CALIFORNIA STATE SCIENCE FAIR
2015 PROJECT SUMMARY

Name(s)
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Project Number
S0523

Project Title
A Systems Biology Approach to Optimize Prediction of Efficacy of Pathway Targeted Therapies in Cancer

Abstract

Objectives/Goals
One of the most challenging problems in the field of medical science is predicting the drugs that will work for specific individuals diagnosed with varying cancer types. Today doctors have many anti-cancer therapeutics to choose from; however, doctors are only able to predict which drug would work primarily based on toxicity levels. The objective of this project is to develop a software tool to effectively test my hypothesis that drugs targeted to a specific pathway are only effective if that pathway is up regulated. These up-regulated pathways can be identified using a data driven approach by analyzing the interaction between proteomic, transcriptomic, and drug response data.

Methods/Materials
I focused on Non-Small Cell Lung Cancer for this research project and used corresponding lung cell data. My procedure consists of three parts: data discovery and analysis, statistical inference, and dynamic visualization software. In data discovery and analysis, relevant data was collected from multiple sources and integrated into a data cube. For statistical inference, various methods such as paired p-values, probability density bell curves, and scatter plots were used to compare fifty-eight common pathways across a pair of cell lines where the same pathway-targeted therapy worked on one cell line and not on the other. Finally, dynamic visualization software was developed to view dynamic models of these pathways.

Results
Of the common pathways, 94.8% were unregulated in the same cell line where the drug had a positive response. Thus I validated my hypothesis and developed an approach to view various biological data such as transcriptomic, proteomic, and drug data as a system and effectively determine the correlation between these data sets as well as visualize dynamic models with the integration of bimolecular signaling networks, protein-protein interactions, and transcription factor regulation.

Conclusions/Discussion
I effectively developed a user-friendly data analysis and visualization software that creates a full pathway analysis for a specific patient based on the patient#s proteomic and transcriptomic tumor analysis. This software can successfully help clinicians narrow down the number of drugs that have a higher probability of working for an individual cancer patient.

Summary Statement
Using translational systems knowledge to dynamically map bio-molecular pathways and data analytics, I developed a data analysis and visualization software that effectively creates a full pathway analysis for a specific patient based on the

Help Received
Dr. Parag Mallick at Stanford helped me understand the various biological datasets, reviewed my methodology and verified the viability of this approach.