The average error and standard error rate (%) in the test set of the microarray data sets are used as performance indicators.

"Combination" refers to using both sets of dominant and dormant genes together for the classifier. Hence, the number of selected genes in the "Combination" case for each fold is \{10, 20, 30, 40, 50\}.

Statnikov et al. [5] had reported Accuracy (%) for the Lung Cancer data set by using all genes as input features fed for several classifiers. Here we used the 1-Accuracy (%) as the error rate listed above for comparison.