Idaho State University | Mathematics and Statistics

Colloquium

High-Dimensional Methylation Data Analysis in Cancer Using Trans-dimensional Markov Chain Monte Carlo

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The analysis of high-dimensional methylation data is increasingly critical in biology and health sciences due to its significant role in cancer development and progression. Various statistical methods and analytical tools have been developed to investigate DNA methylation, particularly in identifying differentially methylated cytosines or regions between groups, such as cancerous versus healthy tissues. However, analyzing high-dimensional methylation data presents substantial challenges, including heavy missing data, low read depths, functional autocorrelation patterns, the presence of multiple covariates, and the need to address multiple comparisons.

In this talk, we will explore these challenges and provide an overview of current methodologies and tools, including two of our recently published approaches. Furthermore, we will introduce a novel method that leverages trans-dimensional Markov chain Monte Carlo techniques with hidden Markov models and binomial emissions tailored for bisulfite sequencing data. We will illustrate the effectiveness of these methods through both simulations and real data analyses on Acute Leukemia and Colorectal Cancer.

Tuesday, Dec. 3
3:45 pm
PS 307

(or) Zoom ID: 839 9607 9478