Project Title: Performance on the Flanker Task in children with ADHD
Supervisor: Annie Dupuis
Supervisor Email: Annie.Dupuis@mdstats.ca
Supervisor Phone: 4169035588
Co-Supervisor: Russell Schachar
Co-Supervisor Contact Details: Russell.Schachar@sickkids.ca
Project Description: Children performed a variant of the Flanker task, a computerized cognitive task measuring the speed and accuracy of responses to a stimulus. Using a game controller, children push the right button when the stimulus is an S or an H and a left button when the stimulus is an M or an N. To increase the difficulty of the task, each stimulus is presented with "flanker" letters, letters to the right and left of the stimulus that are associated with an incongruent response (associated with the opposite response from the stimulus, eg: MMSMM). The task can be performed with and without feedback (an auditory signal indicating if the response was accurate or inaccurate). In addition to speed and accuracy under feedback/no feedback conditions, we also measure the change in response time following errors vs correct responses. We will compare performance on these measures between children with and without ADHD. We will also use cluster analysis to identify distinct patterns of response across the children, for example to identify children using different speed vs accuracy tradeoff strategies.
Statistical methods/analyses to be employed and level of familiarity needed for these methods: Repeated measures analysis (across feedback/no feedback conditions) of continuous (response time) and binomial (accuracy) outcomes (mixed models and generalized mixed models); cluster analysis; the student will be given code that can be adapted for these analyses
Site Location: The Hospital for Sick Children/555 University Avenue
Site Description: The student will work in an office located in the psychiatry department at Sick Kids, in the original hospital building. The student office has 5 desks and a table for meetings.
Statistical software used at this site: SAS is used for running linear models and R is used for cluster analyses and graphs
Project available for MSc and/or PhD: MSc only
Expected availability: flexible
Additional Onboarding Requirements: Proof of immunity to measles, rubella, and chicken pox is required (laboratory evidence of immunity or physician documented vaccination) as well as two stage testing for tuberculosis. Students will need to bring their own laptops with SAS and R.

Project Title: Phenome-wide association study of Cystic Fibrosis Modifier Genes
Supervisor: Lisa Strug
Supervisor Email: lisa.strug@utoronto.ca
Supervisor Phone: 416-813-7654 ext. 301762
Co-Supervisor:
Co-Supervisor Contact Details:
Project Description: We have identified common variation in several genes that contribute to Cystic Fibrosis (CF) disease severity. The majority of these genes are transporters, and we are unaware if variation in the genes impact phenotypes in individuals who do not have CF, that is, individuals without two mutations in the CF causal gene, CFTR. Using 500,000 individuals from the UKBiobank who have been genotyped genome-wide and have detailed, comprehensive phenotypic data, the student will carry out a Phenome-wide association study (PheWAS). A PheWAS correlates the genetic variants of interest with every possible phenotype measured to characterize the clinical impact across the body system of these genes. Ultimately, we will have an improved understanding of the phenotype associated with normal variation in these genes of interest; genes which, with a background of CFTR mutations, can cause severe disease. Understanding of the impact of these variants in a normal CFTR background may also suggest milder CF-related phenotypes not previously appreciated, as well as alternative uses for therapeutics that are designed to target these genes.
Statistical methods/analyses to be employed and level of familiarity needed for these methods: Statistical methods implemented will be multiple logistic and linear regression, principal component analysis, exploratory data analysis. The student will be expected to have good work knowledge of regression methodology and ability to work with large data sets in a Unix environment.
Site Location: SickKids Research Institute, 686 Bay Street
Site Description: The successful candidate will be working amongst other statisticians, bioinformaticians, molecular geneticists, clinical researchers and programmers involved in the Canadian Cystic Fibrosis Gene Modifier Study. The research program is based out of The Hospital for Sick Children Research Institute, with both wet and dry laboratory space and scientists working collaboratively to improve the lives of individuals living with Cystic Fibrosis.
Statistical software used at this site: R, PLINK, Pearl
Project available for MSc and/or PhD: Both MSc and PhD
Expected availability: Flexible
Additional Onboarding Requirements: Several requirements, such as vaccinations facilitated through HR

Project Title: Understanding the Phenotype of Individuals with CFTR Gene Mutations
Supervisor: Lisa Strug
Supervisor Email: lisa.strug@utoronto.ca
Supervisor Phone: 416-813-7654 ext. 301762
Co-Supervisor:
Co-Supervisor Contact Details:
Project Description: Cystic Fibrosis (CF) is a recessive genetic disease: individuals with CF have a CFTR mutation inherited from both their mother and their father. It has long been assumed that individuals with one CFTR mutation, that is a mutation inherited from only one parent, are no different clinically from individuals with no mutations, and this is quite common with a carrier frequency of 1 in 25 live Caucasian births. Recent anecdotal information suggests there may be a CFTR "carrier" phenotype. If there is a carrier phenotype, we would like to characterize it, and recent data made publicly available will allow us to do that. The UKBiobank is a study following more than 500,000 volunteers. These individuals are sampled from across the United Kingdom, were between the ages of 40 and 69 at the time of recruitment, and have comprehensive phenotypic data available on them. Because the carrier frequency of CFTR mutations in this population is anticipated to be quite high (1 in 25), we expect 20,000 individuals who are CFTR mutation carriers; a sample size that should be sufficient to comprehensively characterize the carrier phenotype. Therefore, the student will carry out univariate and multivariate regression modeling to determine the constellation of phenotypes for which individuals who carry a CFTR mutation differ from individuals who do not carry a mutation, as well as implementation of clustering techniques to determine whether carrier and non-carriers can be discriminated on the basis of phenotypes across several organ systems. Understanding if there is a carrier phenotype is important for long term monitoring and clinical care of these patients.
Statistical methods/analyses to be employed and level of familiarity needed for these methods: Experience with univariate and multivariate regression modelling, cluster analysis, PCA
Site Location: SickKids Research Institute, 686 Bay Street
Site Description: The successful candidate will be working amongst other statisticians, bioinformaticians, molecular geneticists, clinical researchers and programmers involved in the Canadian Cystic Fibrosis Gene Modifier Study. The research program is based out of The Hospital for Sick Children Research Institute, with both wet and dry laboratory space and scientists working collaboratively to improve the lives of individuals living with Cystic Fibrosis.
Statistical software used at this site: R
Project available for MSc and/or PhD: Both MSc and PhD
Expected availability: flexible
Additional Onboarding Requirements: Vaccinations and several other requirements facilitated by HR

Project Title: Identifying patients at rapid loss for bone disease
Supervisor: Jenna Sykes
Supervisor Email: sykesj@smh.ca
Supervisor Phone: 416-864-6060 ext. 2031
Co-Supervisor: Dr. Anne Stephenson, Dr. Sanja Stanojevic
Co-Supervisor Contact Details: stephensona@smh.ca, sanja.stanojevic@sickkids.ca
Project Description: Our group works with large population-based registries in cystic fibrosis to examine health outcomes such as survival pre- and post-survival and longitudinal lung function/nutritional trends over time within Canada. The student will use longitudinal data from the Toronto CF Registry data to model patterns of bone loss over time, adjusting for known clinical factors.
Statistical methods/analyses to be employed and level of familiarity needed for these methods: The student will employ Latent Class Mixture Models to these data. No previous knowledge of these models is required; relevant readings will be provided. Knowledge of programming in R would be an asset.
Site Location: St. Michael's Hospital, 30 Bond Street, Toronto
Site Description: Our group involves clinicians, statisticians as well as allied health team members that are involved in the care of patients with cystic fibrosis. The student would work closely with Ms. Jenna Sykes, Dr. Stephenson and Dr. Stanojevic. Ms. Sykes has a MMath in Biostatistics and is a co-author on more than 60 peer-reviewed articles. Dr. Stephenson is an MD/CF physician with a PhD in clinical epidemiology. Dr. Stanojevic has a PhD in applied statistics. We have weekly research meetings that we would encourage the student to attend.
Statistical software used at this site: R version 3.4.3.
Project available for MSc and/or PhD: MSc only
Expected availability: We can be flexible depending on the student's preferred availability.
Additional Onboarding Requirements: Vaccinations are required to be up-to-date.

Project Title: Genome-wide diet-gene interaction analysis for risk of psychiatric comorbidity in inflammatory bowel disease

Supervisor: Dr. Pingzhao Hu

Supervisor Email: pingzhao.hu@utoronto.ca

Supervisor Phone: (204) 789-3229

Co-Supervisor: Dr. Wei Xu

Co-Supervisor Contact Details: wxu@uhnres.utoronto.ca, 416-946-4497

Project Description: Background: Risk factors, such as dietary and genetic factors, have been identified as being associated with the development of inflammatory bowel disease (IBD). IBD causes severe physical symptoms, is associated with psychological comorbidities and may markedly impact on quality of life.
Psychiatric disorders particularly depression and anxiety disorders, occur in up to 40% of patients with IBD. The impact of psychiatric comorbidity (PC) on outcomes in IBD patients represents a critical knowledge gap for patients, clinicians, researchers and decision makers. However, detection of PC in IBD patients can be challenging. There is no information as to whether there are genetic and dietary factors that interact to modify the risk of PC in IBD.
Hypothesis: There exist genetic risk factors that are associated with the development of PC in IBD and diet may modify the effect of genetic variants on risk of PC in IBD.
Objectives: The overarching goals of this project are to perform a genome-wide scan to identify genetic risk loci associated with PC in IBD and to assess dietary factors that interact with genetic variants to modulate the risk of PC in IBD.
Methods: DNA samples from individuals with IBD from the Manitoba IBD Cohort Study were analysed using SNP microarrays. The quality controlled dataset contained 240 IBD samples (94 and 146 of them with and without PC in IBD, respectively) and 1,267,826 SNPs. We have identified more than 5,000 copy number variations (CNVs) from the genetic data of the 240 IBD patients (Frenkel et al. 2017). Food avoidance and sugar intake data of the patients were also collected (Vagianos et al. 2016). The PC status of the IBD patients was assessed (Walker et al. 2008). To identify genetic risk loci for PC in patients with IBD, we will perform allelic genetic association analysis to identify significant SNPs. To test interactions between these dietary factors and more than 1 million genetic variants for risk of PC in IBD, we will first use logistic regression to investigate multiplicative gene-diet interactions, then we will apply a two step-based statistical analytics strategy that involves a screening step based on marginal associations and gene-diet correlations and a testing step for multiplicative interactions, while correcting for multiple testing.

Statistical methods/analyses to be employed and level of familiarity needed for these methods: This is an interdisciplinary project. The student will need to have knowledge in genetics, statistics and machine learning. If the student is not familiar with the technologies, she/he will be trained for the analysis skills and apply them for the project:

1. Unsupervised machine learning approaches (e.g. principal component analysis)
2. Genetic association analysis
3. Gene-diet interaction analysis
4. Multiple testing

Site Location: The student will not work at the site of practicum supervisor (Dr. Pingzhao Hu), but he/she will meet with Dr. Hu by skype one time (1 hour) per week and additional email communications. The student will work at the site of practicum co-supervisor (Dr. Wei Xu) for one afternoon in every week (time to be decided). Depending on the student's performance and interest, it may be possible for the student to do an internship/co-op in 2019 summer (May 1- Aug 31, 2019) with payment $6,000 in Dr. Hu's lab at the University of Manitoba, Winnipeg.
Site Description: The study will need to have his/her own laptop and use it to remotely access the CPU/GPU-based high performing computing platform in Dr. Hu's lab. The platform has installed related data modeling software (R, Matlab, Python, Deep learning tools, PLINK) and will allow the student to perform large-scale deep/machine learning analysis of big genomic and genetic data.
Statistical software used at this site: R, Matlab, Python, Deep learning tools (TensorFlow, etc.), PLINK
Project available for MSc and/or PhD: MSc only
Expected availability: Flexible
Additional Onboarding Requirements: No

Project Title: Deep learning-based cancer cell counting from biomedical images
Supervisor: Dr. Pingzhao Hu
Supervisor Email: pingzhao.hu@utoronto.ca
Supervisor Phone: (204) 789-3229
Co-Supervisor:
Co-Supervisor Contact Details:
Project Description: Detecting cancer cells from biomedical images is an important question in a wide range of biomedical research and clinical practices. Recent advancement of deep learning in processing images makes it possible to evaluate cancer cells from biomedical images faster and more reliable. This is a part of an international collaboration project with investigators from Japan, Germany and Canada. The goal of the student's project is to apply a density estimation-based deep learning (DL; U-net) algorithm (Lempitsky et al. 2010,Xie et al,2018) to automatically enumerate cancer cells within the images. Given that the number of images generated in-house may be not enough to train the DL net, we will apply transfer learning to train the model on other large microscopic based images data set with known cell counts. The U-net algorithm produces density maps for series of input images and cell counting will be examined by solving regression problems. The trained regression model will then be applied to in-house biomedical images (e.g. microscopy images) generated under different conditions. The estimated cancer cell counts will be compared between different conditions. This approach overcomes many limitations of traditional single-cell segmentation based methods, including cell clumping and overlap (i.e. resolving individual cells).
Statistical methods/analyses to be employed and level of familiarity needed for these methods: Although the major analysis is deep learning-based regression analysis, the student should be also familiar with linear regression modeling as a baseline model. The student should also understand the repeated measurement analysis. The student is required to know how to program using Python under Linux environment. Although the student is not necessary to have knowledge in deep learning, some experience in machine learning and manipulating "true big data" will be helpful. The student will have the opportunity to take 1-2 deep learning courses/modules offered by Dr. Andrew Ng in Coursera. Dr. Hu will pay the fee.
Site Location: The student will not work at the site of practicum supervisor (Dr. Pingzhao Hu), but he/she will meet with Dr. Hu by skype one time (1 hour) per week and additional email communications. Depending on the student's performance and interest, it may be possible for the student to do an internship/co-op in 2019 summer (May 1- Aug 31, 2019) with payment $6,000 in Dr. Hu's lab at the University of Manitoba, Winnipeg.
Site Description: The study will need to have his/her own laptop and use it to remotely access the CPU/GPU-based high performing computing platform in Dr. Hu's lab. The platform has installed related data modeling software (R, Matlab, Python, Deep learning tools) and will allow the student to perform large-scale deep/machine learning analysis of imaging data.

Statistical software used at this site: R, Matlab, Python, Deep learning tools (TensorFlow, etc.)
Project available for MSc and/or PhD: Both MSc and PhD
Expected availability: Flexible
Additional Onboarding Requirements: No

Project Title: Effects of Cognitive Bias Modification (CBM) on suicide ideation
Supervisor: Marcos Sanches
Supervisor Email: marcos.sanches@camh.ca
Supervisor Phone: 416 535 8501 ext. 36674
Co-Supervisor:
Co-Supervisor Contact Details:
Project Description: Cognitive Bias Modification (CBM) is an intervention that has been demonstrated to have positive effect on treatment of depression and addiction, but an important outcome that has not been looked at to date is suicide ideation. This study is a randomized trial that gather data before and after the CBM intervention with the aim to test its effect on changing levels of suicide ideation.
Statistical methods/analyses to be employed and level of familiarity needed for these methods: Descriptive analysis and Analysis of Correlated Data - Multilevel Modeling. Some familiarity with regression analysis in general is important as well as with basic concepts in statistics (statistical inference, causal analysis).
Site Location: Centre for Addiction and Mental Health (CAMH), 33 Russell Street, Toronto
Site Description: CAMH is Canada's largest mental health and addiction teaching hospital, as well as one of the world's leading research centres in the area of addiction and mental health. CAMH combines clinical care, research, education, policy development and health promotion to help transform the lives of people affected by mental health and addiction issues. Learn more at www.camh.net
Statistical software used at this site: R, SPSS, SAS, Stata, Mplus
Project available for MSc and/or PhD: MSc only
Expected availability: We are quite flexible with time.
Additional Onboarding Requirements: Usual requirements are Tuberculosis screening and general paperwork.

Project Title: Effect of Adherence to anti-psychotic medication on clinical outcome - a Latent Change Score approach
Supervisor: Marcos Sanches
Supervisor Email: marcos.sanches@camh.ca
Supervisor Phone: 416 535 8501 ext. 36674
Co-Supervisor:
Co-Supervisor Contact Details:
Project Description: The prevailing theory indicates that not taking the medication as prescribed would lead to the worsening of the clinical outcomes in patients in genral. We have followed a specific cohort of patients on anti-psychotic medication and failed to find a direct association between the adherence to medication and clinical outcomes. There are different hypothesis on why that would happen but here we propose to use a more sophisticated model, the Latent Change Score model, to test this association. Such model specifies that the chagne in medication adherence will be associated with changes in clinical outcomes, where the change is defined as a latent variables in the model.
Statistical methods/analyses to be employed and level of familiarity needed for these methods: Latent Variable Modeling. Some knowledge with regression models and latent variable theory is helpful.
Site Location: Centre for Addiction and Mental Health (CAMH), 33 Russell Street, Toronto
Site Description: Centre for Addiction and Mental Health (CAMH) Description: CAMH is Canada's largest mental health and addiction teaching hospital, as well as one of the world's leading research centres in the area of addiction and mental health. CAMH combines clinical care, research, education, policy development and health promotion to help transform the lives of people affected by mental health and addiction issues. Learn more at www.camh.net
Statistical software used at this site: R, SAS, SPSS, Mplus and Stata. This specific project will likely have to be done in Mplus or R.
Project available for MSc and/or PhD: MSc only
Expected availability: Workdays, we are flexible
Additional Onboarding Requirements: CAMH requires TB screening and paperwork.

Project Title: Creating a prognosis model for palliative care cancer patients
Supervisor: Wei Xu
Supervisor Email: Wei.Xu@uhnresearch.ca
Supervisor Phone: 4169464497
Co-Supervisor: Lisa W. Le
Co-Supervisor Contact Details: Lisa.Le@uhnresearch.ca
Project Description: The aim of this project is to develop a prediction model on overall survival. Demographics and clinical variables were collected for patients received palliative care in last ten years, as well as their symptom scores and perform status over time as repeated measures. Our research group has already investigated and developed a predictive model using the cross-sectional data at baseline. This project will explore how these repeated measures can be utilized for predicting prognosis of cancer patients receiving palliative care.
Statistical methods/analyses to be employed and level of familiarity needed for these methods: Survival analysis and repeated measures analysis will be performed. Students will get exposure in developing predictive models. Depending on the student's interest and time available, the student is encouraged to explore some machine learning techniques.
Site Location: 10-502B, 610 University Ave, Toronto, Ontario, M5G 2M9
Site Description: Department of Biostatistics, Princess Margaret Hospital, University Health Network
Statistical software used at this site: SAS, R and others as needed.
Project available for MSc and/or PhD: Both MSc and PhD
Expected availability: Flexible
Additional Onboarding Requirements: TB test by UHN policy

Project Title: Developing prognostic models for assessing Survival outcomes in the Hematology patients data.
Supervisor: Wei Xu
Supervisor Email: wxu@uhnres.utoronto.ca
Supervisor Phone: 4169464497
Co-Supervisor: Eshetu G. Atenafu
Co-Supervisor Contact Details: Eshetu.Atenafu@uhnresearch.ca
Project Description: The student will have the opportunity to learn/advance their Survival analysis skills, how to define different scoring systems using important covariates of interest and suggest different prognostic scores for Hematology patients data. The main outcomes include time to event outcomes and recurrence. Advanced statistical methods such as survival analysis incorporating competing events, binary partitioning to obtain optimum threshold and scoring systems will be developed. Data might be partitioned as learning and validation. The developed prognostic scores will be implemented/validated using the validation dataset and if there are more than one such scores assessment will be performed and a recommendation will be provided based one the performance. The study types include clinical trial and/or retrospective cohort data.
Statistical methods/analyses to be employed and level of familiarity needed for these methods: Survival Analysis, Binary Recursive Partitioning, (Concordance Index (optional))
Site Location: 10-502B, 610 University Ave, Toronto, Department of Biostatistics, Princess Margaret Hospital, University Health Network
Site Description: Department of Biostatistics, Princess Margaret Hospital, University Health Network
Statistical software used at this site: SAS, R and others as needed
Project available for MSc and/or PhD: Both MSc and PhD
Expected availability: Flexible
Additional Onboarding Requirements: TB test by UHN policy

Project Title: Relationships among self-rating scales related to geriatric mental health
Supervisor: Dr. Sandra Gardner
Supervisor Email: sgardner@research.baycrest.org
Supervisor Phone: 416-785-2500 x 3352
Co-Supervisor: Dr. Malcolm Binns
Co-Supervisor Contact Details: mbinns@research.baycrest.org, 416-785-2500 x 3594
Project Description: In-patient and out-patient psychiatric patients at Baycrest completed several self-rating scales related to mood, dignity and health-related quality of life at each of their clinical visits. The purpose of the project is to examine the relationships among the total scale scores across time and identify patients with similar response patterns.
Statistical methods/analyses to be employed and level of familiarity needed for these methods: Longitudinal data analysis, discriminant analysis, clustering
Site Location: Rotman Research Institute, Baycrest Health Sciences Kimel Family Building 3560 Bathurst Street, Toronto
Site Description: Baycrest is a geriatric care facility with a long-term care home as well as an acute care hospital. Baycrest's research focus is brain health and aging and the Rotman Research Institute specializes in the study of human brain function.
Statistical software used at this site: R and SAS
Project available for MSc and/or PhD: MSc only
Expected availability: To be determined
Additional Onboarding Requirements: Baycrest's required online training courses and the Tri-Council Policy online ethics course.

Project Title: Implications of combining data from multiple surveys
Supervisor: Victoria Landsman
Supervisor Email: victoria.landsman@utoronto.ca
Supervisor Phone: 4169272027 ext 2131
Co-Supervisor:
Co-Supervisor Contact Details:
Project Description: As a starting point, we will simulate data to explore the properties of the methods outlined in Schenker et al. (SIM, 2010). These methods have been proposed to improve analyses of self-reported data in one survey using clinically measured data from another survey.
Statistical methods/analyses to be employed and level of familiarity needed for these methods: Working with large scale population data, imputation methods, propensity scores methods, regression models. Although I expect some level of independent work for this project, I will provide all necessary guidance.
Site Location: 481 University Avenue, Suite 800, Toronto
Site Description: Institute for Work and Health (IWH) is a non-profit research organization with the focus on occupational health and safety.
Statistical software used at this site: R
Project available for MSc and/or PhD: Both MSc and PhD
Expected availability: Flexible
Additional Onboarding Requirements: None

Project Title: Use of joint point regression for temporal analysis of trends
Supervisor: Victoria Landsman
Supervisor Email: victoria.landsman@utoronto.ca
Supervisor Phone: 4169272027 etx 2131
Co-Supervisor:
Co-Supervisor Contact Details:
Project Description: In this project we will learn about joinpoint regression analysis which is a powerful regression approach to analyzing trends. This tool has been used worldwide for the temporal analysis of cancer incidence. In this project we will apply the method to the temporal analysis of injuries trends.
Statistical methods/analyses to be employed and level of familiarity needed for these methods: Regression analysis, trends, administrative databases. I will provide all the necessary guidance.
Site Location: 481 University Avenue, Suite 800, Toronto
Site Description: Institute for Work and Health is a non-profit research organization with the focus on occupational health and safety.
Statistical software used at this site: R
Project available for MSc and/or PhD: MSc only
Expected availability: Flexible
Additional Onboarding Requirements: None

Project Title: Using variability in kidney function to predict genes associated with lupus nephritis
Supervisor: Eleanor Pullenayegum
Supervisor Email: eleanor.pullenayegum@sickkids.ca
Supervisor Phone: 4168137654x301031
Co-Supervisor:
Co-Supervisor Contact Details:
Project Description: Lupus is a life threatening, chronic, autoimmune disease where the body's immune system mistakenly attacks healthy tissue. Genes play an important role in determining who will develop lupus. We have genetic data longitudinal, repeated measures on thousands or children and adults with lupus. We are interested in exploring variability of kidney function as a means of identifying genes associated with lupus nephritis. Analysis will involve advanced modelling techniques such as inverse-weighting and the jackknife, so the project is well suited to a doctoral-level student or a student with prior experience of data analysis.
Statistical methods/analyses to be employed and level of familiarity needed for these methods: Inverse-weighting, mixed models, GEE, JackKnife. Some familiarity would be helpful, and a good grasp of regression modelling essential
Site Location: Sick Kids - Peter Gilgan Centre for Research & Learning, 686 Bay Street
Site Description: The work site is a research institute attached to the hospital. As such you will be working in an office environment alongside Scientists, Research Assistants and other Graduate students from a range of disciplines
Statistical software used at this site: R
Project available for MSc and/or PhD: Both MSc and PhD
Expected availability: Flexible
Additional Onboarding Requirements: Immunizations must be up to date and 2-step TB test completed

Project Title: Longitudinal trajectory of patient-reported symptoms in cervical cancer patients
Supervisor: Amy Liu
Supervisor Email: zhihuiamy.liu@uhnresearch.ca
Supervisor Phone: 416-946-4501
Co-Supervisor: Olli Saarela
Co-Supervisor Contact Details: olli.saarela@utoronto.ca
Project Description: Cervical cancer patients treated with chemo-radiotherapy at Princess Margaret Cancer Centre from 2011 to 2016 were assessed for 9 symptoms (pain, tiredness, drowsiness, nausea, lack of appetite, depression, anxiety, shortness of breath, and wellbeing) using the Edmonton Symptoms Assessment System (ESAS) questionnaire. ESAS at baseline (pre-treatment) and at follow-up visits are collected, in addition to other patient and treatment information. The objective is to evaluate longitudinal changes in ESAS. In this practicum project, the student will (i) explore different ways to visualize longitudinal data, (ii) analyze the data using generalized linear mixed models or generalized estimating equations and (iii) investigate factors associated with changes in ESAS.
Statistical methods/analyses to be employed and level of familiarity needed for these methods: Some familiarity with generalized linear mixed models and/or generalized estimating equations.
Site Location: 610 University Avenue, 10th floor
Site Description: The Princess Margaret Cancer Centre is a scientific research centre and a teaching hospital, affiliated with the University of Toronto Faculty of Medicine as part of the University Health Network. The hospital now stands as the largest cancer centre in Canada and one of the five largest cancer centres in the world.
Statistical software used at this site: R and SAS
Project available for MSc and/or PhD: Both MSc and PhD
Expected availability: Flexible
Additional Onboarding Requirements: Possibly.

Project Title: Cardiovascular disease attributable to nutrition-related causes: Estimating future burden and evaluating nutrition policy options for maximizing population health benefit in Canada
Supervisor: Lennon Li [Please note that I have provided two project descriptions, but will be hiring only one student based on their particular interest and ability for one of the two projects. Only one application is required to be considered for both projects]
Supervisor Email: lennon.li@oahpp.ca
Supervisor Phone: 6472607479
Co-Supervisor: Brendan Simth
Co-Supervisor Contact Details: Brendan.smith@oahpp.ca
Project Description: The student will work on a CIHR funded project to analyze the 2004 and 2015 Canadian Community Health Survey (CCHS)-Nutrition component. The nationally-representative CCHS-nutrition surveys provide one of the riches sources of detailed population-level information about food and nutrient intakes available in the world. Directly measured dietary intake will be calculated using the raw 24-hour dietary recall data. The primary exposures of the study are sugar-sweetened beverage and sodium consumption, however there will be flexibility to examine other project-related dietary factors and patterns of interest. In particular, the analyses will examine the variation of usual dietary intakes of nutrients of interest across socioeconomic position (e.g., education and income). The analysis requires the use of the NCI method which uses a two-part model to estimate usual dietary intake on a consumption day for episodically-consumed foods. Time permitting, the student will also be asked to estimate the effect of changing nutrient consumption level on future population and social inequities in CVD incidence (2015-2025) using the Cardiovascular Disease Population Risk Tool (CVDPoRT), a validated population-based risk algorithm.
Statistical methods/analyses to be employed and level of familiarity needed for these methods: In addition to generalized linear models, the two part NCI method will be employed for this work. The first part estimates the probability of consumption using logistic regression with a person-specific random effect. The second part specifies the consumption-day amount using linear regression on a transformed scale, also with a person-specific effect. Parts I and II are linked by allowing the two person- specific effects to be correlated and by including common covariates in both parts of the model. The student will benefit from specialized training on this method, in addition to SAS macros created by the NCI method. Experience analysing 24-hour recall nutrition data is an asset, but not necessary.
Site Location: 480 University Ave
Site Description: Public Health Ontario (PHO) is a crown agency, we keep Ontarians safe and healthy. With our partners in government, public health and health care, we prevent illness and improve health. We provide the scientific evidence and expert guidance that shapes policies and practices for a healthier

Ontario. PHO has locations across Ontario, including 11 laboratory sites. The student will be assigned a cubical at PHO head office
Statistical software used at this site: There is some flexibility. The validate NCI macros are provided in SAS, student can implement in R if comfortable
Project available for MSc and/or PhD: Both MSc and PhD
Expected availability: flexible
Additional Onboarding Requirements: 2 weeks notice for computer and email account

Project Title: The Burden of severe Group A Streptococcus in Ontario
Supervisor: Lennon Li [Please note that I have provided two project descriptions, but will be hiring only one student based on their particular interest and ability for one of the two projects. Only one application is required to apply for both projects]
Supervisor Email: lennon.li@oahpp.ca
Supervisor Phone: 6472607479
Co-Supervisor: Natasha Crowcroft
Co-Supervisor Contact Details: natasha.crowcroft@oahpp.ca
Project Description: Group A streptococci (GAS) are bacterial pathogens that colonize and infect the upper respiratory tract and skin of humans. GAS can cause non-invasive disease such as pharyngitis ('strep throat'), scarlet fever and skin infectious. Invasive GAS occurs when it invades normally sterile parts of the body and can lead to severe infections such meningitis and rarely, death. Incidence of iGAS has been increasing in Ontario. Although most cases are sporadic, there have been several recent community outbreaks in Thunder Bay, Toronto and Middlesex-London. One report on a cluster finds a "striking overabundance of skin and soft tissue infections that did not meet the definition of iGAS disease but which were severe and, for the most part, required hospitalization." This highlights that active surveillance of severe cases of GAS occurs only after invasive infections have been identified, which means that the full pattern of transmission and even some outbreaks may not be captured by existing public health surveillance. Understanding the epidemiology of severe GAS will help inform future GAS interventions, including outbreak response and the potential of a new vaccine that is under development. PHO is therefore conducting a study with the specific objectives to: 1. Describe severe GAS cases in Ontario over time, age, sex and socioeconomic factors 2. Identify geographic clusters (hot spots) of severe GAS to identify areas of highest risk of iGAS 3. Compare severe GAS cases to reported (iPHIS) iGAS cases over time, age, sex, geography and socioeconomic factors The student will work on objective 2. The hypothesis to be explored is that there are more clusters of GAS than identified by current surveillance, which is important because it affects the likely design and impact of interventions. The student is also expected to work with epidemiologists and content experts to learn about the epidemiology of GAS and iGAS, and to gain more experience in communication and presentation skills in real work settings.
Statistical methods/analyses to be employed and level of familiarity needed for these methods: Some experience with Generalized Linear models, time series models. Spatial models will be introduced during the project. Familiarity with R is a must
Site Location: 480 University Ave
Site Description: Public Health Ontario (PHO) is a crown agency, we keep Ontarians safe and healthy. With our partners in government, public health and health care, we prevent illness and improve health. We provide the scientific

evidence and expert guidance that shapes policies and practices for a healthier Ontario. PHO has locations across Ontario, including 11 laboratory sites. The student will be assigned a cubical at PHO head office
Statistical software used at this site: R
Project available for MSc and/or PhD: MSc only
Expected availability: flexible
Additional Onboarding Requirements: Two weeks notice for computer and email account

Project Title: Employment changes in patients with early arthritis following diagnosis: a longitudinal study
Supervisor: Eleanor Pullenayegum
Supervisor Email: eleanor.pullenayegum@sickkids.ca
Supervisor Phone: 4168137665x301031
Co-Supervisor: Lily Lim
Co-Supervisor Contact Details: llim@chrim.ca
Project Description: This study aims to study how patients' employment states change longitduinally, specifically, the transition intensities, probabilities and the duration of time spent in each state, over time. We will seek to identify disease related predictor for the change in states. This is a longitudinal cohort of early arthritis patients (within one year of disease onset), followed longitudinally from the time they are diagnosed, at every clinic visit. Data including sociodemographics, employment states (student, homemaker, part-time, full-time, work disabled), health related quality of life and functional status are collected at baseline and annually. Disease activity (active joint counts) and medical treatment are collected at every visit (irregular schedule).
Statistical methods/analyses to be employed and level of familiarity needed for these methods: Markov Multistate Model. Familiarity not required but ability to learn new methods using published papers and R package manuals is needed - you will have guidance from your supervisor but independent learning is also expected
Site Location: Peter Gilgan Clinical Research and Learning Center, SickKids. 686 Bay Street
Site Description: The successful candidate will be working in a vibrant environment with statisticians, epidemiologists and other students. The candidate can attend weekly high quality epidemiology rounds at the Child Health Evaluative Sciences program or other programs (such as bioinformatics, big data, genetic epidemiology) within the building and gain great exposures to cutting edge scientific methods.
Statistical software used at this site: R
Project available for MSc and/or PhD: Both MSc and PhD
Expected availability: Flexible
Additional Onboarding Requirements: Up to date vaccinations, 2-stage TB test

Project Title: Practice Patterns in Renal Replacement Therapy (RRT or Dialysis) for the Elderly
Supervisor: Gerald Lebovic
Supervisor Email: lebovicg@smh.ca
Supervisor Phone: 14168646060 ext. 7817
Co-Supervisor: Kevin Thorpe
Co-Supervisor Contact Details: kevin.thorpe@utoronto.ca 416.864.5776
Project Description: Elderly patients in the ICU have an increased risk of acute kidney injury which can lead to a greater risk of death. However, utilization of RRT in this population has not been well studied. It is believed that this population is less likely to receive RRT as compared to a younger population. We will examine practice patterns and patient demographics that may be associated with the use of RRT in this population as well as associated outcomes such as mortality. Data has been collected on several hundred elderly subjects at numerous centres across Canada. There are several questions of interest and the student, in conjunction with the supervisor, will choose the most suitable question(s) to work on.
Statistical methods/analyses to be employed and level of familiarity needed for these methods: Multivariable regression models and generalized linear models will be used in some of the analysis. Hierarchical models (i.e. linear mixed model or generalized linear mixed model) will be used to examine practice patterns where subjects are nested within units or hospitals. Time to event analysis will be employed to examine mortality. Depending on the variables used, imputation techniques such as multiple imputation may be used in the analysis.
Site Location: St. Michael's Hospital (250 Yonge Street site)
Site Description: Applied Health Research Centre (AHRC) where both the Supervisor and Co-Supervisor work. The AHRC is an academic research organization working on more than 100 studies.
Statistical software used at this site: Primarly R but SAS too
Project available for MSc and/or PhD: MSc only
Expected availability: Flexible to be determined by supervisor and student
Additional Onboarding Requirements: Brief orientation and some other requirements (will find out)

Project Title: ADHD, ODD, and CD symptom profile agreement
Supervisor: Annie Dupuis
Supervisor Email: Annie.Dupuis@mdstats.ca
Supervisor Phone: 4169035588
Co-Supervisor: Russell Schachar
Co-Supervisor Contact Details: Russell.Schachar@sickkids.ca
Project Description: The diagnoses of attention deficit hyperactivity disorder (ADHD), oppositional defiant disorder (ODD), and conduct disorder (CD) are made on the basis of criteria published in the Diagnostic and Statistical Manual of Mental Disorders, Fifth edition. The presence of symptoms of each disorder is established through questionnaires and interviews, often from more than one informant, such as the child's parent/guardian and teacher. Agreement across multiple informants, or even within the same informant across multiple modes (questionnaire vs interview) is imperfect, complicating the establishment of a final diagnosis. Our lab has data on disruptive behavior symptoms in over 2000 children and adolescents across multiple informants and measurement scales, providing a rich dataset for exploring different patterns of symptom score discrepancies. This project is a non-traditional biostatistics project that would benefit from a creative individual with an interest in applying multivariate methods (factor analysis, cluster analysis) and data visualization to gain a better understanding of the strengths and limitations of our data for classifying participants into different diagnostic groups. We expect that some children will fall into clear diagnostic groups regardless of the informant or type of questionnaire or interview, whereas others will follow distinct patterns in the way their scores vary across the different measurement scales. Atypical subgroups of participants will be examined to determine if they present with elevated rates of learning disabilities or other comorbid disorders. The student should be comfortable with problems that don't have a single "correct" solution! Ultimately, this work will help us develop appropriate classification rules for participants for use in future studies.
Statistical methods/analyses to be employed and level of familiarity needed for these methods: Measures of agreement (absolute agreement, kappa, weighted kappa); factor analysis; cluster analysis; the student will be given code that can be adapted for these analyses
Site Location: The Hospital For Sick Children, 555 University Avenue
Site Description: The student will work in an office located in the psychiatry department at Sick Kids, in the original hospital building. The student office has 5 desks and a table for meetings.
Statistical software used at this site: SAS is used for data manipulation, measures of agreement, and factor analyses; R is used for cluster analysis and figures
Project available for MSc and/or PhD: Both MSc and PhD
Expected availability: flexible
Additional Onboarding Requirements: Note: this is an MSc project but can be a PhD project if the student has a specific interest in multivariate methods and wishes to take the analyses further; Proof of immunity to measles, rubella, and chicken pox is required (laboratory evidence of immuni

Project Title: Clinical Trial Reports
Supervisor: Kevin Thorpe
Supervisor Email: kevin.thorpe@utoronto.ca
Supervisor Phone: 416-864-5776
Co-Supervisor:
Co-Supervisor Contact Details:
Project Description: This project will mainly revolve around the development of standard reporting tools for clinical trials. This includes developing generic tools for producing publication ready tables of results and more detailed statistical reports.
Statistical methods/analyses to be employed and level of familiarity needed for these methods: Methods range from simple unadjusted comparisons of continuous, binary and survival data through multiple regression models appropriate to the same data types.
Site Location: The Applied Health Research Centre, 250 Yonge St. 6th floor
Site Description: The student will have a cubicle in an open office environment.
Statistical software used at this site: R will be the primary tool for this project although SAS and Stata are also used by some individuals in the office.
Project available for MSc and/or PhD: MSc only
Expected availability: Flexible although Friday is to be avoided since I am at the university then.
Additional Onboarding Requirements: To be determined.

Project Title: Ontario Gyne Cancer treatment outcome comparison
Supervisor: Lisa Wang
Supervisor Email: lisawang@uhnresearch.ca
Supervisor Phone:
Co-Supervisor:
Co-Supervisor Contact Details:
Project Description: Through this project, some data problem will be identified and explained. Simulation of this type of data and analysis results will be further explored and summarized.
Statistical methods/analyses to be employed and level of familiarity needed for these methods: Competing risk, cox model and simulation
Site Location: 610 University Avenue, Princess Margaret Cancer Center
Site Description: There will be a work station in the common area or Cubical in the Biotatistics department. A laptop or desk top can be used
Statistical software used at this site: SAS and R
Project available for MSc and/or PhD: Both MSc and PhD
Expected availability: Wednesday or Tuesday
Additional Onboarding Requirements:

Project Title: Analysis of High-dimensional Sequencing Data in Sister Pairs with Early Onset Breast Cancer

Supervisor: Shelley Bull

Supervisor Email: bull@lunenfeld.ca

Supervisor Phone: 416-586-8245

Co-Supervisor: Razvan Romanescu (Post-doctoral Fellow)

Co-Supervisor Contact Details: razvan@lunenfeld.ca

Project Description: Recent progress in next generation sequencing technologies makes it possible to investigate the role of rare variants in disease etiology. Statistical methods to assess association with rare variants are well-developed in the case of unrelated individuals, but few are available for family-based designs. Because rare variants for cancer susceptibility tend to be enriched in families, tests based on affected sib pairs (ASPs) can be more powerful compared to case-control designs. The purpose of the practicum project is to apply and compare test statistics designed for genome wide association study (GWAS) analysis of ASPs in (1) a pilot study of genomic sequencing of 20 sister pairs selected from the Ontario Familial Breast Cancer Registry (OFBCR), and in (2) larger datasets of sister pairs simulated under a statistical genetic model that reflects features of the pilot study data. Use of existing public annotation resources will be required to specify sets of rare variants for analysis of genes and genomic regions. The overall goal of the research is to discover novel variants in susceptibility genes that account for the substantial unexplained component in familial breast cancer susceptibility.

Statistical methods/analyses to be employed and level of familiarity needed for these methods: When working with genetic data the analyst will encounter structural errors related to genotype calling, sequencing platforms, etc. These errors will often cause the analysis models to be misspecified, resulting in type I errors that depart from nominal. The student will analyze the distribution of p-values obtained from GWAS testing and apply genomic corrections to ensure that reported p-values are accurate. This may involve applying a transformation to raw p-values and fitting a simple "empirical" distribution to the results, with the purpose of computing robust critical values for multiple testing.
Familiarity needed with descriptive data analysis, plotting techniques (e.g.. histograms, Q-Q plots, etc), and methods for categorical data analysis (estimation & hypothesis testing), including linear and logistic regression. R programming skills and ability to understand and modify statistical procedure codes.

Site Location: Prosserman Centre for Population Health Research, 60 Murray St., Lunenfeld-Tanenbaum Research Institute, Sinai Health System

Site Description: The Prosserman Centre consists of principal investigators in Biostatistics/Statistical Genetics or Genetic Epidemiology with trainees (grad students & postdocs) and research staff. Office space ("dry" lab) with access to computing resources, including local network and HPC clusters.

Statistical software used at this site: Custom R code (for non-standard methods), plotting techniques implemented in R, use of scripts for automating high-throughput analysis, some use of spreadsheets for examination of large volume output

Project available for MSc and/or PhD: Both MSc and PhD

Expected availability: Wednesdays best, Tuesday or Thursday also suitable
Additional Onboarding Requirements: Students must register in the Research Training Centre in the Research Institute and submit a completed Staff Immunization and Surveillance Policy Information Sheet. The form must be completed by a physician or the occupational health nurse at a prev

Project Title: Application of computationally-intensive methods in large-scale genetic association study of lung cancer

Supervisor: Prof. Shelley Bull

Supervisor Email: bull@lunenfeld.ca

Supervisor Phone: 416-586-8245

Co-Supervisor: Dr. Myriam Brossard (Post-doctoral Fellow)

Co-Supervisor Contact Details: brossard@lunenfeld.ca

Project Description: Typically, genome-wide association studies (GWAS) look for genetic variants associated with complex diseases (eg. lung cancer risk) by testing association of each common genetic variant (SNP) among several millions of variants genotyped and/or imputed on the genome of several thousands of subjects (eg. lung cancer cases & controls). Although, GWAS have succeeded in uncovering numerous variants (in multiple genomic regions) associated with complex diseases, other variants & regions remain to be discovered. To improve power for region/variant discovery, we are currently developing and investigating alternate and more sophisticated methodologies based on region-based statistical methods for joint analysis of multiple variants grouped in pre-specified genomic regions.

As part of this project, we are interested in evaluating whether integration of biological knowledge in region-based tests improves region discovery. The trainee will apply a recent scalable methodology integrating functional information with genome-wide multi-variants regression models for region/variant discovery (bfGWAS, Yang et al, 2017) in genome-wide genetic data from a lung cancer case-control study (McKay et al 2017). Cases and controls (2308 individuals in total) have been genotyped using the Oncoarray platform, and up to 8 million SNP variables imputed from the 1000 Genomes Project reference population. bfGWAS will be applied using 1) default arbitrary region definition, and 2) a more flexible region definition constructed from data. We also plan to evaluate the sensitivity of bfGWAS to different sources of biological annotations and compare the results to another region-based analysis approach we have been developing.

References:

McKay JD et al. Large-scale association analysis identifies new lung cancer susceptibility loci and heterogeneity in genetic susceptibility across histological subtypes. Nat Genet. 2017 Jul;49(7):1126-1132. doi: 10.1038/ng.3892. Epub 2017 Jun 12.

Yang et al. A scalable Bayesian method for integrating functional information in GWAS, American J of Human Genetics, 7 September 2017, 101(3), 404-416.

Software: https://github.com/yjing/bfGWAS

Statistical methods/analyses to be employed and level of familiarity needed for these methods: bfGWAS is formulated as a Bayesian hierarchical variable selection regression model for genome-wide analysis and incorporates biological knowledge through knowledge-specific prior distributions specified on SNP effects. It models the effect-size distribution & probability of causality for regions & variants with different annotations, thus prioritizing association signals based on the quantification of the annotations. For computationally feasible genome-wide Bayesian inference, the method uses a scalable EM-MCMC algorithm that (1) splits

arbitrary the genome in regions of 5,000 to 10,000 consecutive variants, allowing per region-parallelization of MCMC iterations at the Estimation-step and (2) summarizes the posterior effects across all regions & updates annotation-specific posterior estimates at the Maximization-step. This project requires understanding of methods for Bayesian regression and MCMC computation, as well as R programming skills and ability to understand and modify statistical procedure code. Some familiarity with genomic or other large scale data and experience in a linux environment would be useful.
Site Location: Prosserman Centre for Health Research, 60 Murray St., Lunenfeld-Tanenbaum Research Institute, Sinai Health System
Site Description: The Prosserman Centre consists of principal investigators in Biostatistics/Statistical Genetics or Genetic Epidemiology with trainees (grad students & postdocs) and research staff. Office space ("dry" lab) with access to computing resources, including local network and HPC clusters, will be provided.
Statistical software used at this site: Custom software and R code (for non-standard methods), plotting techniques implemented in R, scripts for automating high-throughput analysis (in linux environment), some use of spreadsheets for examination of large volume output
Project available for MSc and/or PhD: PhD only
Expected availability: Wednesday best, Tuesday or Thursday also suitable
Additional Onboarding Requirements: Students must register in the Research Training Centre in the Lunenfeld-Tanenbaum Research Institute and submit a completed Staff Immunization and Surveillance Policy Information Sheet. The form must be completed by a physician or the occupational health

Project Title: Multilevel models to examine the effect of neighbourhood factors on health care access and utilization in Toronto: The Neighbourhood Effects on Health and Well-Being (NEHW) Project
Supervisor: Rosane Nisenbaum
Supervisor Email: nisenbaumr@smh.ca
Supervisor Phone: 416-8646060 extension 77338
Co-Supervisor:
Co-Supervisor Contact Details:
Project Description: Background: There is a large body of evidence in the literature supporting the association of neighbourhood factors and several illnesses, in addition to individual factors. The Neighbourhood Effects on Health and Well-Being (NEHW) Project was conducted to determine how Toronto neighbourhood factors, in addition to individual resident factors, affected residents' health. It included a random sample of 2412 residents from 47 Toronto neighbourhoods (https://www.ncbi.nlm.nih.gov/pubmed/25463919) Objectives: The objectives of this Practicum project are to: Question 1: Examine to what extent neighbourhood stressors (neighbourhood safety, neighbourhood problems) are associated with health care access and utilization in the past 12 months Question 2: Examine to what extent neighbourhood buffers/resources (neighbourhood quality, neighbourhood services and resources) offset the contribution of neighbourhood stressors to health care access and utilization in the past 12 months Question 3: Determine if individual-level characteristics interact with neighbourhood-level variables with respect to health care access and utilization Question 4: Determine if the relationships in #1, #2 and #3 change if census neighbourhood characteristics (e.g. proportion of immigrants, neighbourhood income quintile) are also considered
Statistical methods/analyses to be employed and level of familiarity needed for these methods: Methods: Derivation of health care access and utilization outcomes from individual items Merging Survey data with Census data by neighbourhood name or number Descriptive statistics, graphics Multilevel models (logistic or Poisson) to account for clustering of residents within neighbourhoods
Site Location: Centre for Urban Health Solutions, Li Ka Shing Knowledge Institute, St Michael's Hospital, 209 Victoria Street, 3rd floor, Toronto
Site Description: Please follow the link http://stmichaelshospitalresearch.ca/research-programs/urban-health-solutions/
Statistical software used at this site: SAS or R
Project available for MSc and/or PhD: Both MSc and PhD
Expected availability: Monday, Wednesday or Friday are better, but can accommodate if necessary
Additional Onboarding Requirements: Yes. Because this is a hospital, there is a list of requirements including vaccination, online training and orientation.

Project Title: Quantile Segmented Regression
Supervisor: Rahim Moineddin
Supervisor Email: Rahim.moineddin@utoronto.ca
Supervisor Phone: (416) 946-5860
Co-Supervisor:
Co-Supervisor Contact Details:
Project Description: Project Description: In Interrupted Time Series (ITS) study, a series of observations on the same outcome before and after the introduction of an intervention are measured and used to test immediate (level change) and gradual effects (trend change) of the intervention. The Interrupted Time Series method is able to distinguish the effect of the intervention from secular trend (change that would have happened even in the absence of the intervention). Estimating the intervention effect is done by comparing the trend in the outcome after the intervention to the existing trend in the pre-intervention period, and is achieved through modifications to the standard regression analysis known as segmented regression. Quantile regression is a type of regression analysis used in statistics and econometrics for modelling the conditional median or other quantiles of a continuous outcome measure. In ordinary least square linear regression we model the conditional mean of the outcome measure. Quantile regression is an extension of the linear regression for modelling the conditional quantiles. The primary objective of this project is to use the segmented quintile regression as an alternative interrupted time series method for assessing the impact of an intervention on the quantile of a health outcome measure. We are also interested to investigate the application of the random effect segmented quantile regression in quantile regression for adjusting for the serial correlation among time series data. This project requires some simulation experiments as well as applying the segmented quantile regression methodology on a real data set.
Statistical methods/analyses to be employed and level of familiarity needed for these methods: Methods from linear regression and simulation.
Site Location: 500 University Ave., 3rd Floor, Department of Family and Community Medicine, Research Program.
Site Description: The DFCM, the Department of Family & Community Medicine at the University of Toronto, is an academic setting and is the largest Family Medicine training program in North America. Our department is recognized internationally for its clinical, educational and research excellence. The DFCM Research Program was established in 1995 to create a critical mass of Family Medicine researchers; provide faculty with protected research time; develop research excellence and productivity; and build an infrastructure to support research. The DFCM currently supports 26 researchers through its Investigator Awards Program in order to provide protected research time.
Statistical software used at this site: R
Project available for MSc and/or PhD: Both MSc and PhD
Expected availability: Students have the flexibility to choose any day, Monday to Friday, between 9am to 4pm.
Additional Onboarding Requirements:

Project Title: Inter and Intra class correlation (ICC) for repeated measures.
Supervisor: Rahim Moineddin
Supervisor Email: Rahim.moineddin@utoronto.ca
Supervisor Phone: (416) 946-5860
Co-Supervisor:
Co-Supervisor Contact Details:
Project Description: Measurement is an essential component of scientific research in natural, social, and health sciences. In the past few decades, the situation in clinical research has become more complex. Generally measurements are not 100 percent accurate and the concept of reliability is a fundamental approach to reveal the amount of random and systematic measurement errors. The reliability is generally measured by the ratio of the variability between patients/subjects to the total variability (the sum of patient/subject variability and measurement error) known as ICC. The ICC can be estimated using Analysis of Variance or Random effects model. When the design is complex, for example one rater rates the same patient more than once the classical approach for estimating the ICC is biased. Generalizability theory (G theory) has been used for calculating the ICC for more complex designs. The purpose of this project is replicating the results of G theory using appropriate combination of modelling the random effects and the covariance structure of the residuals to account for the complexity of the study design. In other words we are interested to model the R matrix and use the G matrix components to estimate the ICC for repeated measures. This project involves simulating correlated continuous measures and fitting appropriate mixed models for estimating the ICC for repeated measures as an alternative method.
Statistical methods/analyses to be employed and level of familiarity needed for these methods: Methods from linear mixed models and Generalized Estimation Equations (GEE).
Site Location: 500 University Ave., 3rd Floor, Department of Family and Community Medicine, Research Program.
Site Description: The DFCM, the Department of Family & Community Medicine at the University of Toronto, is an academic setting and is the largest Family Medicine training program in North America. Our department is recognized internationally for its clinical, educational and research excellence. The DFCM Research Program was established in 1995 to create a critical mass of Family Medicine researchers; provide faculty with protected research time; develop research excellence and productivity; and build an infrastructure to support research. The DFCM currently supports 26 researchers through its Investigator Awards Program in order to provide protected research time.
Statistical software used at this site: SAS
Project available for MSc and/or PhD: Both MSc and PhD
Expected availability: Students have the flexibility to choose any day, Monday to Friday, between 9am to 4pm.
Additional Onboarding Requirements:

Project Title: Analysis of a Natural History Cohort in First-Line NSCLC
Supervisor: Matt Kowgier
Supervisor Email: matthew.kowgier@roche.com
Supervisor Phone: 4169340299
Co-Supervisor:
Co-Supervisor Contact Details:
Project Description: The collection of this natural history cohort provides a rich real world data set, including patients screened in over 20 countries and those who do not have adequate tissue for molecular analysis. At baseline, we will have a comprehensive genomic profile on all patients screened for the study, including bTMB and the genomic alterations included in the FACT assay.
Statistical methods/analyses to be employed and level of familiarity needed for these methods: Time-to-event analysis, i.e., survival analysis methods; and, possibly, data mining methods.
Site Location: Roche Canada, 7070 Mississauga Road, Mississauga, ON
Site Description: Near Mississauga Road and 401 West
Statistical software used at this site: R, SAS
Project available for MSc and/or PhD: Both MSc and PhD
Expected availability: Probably Monday or Tuesday or Wednesday
Additional Onboarding Requirements:

Project Title: An artificial neural network for predicting local recurrence among women diagnosed with ductal carcinoma in situ in Ontario

Supervisor: Rinku Sutradhar

Supervisor Email: rinku.sutradhar@ices.on.ca

Supervisor Phone: 416-480-6091

Co-Supervisor: Lawrence Paszat

Co-Supervisor Contact Details:

Project Description: Ductal carcinoma in situ (DCIS) of the female breast is a precursor lesion for infiltrating ductal carcinoma (IDC), although most cases of DCIS will not progress to IDC. The prevalence of DCIS, in the absence of IDC, has greatly increased in the era of mammography. A small percent of women (3.4%), with a diagnosis of DCIS without invasion at the time of initial diagnosis, will die from IDC within 10 years. Some argue that DCIS is over-diagnosed because of the increase in its prevalence among screened populations. Others argue that DCIS is over-treated, given that many cases of DCIS will not recur or progress to IDC. Time-to-event regression models have been used to predict the risk of local recurrence among women diagnosed with DCIS; these models serve as a standard traditional statistical approach for predicting the risk of an outcome occurring over time. Exploring methods which are free of assumptions but still maintain strong prediction ability is important. Artificial Neural Networks (ANN) models, which are completely non-parametric, are being used increasingly in various areas of research. Although analyzing the data using ANN methodology is usually more complex than traditional approaches, ANN models can be more flexible and efficient when the main aim is prediction or classification of an outcome using different explanatory variables.

The objectives of this project are as follows:

1- To develop and validate an Artificial Neural Network (ANN) for predicting the risk of local recurrence following breast conserving therapy with or without radiation among women with ductal carcinoma in situ in Ontario

2- To compare the predictive performance of Artificial Neural Networks against our traditional statistical approach such as time-to-event prediction models that has already been developed.

Statistical methods/analyses to be employed and level of familiarity needed for these methods: Prediction models for time-to-event data, comparing artificial neural network models against traditional survival models; students should be familiar with survival modeling concepts at minimum.

Site Location: Institute for Clinical Evaluative Sciences

Site Description: ICES is a research institute that applies the study of health informatics for health services research and population-wide health outcomes research in Ontario using data collected through the routine administration of Ontario's system of publicly funded health care. Students will be working in an office environment and will have access to a computer for analyzing their project-specific Ontario-wide data.

Statistical software used at this site: R and SAS

Project available for MSc and/or PhD: MSc only

Expected availability: Tuesday, Thursday morning or early afternoon would be best, however this is flexible
Additional Onboarding Requirements:

Project Title: Examining the impact of the Edmonton Symptom Assessment System on health services outcomes among cancer patients in Ontario
Supervisor: Rinku Sutradhar
Supervisor Email: rinku.sutradhar@ices.on.ca
Supervisor Phone: 416-480-6091
Co-Supervisor: Lisa Barbera
Co-Supervisor Contact Details:
Project Description: Since 2007, Cancer Care Ontario, the cancer agency in Ontario, Canada, has systematically collected symptom scores in cancer outpatients by implementing the Edmonton Symptom Assessment System (ESAS) as a standardized tool in all cancer centers. One of the goals of this initiative is to improve symptom management through earlier identification, documentation, and communication of patients' symptoms. The ESAS is a well known and validated tool to screen for the presence and severity of symptoms. The identification of symptoms with this screening tool is meant to prompt a further detailed assessment, with possible intervention depending on the findings. In essence, Ontario has implemented population-wide standardized symptom assessment for cancer outpatients. The primary objective of this project is to evaluate the impact of ESAS screening on several health services outcomes among cancer patients in Ontario. This will be done by examining a matched cohort of patients who do and do not participate in ESAS screening. These patients will then be followed over time to assess their rate of use of health services such as emergency department visits, hospitalizations, palliative care visits etc.
Statistical methods/analyses to be employed and level of familiarity needed for these methods: Survival models and recurrent event models; students should be familiar with survival modeling concepts at minimum.
Site Location: Institute for Clinical Evaluative Sciences
Site Description: ICES is a research institute that applies the study of health informatics for health services research and population-wide health outcomes research in Ontario using data collected through the routine administration of Ontario's system of publicly funded health care. Students will be working in an office environment and will have access to a computer for analyzing their project-specific Ontario-wide data.
Statistical software used at this site: R and SAS
Project available for MSc and/or PhD: MSc only
Expected availability: Tuesday, Thursday morning or early afternoon would be best, however this is flexible
Additional Onboarding Requirements:

Project Title: Exponential Dispersion models for healthcare cost data
Supervisor: Nicholas Mitsakakis
Supervisor Email: n.mitsakakis@theta.utoronto.ca
Supervisor Phone:
Co-Supervisor:
Co-Supervisor Contact Details:
Project Description: Compound models rely on the assumption that the quantity of interest is generated as a sum of (independent and identically distributed) random variables, where the number of summed variables is a random variable itself. An example of this type of distribution is the compound Poisson or Tweedie, which is the distribution of Y where $Y = X1 + \ldots + X$N, where N follows Poisson distribution and Xi are iid Gamma variables. These models have been used in various applications including actuarial studies and survival analysis. However they have been basically ignored for the analysis of health care cost data, even though they seem very suitable: each patient accumulates incurred cost as a sum of individual cost amounts incurred as a result of "episodes" of interactions with the health care system (e.g. hospital visit, physician visit, use of medical technology etc.). One of the advantages of these models is that they can be treated as members of a larger class of models, Exponential Dispersion models. The use of the latter allows for specific deductions and inferences. For example, these models potentially allow the decomposition of the variance into two components, one associated with the frequency (i.e. the distribution of N) and one associated with the "severity" (i.e. the distribution of individual Xi variables). Such distinction can be greatly informative for medical decision making, as it can separate patients with large costs due to frequent health care utilization, from those with infrequently but very costly utilization. The objective of this project is to review Poisson compound models and their representation as exponential dispersion models, focusing on a specific class of them, the Tweedie model, to review existing implemented tools that can be used for fitting these models and to evaluate the benefit of these models in comparison to current practice (e.g. gamma regression models) using synthetic and real medical cost data.
Statistical methods/analyses to be employed and level of familiarity needed for these methods: Tweedie models and simulation methods will be used, no familiarity is needed. Experience with generalized linear models in both practical and theoretical level would be important.
Site Location: Biostatistics Research Unit/ THETA Collaborative within Toronto General Hospital
Site Description: Open space cubicles, students will mostly use their own laptops. They can interact with other students, postdoctoral fellows and researchers/ biostatisticians.
Statistical software used at this site: R
Project available for MSc and/or PhD: PhD only
Expected availability: This can be flexible
Additional Onboarding Requirements: A couple of orientation sessions from UHN (they need to be taken as early as possible)

Project Title: Methods for identifying and describing health state transitions
Supervisor: Nicholas Mitsakakis
Supervisor Email: n.mitsakakis@theta.utoronto.ca
Supervisor Phone:
Co-Supervisor:
Co-Supervisor Contact Details:
Project Description: Disease progression can be described as a series of mutually exclusive and collectively exhaustive health states, where patients are moving through them. Various issues are of interest around the description of the ways patients are transition through the states. One has to do with the way the different pathways patients take can be described. Efficient and informative ways including visualization techniques are of interest. Another issue is related to the estimation of the transition intensities and probabilities, which are often of interest. Those can be potentially estimated with the use of multistate models, however this task is not trivial, especially when the number of health states is large. Finally, the transitions are not always observable and in those cases a method of inferring these transitions is of interest. Hidden Markov Models could offer a solution, if these transitions are associated with other observable variables. In this project, any of these issues may be investigated, with the use of simulated as well as already collected real chart review prostate cancer patient data. Students will discuss with supervisor and select appropriate project of mutual interest.
Statistical methods/analyses to be employed and level of familiarity needed for these methods: Some of the following will be used according to the specific project: exploratory descriptive analysis, network/pathway data analysis, visualization methods, multistate models, Hidden Markov Models
Site Location: Biostatistics Research Unit/ THETA Collaborative within Toronto General Hospital
Site Description: Open space with cubicles for students; student will have the opportunity to interact with other students, postdoctoral fellows, researchers/biostatisticians.
Statistical software used at this site: R
Project available for MSc and/or PhD: Both MSc and PhD
Expected availability: Flexible
Additional Onboarding Requirements: UHN requires a couple of orientation sessions, to be taken as early as possible.

Project Title: Risk of second primary cancers after treatment of breast, colorectal and gynecologic cancer

Supervisor: Hedy Jiang

Supervisor Email: hedy.jiang@cancercare.on.ca

Supervisor Phone: 6479885516

Co-Supervisor:

Co-Supervisor Contact Details: hedy.jiang@cancercare.on.ca

Project Description: The project was funded by the Canadian Centre for Applied Research in Cancer Control Seed Grant. It is one of few studies to examine second cancers in women in Canada. Knowledge of the risk and patterns of second cancers may influence future surveillance and prevention. The identification of patient groups at increased risk for secondary malignancy will lead to the implementation of early intervention and reduction of mortality associated with the second cancer occurrence.

The retrospective cohort comprises women 30 to 74 years of age diagnosed with their first invasive breast, uterus, ovarian and colorectal cancer in Ontario in 2010-11, with follow up to the year 2016. Cases will be identified through the Ontario Cancer Registry, and the characteristics of the patient will be obtained through the Activity Level Reporting databases, including prognostic information such as age at diagnosis, place of residence, chemotherapy, and hospital information. Indicators of rurality and socio-economic status (i.e., household income in 2010) at dissemination area level at diagnosis will be collected from Statistics Canada.

Statistical methods/analyses to be employed and level of familiarity needed for these methods: Logistic regression (familiar); survival analysis (familiar); data management (familiar); SAS and R (familiar)

Site Location: 525 University Ave.

Site Description: CCO is the Ontario government's principal advisor on the cancer and renal systems, as well as on access to care for key health services. We are governed by Ontario's Cancer Act and accountable to the Ministry of Health and Long-Term Care. We equip health professionals, organizations and policy-makers with the most up-to-date cancer knowledge and tools to prevent cancer and deliver high-quality patient care. Our purposes include:

* Collect and analyze data about cancer services and combine it with evidence and research that is shared with the healthcare community in the form of guidelines and standards.
* Monitor and measure the performance of the cancer system.
* Oversee a funding and governance model that ties funding to performance, making healthcare providers more accountable and ensuring value for investments in the system.
* Engage cancer patients and their families in the design, delivery and evaluation of Ontario's cancer system.

Statistical software used at this site: SAS and R

Project available for MSc and/or PhD: Both MSc and PhD

Expected availability: One day per week while students can choose which day to come on-site

Additional Onboarding Requirements: NA

Project Title: Estimation of Ambient Environmental Exposure using Big Data and Analytics
Supervisor: Wendy Lou
Supervisor Email: wendy.lou@utoronto.ca
Supervisor Phone: (416) 946-7804
Co-Supervisor: Erjia Ge
Co-Supervisor Contact Details: erjia.ge@utoronto.ca & (416) 978 7520
Project Description: This project will focus on developing geospatial models for estimating environmental exposures (e.g. PM2.5, NO2, and O3 concentrations) using satellite remote sensing, meteorology, and land use information data etc.—all are available through the Canadian Urban Environmental Health Research Consortium (CANUE; https://canue.ca). The planned activities include (1) reviewing methodology relevant to spatiotemporal distributions for air pollution concentrations, (2) performing analyses using geospatial and machine learning methods, and (3) verifying results using other approaches and analytic tools. Participating student(s) will be working with co-supervisors at DLSPH and CANUE, and will be involved in data analyses, statistical modelling and manuscript preparation.
Statistical methods/analyses to be employed and level of familiarity needed for these methods: Familiarity of statistical methods for spatial correlated data, environmental epidemiology and exposure science would be very helpful, but not required. As examples, advanced geospatial models such as Geographically Weighted Regression and Spatial Interpolation methods would be applied to model spatiotemporal distributions for air pollution concentrations; The Community Multiscale Air Quality Modeling System CMAQ (https://www.epa.gov/cmaq) would be used to generate a hybrid method integrating the above geospatial models and air pollution dispersion models for the estimate. Cross-validation would be performed to assess model predictability.
Site Location: ? Dalla Lana School of Public Health
Site Description: DLSPH, Health Sciences Building
Statistical software used at this site: Various analysis software packages will be used, including primarily R, ArcGIS, or Python.
Project available for MSc and/or PhD: Both MSc and PhD
Expected availability: Weekly one-hour meeting with co-supervisors, and other on-site days/times (3-4 hours/week) to be determined with co-supervisors.
Additional Onboarding Requirements: N/A

Project Title: Development of code for use of Stan for Bayesian meta-analysis
Supervisor: George Tomlinson
Supervisor Email: george.tomlinson@utoronto.ca
Supervisor Phone: 4166347246
Co-Supervisor:
Co-Supervisor Contact Details:
Project Description: The Bayesian approach to meta-analysis has numerous advantages over the classical approach. For some meta-analyses though, implementations of the Bayesian approach using software such as OpenBUGS or JAGS are very slow to run. The language Stan (http://mc-stan.org) is a relative newcomer for fitting Bayesian models and on some complex problems runs an order of magnitude faster than OpenBUGS or JAGS. The aim of this project is to develop a set of programs in R and Stan that can be used to run Bayesian meta-analyses. These will start with standard meta-analyses of studies with binary or continuous outcomes and range through increasingly complex settings (meta-analysis of diagnostic tests, meta-regression, network meta-analysis), depending on the student's rate of progress.
Statistical methods/analyses to be employed and level of familiarity needed for these methods: The student should be have very good knowledge of R; familiarity with other programming languages will make it easier to learn Stan. Training in Bayesian methods and meta-analysis will be useful, but some of this will be given as part of the practicum.
Site Location: University Health Network - Toronto General Site
Site Description: The work site is the offices of THETA/BRU (Toronto Health Economics and Technology Assessment/Biostatistics Research Unit). At the BRU, there are three PhD biostatisticians and 4 MSc biostatisticians who work with other researchers at UHN on a variety of medical research projects, some of which are meta-analyses. THETA houses a large number of graduate students in health economics, health technology assessment and health services research.
Statistical software used at this site: R (and various R packages), and Stan will be used for the project
Project available for MSc and/or PhD: Both MSc and PhD
Expected availability: Weekly meetings with supervisor - we can provide a workspace if needed for 0.5 days per week.
Additional Onboarding Requirements: There are standard procedures for anyone working as a student at UHN

Project Title: Breastfeeding duration in TARGet Kids! registry
Supervisor: Dr. Charlie Keown-Stoneman
Supervisor Email: KeownStonemC@smh.ca
Supervisor Phone: 4168646060 x7837
Co-Supervisor:
Co-Supervisor Contact Details:
Project Description: In this project the student will work with the primary biostatistician involved in the TARGet Kids registry. TARGet Kids! is a multi-disciplinary research network that collects longitudinal health exposures in Canadian children to advance evidence for community-based prevention and population-level health promotion (www.targetkids.ca). The student will be involved in analysis planning, data cleaning/prepping, analysis, and presenting results using the TARGet Kids! data. The main goal of this project is to investigate the possible associations between the time at which children stop breastfeeding (possibly right-censored) and other variables collected within the TARGet Kids! registry, such as zBMI. The student will be involved in the analysis planning stage to decide on possible exposures/covariates in the model, some of which may be time-varying.
Statistical methods/analyses to be employed and level of familiarity needed for these methods: Survival/time-to-event analysis, some familiarity an asset
Site Location: Applied Health Research Centre (AHRC): 6th floor 250 Yonge Street, Toronto ON (above the Eaton Centre)
Site Description: The AHRC is a leading not-for-profit academic research organization (ARO) fully integrated with the Li Ka Shing Knowledge Institute of St. Michael's Hospital. Established in 2009, the AHRC is the only University of Toronto (U of T) affiliated not-for-profit ARO in Toronto.
Statistical software used at this site: R (possibly SAS)
Project available for MSc and/or PhD: MSc only
Expected availability: Fridays (time of day flexible)
Additional Onboarding Requirements: TBD

Project Title: Genetics of C-peptide in diabetes
Supervisor: Andrew Paterson
Supervisor Email: andrew.paterson@sickkids.ca
Supervisor Phone: 416 813 6995
Co-Supervisor:
Co-Supervisor Contact Details:
Project Description: C-peptide is one of the important measures used to separate types of diabetes. Here, we will use C-peptide measures from people with diabetes to identify genetic variants associated with differences between people. C-peptide measures are rather unusual, since many people with diabetes have levels that are below detection, making the use of common statistical methods inappropriate. We will perform genome-wide association to identify genetic variants that are associated with differences in C-peptide between people, as well as differences in the rate of change of C-peptide levels over time.
Statistical methods/analyses to be employed and level of familiarity needed for these methods: linear regression, tobit regression
Site Location: 686 Bay St, The Hospital for Sick Children Research Institute
Site Description: Sickkids research institute is the premier pediatric research facility in Canada
Statistical software used at this site: R
Project available for MSc and/or PhD: Both MSc and PhD
Expected availability: Flexible
Additional Onboarding Requirements: Vaccinations required

Project Title: genetic analysis of renal function in type 1 diabetes
Supervisor: Andrew Paterson
Supervisor Email: andrew.paterson@sickkids.ca
Supervisor Phone: 416 813 6994
Co-Supervisor:
Co-Supervisor Contact Details:
Project Description: People with type 1 diabetes are at increased risk for damage to their kidneys. We typically measure kidney disease using the amount of protein in the urine, as well as the level in the blood of a chemical that is excreted by the kidneys. Usually these measures have been considered separately. Here we plan to consider them together. We will identify genetic variations from across the genome that are associated with either or both measures. This will be a genome-wide association study
Statistical methods/analyses to be employed and level of familiarity needed for these methods: linear regression
Site Location: 686 Bay Street, The hospital for sick children research institute
Site Description: Sickkids research institute is one of the best in Canada
Statistical software used at this site: R and perhaps SAS.
Project available for MSc and/or PhD: Both MSc and PhD
Expected availability: Flexible
Additional Onboarding Requirements: vaccinations

Project Title: Components of Cognitive function and their relationship to genetics and nutrients in Women's Health Initiative Study
Supervisor: rafal kustra
Supervisor Email: profKustra@gmail.com
Supervisor Phone:
Co-Supervisor:
Co-Supervisor Contact Details:
Project Description: Genetics grouping involving two genes and intake of Zinc and Antioxidants has been shown to alter the risk of Age-Related Macular Degeneration (AMD). AMD and Dementia-spectrum diseases (including Alzheimer's Disease) have previously been shown to co-occur and to have some of the same genetic risk factors. We have just published our findings that show a similar interaction of Zinc intake and genetics as risk factors of Cognitive Decline in Women's Health Initiative sub-cohort of over 7000 women. In this project we want to investigate dependence of various sub-components of cognitive function and zinc intake-genetics interaction in the same cohort.
Statistical methods/analyses to be employed and level of familiarity needed for these methods: Ability to work with medium-sized data (about 25000 records). Interest in learning about research in Cognition and Dementia. This is a longitudinal data and in our initial study we used repeated-measures logistic regression with some non-linear effects (for Age), though other methods may be contemplated.
Site Location: HSB
Site Description: HSB - either student lab, a desk outside my office (in HSB) or my lab (after it gets moved to new location within HSB)
Statistical software used at this site: R
Project available for MSc and/or PhD: Both MSc and PhD
Expected availability: Flex
Additional Onboarding Requirements: No

Project Title: Relationships among spatio-temporal neuroelectric activity related to early cognitive impairment
Supervisor: Dr. Malcolm Binns
Supervisor Email: mbinns@research.baycrest.org
Supervisor Phone: 416-785-2500 x 3594
Co-Supervisor: Dr. Sandra Gardner
Co-Supervisor Contact Details: sgardner@research.baycrest.org, 416-785-2500 x 3352
Project Description: Out-patient neurology patients at Baycrest completed neuroelectric imaging studies recording longitudinal electrical signals from multiple scalp locations. The purpose of the project is to examine the spatial and temporal relationships of signals and use these relationships to identify patients with specific response patterns.
Statistical methods/analyses to be employed and level of familiarity needed for these methods: data analysis, discriminant analysis, principal component analysis
Site Location: Rotman Research Institute, Baycrest Health Sciences Kimel Family Building 3560 Bathurst Street, Toronto
Site Description: Baycrest is a geriatric care facility with a long-term care home as well as an acute care hospital. Baycrest's research focus is brain health and aging and the Rotman Research Institute specializes in the study of human brain function.
Statistical software used at this site: R and SAS
Project available for MSc and/or PhD: MSc only
Expected availability: To be determined
Additional Onboarding Requirements: Health & Safety, WHMIS, Research Ethics online training, Two-step TB skin test.

Project Title: Variation along continuous neuroelectric activity related to early cognitive impairment
Supervisor: Dr. Malcolm Binns
Supervisor Email: mbinns@research.baycrest.org
Supervisor Phone: 416-785-2500 x 3594
Co-Supervisor: Dr. Sandra Gardner
Co-Supervisor Contact Details: sgardner@research.baycrest.org, 416-785-2500 x 3352
Project Description: Out-patient neurology patients at Baycrest completed neuroelectric imaging studies recording longitudinal electrical signals from multiple scalp locations. The purpose of the project is to examine variation in functional forms of digitized signals and use these relationships to identify patients with specific response patterns.
Statistical methods/analyses to be employed and level of familiarity needed for these methods: Longitudinal data analysis, discriminant analysis, principal component analysis
Site Location: Rotman Research Institute, Baycrest Health Sciences Kimel Family Building 3560 Bathurst Street, Toronto
Site Description: Baycrest is a geriatric care facility with a long-term care home as well as an acute care hospital. Baycrest's research focus is brain health and aging and the Rotman Research Institute specializes in the study of human brain function.
Statistical software used at this site: R and SAS
Project available for MSc and/or PhD: MSc only
Expected availability: To be determined
Additional Onboarding Requirements: Health & Safety, WHMIS, Research Ethics online training, Two-step TB skin test.