One Page Research Experience

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Website

GitHub

My interdisciplinary research unites two strands of recent, significant scientific inquiry: Computer science and biological science. My research focuses on biomedical informatics with cancer approaches. Our recent articles discuss the potential biomarkers for metastatic breast and lung cancers. The study design of all these projects was based on publicly available transcriptomics data, like GEO and TCGA. Therefore, we performed various in-silico analyses to reach the most critical differentially expressed genes (DEGs) in two comparable cohorts.

Moreover, we studied multiple pathways and transcription factors closely related to our DEGs. To validate those genes, we utilized survival analysis to demonstrate how dysregulation of the DEGs could affect metastasis progression. I suggest developing protein-protein and gene-gene interaction networks to reach our dataset's most comprehensive perspective of critical genes. I gained experience in computational analyses for RNASeq and Microarray data, resulting in two peer-reviewed articles in PLoS One[1] and Scientific Reports[2].

I see these two projects as the starting point for my long-term research goal of expanding the field of study of computational cancer research. I firmly believe that with the power of computers, we can overcome cancer way earlier than we expect. My future research projects include a comprehensive study on Pan-Cancer expression networks with a machine-learning approach [3].

My intellectual curiosity in virology motivated me to join an international research group headed by professor Youping Deng from the University of Hawaii. In this project, we utilized a massive dataset from the GISAID database, using COVID-19 sequences with region and date tags, which let us track mutation patterns in different regions and monitor a timeline of COVID-19 mutations globally. I learned a lot of techniques in genomics data science in this project. All the manuscripts are currently in the reviewing process.

With this training and experience, I designed a web service that addresses all the issues and bugs I faced in my research experiences. The service is divided into three major types, genomics, proteomics and high throughput data analyses; however, the first and only available tool at the moment is Express-A[4]. The tool is capable of analyzing expression data with an interactive approach. In graduate school, I want to develop these tools to hopefully make a turning point in biology research, specifically cancer biology.

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[1] https://doi.org/10.1371/journal.pone.0260584

[2] https://doi.org/10.1083/S41598-022-22252-7

[3] https://github.com/Arshammik/Lung-Cancer-TCGA-

[4] https://express-a.canobo.org/#/