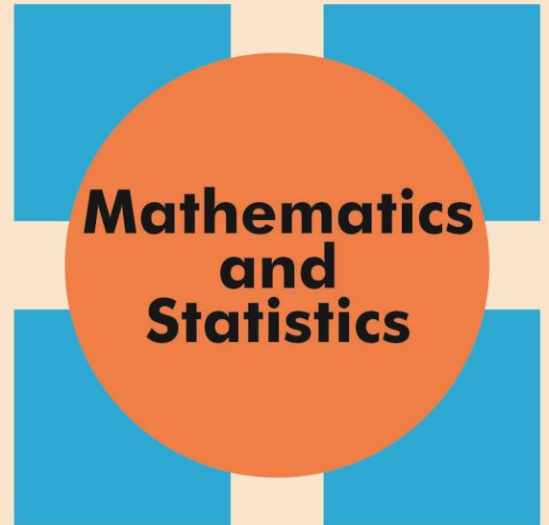


COLLOQUIUM

Kevin McGregor
York University

Community modelling techniques in microbiome data



Date: Friday, Dec. 1st

Time: 3:30PM

Zoom link: <https://uregina-ca.zoom.us/j/94223382852?pwd=UzdqSG52UkITm9GNVFvRGZKMlhHUT09>

Password: 767870

Abstract:

The microbiome is the collection of microorganisms colonizing the human body and plays an integral part in human health. Community modelling is an important kind of analysis in microbiome studies, as species in the human microbiome are known to be metabolically linked. In this talk, I will outline various statistical techniques I have developed in recent years to perform community modelling in the microbiome, including both co-occurrence estimation and Bayesian dimension reduction techniques. These methods will be highlighted in metagenomic sequencing data from a pediatric multiple sclerosis dataset from Dr. Heather Armstrong at the University of Manitoba. I will also show how such techniques are applicable in other count-based sequencing platforms such as single-cell RNA-sequencing data.