

MINDYViewer Documentation

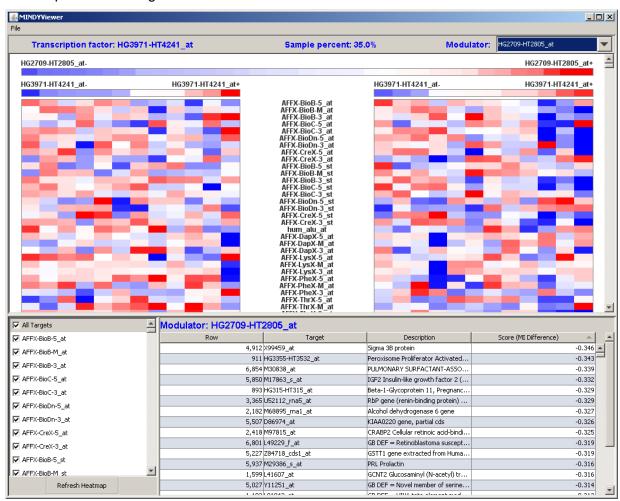
Description: Views the results of MINDY

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Release: 1.0

Summary:

The MINDYViewer module displays analysis results generated by the MINDY (<u>M</u>odulator <u>Inference</u> by <u>Network</u> <u>Dy</u>namics) module. This implementation uses results from the MINDY heatmap visualizer in geWorkbench.



The heatmap on the left contains the specified percentage of samples where the modulator is least expressed. The heatmap on the right contains the specified percentage of samples where the modulator is most highly expressed. In both heatmaps, the samples are sorted based on the expression level of the transcription factor (from lowest to highest expression value). As shown in the legends above the heat maps, dark blue represents the lowest expression values and dark red the highest expression values.



The table below the heatmaps lists the conditional MI difference for each target gene. This value, which ranges between -1 and 1, is interpreted as follows:

score < 0, MI between the transcription factor and the target gene is greater when the specified modulator gene is highly expressed; the modulator inhibits the transcription factor/target interaction

score = 0, MI between transcription factor and target gene is not statistically different when the specified modulator gene is least and highly expressed; the modulator does not modulate the transcription factor/target interaction

score > 0, MI between transcription factor and target gene is greater when the specified modulator gene is least expressed; the modulator enhances the transcription factor/target interaction

Operations:

If you have analyzed more than one modulator gene, use the Modulator drop-down list at the top of the window to select the modulator to display.

To display a subset of the target genes, use the Target list (bottom left) to select the genes and then click the *Refresh Heatmap* button.

To save the heatmaps to an image file (.png format), display the desired subset of target genes and then select *File>Save Image*. Attempting to save a heatmap image with all target genes displayed may generate an out-of-memory error.

For a description of the transcription factor, move your cursor over the name of the transcription factor (above the heatmaps). For a description of the modulator gene, move your cursor over the name of the modulator (above the table).

References:

- Wang K, Nemenman I, Banerjee N, Margolin AA, Califano A, Genome-wide Discovery of Modulators of Transcriptional Interactions in Human B Lymphocytes. Proceedings of the 10th Intl. Conf. on Res. In Comp. Mol. Biol. (RECOMB), Venice Apr. 2006.
- http://www.geworkbench.org

Parameters:

Name	Description
dataset.file	Input fileres, .gct
mindy.file	Output from MINDY modulemindy

Platform dependencies:

GenePattern

Module type: Visualizer

CPU type: any OS: any

Java JVM level: 1.5

Language: Java