

Preface

Less than 50% of diagnosed cancers are cured using current treatment modalities. Many common cancers can already be fractionated into such therapeutic subsets with unique prognostic outcomes based on characteristic molecular phenotypes. It is widely expected that treatment approaches of complex cancer will soon be revolutionized by combining molecular profiling and computational analysis, which will result in the introduction of novel therapeutics and treatment decision algorithms that target the underlying molecular mechanisms of cancer.

The sequencing of the human genome was the first step in understanding the ways in which we are wired. However, this genetic blueprint provides only a “parts list”, and neither information about how the human organism is actually working, nor insight into function or interactions among the ~30 thousand constitutive parts that comprise our genome. Considering that the 30 years of worldwide molecular biology efforts have only annotated about 10% of this gene set, and we know even less about proteins, it is comforting to know that high-throughput data generation and analysis is now widely available.

By arraying tens of thousands of genes and analyzing abundance of and interaction among proteins, it is now possible to measure the relative activity of genes and proteins in normal and diseased tissue. The technology and datasets of such profiling-based analyses will be described along with the mathematical challenges that face the mining of the resulting datasets. We describe the issues related to using this information in the clinical setting, and the future steps that will lead to drug design and development to cure complex diseases such as cancer.

Cancer Informatics in the Post Genomic Era

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