

## **Yeast Transcription Networks: Structure, Dynamics, and Evolution**

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Yeast has evolved a complex transcriptional regulatory network to control its gene expression in response to changes in environment. We are interested in how the network is structured and what are the functional and evolutionary constraints. To answer how, we have developed a number of computational algorithms to systematically reconstruct the network using sequence and functional genomics data. To analyze the functional constraints, we have developed an experimental system to study the dynamics of gene regulation quantitatively at the pathway/network level in single cells. The quantitative measurements are then combined with mathematical modeling to gain insight into how the system functions. To analyze the evolutionary constraints, we study evolution of transcription factors and cis-regulatory sequences via comparative genomics to derive the basic modes of evolutionary changes in transcriptional circuitry.