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- Schemenner, R.W., Huber, J.C. and Cook, R.L. (1987), "Geographic Differences and the Location of New Manufacturing Facilities," Journal of Urban Economics, Vol. 21, No. 1, pp. 83-104.

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AN EFFICIENT MINING PROCEDURE FOR GENE SELECTION BY USING SELECT ATTRIBUTES

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ABSTRACT

We propose a novel gene selection algorithm based on select attributes. The proposed algorithm eliminates gene redundancy automatically and yields a very small number of cancer related genes. Using the selected genes on the cancer classification, the robust classification accuracy has been produced across different types of classification methods. By comparing the number of selected genes and the classification accuracy obtained by our methods with others, our gene selection algorithm is very competitive compared to most recent gene selection methods. In addition, it has been convinced by the literature research that our identified genes are biologically relevant to cancer. Therefore our method will be a useful supplementary tool for the future studies in the application of microarray datasets.

KEYWORDS
Classification, DNA Microarray, Gene Selection, Select attribute, WEKA.

1. INTRODUCTION

The main reason for gene mining is to find and separate genes that are characterized for conferring essential traits. The availability of molecular biological technique is more. It has allowed for rapid development and identification of nucleic acid derived sequence.

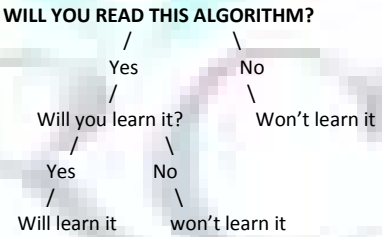
WHERE IS GENE LOCATED*?*

A cell is made up of chromosomes. 23 pairs of chromosomes present in a single cell. The Chromosome is made up of genes. The genes consist of DNA which is made up of four chemical letters .i.e A, C, T, G. In a cell both DNA and RNA are present. Both did a replication process.DNA was convert into RNA is called transcription process. RNA was convert into DNA is called reverse transcription process. Protein was obtained from the RNA with the help of translation process. The advantages of gene mining is, it is used in clonning method,pregnancy cases,agriculture. The disadvantage of gene mining is,high tech,costly. In this paper large number of attributes are present,so using the select attributes and then classify with various algorithm it produce different output for various algorithms.compare all output and find which one is low output, it is the final accuracy. Furthermore, using the selected genes on the cancer classification, the robust classification accuracy has been produced by some different classification methods.

2. METHODS USED FOR GENE MINING

2.1 **CLASSIFICATION**

Classification is a data mining algorithm that creates a step-by-step guide for how to determine the output of a new data instance. The tree it creates is exactly that: a tree where by each node in the tree represents a spot where a decision must be made based on the input, and you move to the next node and the next until you reach a leaf that tells you the predicted output. Sounds confusing, but it's really quite straightforward. Let's look at an example.



This simple classification tree seeks to answer the question "Will you understand classification trees algorithm?" At each node, you answer the question and move on that branch, until you reach a leaf that answers yes or no. This model can be used for any unknown data instance, and you are able to predict whether this unknown data instance will learn classification trees by asking them only two simple questions. That's seemingly the big advantage of a classification tree it doesn't require a lot of information about the data to create a tree that could be very accurate and very informative.

2.2. **GAUSSIAN PROCESS**

Implements Gaussian process for regression without hyper parameter tuning. To make choosing an appropriate Noise level easier, this implementation applies normalization / standardization to the target attribute as well. Missing values are replaced by the global mean / mode. Nominal attributes are converted to binary ones.

2.3. **LINEAR REGRESSION**

Regression is the easiest technique to use, but is also probably the least powerful.. This model can be as easy as one input variable and one output variable.Of course, it can get more complex than that, including dozens of input variables. In effect, regression models all fit the same general pattern. There are a number of independent variables, which, when taken together, produce a result a dependent variable. The regression model is then used to predict the result of an unknown dependent variable, given the values of the independent variables.

2.4. **MULTILAYERED PERCEPTRON**

It is a feed forward artificial neural network model that maps sets of input data onto a set of appropriate output. An MLP consists of multiple layers of nodes in a direct graph, with each layer fully connected to the next one. Except for the input nodes, each node is a neuron with a non linear activation function. MLP

utilizes a supervised learning technique called back propagation for training the network. MLP is a modification of the standard linear perceptron and can distinguish data that is not linearly separable.

2.5. **SMO REG**

SMO reg implements the support vector machine for regression. The parameters can be learned using various algorithms. The algorithms is selected by setting the reg optimizer. The most popular algorithm(reg smo improved) is due to shevade, keerthi et al and this is the default reg optimizer.

3. NUMERICAL EXPERIMENTS

In order to exam our algorithm, we carry out some experiments on datasets, namely Breast cancer datasets. Breast cancer dataset have an attribute is 11 and instance is 699. Using select attributes, select few attributes out of 11 attributes and classify with various algorithm. Find the output. Do the procedure repeatly until the output becomes low. This process is called as selecting best method by various search models. Use all methods and find best method.

3.1 **Find accuracy**

Breast cancer datasets

Instance 699

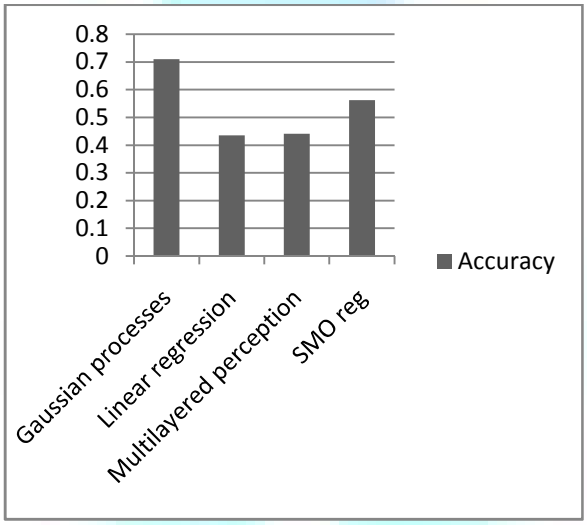
Attributes 11

There are Sample code number, Clump thickness, Uniformity of cell size, Uniformity of cell shape, Marginal adhesion, Single epithelial cell size, Bare nuclei, Bland chromatin, Normal nucleoli, Mitoses, Class. In select attributes, cross validation is select in the attributes select mode. Then number of folds are represent in %. Here choose only four attributes there are clump thickness, bare nuclei, bland chromatin, class.

TABLE 1: SELECT ATTRIBUTES 4

Algorithm	Accuracy
Gaussian processes	0.7105
Linear regression	0.4353
Multilayered perception	0.4408
SMO reg	0.562

FIG. 1: GRAPH FOR 4 ATTRIBUTES

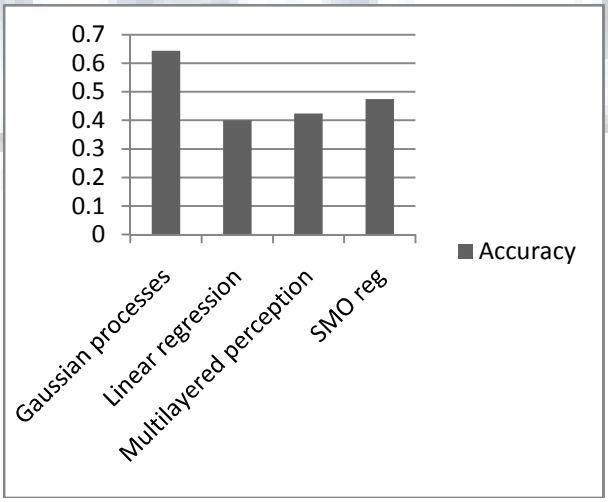


Here choose only five attributes. They are clump thickness, Uniformity of cell size, Bare nuclei, Bland chromatin, Class.

TABLE 2: SELECT ATTRIBUTES 5

Algorithm	Accuracy
Gaussian processes	0.6444
Linear regression	0.4003
Multilayered perception	0.4243
SMO reg	0.4747

FIG. 2: GRAPH FOR 5 ATTRIBUTES

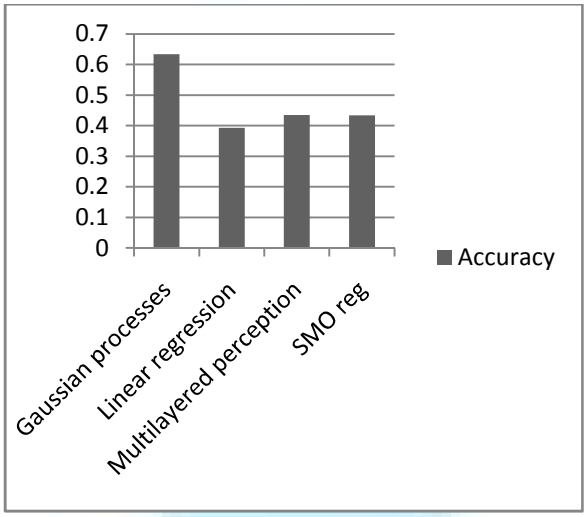


Here choose only six attributes. They are Clump thickness, Uniformity of cell size, Bare nuclei, Bland chromatin, Normal nucleoli, Class.

TABLE 3: SELECT ATTRIBUTES 6

Algorithm	Accuracy
Gaussian processes	0.6342
Linear regression	0.3933
Multilayered perception	0.4351
SMO reg	0.4335

FIG. 3: GRAPH FOR 6 ATTRIBUTES

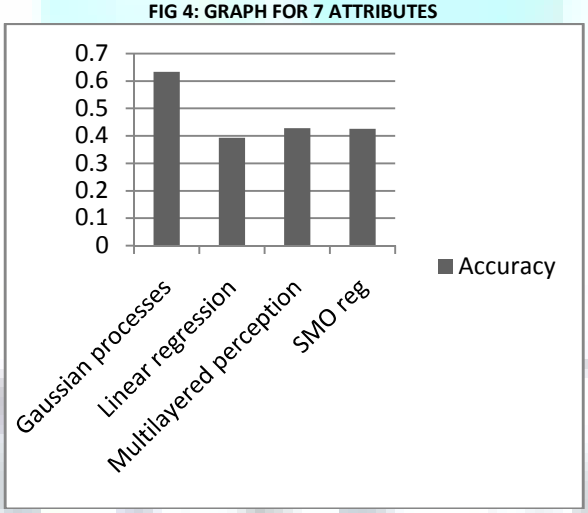


Here choose only seven attributes. They are clump thickness, uniformity of cell size, uniformity of cell shape, bare nuclei, bland chromatin, normal nucleoli, class.

TABLE 4: SELECT ATTRIBUTES 7

Algorithm	Accuracy
Gaussian processes	0.6338
Linear regression	0.3929
Multilayered perception	0.4284
SMO reg	0.4262

FIG 4: GRAPH FOR 7 ATTRIBUTES



4. COMPARISON WITH PREVIOUS WORK

The gene selection problem and classification problem have been studied by several authors. For comparison, we list the number of selected genes and classification accuracy obtained by different methods and it is listed above. Here select few attributes and find the accuracy. When the accuracy becomes low, this process is stopped.

5. BIOLOGICAL INTERPRETATION OF THE SELECTED GENES

In this section, explain about the genes in this datasets selected by the algorithm and analyze their relationship with the occurrence of disease, which are based on the identified genes closely correlated with the pathogenesis of specific or general diseases.

In summary, the majority of the genes selected by our method are relevant to the pathogenesis of disease. Some of them have definite biological meaning while the others remain to be explored. It reflects the complexity of cancerous pathogenesis.

6. CONCLUSION

Gene selection procedure is conducted on the microarray datasets through these algorithms. It can reduce the gene redundancy automatically and collect a very small number of related genes. By using the selected genes on the classification, rather high classification accuracy is obtained. The number of selected genes

and the classification accuracy obtained by our methods was compared with others, our gene selection algorithms are very hard or difficult compared to most recent gene selection methods.

7. ACKNOWLEDGMENT

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