

Inferring a Plausible Mouse Immune Response Network from Microarray Time Series Data

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Abstract. In this paper, we inferred a plausible IL-2 stimulated immune response gene network for mouse T cell by clustering the time series microarray and literature mining. First, we clustered the time series microarray data into 23 co-expressed gene groups, and discretized gene expression of each gene group into discrete Boolean states. Hence, we got 12 distinct Boolean states of gene expression groups. We then mined the PubMed database to find out the previous known regulatory interactions between the selected key genes for the 12 co-expressed gene groups. We used Boolean network dynamical model to simulate the dynamic gene expression of the gene network. A plausible immune response gene network was obtained by conjecturing a gene network topology which is consistent with biological function requirement, i.e. the same gene expression as microarray data, and robustness of gene network under external perturbations, which was defined as basin size of the biological steady state.

Keywords: Boolean network, immune response network, robustness, network reconstruction

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