

Data Science Seminar Series

Thursday, February 17, 3:30-4:30 pm, S375

TITLE

Inference of ancient polyploidy using Gene pair similarity

SPEAKER

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ABSTRACT

A genome contains all genes defining a species and is almost identical from one organism to another. The slight differences account for individual genetic variation within a population as well as genetic distinctions between different populations of the same species. In some phylogenetic domains, such as the yeast or fish or, especially, plants, the genome of species can be seen to have irrevocably doubled or tripled some time ago through a process called polyploidization. An essential type of evidence in analyzing ancient polyploidization events is the distribution of coding sequence similarities between two homologs genes in a genome. At the same time, the polyploidization events, such as whole-genome doubling (WGD), tripling (WGT),..., will be predicted using a Maximum Likelihood transition point in the similarities between the two events as a discriminator for the hypothesized origin of each similarity. This work will discuss the theory behind gene pair similarity and the practical implementation of models.

BIOGRAPHY

Dr. Yue Zhang received Ph.D. degree from Department of Mathematics of University of Ottawa. She is an Assistant Professor in the Department of Mathematics and Statistics at TRU. Her research interests focus on comparative genomics by employing methods of mathematics and statistics. Before joining TRU, she worked as a research associate at the Canada's Michael Smith Genome Sciences Centre. Her research approach is largely based on probability modelling, statistics, data science, algorithms, and other types of mathematics, and deals with large datasets.