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Modeling and Estimation of Gene Regulatory Networks and Environmental Stress Response

This talk investigates the dynamics of gene regulatory networks governing cold shack response in budding yeast, Saccharomyces cerevisiae, through the use of a differential equation model. The inverse problem of determining model parameters from observed data is our primary interest. We fit the differential equation model to microarray data from a cold shock experiment using a Bayesian maximum likelihood approach, and we discuss future efforts involving gene deletion experiments and related modeling problems.