

Key gene pathways shared by multiple cancers: Functional genomics analysis using machine learning

Katie Gao^{1*} and Yi Huang²

¹Centennial High School, USA

²Department of Mathematics and Statistics, University of Maryland, USA

Despite a wealth of literature on identifying gene signatures for individual types of cancer, little has been reported regarding the comparison of gene signatures across multiple cancers to identify potential common-cancer gene signatures. We hypothesize that multiple cancers can be triggered and/or regulated by similar gene pathways; additionally, we aim to identify promising gene signatures to aid the diagnostic screening of multiple cancers in a more timely and accurate fashion. The advent of the big data era for cancer functional genomics, powered by high-throughput technologies (such as microarrays) and machine learning, has opened up a new path to study these hypotheses. The goals of this study are: (1) to collect gene signatures for individual cancers and evaluate their predictive ability across multiple cancers; (2) to identify potential common gene pathways for multiple cancers; and (3) to construct a meta-classifier to predict multiple cancers. We utilized 14 publicly available microarray gene expression datasets for a variety of cancers from the NCBI-GEO database. Our machine learning analysis indicated high predictive accuracy among the gene signatures identified from the datasets of breast, mammary gland, endometrial, and female non-smoker lung cancers; the results suggest a promising underlying genetic commonality. We will also present enrichment analysis of the predictive genes and demonstrate the relationship among gene pathways across multiple cancers. Our computational algorithm for the meta-classifier of multiple cancers will be shown at the end.

Biography:

Katie Gao is a junior at Centennial High School in Ellicott City, MD. She has been conducting research internship with Prof. Yi Huang at UMBC. She has always been deeply involved in science and has collected a few accolades along the way, including finishing top 20 at the 2016 National Brain Bee Championship and qualifying for the 2016 National Chemistry Olympiad.

Yi Huang is an Associate Professor at UMBC's Department of Mathematics and Statistics. She earned Ph.D in Biostatistics at Johns Hopkins University. Her research specializes in biostatistical methodology development and application in many areas of biomedical and health policy research.