Elucidation of the sequential transcriptional activity in *Escherichia coli* using time-series RNA-seq data

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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, the ability to study the sequential changes of the transcriptome comes. Here, we present a new method to augment regulation networks accumulated in literature with transcriptome data gathered from time-series experiments to construct a sequential representation of transcription factor activity. We apply our method on a time-series RNA-Seq data set of *Escherichia coli* as it transitions from growth to stationary phase over five hours and investigate the various activity in gene regulation process by taking advantage of the correlation between regulatory gene pairs to examine their activity on a dynamic network. We analyse the changes in metabolic activity of the *pagP* gene and associated transcription factors during phase transition, and visualize the sequential transcriptional activity to describe the change in metabolic pathway activity originating from the pagP transcription factor, phoP. We observe a shift from amino acid and nucleic acid metabolism, to energy metabolism during the transition to stationary phase in *E. coli*.

Biography

Pui Shan Wong completed her Master's degree in Bioinformatics at University of Auckland, New Zealand. She is now working at National Institute of AIST in Japan under the Biotechnology Research Institute for Drug Discovery and has started her career with six publications.

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