

Discrete Mathematics Seminar

Time: Friday, 11 April 2014, 1:00-2:00 PM
Room: 238 Derrick Hall
Title: Identifying DNA methylation patterns using statistical and computational methods
Speaker: Dr. Shuying Sun, Mathematics Department

Abstract:

DNA methylation is one of the most common molecular changes in cells. It involves the addition of a methyl group to the 5' cytosine (C). This epigenetic event plays an important role in regulating gene expression. Therefore, it is important to study DNA methylation patterns such as hemimethylation (i.e., methylation only occurs on one DNA strand) and differential methylation between two groups. With next generation sequencing (NGS) technologies, it is now possible to identify different methylation patterns by considering methylation at the single CG site level in an entire genome. However, it is challenging to identify DNA methylation patterns in large and complex NGS data. In order to address this difficult question, we have developed a computational pipeline (HMPL) to identify hemimethylation patterns and a new hidden Markov model-based statistical approach to identify differentially methylated regions. In this presentation, we will introduce our methods and compare them with currently those available, using both simulated data and real sequencing data.