

Are We There Yet? Genomic Profiling and Mechanism in Cancer Research

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Abstract

The advent of the human genome sequence and genomic profiling technologies has impacted all of biomedical research. The effect has been particularly great on cancer research because cancer is a disease uniformly characterized by disturbed genome function. Studies which take a whole genome view of cancer are transforming the classification of tumors, enhancing understanding of tumorigenesis and promising to affect patient care. However, the development of large sets of genomic data has challenged cancer biologists who as a rule have never encountered data on this scale. Implementation of conventional statistical techniques has brought a level of order to the biologist's desktop, but significant problems remain to be solved. The challenge remains to extract the maximum useful

information from genomic data. This requires both new algorithmic approaches which can accommodate the complexity of the underlying rules of genome function and effective strategies for linking different types of genomic data to each other and to external sources of gene and genome annotation. Progress in this arena will be necessary to fully realize the potential of genomics to impact on our ability to intervene in the clinical arena. Of particular importance will be approaches which help identify critical genes and pathways which are essential to tumor growth and survival. Examples will be presented which illustrate the boundaries of conventional analyses based on studies of tumor profiling at the expression and gene copy number level as well as experimental models designed to explore the function of specific pathways.