

# Identification of Stable Genetic Networks Using Convex Programming

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Gene regulatory networks capture interactions between genes and other cell substances, resulting in various models for the fundamental biological process of transcription and translation. The expression levels of the genes are typically measured in mRNA concentrations in micro-array experiments. In a so called genetic perturbation experiment, small perturbations are applied to equilibrium states and the resulting changes in expression activity are measured. This paper develops a novel algorithm that identifies a sparse stable genetic network that explains noisy genetic perturbation experiments obtained at equilibrium. Our identification algorithm can also incorporate a variety of possible prior knowledge of the network structure, which can be either qualitative, specifying positive, negative or no interactions between genes, or quantitative, specifying a range of interaction strength. Our method is based on a convex programming relaxation for handling the sparsity constraint, and therefore is applicable to the identification of genome-scale genetic networks.