1046-62-1572 Nabin K. Shrestha* (nmanandh@mail.usf.edu), 4102 Skipper Road, Apt. 209, Tampa, FL 33613, and K. M. Ramachandran, 4202 E. Fowler Avenue, PHY 114, University of South Florida, Department of Mathematics and Statistics, Tampa, FL 33620. Behrens Fisher's Distribution for selecting Genes and its Application in Cancer Classification.

Microarray expression experiments allow the recording of expression levels of thousands of genes simultaneously. Such data have been useful for classifying different types of cancers. Majority of literature on this topic assumes equality of variance between control and treatment samples. Because the variance of the expression levels in different classes are generally different due to the nature and response of the mRNA at the different conditions, the classification methods should take account of this information. In this paper, we have proposed a new method of selecting informative genes based on the Bayesian Version of Behrens-Fisher distribution. We have found that the proposed method selects the genes that are useful for classification and gives the better classification result by improving classification accuracy. The efficiency of this method has been demonstrated by applying them in three real microarray data. We have compared our result with some of the other popular methods that are found in the literature. (Received September 16, 2008)