This special issue consists of recent advances in computational methods, algorithms, and applications in biomarker discovery and systems biology research.

Computational biology is essential in the process of translating biological knowledge into clinical practice, as well as in the understanding of biological phenomena at different organizational and complexity scales. A key contribution of computational biology is the discovery of biomarkers for predicting clinical outcomes. The complexity of human biological systems and imperfect instrumentations of high-throughput biological instruments/results have created significant hurdles in biomarker development. This process involves the predictive modelling and integration of different types of data and knowledge for screening, diagnostic or prognostic purposes. Moreover, this requires the design and combination of different methodologies based on statistical analysis and machine learning. The articles in this special issue will introduce key computational approaches and applications to biomarker discovery and systems biology research.

Topics of interest for the Special Issue include:

- Computational methods for cancer biomarker discovery
- LC-MS data analysis and proteomics
- Data analysis methods for next generation sequencing/SNP/genotype/epigenetic data
- Data integration and TCGA data processing
- Deep sequencing data analysis
- Modeling of genetics networks and signaling pathways
- Dynamics and control of gene regulatory networks
- Differential analysis of molecular regulatory networks
- System level prognosis and diagnosis
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