

Abstract Submitted  
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**Determining Regulatory Networks Governing the Differentiation of Embryonic Stem Cells to Pancreatic Lineage** IPSITA BANERJEE, University of Pittsburgh — Knowledge of pathways governing cellular differentiation to specific phenotype will enable generation of desired cell fates by careful alteration of the governing network by adequate manipulation of the cellular environment. With this aim, we have developed a novel method to reconstruct the underlying regulatory architecture of a differentiating cell population from discrete temporal gene expression data. We utilize an inherent feature of biological networks, that of sparsity, in formulating the network reconstruction problem as a bi-level mixed-integer programming problem. The formulation optimizes the network topology at the upper level and the network connectivity strength at the lower level. The method is first validated by *in-silico* data, before applying it to the complex system of embryonic stem (ES) cell differentiation. This formulation enables efficient identification of the underlying network topology which could accurately predict steps necessary for directing differentiation to subsequent stages. Concurrent experimental verification demonstrated excellent agreement with model prediction.

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