

## Computational Advances in Cancer Informatics (A)

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## Supplement Aims and Scope

Cancer Informatics represents a hybrid discipline encompassing the fields of oncology, computer science, bioinformatics, statistics, computational biology, genomics, proteomics, metabolomics, pharmacology, and quantitative epidemiology. The common bond or challenge that unifies the various disciplines is the need to bring order to the massive amounts of data generated by researchers and clinicians attempting to find the underlying causes and effective means of treating cancer.

The future cancer informatician will need to be well-versed in each of these fields and have the appropriate background to leverage the computational, clinical, and basic science resources necessary to understand their data and separate signal from noise. Knowledge of and the communication among these specialty disciplines, acting in unison, will be the key to success as we strive to find answers underlying the complex and often puzzling diseases known as cancer.

Authors of articles in this supplement were asked to focus on computational advances, including one or more of the following topics:

- Gene Set Enrichment Analysis
- Hybrid Computing
- Efficient Cloud Storage and Retrieval
- Matching of Expression Patterns
- Multi-Modal Analysis
- Splice Variations and Chip Seq System Algorithms
- Rapid High-Throughput Analysis
- Computational Molecular Profiling
- Digital Gene Expression Analysis
- De Novo Genome Assembly and Re-Sequencing Computational Methods
- Computational Drug Repurposing
- Accelerated Next Generation Sequencing Technologies and Search Engines
- Post-Transcriptional Pattern Recognition
- Computational Advances in High-Content Platform Analysis
- Data visualization Software Development
- Machine Learning and Integrative Computer Approaches for Cancer Omics Research



Computational method is playing an increasingly more important role in cancer research. The advances of text mining<sup>1-3</sup>, microRNA<sup>4,5</sup>, pathway analysis<sup>6,7</sup>, and whole genome sequencing<sup>8</sup> shed light on improving medical practices using fine-grained information of individual patients but there is a long way to go towards personalized medical practices. We still cannot provide optimal treatment for many cancer patients<sup>9</sup> and we have not accurately identified relationships between molecular subtypes and prognosis and treatment response. To improve treatment, we need to learn which pathways are altered in a given cancer, determine how they are changed, identify therapeutic targets on the pathways, and discover therapies that can reverse the damage.

Biomedical science is entering a “big data” era, and the catalogue of genomic variants in the human population is expanding rapidly in the decades to come. There has been an explosion of new genomic and proteomic datasets, which provide us with unprecedented and rich resources to discover the underlying mechanisms. There are also abundant data concerning SNPs, somatic mutations, copy number, methylation levels, and expression levels in cancerous and noncancerous tissue. To fully exploit these data, we need advanced biomedical informatics methodology that can extract useful knowledge efficiently. The main objective of this special issue is to bring researchers together from different areas of cancer informatics to exchange ideas, disseminate novel research methodologies, and promote cross-disciplinary collaborations. The issue is therefore broad to cover various aspects of informatics and medical analyses, a unique combination that is appreciated by researchers in the field. Just to highlight a few articles, Kim et al systematically compare different feature selection and predictive models to identify a set

of highly predictive features to predict novel pre-miRNAs in renal cancer study. Neapolitan et al use Bayesian networks to infer aberrant signaling pathways in ovarian cancer using The Cancer Genome Atlas (TCGA) data. Hua et al evaluate gene set enrichment analysis via a hybrid model. Lu et al integrate protein phosphorylation and gene expression data to infer signaling pathways.

It is more imperative than ever to work together in cancer informatics to reveal insightful biological functions and their underlying mechanisms. We appreciate the opportunity to lead and contribute to this special issue.

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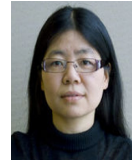
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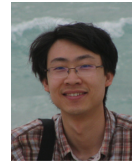
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