

Reverse Engineering Genetic Networks: a computational and experimental approach - (session: Novel Algorithms for Bioinformatics)

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Genes, proteins and metabolites are organized into extensive networks that enable a cell to respond, adapt and communicate with its environment. The extent and complexity of such networks can hinder attempts to elucidate their structure and function. To address this problem, we have developed an approach that uses systematic transcriptional perturbations to construct a first-order model of a gene and protein regulatory network. We applied this method to a nine-gene subnetwork of the SOS pathway in *Escherichia coli* and obtained an accurate model of the regulatory interactions. Using the recovered model, we correctly identified the major regulatory genes and the genes that directly mediate Mitomycin C activity in the subnetwork. This approach, which is experimentally and computationally scalable, provides a novel framework for elucidating the functional properties of genetic networks and identifying the mechanisms of action of pharmacological compounds.