Mentor
Qingling Duan, Ph.D.
Email: qingling.duan@queensu.ca

Project Title
Network analysis of gene expression data

Background and significance
Transcriptomics refer the quantitative and qualitative characterization of gene expression (ribose nucleic acids, RNA) and represents a genome-wide, non-hypothesis driven approach to study biological systems and human diseases. Analysis of gene expression profiles have focused on the differential expression of single genes between disease states or treatment groups. However, genes are not expressed in isolation but instead interact within pathways or networks. Network based approaches for the analysis of gene expression data will identify groups of interrelated genes that may be serve as better predictors of disease risk or drug response phenotypes than single genes.

Project objective
The aim of this project is to identify pathways and co-expression networks using transcriptomics data.

Skills developed
The student will learn methods for processing and analysis of biomedical data.

Preferred Pre-requisites
Fluency in UNIX, R, Biomedical computing/informatics

Project type
Undergraduate project