

Differential Equations and Applied Math Seminar

Texas State University

2-3pm April 17, 2015

329 Derrick Hall

Speaker: Brittany Enfield, Texas State University
Honor's Thesis Research with Advisor Dr. Shuying Sun

Title: Identifying hemimethylation sites in breast cancer cell lines using statistical methods

Abstract: Many cancer studies using microarray technologies have shown a correlation between DNA methylation and tumor growth. These array-based studies often assume symmetric methylation on both strands of DNA since microarray technologies lack the ability to obtain methylation levels of the forward and reverse DNA strands at single CpG sites. However, asymmetric methylation, or hemimethylation, does exist and has been reported in several cancer studies. Due to the limitation of previous DNA methylation sequencing technologies, researchers could only study hemimethylation on specific genes, but the overall genomic hemimethylation landscape remains relatively unexplored. With the development of advanced next generation sequencing techniques, we can now measure methylation levels on both the forward and reverse strands at single CpG sites in an entire genome. Identifying and studying hemimethylation sites along DNA may potentially reveal regions related to undergoing tumor growth. For our research, we identify hemimethylated CpG sites using statistical tests, map them to their corresponding genes and promoter regions, and then study the functions of these sites, especially those related to cancer. In particular, we compare hemimethylated CpG sites from 16 normal cell samples and 7 breast cancer cell lines. This is done by performing the two-sample t-test on each CpG site and identifying hemimethylated sites as those with p-value less than .05 and absolute mean difference greater than 0.6. CpG sites showing hemimethylation in the cancer cell lines are then mapped to nearby genes and promoter regions. Finally, we study the functions of genes and promoters with a high incidence of hemimethylation in the cancer cell lines. Our results reveal that hemimethylation does occur across the entire genome with notably higher numbers in the breast cancer cell lines than in the normal cell samples. In addition, several of the highly hemimethylated genes and promoter regions may influence tumor growth or suppression. These genes may also indicate a progressing transition to a new tumor stage.

Interested faculty and graduate students are encouraged to attend.