University of Manitoba

Pacific Institute for the Mathematical Sciences

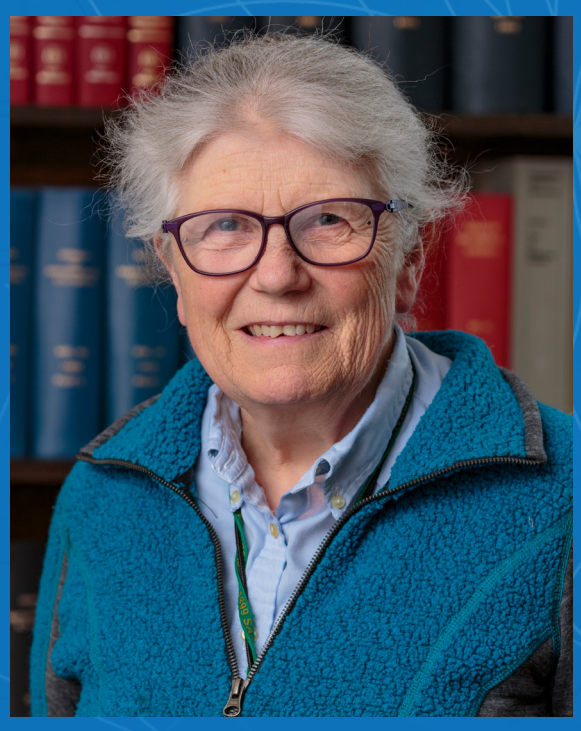
PIMS - UMANITOBA LECTURE

ELIZABETH THOMPSON

Wednesday, November 20, 2019
4:00 pm

Robert B. Schultz Lecture Theatre
University of Manitoba

VARIATION IN THE DESCENT OF GENOME: MODELING AND INFERENCE.



Elizabeth Thompson

Professor Emerita of Statistics
University of Washington

Biography

Elizabeth Thompson received her B.A. and Ph.D. in mathematics from Cambridge University, UK. After postdoctoral work in genetics at Stanford University, she joined the mathematics faculty of the University of Cambridge in 1976. She was a Professor of Statistics at the University of Washington from 1985 until her (semi-) retirement in 2018. Her research is in the development of methods for model-based likelihood inference from genetic data on both humans and other species, including inference of relationships among individuals and among populations. Dr. Thompson has received an Sc.D degree from the University of Cambridge, the Jerome Sacks award for cross-disciplinary statistical research, the Weldon Prize for contributions to Biometric Science, and a Guggenheim fellowship. She is an honorary fellow of Newnham College, Cambridge, and an elected member of the International Statistical Institute, the American Academy of Arts and Sciences, and the US National Academy of Sciences.

Abstract

In meiosis, DNA is copied from parents to offspring, so that individuals who share common ancestors may have identical DNA copies from those ancestors through repeated meioses. This identical-by-descent (IBD) DNA underlies the similarities between relatives, at both the family level and at the population level. However, the process of meiosis is quite variable, and DNA is inherited generation-to-generation in large segments. The patterns of IBD genome among relatives are complex, and in remote relatives segments of IBD DNA are rare but not short. Modern genetic data on millions of markers across the genome allows estimation of shared DNA, but accurate estimation requires modelling the processes that give rise to these complex IBD patterns. IBD must be estimated jointly among individuals and across the genome. Pedigree information, if available, provides prior probabilities of IBD patterns. Where inferred IBD is discordant with pedigree information, there is potential to detect selection or other processes distorting the outcomes of the meiotic process.

MORE DETAILS: HTTPS://WWW.PIMS.MATH.CA/SCIENTIFIC-EVENT/191120-PUDLET