

**“Cloud-Scale Genomic Signals Processing Classification
Analysis for Gene Expression Microarray Data”
Benjamin Harvey, PhD Student, Computer Science
Bowie State University**

Thursday, Oct. 23, 2014 @ 3:30 - 4:45 PM, CSB - Room 309

Benjamin Harvey is a doctoral student of the Computer Science Department at Bowie State University. He holds a M.Sc. in Computer Science from Bowie State University, a Cryptologic Computer Science Certificate from the University of Maryland Baltimore County in conjunction with the Naval Post-Graduate School, and a B.S. in Pre-Med./Computer Science from Mississippi Valley State University. He currently holds a position with the Department of Defense as a cryptologic computer scientist and network evaluator. He brings over 5 years of experience designing and implementing intelligence, cloud, and healthcare software solutions with over 4 years of experience researching genetics and bioinformatics clinical technologies.

Abstract: As microarray data available to scientists continues to increase in size and complexity, it has become overwhelmingly important to find multiple ways to bring inference through analysis of DNA/mRNA sequence data that is useful to scientists. Though there have been many attempts to elucidate the issue of bringing forth biological inference by means of wavelet preprocessing and classification, there has not been a research effort that focuses on a cloud-based classification analysis of microarray data using Wavelet thresholding in a Cloud environment to identify significantly expressed features. A novel methodology that uses Wavelet based Denoising to initialize a threshold for determination of significantly expressed genes for classification is discussed. Additionally, this research was implemented and encompassed within cloud-based distributed processing environment. The utilization of Cloud computing and Wavelet thresholding was used for the classification 14 tumor classes from the Global Cancer Map (GCM). The results proved to be more accurate than using a predefined p-value for differential expression classification.

Contact Dr. Soo-Yeon Ji (sji@bowiestate.edu) if you have any question.