Personalized and precision medicine: Integrating big data into biomarker discovery & drug development

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In recent years, there has been rapid growth of large-scale cancer genomic and phenotypic data, and publicly available high-throughput screening data for thousands of small molecules. Consequently, computational-aided drug development has emerged as a new way to nominate drugs in the battle against a number of cancers. Our hypothesis is that computational-aided virtual drug screens will enable fast nomination of efficacious drug candidates while simultaneously identifying drug mechanisms of action. This approach represents a departure from the more traditional approach of chemical screening against individual gene targets. The development and application of such methods to various hard to treat cancers can enable the rapid, data driven selection of new therapeutic strategies for these deadly diseases. Our long-term goal is to provide new therapeutic options along with companion biomarkers for patients with hard to treat cancers, and subsequently to reduce disease-associated mortality.

More information about the Huang lab can be found online at http://huang-lab.umn.edu