

CSI Results Visualisation

A results visualisation tool has been developed in order to help you explore some common features output from the CSI model. Roughly, the tool allows you to visualise the resulting marginal and MAP networks, applying thresholds as appropriate. One can also view the model predictions while comparing them to the input data.

The main display is broken into three main sections; the top right of the page displays the network, the top left shows a table of genes and various attributes associated with them, at the bottom of the page a series of plots show a selected gene and its parents. The menu-bar at the top of the page allows some other operations to be performed.

Network Graph

The top right of the page displays a directed graph showing all the selected genes with arrows pointing from “parental” genes to their targets. The plot can be dragged after clicking with the mouse and zoomed by “scrolling”. Hovering over a node displays its name, while clicking on it allows it to be rearranged within the graph.

The actual nodes and edges displayed within the graph is a representation of the graph with the current options applied, with a number of controls in other sections controlling what’s displayed.

$$\sum_i x_i$$

Table of Genes

The table in the top right of the page displays a list of genes and various attributes associated with them. The checkbox shows which genes are selected to be displayed within the network graph and can be toggled individually or across all genes by clicking on different checkboxes. The other columns show results from the model that are helpful in extracting information from its fit.

All columns can be sorted by clicking on their title, clicking on the same column a second time will reset the sort. Sorting by any column and then inspecting the top and bottom genes can be informative, either of biologically relevant information or of the model misinterpreting the input data and further preprocessing.

Number of Parents and Children

The columns titled `Prnt` and `Chld`

Manual Result Extraction

In order to open CsiVis the HDF5 results from CSI need to be transformed into a JSON file. This process happens automatically within the iPlant App, but can be triggered manually by running a command like:

```
python csi-postprocess.py output.h5 -v > output.json
```

This command executes the Python script `csi-postprocess.py`, telling it to take the complete results from the HDF5 formatted file `output.h5`, extract the *better* models and predictions and write them out to `output.json`. The `-v` option causes output to be *verbose*, that is it displays some progress messages.

A few options exist to control this extraction process, and these can be seen by running:

```
python csi-postprocess.py --help
```

A more complete set of results can be viewed by running:

```
python csi-postprocess.py -v output.h5 \  
    --weight 1e-6 --predict 1e-3 > output.json
```

will cause models with even lower probabilities to be written to the JSON file, as well as more predictions. The trade off is larger JSON file size which can cause issues when loading CsiVis in a web browser.