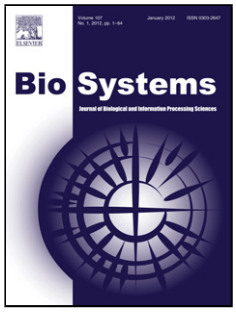

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Predicting link directionality in gene regulation from gene expression profiles using volatility-constrained correlation

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Abstract

To uncover potential disease molecular pathways and signaling networks, we do not only need undirected maps but also we need to infer the directionality of functional or physical interactions between cellular components. A wide range of methods for identifying functional interactions between genes rely on correlations between experimental gene expression measurements to some extent. However, the standard Pearson or Spearman correlation-based approaches can only determine undirected correlations between cellular components. Here, we apply a volatility-constrained correlation method for gene expression profiles that offers a new metric to capture directionality of interactions between genes. To evaluate the predictions we used four datasets distributed by the DREAM5 network inference challenge including an in silico-constructed network and three organisms such as *S. aureus*, *E. coli* and *S. cerevisiae*. The predictions performed by our proposed method were compared to a gold standard of experimentally verified directionality of genetic regulatory links. Our findings show that our method successfully predicts the genetic interaction directionality with a success rate higher than 0.5 with high statistical significance.

1 Introduction

Unveiling the comprehensive map of interactions between cellular components may lead to elucidate genetic roots of a disease and to unlock