

Abstract Submitted
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Identification of driving network of cellular differentiation from single sample time course gene expression data. YE CHEN, The National Heart, Lung, and Blood Institute (NHLBI), NATHANIEL WOLANYK, University of Alabama at Birmingham, TUNC ILKER, SHOUGUO GAO, XUJING WANG, The National Heart, Lung, and Blood Institute (NHLBI) — Methods developed based on bifurcation theory have demonstrated their potential in driving network identification for complex human diseases, including the work by Chen, et al. Recently bifurcation theory has been successfully applied to model cellular differentiation. However, there one often faces a technical challenge in driving network prediction: time course cellular differentiation study often only contains one sample at each time point, while driving network prediction typically require multiple samples at each time point to infer the variation and interaction structures of candidate genes for the driving network. In this study, we investigate several methods to identify both the critical time point and the driving network through examination of how each time point affects the autocorrelation and phase locking. We apply these methods to a high-throughput sequencing (RNA-Seq) dataset of 42 subsets of thymocytes and mature peripheral T cells at multiple time points during their differentiation (GSE48138 from GEO). We compare the predicted driving genes with known transcription regulators of cellular differentiation. We will discuss the advantages and limitations of our proposed methods, as well as potential further improvements of our methods.

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