Abstract

Support Vector Machine (SVM) is a reliable method for performing classification and regression especially in supervised machine learning. However, SVM has scalability issues in compute time and memory usage. Therefore, there are many proposals for Parallel Support Vector Machine (PSVM) for mining large-scale data. In this study, the authors conducted a PSVM concept test with SMO decomposition that could be handled and classified cancer using microarray data. The author applies the Sequential Minimal Optimization (SMO) technique which uses lagrange multipliers to solve quadratic programming (QP) problems that arise during training. To test the concept of SMO decomposition, the data set will be broken down into several subsets and then independently conduct SMO training for each subset and combine each training result into one SMO classification model. Evaluation is done by comparing the accuracy and performance of SMO decomposition and non-decomposition SMO. Evaluation increased SMO decomposition 75% and non-SMO decomposition 63% as well as SMO decomposition training time 5.7 times faster according to non-SMO decomposition

Keywords: Microarray, Suport Vector Machine (SVM), Parallel Suport Vector Machine (PSVM), Sequential Minimal Optimization(SMO)