

Causal Graphical Models for Discovering Gene Regulations

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**ABSTRACT**

I will present several causal graphical models for discovering gene regulations from observational genomic data in an exploratory fashion. Our methods are specifically tailored to common features of genomic data including high level of noise, high skewness, zero-inflation, sample heterogeneity, feedback loops, and presence of unmeasured confounders. Our theories show that causal structure is identifiable under all the presented causal graphical models with purely observational data. I will provide intuition as to why causality is identifiable under different scenarios and demonstrate the practical utility using multiple real datasets with known causal structure.