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Support Vector Machines and Relevance Vector Machines and Their Usage

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The researchers sought to use to supervised machine learning algorithms to determine the minor set of genes that can provide exact cancer from the microarray data [1]. The importance of getting the minimum subset significantly stimulate the need for additional studies on the likely biological relationship that between the small number of genes together with the onset of cancer and drug development; it helps to considerably reduce the cost incurred in testing cancer since it streamlines the gene expression tests to cover a minimal amount of genes [2-3]. In addition, a minimal subset helps reduce noise arising from extraneous genes and the associated computational problem [4]. The researchers have suggested a method that includes two major steps such as using the Analysis of Variance (ANOVA) ranking scheme to select the most significant genes and a superior classifier was used to determine all the modest combinations of the main genes [5]. The researchers used both the Relevance Vector Machine (RVM) classifier and the Support Vector Machine (SVM) to increases the accuracy of cancer genes classification and the drug prediction [6]. The findings of the experiment prove that the suggested method performs excellently or it achieves accurate cancer classification in comparison to the common conventional techniques [7].

According to the article, researchers are successful applying the micro array data analysis in many biological areas such as determining the pertinent genes which helpful in making cancer diagnosis and prognosis as well as assist in development of therapies or drugs [8]. Besides, the analysis is applied in identifying the unidentified impacts of a certain cancer therapy and making cancer classification by prediction and classification [9]. Despite applying the techniques such as the Generalized Singular Value Decomposition (GSVD), Singular Value Decomposition (SVD), Principal Component Analysis (PCA), and the Support Vector Machines (SVMs), researchers always find some missing values which can be regarded as a critical preprocessing step [10]. During gene expression, data is lost owing to errors during experiments in the lab, slides which contain scratches or dirt, image corruption, and insufficient resolution [11].

In the study, the researchers propose a useful technique that combines Relevance Vector Machine classifier and the Support Vector Machine to accurately perform classification of cancer by utilizing a combination of two gene expression in lymphoma dataset [12]. The two-step cancer classification involves the use of a scoring scheme to rank and retain all the genes in the training dataset with the highest score [13]. Then, the researchers used a superior classifier like the RVM classifier and SVM to test all the gene combinations. The Support Vector Machines (SVMs) usually optimizes the margin between two datasets by creating a dividing hyper plane in the space [14-15]. Besides, they typically perform excellently in tasks which involve pattern recognition since they are regarded as linear classifiers with the ability to detect the optimal hyper plane that optimizes the margins that exist between patterns [16]. Furthermore, the support vector machines are widely applied to perform analysis of gene expression data [17]. In this case, the researchers used several support vector machines that contained essential kernel functions. Additionally, the scholars conducted five-fold cross-validation (CV) to adjust the parameters of the support vector machine as provided in the training data [18]. The research also entails the cross-validation precision for entire sets of data and chooses the minor CV error. The figure 1 below indicates the CV process [19].

The researchers unsystematically divide the data set into two namely the training and testing (F1 and F2 respectively); besides, the samples of the training data are relied on to rank the genes [20]. Then two genes among the twenty are used to produce a combination labeled (FC1) which is then arbitrarily clustered into five groups from fc1 to fc5 [21]. Subsequently, the researchers chose a single group which is then tested. The remaining four groups are utilized as support vector classifiers. Additionally, the continued to produce combination to a point at which superior precision is obtained [22]. Lastly, they carried the drug prediction using the fitted support vector machine. The study proved that both the SVM is a highly effective classifier while the CV and the Analysis of Variance (ANOVA) are incredibly important ranking schemes with particularly when used to find the smallest subsets if gene to make precise classification of cancer [23]. The newly proposed technique subdues the main drawback related to the SVM technique. The application of the Relevance Vector Machine is usually minimal in comparison to the use of the support vector machine given its high or more significant number of vectors [24]. The researcher did the experiments for the suggested method by utilizing a lymphoma dataset; also, they relied on the K-means method for conducting clustering of the twenty chosen genes [25]. The findings from the experiment reveal that the use of the Relevance Vector Machine classifier can significantly assist in performing accurate cancer classification as compared to other traditional techniques.

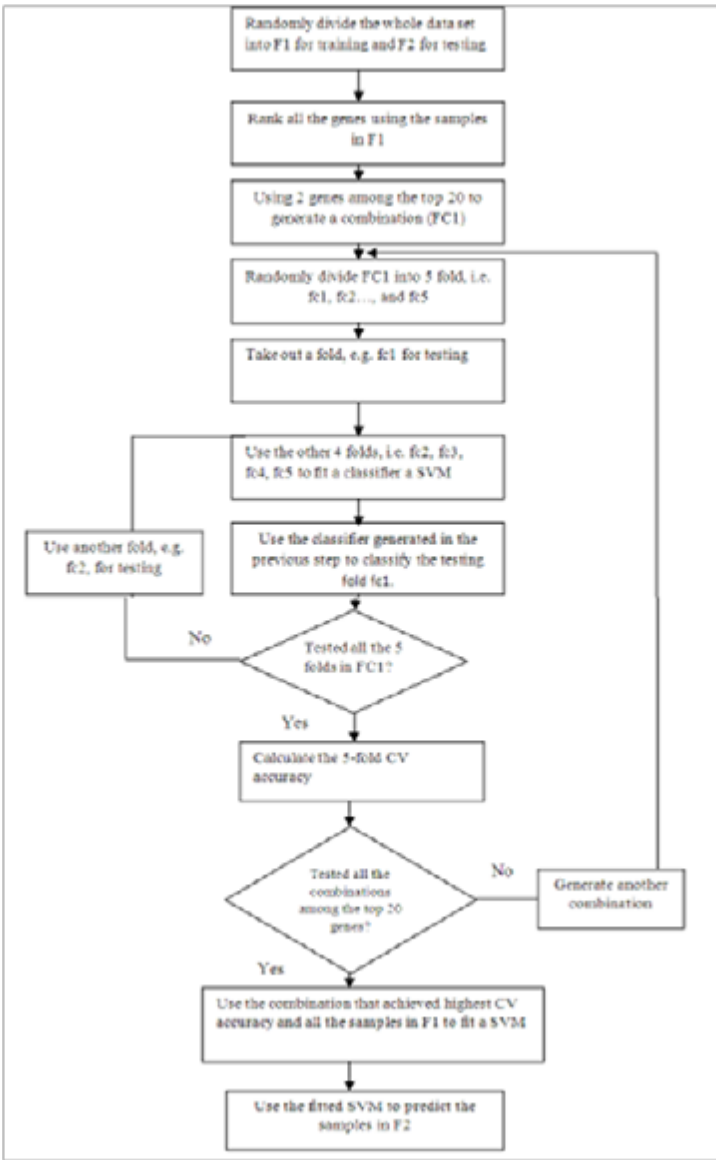

Figure 1: Cross Validation Process (Source: Bharathi A, Natarajan AM (2011) Cancer Classification Using Support Vector Machines and Relevance Vector Machine Based on Analysis of Variance Features, Journal of Computer Science 7: 1393).

References

1. Bharathi A, Natarajan A M (2011) Cancer Classification Using Support Vector Machines and Relevance Vector Machine Based On Analysis of Variance Features. Journal of Computer Science 7: 1393.
2. Alter O, Brown PO, Botstein D (2003) Generalized Singular Value Decomposition for Comparative Analysis of Genome-Scale Expression Data Sets of Two Different Organisms. Proc Natl Acad Sci 6: 3351-3356.
3. Swathi M (2017) Drug Prediction of Cancer Genes Using SVM. Enliven: Pharmacovigilance and Drug Safety 4: 001.
4. Carin L, Dobeck GJ (2003) Relevance Vector Machine Feature Selection and Classification for Underwater Targets. In Oceans. Proceedings 2: 1110.
5. Chen Liao, Shutao Li (2007) A Support Vector Machine Ensemble for Cancer Classification Using Gene Expression Data. Berlin, Germany.
6. Chen Liao, Shutao Li, Zhiyuan Luo (2007) Gene Selection Using Wilcoxon Rank Sum Test and Support Vector Machine for Cancer Classification. Berlin, Germany.
7. Chen S, Gunn SR, Harris CJ (2001) The Relevance Vector Machine Technique for Channel Equalization Application. IEEE Trans Neural Netw 6: 1529-1532.
8. Cheng Cun-gui, Lu-yao Cheng, Run-sheng Xu (2007) Classification of FTIR Gastric Cancer Data Using Wavelets and SVM. In Natural Computation 2: 543-547.
9. Swathi M (2017) Clustering Enhancement Using Similarity Indexing to Reduce Entropy. Enliven: Bioinform 4: 001.

10. El-Naqa I, Yongyi Yang, Wernick MN, Galatsanos NP, Nishikawa RM (2002) A Support Vector Machine Approach for Detection of Micro Calcifications. IEEE Transactions on Medical Imaging 21: 1552-1563.
11. Isabelle Guyon, Jason Weston, Stephen Barnhill, Vladimir Vapnik (2002) Gene Selection for Cancer Classification Using Support Vector Machines. Machine learning 46: 389-422.
12. Jose Crispin Hernandez Hernandez, Béatrice Duval, Jin-Kao Hao (2007) A Genetic Embedded Approach for Gene Selection and Classification of Microarray Data. European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics: 90-101
13. Swathi M (2018) Enhancement of K-Mean Clustering for Genomics of Drugs. Enliven: J Genet Mol Cell Biol 5: 001.
14. Lee Y, Lee CK (2003) Classification of Multiple Cancer Types by Multicategory Support Vector Machines Using Gene Expression Data. Bioinformatics 19: 1132-1139.
15. Song M, Rajasekaran S (2010) A Greedy Algorithm for Gene Selection Based on SVM and Correlation. Int J Bioinform Res Appl 6: 296-307.
16. Murat Cinar, Mehmet Engin, Erkan Zeki Engin, Ziya Atesci Y (2009) Early Prostate Cancer Diagnosis by Using Artificial Neural Networks and Support Vector Machines. Expert Systems with Applications 36: 6357-6361.
17. Shutao Li, Xixian Wu, Xiaoyan Hu (2008) Gene Selection Using Genetic Algorithm and Support Vectors Machines. Soft Computing 12: 693-698.
18. Michael E.Tipping (2001) Sparse Bayesian Learning and the Relevance Vector Machine. Journal of Machine Learning Research 1: 211-244.
19. Furey TS, Cristianini N, Duffy N, Bednarski DW, Schummer M, et al. (2000) Support Vector Machine Classification and Validation of Cancer Tissue Samples Using Microarray Expression Data. Bioinformatics 16: 906-914.
20. Statnikov A, Wang L, Aliferis CF (2008) A Comprehensive Comparison of Random Forests and Support Vector Machines for Microarray-Based Cancer Classification. BMC Bioinformatics 9: 319.
21. Lee Y, Lee CK (2003) Classification of Multiple Cancer Types by Multicategory Support Vector Machines Using Gene Expression Data. Bioinformatics 19: 1135.
22. Mehmet Fatih Akay (2009) Support Vector Machines Combined with Feature Selection for Breast Cancer Diagnosis. Expert Systems with Applications 36: 3240-3247.
23. Cheng-Lung Huang, Chieh-Jen Wang (2006) A GA-Based Feature Selection and Parameters Optimization for Support Vector Machines. Expert Systems with Applications 31: 231-240.
24. Peng S, Xu Q, Ling XB, Peng X, Du W, et al. (2003) Molecular Classification of Cancer Types from Microarray Data Using the Combination of Genetic Algorithms and Support Vector Machines. FEBS Lett 2: 358-362.
25. Noble WS (2006) What Is a Support Vector Machine?. Nat Biotechnol 12: 1565-1567.
26. Chu F, Wang L (2005) Applications of Support Vector Machines to Cancer Classification with Microarray Data. Int J Neural Syst 15: 475-484.
27. Liu Y (2004) Active Learning with Support Vector Machine Applied to Gene Expression Data for Cancer Classification. J Chem Inf Comput Sci 44: 1936-1941.
28. Garnett MJ, Edelman EJ, Heidorn SJ, Greenman CD, Dastur A et al. (2012) Systematic Identification of Genomic Markers of Drug Sensitivity in Cancer Cells. Nature 7391: 570.