

EURASIP Journal on Bioinformatics and Systems Biology

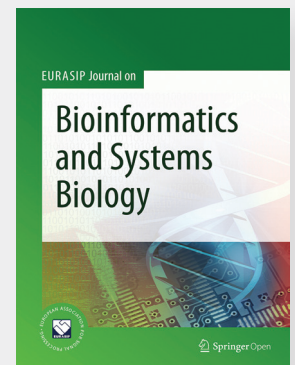
Special Issue on
Statistical reverse engineering methods for
high-throughput molecular data

With the recent advancement in the high-throughput technologies, molecular biology is rapidly evolving into a quantitative science. This achievement led to an increased role of reverse engineering methods in making sense of this high-dimensional data. The development and application of such methods will guide new experiments, shed new light on existing hypotheses and will eventually trigger new discoveries that have been difficult to achieve using the traditional biochemical approaches alone. This special issue will focus on statistical reverse engineering methods for high-throughput molecular data.

We invite all scientists working in the field of statistics, systems biology, bioinformatics and engineering to contribute original research articles and tutorial papers to this special issue. All submitted manuscripts will be peer-reviewed.

Potential topics include, but are not limited to:

- Inference for probabilistic graphical models
- Dynamic Bayesian networks
- Causal inference from observational data
- Methods dedicated to time-resolved data (e.g. Granger causality)
- Scalable algorithms and parallelization for inference
- Special methods for single-cell high-throughput data (single-cell DNA/RNA sequencing, mass cytometry)
- Special methods for reconstructing signaling pathways (e.g. from protein-arrays, mass-spectrometry)



Call for
Papers

Submission Instructions:

Before submission authors should carefully read over the Instructions for Authors, which are located at bsb.eurasipjournals.com/authors/instructions. Prospective authors should submit an electronic copy of their complete manuscript through the SpringerOpen submission system at editorialmanager.com/jbsb according to the submission schedule. They should choose the correct Special Issue in the "sections" box upon submitting. In addition, they should specify the manuscript as a submission to the "Special Issue on Statistical reverse engineering methods for high-throughput molecular data" in the cover letter. All submissions will undergo initial screening by the guest editors for fit to the theme of the special issue and prospects for successfully negotiating the review process.

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Submission Schedule

Manuscripts due:

March 1, 2016