

Model-free Identification of Relevant Variables From Response Data

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In several problems in biology it is of interest to identify from a large set of genes which genes are involved in a phenotypic response such as limb regeneration, tumor reduction, etc. In many cases experimental data consists of external perturbations applied to the system such as the introduction of a chemical. We present a model-free approach to identify candidate genes when an external perturbation causes a change in phenotype. Our approach consists of identifying "bifurcation-like" behavior of a subnetwork of genes/variables when a change in phenotype is observed. The variables that exhibit this behavior are candidates to be in the subnetwork. We explore this approach first with a toy network to highlight the features and possible limitations. We then validate the approach with an in-silico network. Finally, we apply the approach to real data.