A Novel Pan-Cancer Approach to Quantify Tumor Mutational Burden and Clinical Data Predictors for Immunotherapy Response towards Personalized Medicine

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Cancer is among the leading causes of death around the world. Immunotherapies have the potential to improve cancer survival by utilizing the immune system for treatment and reducing radiation and recurrence. Further, cancer immunotherapy has shown promising results across an increasing number of cancers such as lung cancer and melanoma. However, only 20-40% of patients currently respond to immunotherapy despite advances in the treatment. The reasons for this disparity are often attributed to patient and tumor heterogeneity. Differences in patients could cause their immune system to better respond to immunotherapy and differences in the mutations of tumors could allow the immune system to better identify and destroy cancer cells. Predicting which patients will likely respond to immunotherapy would greatly improve patient care through personalized decision-making and save crucial time. Currently, crucial factors in the ability to quantify predictors for immunotherapy response and measure reliability across cancer histological subtypes and immunotherapies are missing, preventing improvement in care. My research proposes a novel tool to robustly quantify clinical/patient predictors and tumor mutational burden (TMB) to predict pan-cancer response to immunotherapy. To quantify the TMB and factor in patient data, my research leverages comprehensive genotype profiling and develops an innovative pipeline to remove artifacts, identify somatic point mutations, and mutational hotspots, and utilize machine learning. Data analysis using pan-cancer dbGaP patients suggests TMB in combination with clinical data is a useful predictor of immunotherapy response with an accuracy of 88%. Future work will explore the host genotype in its potential relationship to immunotherapy response.

Awards Won:

Third Award of $1,000