Reconstructing Gene Networks by A Data-driven Response Surface Method

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Abstract

Xu *et al.* (2001) introduced an interesting response surface model to reconstruct gene networks from microarray data. However, the fixed surface approach failed to find meaning Activator-Repressor-Target gene triplets in Yeast data sets (Spellman *et al.*, 1998). We proposed a data-driven response surface model. The innovation is two-fold: 1. the surface is constructed by data and 2. it allows a time-lag for the activator and repressor genes to act on the target gene. Using the alpha Yeast data set, part of the networks reconstructed are consistent with existing biology knowledge. While some novel parts are yet to be verified by RT-PCR.