

# GenePattern

## MINDY Documentation

**Description:** Runs the MINDY algorithm  
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**Release:** 1.0

### Summary:

The MINDY (**M**odulator **I**nference by **N**etwork **D**ynamics) algorithm computationally infers genes that modulate the activity of a transcription factor at post-transcriptional levels. For a complete description of the MINDY algorithm see Wang, et. al. (2006). Briefly, the algorithm uses mutual information (MI) to measure the mutual dependence of the transcription factor (TF) and its target gene. It computes the following values:

- **unconditional MI** measures the MI of the TF and its target gene across all samples
- **conditional MI** measures the MI of the TF and its target gene across the subset of samples in which the modulator gene is most (or least) expressed
- **conditional MI difference** measures the difference between the conditional MI of the TF and its target gene when the modulator gene is most expressed and when it is least expressed:

$$\begin{aligned} \text{conditional MI difference} = \\ & (\text{MI of TF and target gene when the modulator is most expressed}) - \\ & (\text{MI of TF and target genes when the modulator is least expressed}) \end{aligned}$$

A conditional MI difference that is statistically different than 0 indicates that the modulator gene modulates the interaction of the TF and its target gene.

This implementation uses the MINDY code developed for geWorkbench.

### 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 10<sup>th</sup> Annual Intl. Conf. on Res. In Comp. Mol. Biol. (RECOMB), Venice Apr. 2006. ([http://arxiv.org/PS\\_cache/q-bio/pdf/0510/0510030v2.pdf](http://arxiv.org/PS_cache/q-bio/pdf/0510/0510030v2.pdf))
- <http://www.geworkbench.org>

### Parameters:

Name	Description
input.file	Input file - .res, .gct
modulator.list	A file containing a list of genes (one gene per line) which are possible modulators of the transcription factor. The greater the number of genes in the list, the more time the analysis

# GenePattern

	requires.
dpi.transcription.factor.list	Used with the <i>dpi.tolerance</i> parameter. A file containing a list of all genes (one gene per line) that are annotated as transcription factors. Specifying transcription factors allows the Data Processing Inequality (DPI) to be applied more intuitively when reconstructing the transcriptional interaction network. As a result, indirect interactions of a transcription factor via another transcription factor will be removed from result. For a discussion of the DPI, see section 2.3 in Wang, et. al. (2006).
transcription.factor	The transcription factor.
sample.percentage	Percentage of the samples to use for calculating the least and most expressed states of the modulator gene(s).
conditional.mi.threshold	Threshold for a conditional mutual information (MI) estimate to be considered statistical different from zero. For example, a value of 0.20 filters out target genes with a conditional MI score of less than 0.20. By default, no threshold is set.
conditional.mi.p.value	Ignored if <i>conditional.mi.threshold</i> is specified. Significance level for a conditional mutual information (MI) estimate to be considered statistically different from zero. This is a value between 0 and 1, with 1 indicating no threshold. By default, the value is 1.
dpi.tolerance	Used with the <i>dpi.transcription.factor.list</i> parameter. The percentage of MI score calculations to consider as sampling error. For example if three genes A, B, C form a loop with gene pairs AB, BC, and AC. Then gene pair AB would be removed if: $(MI \text{ of gene AB}) \leq (1-e) (MI \text{ of gene AC})$ $(MI \text{ of gene AB}) \leq (1-e) (MI \text{ of gene BC})$ where <i>e</i> is <i>dpi.tolerance</i> . Corresponding calculations would be done for gene pair BC and AC. The DPI tolerance is normally between 0 and 0.15 since values larger than 0.15 yields higher false positives.
unconditional.mi.threshold	Threshold for an unconditional mutual information (MI) estimate to be considered statistical different from zero. For example, a value of 0.20 filters out target genes with an unconditional MI score of less than 0.20. By default, no threshold is set.
unconditional.mi.p.value	Ignored if <i>unconditional.mi.threshold</i> is specified. Significance level for an unconditional mutual information (MI) estimate to be considered statistically different from zero. This is a value between 0 and 1, with 1 indicating no threshold. By default, the value is 1.

# GenePattern

output.file	The name of the output file - .mindy
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# GenePattern

## Output File:

1. MINDY (.mindy) result file. The .mindy file format is:

transcription factor:	<i>transcription factor</i>			
sample per condition:	<i>sample percentage</i>			
Target	<i>Modulator1</i>	<i>Modulator2</i>	<i>Modulator3</i>	...
<i>target1</i>	score (T1-M1)	score (T1-M2)	score (T1-M3)	
<i>target2</i>	score (T2-M1)	score (T2-M2)	score (T2-M3)	
<i>target3</i>	score (T3-M1)	score (T3-M2)	score (T3-M3)	
...	...	...	...	

The transcription factor and sample per condition values appear on the first two lines.

The remaining lines define a table with modulators as the column names and targets as the row names. The score is the conditional MI difference, which is interpreted as follows:

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

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

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

Use the MINDYViewer module to display the analysis results graphically.

## Platform dependencies:

<b>Module type:</b>	Pathway Analysis
<b>CPU type:</b>	any
<b>OS:</b>	any
<b>Java JVM level:</b>	1.5
<b>Language:</b>	Java