Construction of the Large Scale Biological Networks from Microarrays

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Abstract : One of the sustainable goals of the system biology is understanding gene-gene interactions. Hence, gene regulatory networks (GRN) need to be constructed for understanding the disease ontology and to reduce the cost of drug development. To construct gene regulatory from gene expression we need to overcome many challenges such as data denoising and dimensionality. In this paper, we develop an integrated system to reduce data dimension and remove the noise. The generated network from our system was validated via available interaction databases and was compared to previous methods. The result revealed the performance of our proposed method.

Keywords: gene regulatory network, biclustering, denoising, system biology

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