Personalization of Cancer Therapy: 
the roles of mathematics, physics, 
engineering, and post-genomic technology

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4 pm Friday 
September 5th, 2008 
5.521 Levin Hall

Abstract: The Vision: Each patient should be treated according to the molecular profile of his or her cancer. Despite the Genome Project and despite major advances in high-throughput molecular profiling technologies, that vision has been hard to realize. One reason, among many, is the parochialism of most biomedical research. Biomedical technologies have advanced, but concepts and perspectives from mathematics, physics, and engineering have not yet been incorporated optimally. The Keck Center represents an important antidote to that situation. My multidisciplinary research group and its collaborators have profiled cancer cells at the DNA, RNA, protein, and small-molecule levels using >30 different types of microarrays and other high-throughput technology platforms – in the process developing the ‘Miner Suite’ of web-based bioinformatics tools and identifying candidate biomarkers and anticancer drugs. I’ll discuss that work in relation to three major genomic and bioinformatics programs of the National Cancer Institute (caBIG, TCGA, and CGEMS).