



BioMed Research International

Special Issue on

## Integrated Analysis of Multiscale Large-Scale Biological Data for Investigating Human Disease

# CALL FOR PAPERS

Integrating large-scale data obtained from multiscales is essential for understanding the molecular basis of complex diseases and providing useful therapeutic targets. Several large projects, such as The Cancer Genome Atlas (TCGA), Cancer Cell Line Encyclopedia (CCLE), Genotype-Tissue Expression (GTEx), and Molecular Taxonomy of Breast Cancer International Consortium (METABRIC), have measured the somatic mutation, copy number variation (CNV), mRNA expression, microRNA expression, and methylation data and made them publicly available. Recently, many statistical methods and analysis tools have been developed based on these multiscale large-scale data. A special issue of research or review articles in these research fields is important and timely. The potential contributors for the special issue are oncologist, computational biologists, mathematical biologists, bioinformaticians, systems biologists, and computational pharmacist. We invite authors to contribute original research articles as well as review articles to this special issue.

Potential topics include, but are not limited to:

- ▶ Subtype stratification of patients
- ▶ Multiscale network construction
- ▶ Network module identification
- ▶ Predictive model of disease state
- ▶ Biomarker discovery
- ▶ Combinatorial drug discovery
- ▶ Translational medicine
- ▶ Novel computational methods in large biology data analysis
- ▶ Inferring gene function from expression data
- ▶ Inferring gene function from genome sequence data
- ▶ Integrating expression data with other genome-wide data for functional annotation
- ▶ Integrating expression data from different organisms

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### First Round of Reviews

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