Yeast is the one of the most well-characterized eukaryotic model organism, in terms of network biology and functional genomics. The yeast interactome is the closest to completion and extensive functional genomic studies have given rise to a myriad of datasets related to yeast fitness and genotype-phenotype relationship, including conditional genetic mutations, synthetic lethality, epistasis, ribosome profiling and gene expression. Together with yeast’s simplicity as an organism, this means that we can go beyond simple network connectivity and investigate spatial and temporal aspects of network biology in yeast.

The Gerstein Lab’s expertise in data integration, network science and yeast interactome ideally positions us for this endeavor. We have developed many network-science-based,1–4 machine-learning5–7 and statistical approaches8–11 for building biological networks from heterogeneous biological datasets from human, yeast and other model organisms. We have also participated in large-scale construction of draft regulatory networks for human and other model organisms based on the mod/ENCODE datasets.9,10,12 Further, we developed methods to analyze networks in yeast, such as the identification of functional modules.13–15 For example, by mapping gene-expression data onto the regulatory network of yeast, we identified different sub-networks that are active in different conditions.16,17 Additionally, we have used networks as a framework for integrating a great variety of genomic variation data across individuals and organisms, including yeast, and studying their impact on biological systems.18–20

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