Project #1: immune gene expression in prostate cancer

Recent reports, including ours, have suggested that certain cancers such as muscle invasive bladder and prostate cancer can be classified into distinct genomic and immune transcriptome associated molecular subtypes that also exhibit variability in prognosis.
Prostate cancer has been recently classified into 2 types of luminal- (Luminal A and B), and basal-like molecular subtypes using PAM50 gene expression [2].
Hypothesis: Luminal A, Luminal B, and Basal molecular subtypes of prostate cancer are distinguishable based upon differential gene expression.
Objective: Investigate and identify different immune gene expression patterns associated with luminal- and basal-like molecular subtypes using a novel machine-learning algorithm with an in house immune-panel of genes.

Project #2: Genomic data analysis and visualization GUI

Analysis of a genomic data often involves pre-processing, quality control, normalization, feature selection and classification and differential expression analysis. Many methods exist, however, the best technique depends on the dataset. Therefore, it is often required to try different techniques to select the one that works best for a given dataset.
This project involves development of a user-interface for a yet-to-be-published feature selection algorithm. The objective is to design and implement a user-friendly user interface that would run the algorithm for different genetic data types. The interface would be published online for other researches to use.