

**Joint Seminar Series of the
CENTRE FOR RESEARCH IN MOLECULAR MODELING and the DEPARTMENT OF
CHEMISTRY AND BIOCHEMISTRY**

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Our inherent inability to predict outcome in some breast carcinoma

This talk will introduce the use of bioinformatics to understand and cope with the molecular heterogeneity of breast cancer. In particular, we will explore the different modes of molecular subtyping for this disease, and explain how this patient subtype has confused and confounded a tremendous amount of basic research in molecular oncology. We will also sketch a method for coping with this heterogeneity so that we may identify biomarkers more likely to have clinical utility. We will explain why these methods are important components underlying precision medicine.



Dr. Mike Hallett completed his Ph.D. at the University of Victoria (1992-94) where he developed algorithms related to DNA mapping and sequencing. He was then a postdoctoral researcher at the ETH in Zuerich (1995-2000) where he explored genome evolution. In particular he was interested in designing phylogenetic approaches that incorporate gene duplication, loss and lateral transfer in the reconstruction process. He then served as professor at McGill University (2000-2016) in Biochemistry, Computer Science and within the Cancer Centre where his primary focus was towards the systems biology of breast cancer. He joined Concordia Biology in 2017.