A study for examining the efficacy of detecting genotype-phenotype associations using deep learning models for Single Nucleotide Polymorphisms (SNP) data with variable importance measure. Different levels of linkage disequilibrium and gene-gene interactions are considered using simulated SNP datasets. CNN model was created, 10-fold cross validation was performed for each type of datasets, Permutation variable importance (PVI) and Microablation variable importance (MVI) are measured.

Statistical test is then performed on the result from CNN model, compared to the results from multilayer perception network by stochastic gradient descent (mlpSGD) model and deep belief network (DBN) model.