

GENE EXPRESSION DATA ANALYSIS USING DATA MINING ALGORITHMS FOR COLON CANCER

Archana Mishra¹, Rachna Devi², Sachin Shrivastava³

¹M.Tech Student, ^{2,3}Assistant Professor, Department of Computer Science & Engineering, SCET, Palwal (India)

ABSTRACT

The concept of Data mining is used in various medical applications like tumor classification, protein structure prediction, gene classification, cancer classification based on microarray data, clustering of gene expression data, statistical model of protein-protein interaction etc. Adverse drug events in prediction of medical test effectiveness can be done based on genomics and proteomics through data mining approaches. Cancer detection is one of the hot research topics in the bioinformatics. Data mining techniques, such as pattern recognition, classification and clustering is applied over gene expression data for detection of cancer occurrence and survivability. Classification of colon cancer dataset using weka library, in which Logistics , Ibk, Kstar, NNge, ADTree , Random Forest Algorithms etc had shown 100 % correctly classified instances, followed

by Navie Bayes classification and PART with 97.20 % accuracy. Kappa Statistic for Logistics , Ibk, Ks tar, NNge, ADTree, Random Forest has shown Maximum. Mean absolute error and Root mean squared error are shown low for Logistics , Ks tar and NNge. Using various Classification algorithms the cancer dataset can be easily analyzed in order to obtain the better results.

Keywords: Data Mining, Colon Cancer, Dataset, ROC.

I. INTRODUCTION

In general, Data Mining refers to collecting or mining or extracting knowledge from large amounts of data used in finding new interesting patterns and relationship related to the extracted data, discovering meaningful new correlations, patterns, and trends by digging into large amounts of data stored in the warehouses. It requires intelligent technologies and the compliance to explore the possibility of hidden knowledge that exists in the data. Data mining algorithms and machine learning have exponential complexity and sometimes require parallel computation [1,2].

It is observed that rapid developments in the field of Genomics and Proteomics have created huge biological data to be analyzed. Making sense of the large biological data or analyzing the data by inferring structure or generalization from the data has a great potential to increase the interaction between data mining and bioinformatics. Bioinformatics and data mining provide exciting challenging research and application in the areas of computational sciences [3].

The Waikato Environment for Knowledge Analysis (WEKA) provide a comprehensive collection of machine learning algorithms and data pre-processing tools to researchers and practitioners on new data sets [8, 9, 10]. Orange is an open source component based data mining and machine learning software suite for explorative data analysis , visualization, and scripting interface in Python, providing direct access to all its

power for fast programming of new algorithms and developing complex data analysis procedures [4]

Cancer is a class of diseases characterized by out-of-control cell growth. It originates from small, noncancerous (benign) tumors called adenomatous polyps that form on the inner walls of the large intestine. Colon cancer cells will invade and damage healthy tissue that is near the tumor causing many complications. These cancer cells can grow in several places, invading and destroying other healthy tissues throughout the body. This process itself is called metastasis, and the result is a more serious condition that is very difficult to treat. Rectal cancer originates in the rectum, which is the last several inches of the large intestine, closest to the anus. Colon cancer each year and it is the third most common cancer caused. Risk factors include a diet low in fiber and high in fat, certain types of colonic polyps, inflammatory bowel disease (such as Crohn's disease or ulcerative colitis), and certain hereditary disorders [5][6]

The classification is done in order to fulfill various purposes like Predicting of tumor cells into benign or malignant, classifying the secondary structure of proteins into alpha-helices, beta-sheets or random coils, Categorizing news stories as finance, weather, entertainment, sports, etc [7].

Association rule mining solves the problem of how to search efficiently for those dependencies. Single & Multidimensional Association Rules are used to solve the problem. The prediction system has two stages: feature selection and pattern classification stage. The feature selection can be considered as the gene selection, which is to get the list of genes that might be informative for the prediction of tumor suppressor genes (TSGs) and proto-oncogenes by statistical, information theoretical methods. A classifier makes decision to which category the gene pattern belongs at prediction stage [8][9].

II. MATHEMATICAL MODEL

2.1 System Requirements for the Present Work

Processor : Intel® Core™ i3 CPU M 370 @ 2.40 GHz 2.40 GHz, Installed memory (RAM) : 4.00 GB (3.80 usable), Mother Board : HP Base Board, Hard Disk : 500 GB, OS : Windows 7 Professional (x64) (build 7600) and software such as WEKA and Orange.

2.2 Classification Algorithms

2.2.1 Bayesian Network

Bayesian networks are graphical representation for probabilistic relationships among a set of random variables. A Bayesian network is an annotated directed acyclic graph (DAG) G that encodes a joint probability distribution [10].

Algorithm

Step1: Given a finite set $X = (X_1, \dots, X_n)$ of discrete random variables where each variable X_i may take values from a finite set, denoted by $\text{Val}(X_i)$.

Step2: The nodes of the graph correspond to the random variables X_1, \dots, X_n . The links of the graph correspond to the direct influence from one variable to the other. If there is a directed link from variable X_i to variable X_j . Variable X_i will be a parent of variable X_j .

Step3: Each node is annotated with a conditional probability distribution (CPD) that represents $P(X_i | Pa(X_i))$ where, $Pa(X_i)$ denotes the parents of X_i in G . The pair (G, CPD) encodes the joint distribution $p(X_1, \dots, X_n)$. A unique joint probability distribution over X from G is factorized as: $P(X_1, \dots, X_n) = \prod_i (P(X_i | Pa(X_i)))$.

2.2.2 Naive Bayesian Algorithm

Naïve Bayesian classifier (Langley, 1995) is based on Bayes conditional probability rule is used for performing classification tasks, assuming attributes as statistically independent. All attributes of the dataset are considered independent and strong of each other.[11]

Algorithm

Step1: probability for each class is calculated in the dataset using $P(C=C_j)$.

Step2: For each value x_i of each attribute a_i , probability is calculated using $P(X_i|C=C_j)$

Step3: Classify a new sample to class c_j that have maximum probability $P(C = C_j/X_1, \dots, X_n)$ using Naïve-Bayes Classifier given below here denominator does not depend upon the value of C_j as:

$$P(C = C_j | X_1, \dots, X_n) = \frac{P(C = C_j) \prod_i P(X_i | C = C_j)}{\sum_j P(C = C_j) \prod_i P(X_i | C = C_i)}$$

2.2.3 Random Forest

Leo Breiman and Adele Cutler, 2001 developed Random forest algorithm, is an ensemble classifier that consists of many decision tree and outputs the class that is the mode of the class's output by individual trees. Random Forests grows many classification trees without pruning.[12]

Algorithm

Step1: Let N be the number of training cases, and let M be the number of variables in the classifier. Choose m as input variables, to be used to determine the decision at a node of the tree; m should be much less than M .

Step2: Recurse training set for this tree by choosing N times with replacement from all N available training cases (take a bootstrap sample). Rest of the cases to be estimated as error of the tree by predicting their classes.

Step3: For each node in the tree, randomly choose m variables, which should be based on the decision at that node.

Step4: Calculate the best split based on these m variables in the training set. The value of m remains to be constant during forest growing. Random forest is sensitive to the value of m .

Step5: Each tree is grown to the largest extent possible, into many classification trees without pruning, in constructing a normal tree classifier.

III. METHODOLOGY

We will take following steps for our Methodology

Step1. We will take a dataset of Gene based Disease (we have taken colon cancer dataset) where the Dataset has two classes i.e Positive and Negative.

Step2. Normalization process is required to be applied using Min-Max algorithm, in order to get the Dataset values in a specific range.

Step3. PCA algorithm, we will apply the knowledge discovery processes and perform feature extraction in order to identify the most relevant variables and determine the complexity and/or the general nature of Disease patterns.

Step4. We will get a reduced dataset so as to perform further operations on it. Through the reduced dataset, classifiers are to be found out which will help in training the machines through some technique.

Step5. We have used J48 And Navie Bayes Classification Algorithm for machine learning. Once the machine learning is done, different association of genes are classified into different classes.

Step6. Testing is to be performed by giving sample inputs to the machine, which will in return give the output if the particular gene set has got colon cancer or not. Thus, if the result is Positive, it means the

person is suffering from particular disease and if result is Negative then the person is not having colon cancer.

Step7. On the basis of the various parameters after comparisons among the results.

IV. RESULTS AND DISCUSSIONS

4.1 Results for Classification Using J48

Colon Cancer attribute has been chosen randomly for colon-cancer-kent-ridge data set. J48 is applied on the data set and the confusion matrix is generated for class gender having two possible values i.e. YES or NO.

Confusion Matrix:

a b classified as

33 72 | a = YES

25 170 | b = NO

For above confusion matrix, true positives for class a=YES is 33 while false positives is 72 whereas, for class b=NO, true positives is 170 and false positives is 25 i.e. diagonal elements of matrix $33+170 = 203$ represents the correct instances classified and other elements $25+72 = 97$ represents the incorrect instances.

True positive rate = diagonal element/ sum of relevant row

False positive rate = non-diagonal element/ sum of relevant row

Hence,

TP rate for class a = $33/(33+72) = 0.314$

FP rate for class a = $25/(25+170) = 0.128$

TP rate for class b = $170/(25+170) = 0.871$

FP rate for class b = $72/(33+72) = 0.685$

Average TP rate = 0.677

Average FP rate = 0.491

Precision = diagonal element/sum of relevant column

Precision for class a = $33/(33+25) = 0.568$

Precision for class b = $170/(170+72) = 0.702$

F-measures = $2 * \text{precision} * \text{recall} / (\text{precision} + \text{recall})$

F-measure for class a = $2 * 0.568 * 0.314 / (0.568 + 0.314) = 0.404$

F-measure for class b = $2 * 0.702 * 0.871 / (0.702 + 0.871) = 0.778$

4.2 Results for Classification Using Naïve Bayes Multinomial

Here same, Colon Cancer attribute has been chosen randomly for colon-cancer-kent-ridge data set. Naive Bayes is applied on the data set and the confusion matrix is generated for class gender having two possible values i.e. YES or NO.

Confusion Matrix:

a b , Al' classified as

19 3 | a = YES

5 35 | b = NO

For above confusion matrix, true positives for class a=YES is 19 while false positives is 3 whereas, for class b=NO, true positives is 5 and false positives is 35 i.e. diagonal elements of matrix $5 + 35 = 40$ represents the correct instances classified and other elements $8+17 = 25$ represents the incorrect instances.

TP rate for class a = $19/(19+3) = 0.864$

FP rate for class a = $5/(5+35) = 0.125$

TP rate for class b = $35/(35+5) = 0.875$

FP rate for class b = $3/(19+3) = 0.136$

Average TP rate = 0.871

Average FP rate = 0.132

Precision = diagonal element/sum of relevant column

Precision for class a = $19/(19+5) = 0.792$

Precision for class b = $35/(35+5) = 0.921$

F-measures = $2 * \text{precision} * \text{recall} / (\text{precision} + \text{recall})$

F-measure for class a = $2 * 0.792 * 0.864 / (0.792 + 0.864) = 0.826$

F-measure for class b = $2 * 0.921 * 0.875 / (0.921 * 0.875) = 0.897$

4.3 Comparative Result Analysis

Parameters	NB-Multinomial	J48
Correctly Classified Instances	54 (87.0968%)	45 (72.5806%)
Incorrectly Classified Instances	8 (12.9032%)	17 (27.4149%)
Kappa statistic	0.7238	0.4411
Mean absolute error	0.129	0.2938
Root mean squared error	0.3592	0.5167
Relative absolute error	28.0752%	91.9087%
Root Relative squared error	75.0075%	107.8894%
Total Number of Instances	62	62
Confusion Matrix	a b 19 3 5 35	a b 17 5 12 28

Table 4.1: Table to Show Comparison Between Classification Algorithms

IV. CONCLUSION

From above experimental work we can conclude that correct instances generated by J48 and NaïveBayesMultinomial, as well as performance evolution proves that the, NaïveBayesMultinomial is a simple classifier technique to make a decision tree. Efficient result has been taken from bank dataset using weka tool in the experiment. J48 classifier also shows good results. The experiment results shown in the study are about classification accuracy and cost analysis. NaïveBayesMultinomial gives more classification accuracy for class mortgage in bank dataset having two values Yes and No. Though here in this example, cost analysis valued same

for both the classifier, with gender attribute, we can prove that NaïveBayesMultinomial is cost efficient than the J48 classifier.

REFERENCES

- [1] Mohammed J. Zaki, Shinichi Morishita, Isidore Rigoutsos, "Report on BIODDD04: Workshop on Data Mining in Bioinformatics", in SIGKDD Explorations, vol. 6, no. 2, pp .153-154, 2004.
- [2] J. Li, L. Wong, Q. Yang, "Data Mining in Bioinformatics", IEEE Intelligent System, IEEE Computer Society . Indian Journal of Computer Science and Engineering, vol 1 no 2, pp . 114-118, 2005.
- [3] R. P. Kumar, M . Rao, D. Kaladhar, "Data Categorization and Noise Analysis in Mobile Communication Using Machine Learning Algorithms", Wireless Sensor Network, vol. 4, no.4, pp . 113-116, 2012.
- [4] Mark H. E. Frank, Geoffrey Holmes, Bernhard Pfahringer, Peter Reutemann, Ian H. Witten, "The WEKA data mining software: an update", SIGKDD Explorations, vol. 11, no.1, pp .10-18, 2009.
- [5] D. J. Hand, "Statistics and data mining: intersecting disciplines", SIGKDD Explorations, vol. 1, no. 1, pp . 16-19, 1999.
- [6] C Apte, E Grossman, E Pednault , B Rosen, F Tipu, B White, "Insurance risk modeling using data mining technology", Proceedings of PADD99: The Practical Application of Knowledge Discovery and Data Mining, pp .39-47, 1999.
- [7] Liu, Bing, Chee Wee Chin, Hwee Tou Ng. "Mining topic-specific concepts and definitions on the web." Proceedings of the 12th international conference on World Wide Web. ACM , pp .251-260, 2003.
- [8] M. K. Jakubowski, Q. Guo, M. Kelly , "Tradeoffs between lidar pulse density and forest measurement accuracy", Remote Sensing of Environment , vol. 130, pp . 245-253, 2013.
- [9] E. Frank, M . Hall, L. Trigg, G. Holmes, I. H. Witten, "Data mining in bioinformatics using Weka ", Bioinformatics, vol. 20, no. 15, pp . 2479-2481, 2004.
- [10] M . Hall, E. Frank, G. Holmes, B. Pfahringer, P. Reutemann, I.H. Witten, "The WEKA data mining software: an update ACM SIGKDD Explorations Newsletter, vol. 11, no. 1, pp .10-18, 2009.
- [11] Tomaž Curk, Janez Demšar, Qikai Xu, Gregor Leban, Uroš Petrovič, Ivan Bratko, Gad Shaulsky , Blaž Zupan, "Microarray data mining with visual programming", Bioinformatics, vol. 21, no. 3, pp . 396-398, 2005.
- [12] R. W. Burt , J. S. Barthel, K. B. Dunn, D. S. David, E. Drelichman, J. M . Ford, et al, "Colorectal cancer screening", Journal of the National Comprehensive Cancer Network, vol. 8, no. 1, pp . 8-61, 2010.
- [13] David Cunningham, Wendy Atkin, Heinz -Josef Lenz , Henry T Lynch, Bruce Minsky , Bernard Nordlinger, Naureen Starling, "Colorectal cancer", The Lancet , vol. 375, no. 9719, pp . 1030-1047, 2010.
- [14] R. A. Smith, V. Cokkinides, D. Brooks, D. Saslow, O. W. Brawley , "Cancer screening in the United States, 2010: a review of current American Cancer Society guidelines and issues in cancer screening", CA: a cancer journal for clinicians, vol. 60, no.2, pp . 99-119, 2010.
- [15] K. Mehmed, "Data Mining: Concepts, Models, Methods And Algorithms." IEEE Computer Society, IEEE Press, 2003.
- [16] W. J. Frawley , G. Piatetsky -Shapiro, C. J. Matheus, "Knowledge discovery in databases: An overview", AI magazine, vol. 13, no. 3, pp . 57, 1992.
- [17] H. Lieberman, D. Maulsby , "Instructible agents: Software that just keeps getting better", IBM Systems Journal, vo. 35, no. 3.4, pp . 539-556, 1996.

- [18] R. Rada, "Expert systems and evolutionary computing for financial investing: A review", Expert systems with applications, vol. 34, no. 4, pp . 2232-2240, 2008.
- [19] Cho Sung-Bae, Hong-Hee Won, "Machine learning in DNA microarray analysis for cancer classification", In Proceedings of the First Asia-Pacific bioinformatics conference on Bioinformatics, vol. 19, pp . 189-198. 2003.