

Elucidation of the Sequential Transcriptional Activity in Escherichia coli Using Time-Series RNA-Seq Data

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Abstract : Functional genomics and gene regulation inference has readily expanded our knowledge and understanding of gene interactions with regards to expression regulation. With the advancement of transcriptome sequencing in time-series comes the ability to study the sequential changes of the transcriptome. This method presented here works to augment existing regulation networks accumulated in literature with transcriptome data gathered from time-series experiments to construct a sequential representation of transcription factor activity. This method is applied on a time-series RNA-Seq data set from Escherichia coli as it transitions from growth to stationary phase over five hours. Investigations are conducted on the various metabolic activities in gene regulation processes by taking advantage of the correlation between regulatory gene pairs to examine their activity on a dynamic network. Especially, the changes in metabolic activity during phase transition are analyzed with focus on the pagP gene as well as other associated transcription factors. The visualization of the sequential transcriptional activity is used to describe the change in metabolic pathway activity originating from the pagP transcription factor, phoP. The results show a shift from amino acid and nucleic acid metabolism, to energy metabolism during the transition to stationary phase in E. coli.

Keywords : Escherichia coli, gene regulation, network, time-series

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