Transcription factors control gene expression by binding to regulatory DNA sequences upstream of genes.

- Activators increase gene expression.
- Repressors decrease gene expression.
- Transcription factors are themselves proteins that are transcribed by genes.

The model, called GRNmap, consists of a set of transcription factors that regulate the level of expression of a set of target genes, which can include other transcription factors.

- The dynamic of a GRN is how the expression of genes in the network change over time.

**Yeast respond to the environmental stress of cold shock by changing gene expression**

- Little is known about how transcription factors regulate RNA response.
- The yeast genome is the global transcriptional response to cold shock, where the network of genes that are upregulated under cold shock are called the cold-shock pathway.

The transcription factor deletion strains (ΔCIN5, ΔSWI4) are the key players in the cold-shock pathway.

- The ΔCIN5 strain is the most critical for growth at cold temperatures.
- The ΔSWI4 strain has the largest number of genes that are upregulated under cold shock.

**The fit of the model parameters is close to the minimum theoretical least squares error**

- Least squares error (LSE) represents the error between the model output and the observed data.
- The model fit is the ratio of the least squares error to the total variation in the data.

**The individual parameters reveal details about the behavior of individual genes**

- Upper left: The 60-degree in the network, with the source node is ASH1.
- Lower left: The 0-degree in the network, with the target node is YHP1.

**Conclusions and Future Directions**

- DNA microarray data from the ΔHap4 deletion strain subjected to cold shock was analyzed using an ANOVA test, the GRNmap database, and ordination analysis in order to better understand how genes are regulated during cold shock.

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**References**