Network and Pathway Analysis of Cancer Susceptibility (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.

The focus of bioinformatics in cancer research has shifted from generating ranked lists of genes associated with a particular clinical outcome to systematic analysis of critical signaling pathways and molecular networks in pathogenesis (1;2). This Supplement Issue of Cancer Informatics introduces cutting-edge computational methods developed for pathway and network-based analysis of cancer susceptibility and metastasis, including integrative regulatory networks of DNA copy number and expression profiles (3;4), co-expression network analysis of lncRNAs (5) and E2F-responsive genes (6), modeling the Notch signaling pathway in colon cancer therapy (7), functional genomic analysis in cancer prognosis (8), dysregulated pathways (9), and microRNA profiling of induced pluripotent stem (iPS) cells (10). As pointed out in the comprehensive review of molecular network analysis

provided in this Supplement Issue (11), the future directions of systematic analysis of cancer susceptibility and metastasis are to utilize multi-level molecular profiles and to combine different computational methods in the analysis, in order to dissect important biological pathways and network modules in cancer initiation and progression.

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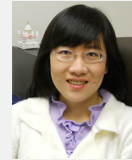
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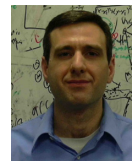
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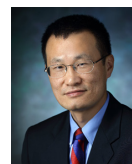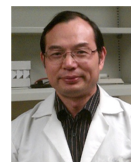
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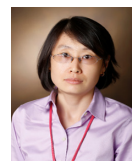
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