



The rising STAR of Texas

Discrete Mathematics Seminar

Time: Friday, April 22, 2022, 1:00-2:00 PM (Central Time)
Title: Statistical Analysis of Tumor Suppressor Genes' Methylation Patterns in Various Breast Cancer Samples
Speaker: Dr. Shuying Sun, Department of Mathematics, Texas State University
Room: 330 Derrick Hall

For people who cannot come, this talk can also be accessed virtually

Zoom Link: <https://txstate.zoom.us/j/99924628868?pwd=czdJWVpWOHZIZE0vbHBQL1pWell6QT09>
ID: 999 2462 8868
Passcode: **753321**

Abstract:

DNA methylation is an epigenetic event. It occurs when a methyl group is added to a cytosine base that is paired with a guanine (i.e., a CG site) in a human genome. DNA methylation plays an important role in regulating gene expression. Many tumor suppressor genes are found to be methylated and associated with breast cancer. However, it is unclear how their methylation patterns change among different breast cancer samples such as tumor, matched normal, living, and dead samples. In this study, we present our statistical analysis results on these genes' methylation patterns in breast cancer patients using publicly available data. In particular, we analyze the differential methylation and co-methylation patterns of these genes by studying their methylation levels or states carefully. We compare tumors with normal samples; we also compare living patients with dead samples. We then show genetic pathway and network analyses of differentially methylated and highly co-methylated genes. Our findings will provide researchers with a new and improved understanding of tumor suppressor genes' methylation patterns in breast cancer.