

# Special Issue on Computational Molecular Networks and Network Pharmacology

## CALL FOR PAPERS

For biomedical research relying on systems biology approaches, two major subdomains might have profound impacts: the molecular network for understanding the principles of regulations at multiple levels and network pharmacology to investigate the effect of small molecules on gene dynamics.

With the development of high-throughput sequencing and profiling techniques for genes and proteins and metabolites, massive amounts of omics data have been accumulated rapidly for biomedical research, especially for the clinical practices including but not limited to cancers, digestive diseases, and respiration diseases. The molecular networks represent the major method to integrate and interpret these biomedical big-data from the systems biology perspective. For example, the gene regulation network would contain the rich information about the dynamics of the gene-gene regulations and their relationships with diseases. The bioinformatics analyses on these molecular networks would also reveal important biological principles that might be hidden in the biomedical big-data.

Network pharmacology approach essentially investigates the “perturbation” of small molecules on the network, which would be important for drug-screening. This approach is useful for understanding the complex molecular network by means of network response to those small molecules such as chemical drugs, yet currently the analytical methods are lacking, making drug screening still laborious.

Therefore, we are emphasizing analytical method development for molecular networks and network pharmacology for a broad area of applications. Any computational methods towards better interpretation of molecular networks, as well as those methods related to network pharmacology, would be desired.

We are inviting investigators to submit original research papers and review articles that will stimulate the continuing efforts in the following areas.

This special issue would also be affiliated with the workshop Molecular Networks and Network Pharmacology on the IEEE International Conference on Bioinformatics and Biomedicine (BIBM), which will be held on December 15–18, 2016, at the Kylin Villa, Shenzhen, Guangdong, China.

Potential topics include but are not limited to the following:

- ▶ Methods for understanding gene-gene regulation networks
- ▶ Methods for understanding protein-protein interaction networks
- ▶ Methods for understanding species-species interaction networks for communities
- ▶ Algorithms for decoding small molecule-gene coregulation networks
- ▶ Applications of molecular network methods for understanding key biomedical questions
- ▶ Methods for solving problems are associated with communications between cells or cells with extracellular components
- ▶ Using network pharmacology approaches for drug screening applications

Authors can submit their manuscripts through the Manuscript Tracking System at <http://mts.hindawi.com/submit/journals/bmri/computational.biology/mnnp/>.

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