Computational and Mathematical Methods in Medicine

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Special Issue on
Network Models for the Joint Analysis of Omics Data

CALL FOR PAPERS

In recent years, it has been supposed that a comprehensive understanding of a biological system can come only from a joint analysis of all omics data. Collecting, analyzing, recording, and using omics data are no small feat, particularly because these processes include people. They also include patient consent and understanding, use of electronic medical records, obtaining and managing samples, ensuring accuracy of the data, maintaining a clinical lab, advancing bioinformatics hardware and software, and employing both computational learning and human judgment to interpret the massive amount of information these tools generate. Omics data illustrate various aspects of cellular functioning and the recent technological progress in high-throughput biology has facilitated their collection. A starting point for analyzing multilayer omics data is to use network models.

A network (or graph) consists of nodes (or vertices) and links (or edges). In biological networks, nodes usually describe discrete biological objects at a molecular (e.g., genes, proteins, metabolites, and drugs) or phenotypic level (e.g., diseases), whereas edges describe physical, functional, or chemical associations between pairs of objects. So far, networks have been one of the most widely used statistical tools for modeling and analyzing single layer omics data. Specifically, these tools applied to studies of protein-protein interaction (PPI) networks, gene interaction (GI) networks, metabolic interaction (MI) networks, and gene coexpression (Co-Ex) networks have provided relevant biological knowledge from these different aspects of molecular machinery inside a cell. However, a more comprehensive understanding of a biological system is supposed to be achieved by a joint, integrative analysis of all these networks. To reach this purpose, data integration methodologies have to satisfy several challenges. These challenges arise due to different sizes, formats, and dimensionalities of the data being integrated, as well as owing to their complexity, noisiness, information content, and mutual concordance, that is, the level of agreement between datasets.

The main goal of this special issue is to publish papers that extract additional biological knowledge from multiple omics data that cannot be gained from any single dataset alone. In addition, we are particularly interested in manuscripts that discuss the recent advancement in approaches that integrate results from omics data and information generated from medical approaches to uncover novel biomedical information. The information not only would help the individual, but also might provide a wealth of information for comparative analyses between individuals and groups, revealing patterns of risk and response to treatment for individuals and populations.

Potential topics include but are not limited to the following:

- Statistical methods for network reconstruction using omics data
- Network models for patient-specific data integration
- Modular networks and condition specific regulators
- Bayesian networks for multiple omics data analysis
- Nonparametric network-based models for multiple omics data analysis
- Cluster analysis of multiple omics data
- Penalized likelihood network-based approaches for multiple omics data

Authors can submit their manuscripts through the Manuscript Tracking System at https://mts.hindawi.com/submit/journals/cmmm/nmjad/.

Papers are published upon acceptance, regardless of the Special Issue publication date.

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