

**2013 IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology
(IEEE CIBCB 2013)**

Special Session on Computational Intelligence in Genetic Regulatory Network

Motivation:

The reconstruction of genetic regulatory network (GRN) from data is a very important topic in bioinformatics. It can help us to understand the mechanism of life and design personalized drugs, and treat genetic diseases.

However, there are challenging issues that prevent us from striding towards our goal due to the complex nature of metabolic molecular systems and the limitation of current data. First of all, the complexity of dynamic molecular interactions is a challenge to be represented mathematically. Secondly, microarray time-series data are the most common data used to learn the GRN. These data are very noisy and might be redundant. Thirdly, probabilistic graphical models, for example Bayesian networks, are very common approaches learning on time-series (or static) data. They often suffer from the well-known curse of dimensionality. That is the number of parameters of the model goes exponentially as the complexity of interactions increases. Current available data usually only comprise tens of instances (time points or other conditions) but thousands of genes. Moreover, the time-delays of different interactions are different. This implies that we have to consider the orders of interactions when designing a model to learn on data with imperfect discrete sampling rates.

We believe that Computational intelligence (CI) can effectively address these challenging issues. For example, the structures of graphical models can be well-represented and explored by various CIs for instance evolutionary and Markov chain Monte Carlo methods. And non-negative matrix factorizations can discover underlining biological patterns.

This special session is soliciting high-quality papers of original research and application papers that have not been published elsewhere and are not under consideration for publication elsewhere. All papers will be rigorously reviewed by at least 3 reviewers. Accepted papers will be published in the CIBCB 2013 proceedings (with ISBN number), included in the IEEE Xplore digital library, and indexed by EI/Compendex. This special session is of clear interest to the computational intelligence community, the statistical learning community, as well as the biology community.

Topics:

The topics of this special session include, but are not limited to:

- * genetic regulatory network
- * transcriptional regulatory network
- * (aberrant) pathway analysis
- * learning on integrated data

- * clustering, biclustering, and triclustering of gene expression profiles
- * gene selection
- * network based systems biology

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