



Department of Mathematics and Statistics

Colloquium

Wednesday March 14

AMB 164 4:00 - 5:00 pm

Multivariate Association Analysis with Somatic Mutation Data

Yang Liu

Fred Hutchinson Cancer Research Center

Abstract

Abstract: Somatic mutations are the driving forces for tumor development, but it is challenging to analyze somatic mutations, because the majority of somatic mutations occur at low frequencies. Furthermore, cancer is a complex disease and is often accompanied by multiple traits; how to jointly analyze these traits to identify important somatic mutations poses additional challenges. In this talk, I will introduce a statistical approach, named as SOMAT, for detecting somatic mutations associated with multiple cancer-related traits. The approach provides a flexible framework for analyzing continuous, binary, or a mixture of both types of traits, and is statistically powerful and computationally efficient. In addition, we propose a data-adaptive procedure for effectively combining test statistics to enhance statistical power. The advantage of SOMAT is demonstrated through both simulations and an exome-sequencing study.

Refreshments at 3:45