Mentor
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Computational Genomics Laboratory

The overarching goal of my research program at Queen's University is to identify and characterize genomic factors that determine risk for multi-factorial diseases or modulate variable drug response. My lab is currently working on multiple disease models including ovarian and breast cancers, asthma, COPD, sleep disordered breathing, chronic pain as well as variable responses to chemotherapy and biologics for severe asthma. Specifically, we have developed pipelines for the analyses of pan-omics data from human populations to determine the interaction between genomic variants with environmental exposures and how these contribute to differences in gene expression, DNA methylation, and disease risk or drug efficacy. My research program is situated in both the School of Computing and the Department of Biomedical & Molecular Sciences. My trainees have backgrounds in various disciplines including but not limited to life science, computer science, biochemistry and epidemiology. Research opportunities in my Computational Genomics Laboratory spans the processing of biological samples to various genotyping platforms and integrative analyses of multiple biomedical datasets. The projects listed here are examples that are currently available for CISC 499:

1. **Genome-wide association studies (GWAS) of chronic obstructive pulmonary disease (COPD):** Numerous genetic and non-genetic risk factors have been previously correlated with COPD, however, few causative variants have been identified. This weakens the concept of genetic testing and precision medicine. The goal of this project is to identify potentially causative variants, which could account for the previous correlations. The student will learn to apply various bioinformatics tools and software as well as large genomic databases such as 1000 Genome Project and the UK Biobank data to identify and characterize novel genetic variants correlated with COPD.
2. **Asthma ontology:** Like COPD, hundreds of genes have been correlated with asthma. In fact, my lab has compiled a list of over 500 associated genes for asthma or a related phenotype (e.g., lung function, drug response). This was the result of manual curation of the existing literature, which was labor-intensive. However, such a comprehensive list is not available elsewhere and has proven to be a very valuable research tool for ongoing projects in my lab. We believe that this list could be further integrated with clinical outcomes, treatments, environmental factors ad other aspects of current knowledge in asthma in a structured manner such as an ontology that represents these findings in a standardized semantic framework. This would allow researchers to easily and quickly retrieve information that would greatly enhance clinical and biomedical research in asthma.
3. **Genetic and environmental interaction in modulating risk for allergic diseases among children.** In addition to DNA sequence variations, epigenomic changes (i.e. DNA methylation) have been shown to predispose to various diseases including asthma and atophy. Unlike DNA sequence variations, however, epigenomics are subject to change over time and influenced by environmental exposures. The goal of this project is to determine the role of epigenomic changes in predisposing to allergic asthma and how these may be regulated by in-utero environmental exposures (during pregnancy). The student will use data available from the Kingston Allergy Birth Cohort (KABC), which is a unique childhood population collected at the Kingston General Hospital (Dr. Anne Ellis) that serves both rural and urban residents with diverse socioeconomic status (SES) and environmental exposures.