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Linear Dynamic Model of Gene Regulation Network of Yeast Cell Cycle

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Gene expression in a cell is regulated by mutual activations or repressions between genes. Identifying the gene regulation network will be one of the most important research topics in the post genomic era. We propose a linear dynamic model of gene regulation for the yeast cell cycle. A small gene network consisting of about 40 genes is reconstructed from the analysis of micro-array gene expression data of yeast S. cerevisiae published by P. Spellman et al. We show that the network construction is consistent with the result of the hierarchical cluster analysis.