Project 1

Diffuse Large B-cell Lymphoma (DLBCL) is the most common non-Hodgkin lymphoma. Current treatment with R-CHOP chemotherapy produces a five-year overall survival of 50-60%. The ability to identify cases of DLBCL that do not respond to the chemotherapy would allow clinicians to identify patients who are likely to benefit from novel, perhaps experimental therapies. In this project we will investigate the role of certain short segments of genomic DNA that regulate gene transcription in DLBCL. We will use publically available datasets of DLBCL cases that includes somatic mutations, gene expression, miRNA expression and DNA methylation data. We will apply bioinformatics and gene expression analysis techniques to study currently-known somatic mutations in specific DNA regions in DLBCL cases and the expression levels of the genes and miRNAs that are regulated by these enhancers. The hypothesis is that patients who do not respond to current chemotherapy treatment have distinct patterns of mutations that regulate genes involved in B-cell development and/or function.

Project 2

miRNAs are small (19-24 nt long) , non-coding RNA molecules that regulate gene expression. In recent years these small molecules have been investigated as potential biomarkers and predictors of recurrence and/or survival in cancer and other diseases. This project is on the analysis of pathogenic human miRNA in approximately 7000 human samples taken from different tissues. The pathogenic human miRNAs are derived by aligning sequences that don't match the human genome against pathogen genomes stored in existing public database. We are interested in investigating the presence of pathogenic miRNA (bacteria or viruses) in different tissue types and possible prevalence in certain diseases or conditions. The candidate will be also trained in accessing these pathogenic genomes and aligning sequences.

Project 3

miRNAs are small (19-24 nt long) , non-coding RNA molecules that regulate gene expression by targeting a set of mRNA. In recent years these small molecules have been investigated as potential biomarkers and predictors of recurrence and/or survival in cancer and other diseases. This project is on an implementation of a miRNA-mRNA mapping algorithm. The algorithm would allow to identify mRNAs that are targeted by a given miRNA