# Speakers: 2017 BTI Interns

March 27, 2018, 2-3 p.m.
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**Yao Li**
Mentor: Dr. Juri Reimand, OICR
Title: Predicting long-range regulatory interactions through gene co-expression analysis across multiple cancer types

Abstract: It is important to explore the insights of gene regulation in cancer. Increasing evidence suggests that genes connected by chromatin loops are transcriptionally co-regulated; co-expression analysis can therefore be used to better understand these regulatory principles and gene function. Using high-throughput transcriptomic data from large scale projects such as the Pancancer Analysis of Whole Genomes (PCAWG), we systematically identified gene pairs associated with long range regulatory interactions. It was found that several subsets of genes are opposite in regulatory patterns for those in tumors and in normal tissues. We hypothesized that gene pairs are dysregulated in cancer if they are differentially co-expressed in healthy individuals. We also found that genes which are proximal to each other in three-dimensional space are more likely to be co-expressed with each other than randomly sampled pairs of genes. In this talk I will present a method based on the three-dimensional conformation of the genome for a better understanding of the regulatory principles and the gene functions. Survival analysis with pathway enrichment are used with high-throughput transcriptomic data from large scale projects.

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**Faith Lee**
Mentor: Drs. Rinku Sutradhar, ICES
Title: Examining the uptake of the Edmonton Symptom Screening Assessment among cancer patients in Ontario

Abstract: There is huge potential in mining population-level health data to derive and evaluate insights on health care delivery and outcomes. Linking data from different provincial databases allows us to detect if there are any trends or patterns between an outcome of interest and certain characteristics. In 2007, Ontario's regional cancer centers began using ESAS (Edmonton Symptom Screening Assessment) to better understand the conditions of cancer patients at palliative centers. In this study, we seek to understand longitudinally and evaluate the factors associated with ESAS uptake among cancer patients seen at centres where ESAS are provided. Better understanding on these associations can suggest which groups of individuals we should target to encourage ESAS uptake. We found ESAS uptake to be significantly associated with cancer type, income quintile among other factors. Chart audit data pertaining to some ESAS surveys collected in 2017 was also visualized to see which symptoms are common and to see if health care providers provided intervention. In this talk, I will talk about the analytical framework and methodology to understand associations between ESAS uptake among cancer patients and characteristics of interest in Ontario. If time permits, I would also briefly introduce the use of multistate models to analyze cervical cancer screening patterns.

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**Dongyang (Dawn) Yang**
Mentor: Dr. Wei Xu, UHN/PMH
Title: The Effect of Two BRM Promoter Polymorphisms on Survival in Head and Neck Squamous Cell Carcinomas

Abstract: The SWI/SNF chromatin remodeling complex is an important regulator of gene expression that has been linked to cancer development. The identification of cancer biomarkers can improve understanding of tumor biology and pave the way for targeted prevention, screening and therapy. Two identified insertion polymorphisms in the BRM promoter (BRM-741 and BRM-1321) could serve as biomarkers to identify individuals who are at increased risk of cancer and may benefit from future targeted interventions. Targeting the head and neck squamous cell carcinoma (HNSCC) patients, it was shown that loss of BRM expression is found in HNSCC at a similar proportion as other solid cancer types and that two BRM promoter polymorphisms are potential susceptibility markers of HNSCC. In this talk, I will present a study to examine BRM expression's effect on survival of HNSCC. Survival analysis combined with genetic models are used.

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**Fangya Mao**
Mentor: Dr. Bingshu Chen, CCTG
Title: Biomarker Analysis with Cancer Clinical Trials Data

Abstract: Biomarkers can be used to establish cancer diagnosis, indicate cancer prognosis and predict cancer treatment responses. A prognostic biomarker relates to the natural history of a disease, indicating the likely course of the disease in an untreated individual. For example, a prognostic biomarker identifies patients who will relapse and experience recurrence of their cancer disease regardless the treatment they received. A predictive biomarker is defined as an indicator to identify sub-populations of patients who are most likely to respond to a certain treatment. It is natural to regard a biomarker as a likely mediator of treatment effect, or sometimes a surrogate marker for disease progression. Therefore, in clinical trials it is important to study on how treatment would affect biomarkers related with the disease process of interest, which can shed light on the mechanism of treatment action. I will talk about the statistical methods (non-parametric and parametric) utilized in correlative studies in MA.32 (A phase III Randomized Trial of Metformin versus Placebo on Recurrence and Survival in Early Stage Breast Cancer) with this principal and present some corresponding results.