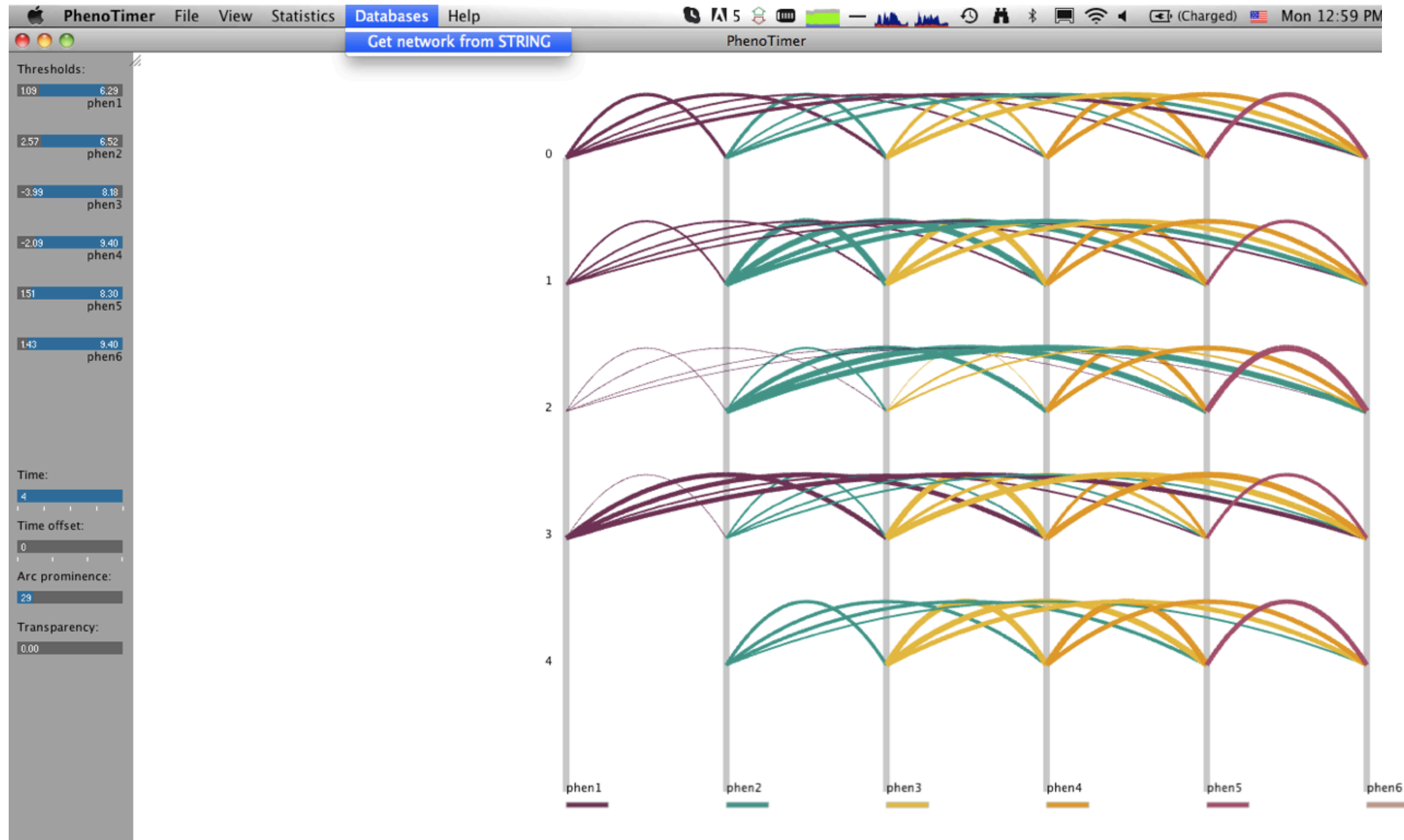


other networks (e.g. PPI)

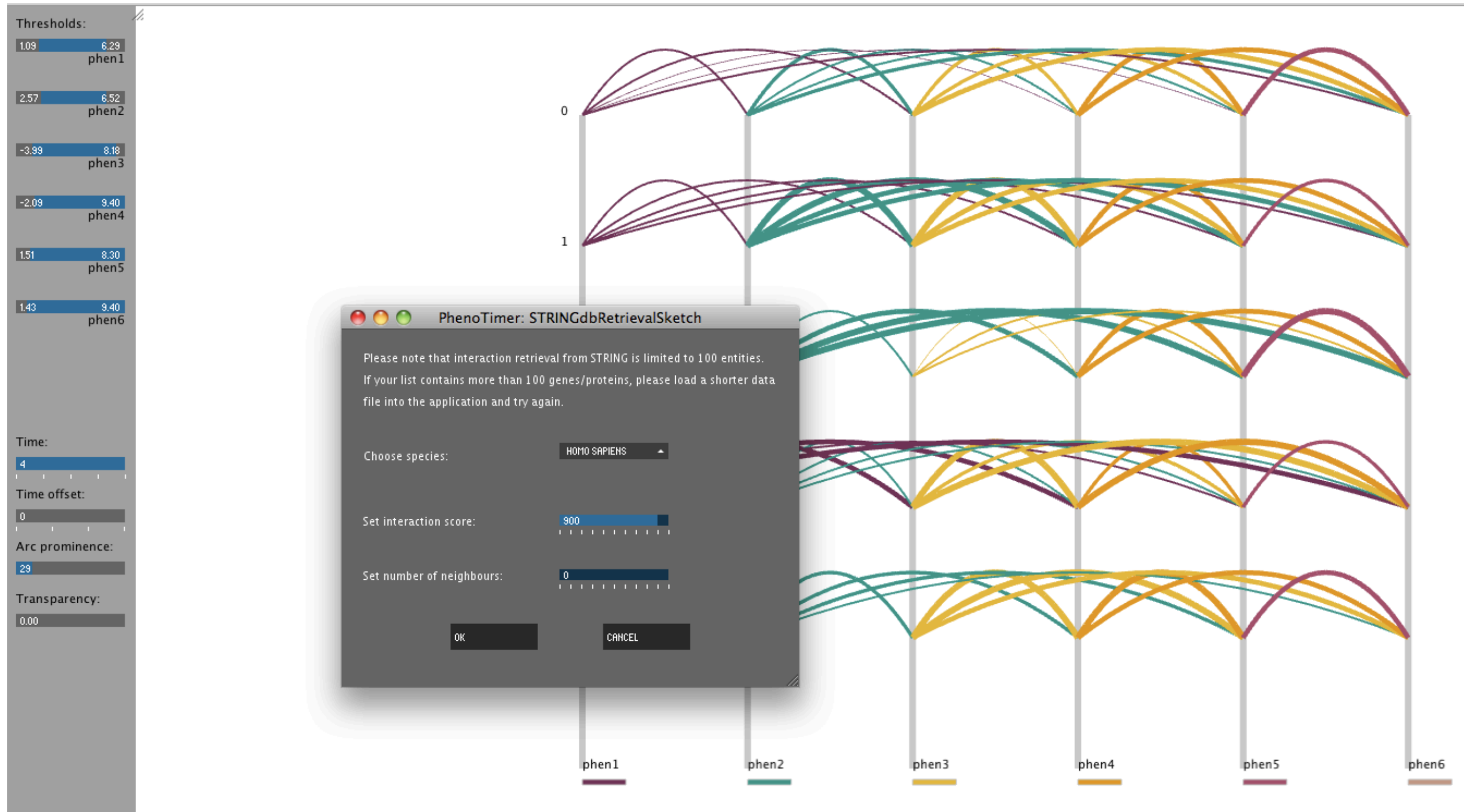


displaying networks

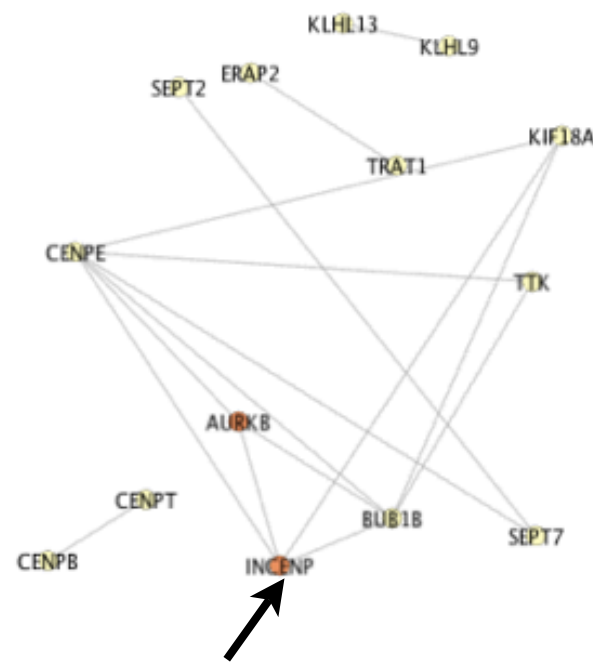
# Loading networks: retrieving network from STRING database



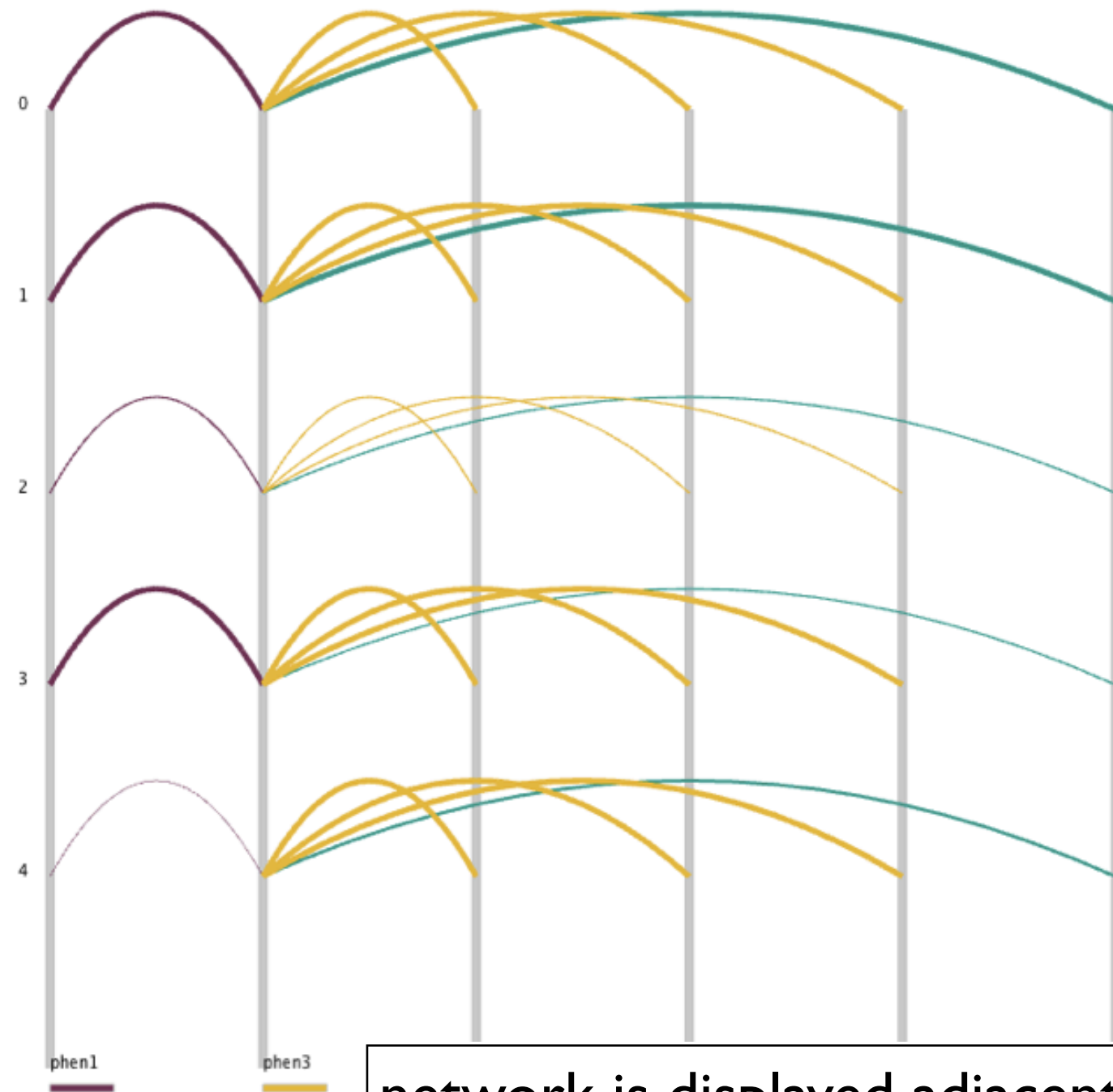
# Loading networks: retrieving network from STRING database



# Dynamic network construction and highlighting

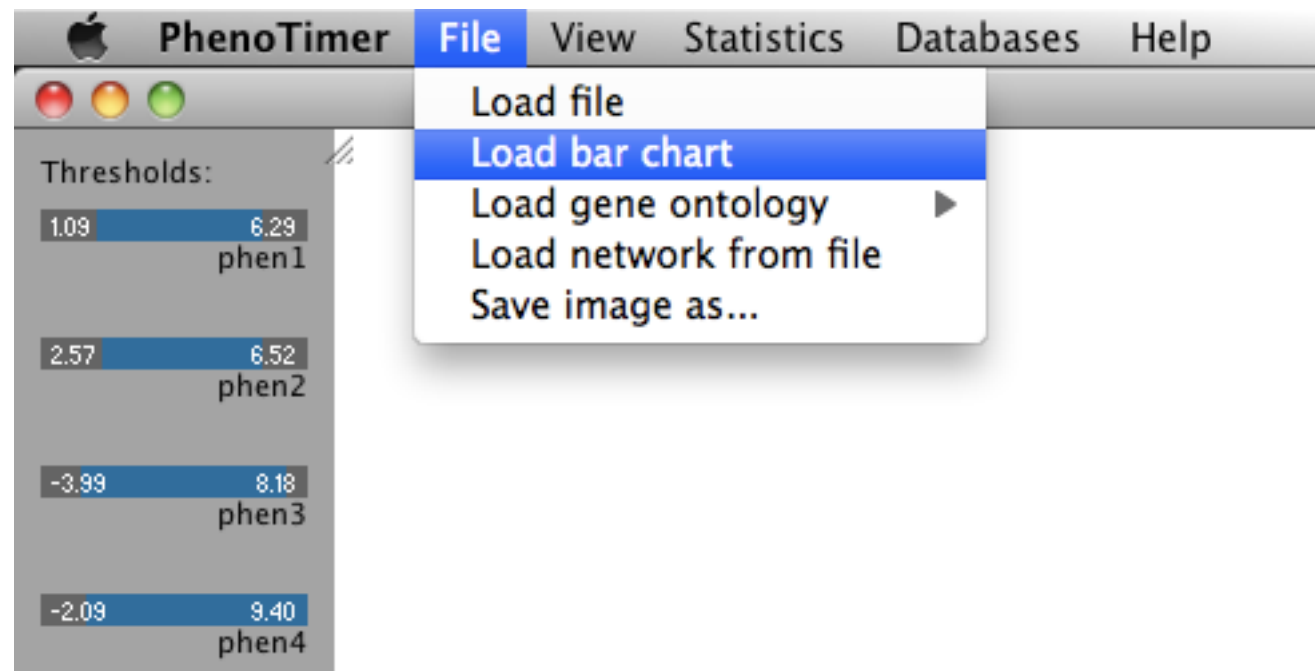


nodes involved in the connections are highlighted at each time point

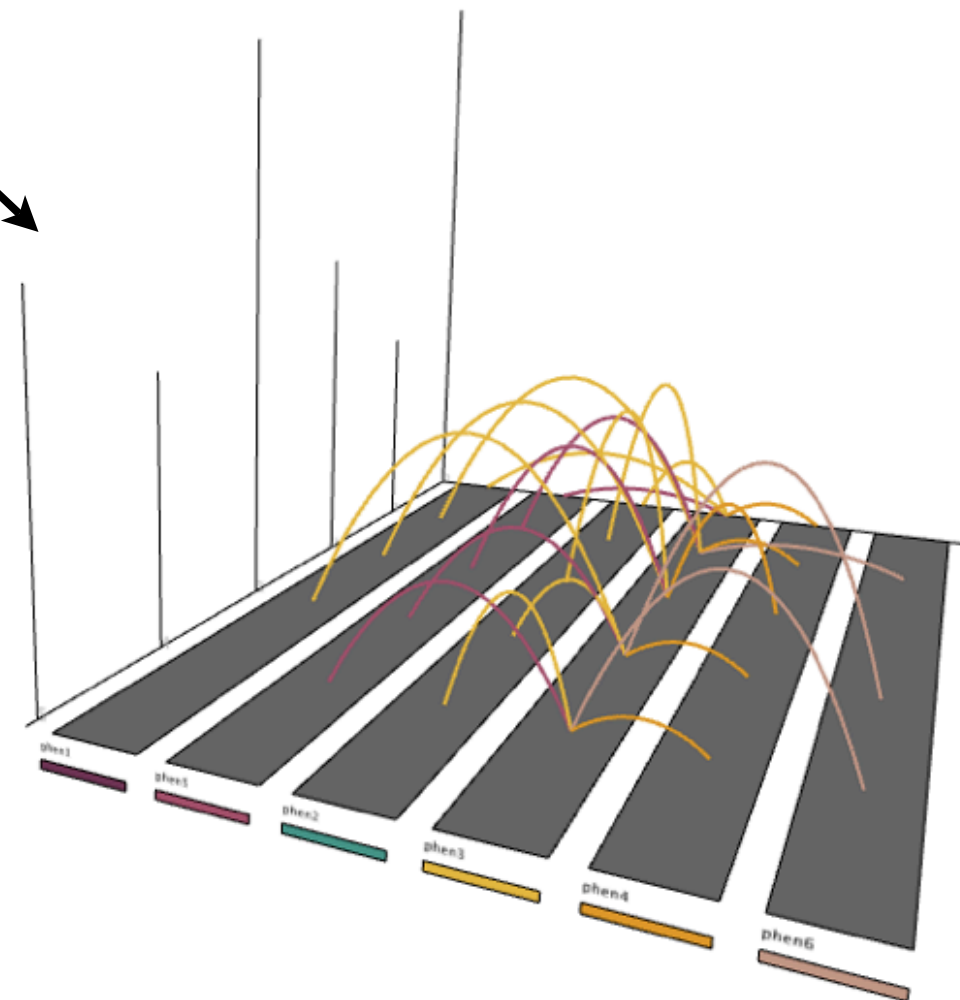


network is displayed adjacent to the plot

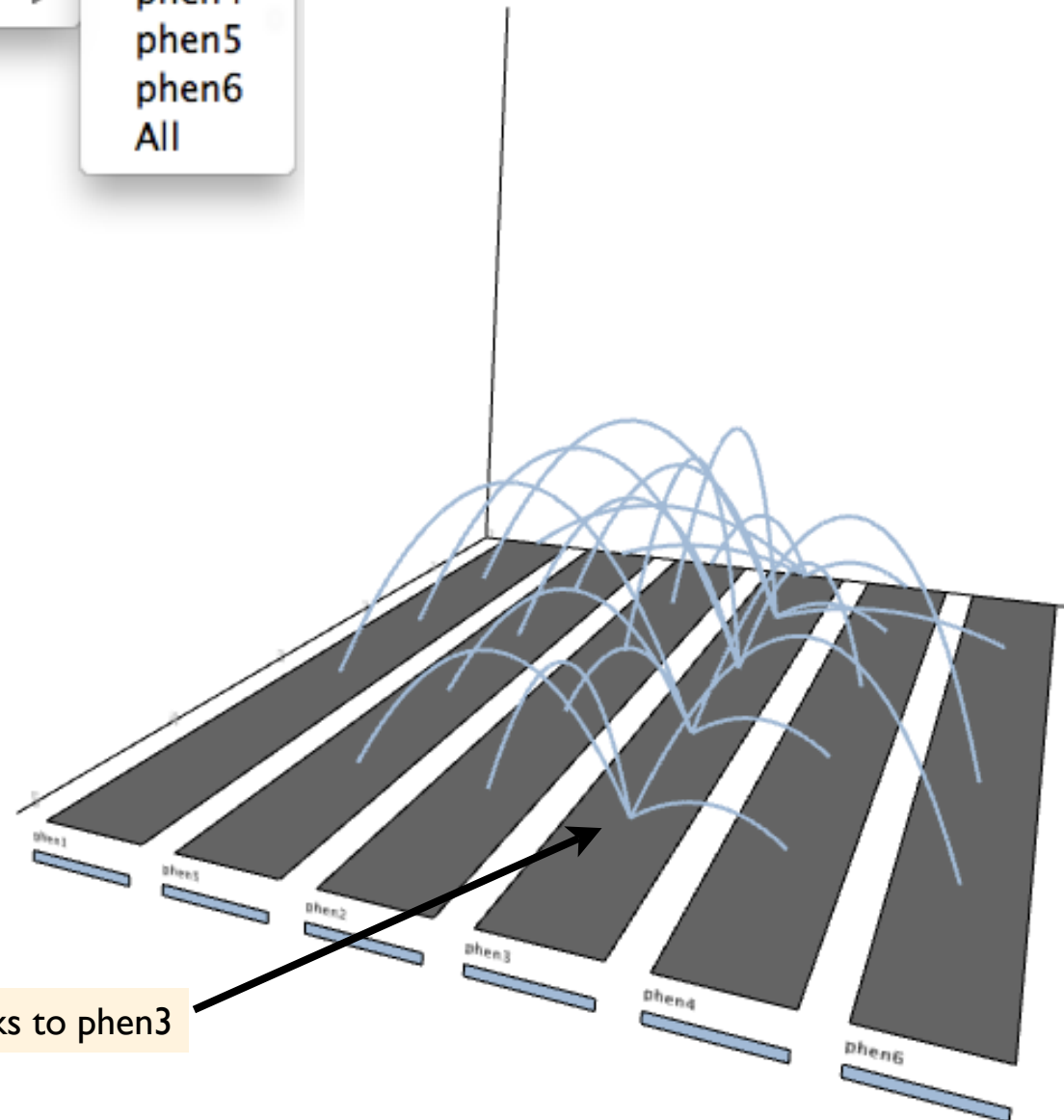
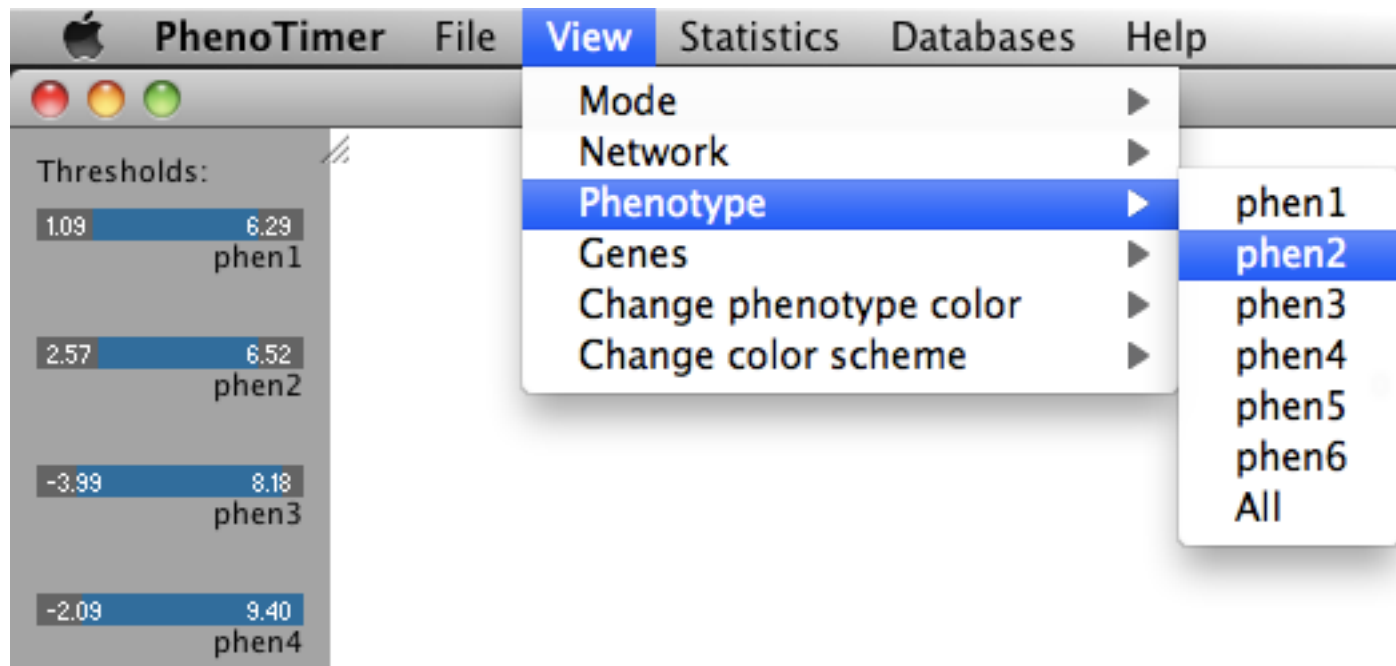
# Loading a bar chart



with bar chart loaded



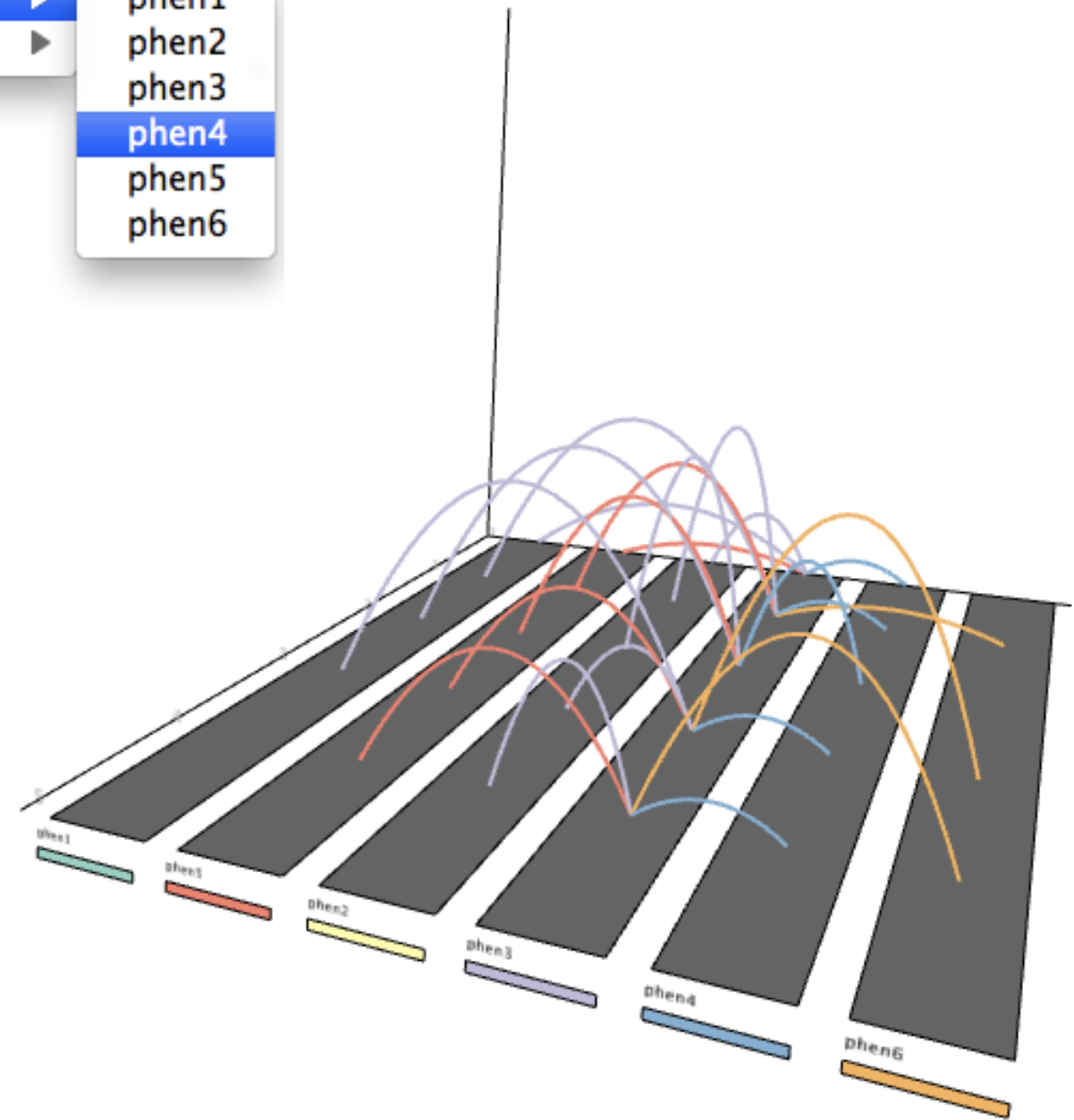
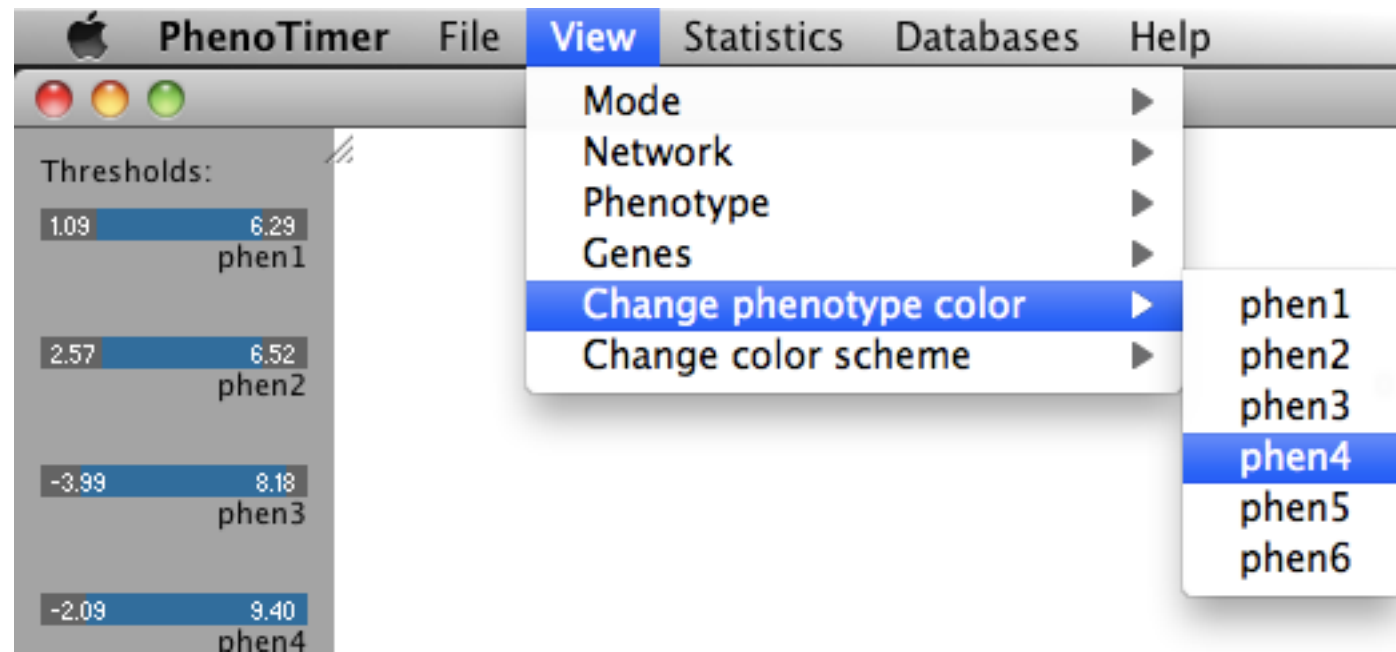
# Show connections to a single phenotype (or to all)



showing only links to phen3

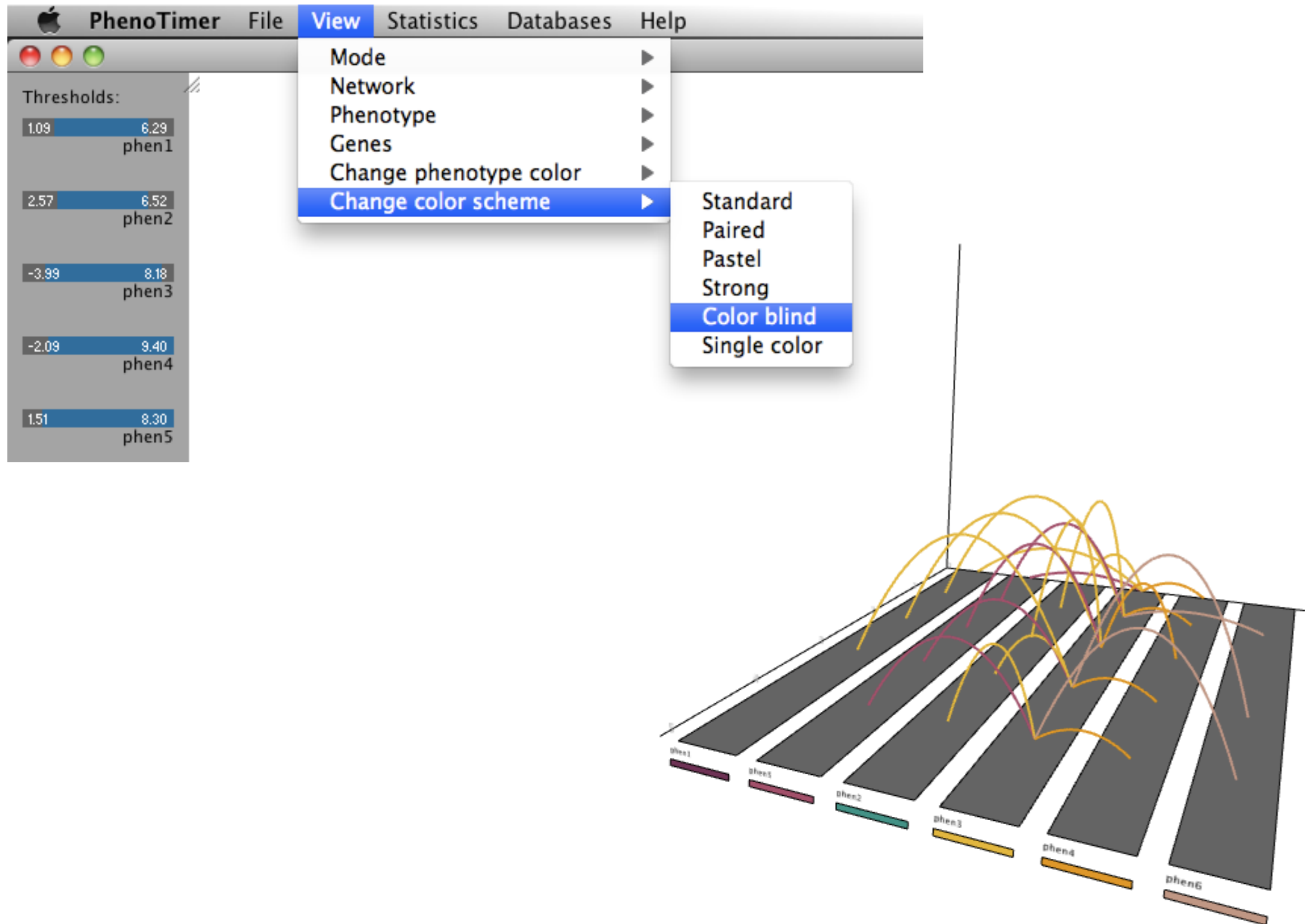


# Changing the arc colors for a phenotype of choice

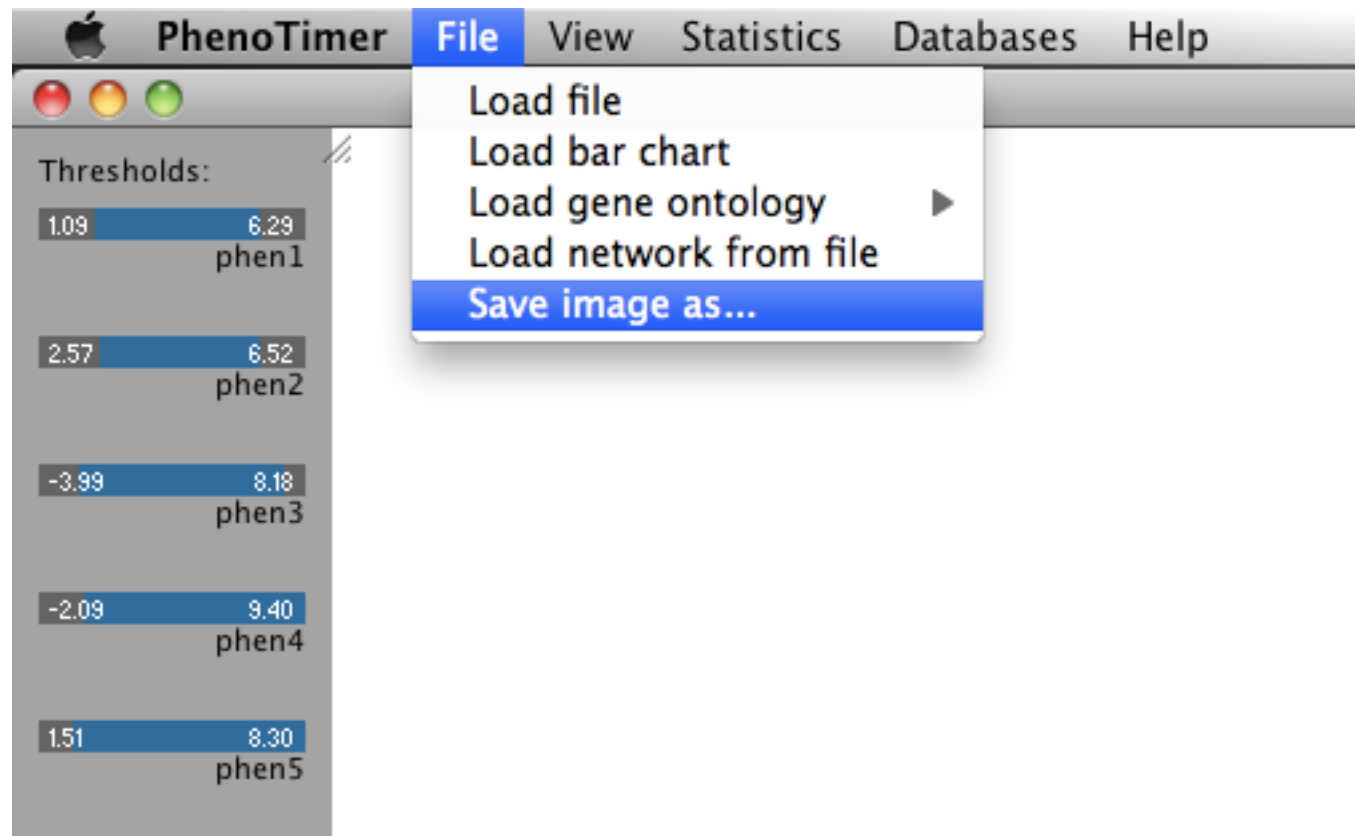




# Changing the color scheme for all arcs and phenotypes



# Saving plot images



# Getting help

The screenshot displays the PhenoTimer application window. The top menu bar includes 'PhenoTimer', 'File', 'View', 'Statistics', 'Databases', and 'Help'. The 'Help' menu is open, showing options: 'Search', 'Quick help', and 'About'. On the left, a 'Thresholds' panel lists six phenotypes (phen1 to phen6) with their respective value ranges. Below this, 'Time' is set to 4, 'Time offset' to 0, 'Arc prominence' to 29, and 'Transparency' to 0.00. The main window features a 3D visualization of time-resolved phenotypic connections, represented by colored arcs connecting different phenotypes. A help dialog box is overlaid on the visualization, providing instructions on view modes, shortcuts, and keypresses. The dialog box includes a 'CLOSE' button in the top right corner. At the bottom of the dialog, it provides a URL for more information: <http://phenotimer.org/>.

PhenoTimer 1.0 visualizes time-resolved phenotypic connections in a genetic context. Five view modes are offered for the user: 3D arc mode, 2D arc mode, circular, heat map, line plot. The modes can be used complementarily.

Shortcuts:

- Mouse dragged + keypressed 'r' → rotate figure
- Mouse dragged + keypressed 'm' → translate (move) figure

Keypressed:

- z → zoom in
- x → zoom out
- t → switch between display of a single time point or the whole trail

For more information, please visit: <http://phenotimer.org/>

Thresholds:

Phenotype	Min	Max
phen1	1.09	6.29
phen2	2.57	6.52
phen3	-3.99	8.18
phen4	-2.09	9.40
phen5	1.51	8.30
phen6	1.43	9.40

Time: 4

Time offset: 0

Arc prominence: 29

Transparency: 0.00



For questions or comments, contact us at: [secrier@embl.de](mailto:secrier@embl.de)

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