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BIOMOLECULAR NETWORKS: FROM ANALYSIS TO SYNTHESIS

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1. Introduction

The study of biological networks is a very challenging research area in biocomputing. This field is of utmost importance, however. These networks underlie much of the emerging fields of synthetic and systems biology, which are revolutionizing molecular biology. Here, we use the term "biological networks" both to refer to biomolecular networks (e.g., gene regulatory networks) and to supporting knowledge representation networks (e.g., Gene Ontology).

There have been numerous recent advancements in synthetic biology. In academia, the Registry of Standard Biological Parts has been developed based on the concept of BioBricks, allowing scientists to browse through standardized and interchangeable biological parts for building synthetic biological systems. In the corporate world, the company Codon Devices is aiming to commercialize DNA synthesis on demand. Another milestone in the field is the first description of the

RNA ribo-regulator and other biological circuit components, such as the genetic toggle switch. Such progress has led to the development of engineered simple genetic circuits that mimic other common devices like oscillators and feedback loops[1]. Other recent achievements include the development of non-native behaviors like optimized drug synthesis and programmed spatial formation[2].

Although scientists have made significant progress in the development of synthetic and systems biology, the fields must still overcome several challenges related to biological networks[3]. To this end, this session offers novel methodologies in two general areas: namely, in inferring network structure from vast amounts of data and in utilizing these networks for pressing applications.

2. Session Papers

Eliciting the structure of a biological network is a fundamental issue. **Kuchaiev and Przulj** introduce a novel generative model of protein-protein interaction networks that accepts only the high-confidence portion of a network but is able to reproduce other low-confidence network features. **Tari *et al.*** propose a new paradigm to determine network structure, which allows biologists to construct networks tailored to their specific needs using Medline abstracts. **Costello *et al.*** present a novel data-driven methodology that synthesizes an ontology from gene-gene interactions and annotations regarding those genes.

Biological networks are dynamic entities which are highly dependent on cellular state. **Sen *et al***. produce gene regulatory networks that are intrinsically state-dependent and offer context-specific annotation in addition to gene-gene interactions. **Roy *et al.*** develop a novel technique to infer functional networks from condition-specific responses and examine gene ontology enrichment of their inferred networks among different cell types.

We also seek to understand how biological networks change over time and across species. **Cheng and Riedel** offer a methodology, based on a stochastic simulation with time-varying inputs, which allows insight and validation into the time-dependent dynamics of a system. **Tian and Samatova** develop a fast algorithm based on connected components that identifies maximally conserved regions across species.

Identification of biomarkers is a substantial application of biological networks. Using a network paradigm, **Dudley and Butte** identify protein biomarkers through a novel methodology which integrates biofluids proteome data and inter-disease genomic

relationships. **Sachs *et al.*** extend the Bayesian Network methodology, often used to identify biomarkers, by allowing cyclic pathways in the biological system to be modeled.

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References

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