Presentation for the Symposium on BEER *October 2019*

Classification of Coronary Artery Disease in Non-diabetic Patients using Artificial Neural Networks

Demond Handley[1]

[1] *Department of Mathematics, Illinois State University, Normal, IL 61761*

`dlhandl@ilstu.edu`

Coronary Artery Disease (CAD) is one of the most common forms of Cardiovascular Disease, with over three million new cases being reported each year. Gene expression values were collected from peripheral blood samples in 640 non-diabetic patients to develop an age, sex gene expression score (ASGES) algorithm to test for CAD. In a previous study, AGES was developed based on ridge regression, where the predictors were age, sex and twenty-three genes, clustered into six metagenes according to cell type, while the model outcome was disease state. Machine learning and deep learning techniques have proven useful when classifying disease types based on genetic information. We split the data into two sets according to sex. Recursive Feature Elimination is used to eliminate metagenes which contribute little to explaining the variance. A feed forward neural network was implemented to predict CAD and we compare the mechanistic of the model to the previously developed ridge regression algorithm. Sensitivity, Specificity, negative predictive values (NPV), accuracy, error, receiver operator characteristic (ROC) curve and area under the curve (AUC) were reported.

Keywords: Machine Learning, Neural Network, Genes, Regression, Coronary Artery Disease, Classification, Deep Learning, Cardiovascular Disease.