Thesis Defense - Bader Abdulrahman Alharbi, PhD, Bioinformatics and Computational Biology
May 10, 2021 11:00 AM - 1:00 PM
VIEW EVENT
All are invited to attend the defense. For more information please contact Graduate Coordinator at kharrism@gmu.edu.

Candidate: Bader Abdulrahman Alharbi

Program: PhD, Bioinformatics and Computational Biology

Date: Monday, May 10, 2021

Time: 11:00 AM

Place: https://gmu.zoom.us/j/99018752622?pwd=S1puc2V3cjFsL01KUm9yMmJteTZtdz09

Title: Computational Analysis of the Phenotypic Significance of Individual DNA Methylation Sites

Committee Chair: Dr. M. Saleet Jafri

Committee Members: Dr. Robert Lipsky, Dr. Nadine Kabbani

ABSTRACT:

DNA methylation is considered essential for epigenetic control of the genome by suppressing the expression of genes upstream and downstream from the methylation site. The quantification of 5-methyl cytosine (5-mC) in the genome through genome-wide methylation profiling has been a major focus in epigenetic studies. However, these efforts are inconsistent since some studies show that genes with statistically higher levels of methylation were not always downregulated. Investigative efforts to examine the patterning and outcome of differentially methylated loci have been sparse. This study's underlying hypothesis is that individual methylation sites near a gene are essential for regulating its expression. We used targeted enrichment methylation data from five different tissue types in Rattus norvegicus to examine differential tissue methylation. This novel methylation data focused our analysis on specific position-based 5-mC patterns using computational methods such as dimensionality reduction and statistical and graphical visualization. This study resulted in several significant findings: 1) Although there were many methylation differences, the methylation levels from 17 unique single methylation sites are sufficient to segregate tissues. 2) The magnitude of the site methylation differences was cataloged and used to differentiate between gene expression profiles. 3) A detailed mapping of all methylation site locations was obtained and showed that such sites correlated with gene expression and tend to cluster near the transcription start site. 4) A novel tool was created, making the cataloging and analysis of the approximately 1 million methylation sites tractable, creating an alternative to the previously employed method of analyzing regional methylation status.