

e-ISSN: 2319-8753 | p-ISSN: 2347-6710

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International Journal of Innovative Research in SCIENCE | ENGINEERING | TECHNOLOGY

# INTERNATIONAL JOURNAL OF INNOVATIVE RESEARCH

IN SCIENCE | ENGINEERING | TECHNOLOGY

Volume 11, Issue 7, July 2022

INTERNATIONAL STANDARD SERIAL NUMBER INDIA

## Impact Factor: 8.118

9940 572 462

6381 907 438

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e-ISSN: 2319-8753, p-ISSN: 2347-6710 www.ijirset.com | Impact Factor: 7.569



Volume 11, Issue 7, July 2022

DOI:10.15680/IJIRSET.2022.1107168

### Lung Cancer Detection Using Machine Learning Techniques

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**ABSTRACT:** In a large data source, Machine learning has improved to involve artificial intelligence, and it is used to give solutions for many problems in knowledge and data engineering. One common application of machine learning is the prediction of an outcome based upon existing data. The machine learns patterns from the existing dataset, and then applies them to an unknown dataset in order to predict the outcome. Classification is a powerful machine learning technique that is commonly used for prediction. Some classification algorithms predict with satisfactory accuracy, whereas others exhibit a limited accuracy. This proposed method investigates a method termed Logistic Regression Technique, which is used for improving the accuracy of weak algorithms. Other classifiers like Random Forest Classifier: Existing 1, SGD Classifier: Existing 2. Implementation with this tool were performed using a lung cancer disease dataset. A comparative analytical approach was done to determine how the regression technique can be applied for improving prediction accuracy in lung cancer prediction. The focus of this method is not only on increasing the accuracy of weak classification algorithms, but also on the implementation of the algorithm with a medical dataset, to show its utility to predict disease at an early stage.

#### I. INTRODUCTION

Lung Cancer is ended up being a cataclysmic danger to the humankind and is fundamental driver of passing among other tumor related losses. The nearness of singular pneumonic knobs in human lungs as generous or threatening decides the gravity of lung disease. Computer supports the findings of lung data has been a progressive advance in the early diagnosing of lung infections. The 10190best technique for actualizing PC supported conclusion for therapeutic picture examination is first to pre-process the picture with a specific end goal to portion it. The initial phase in computers helped conclusion of lung figured tomography. Understanding the picture is by and large to first portion the locale of enthusiasm, for this situation lung, and afterward examine independently every region got, for a tumor, disease, hub identification or other pathology for finding.

Lung detection on medical images forms an essential step in solving several practical applications such as diagnosis of the tumours and registration of patient images obtained at different times. Segmentation algorithms form the essence of medical image applications such as radiological diagnostic systems, multimodal image registration, creating anatomical atlases, visualization, and computer -aided surgery.

Appropriate treatment for lung cancer patients primarily depends on the type of lung carcinoma, such as small cell lung cancer (13%) or non-small cell lung cancer (84%). The most common non-small cell lung cancer can be divided into several main types that named based upon the tumor cells, like adenocarcinomas and squamous cell carcinomas. The small cell lung cancer occurs rarely where the percentage also is very less.

This project is based on demos copy technology is used for malignant melanoma Lung cancer detection. In this system different step for melanoma Lung cancer lesion characterization i.e., first the Image Acquisition Technique, pre-processing, segmentation, define feature for Lung cancer Feature Selection determines lesion characterization, classification methods.

#### **II. RESEARCH METHODOLIGIES**

#### 2.1 EXISTING SYSTEMS

The most important application of microarray in gene expression analysis is to classify the unknown tissue samples according to their gene expression levels with the help of known sample expression levels. In this paper, we present a nonparallel plane proximal classifier (NPPC) ensemble that ensures high classification accuracy of test

e-ISSN: 2319-8753, p-ISSN: 2347-6710 www.ijirset.com | Impact Factor: 7.569



Volume 11, Issue 7, July 2022

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samples in a computer-aided diagnosis (CAD) framework than that of a single NPPC model. For each data set only, a few genes are selected by using a mutual information criterion.

Then a genetic algorithm-based simultaneous feature and model selection scheme is used to train a number of NPPC expert models in multiple subspaces by maximizing cross-validation accuracy. The members of the ensemble are selected by the performance of the trained models on a validation set. Besides the usual majority voting method, we have introduced minimum average proximity-based decision combiner for NPPC ensemble. The effectiveness of the NPPC ensemble and the proposed new approach of combining decisions for cancer diagnosis are studied and compared with support vector machine (SVM) classifier in a similar framework.

A hybrid CAD method of cancer classification taking the advantage of both filter and wrapper methods. A fast dimensionality reduction step is carried out by selecting a small set of genes by the MRMR ranking method. Then we used the wrapper method (for improved classification accuracy) on this small set of genes to reduce the computational burden. We have selected nonparallel plane proximal classifier (NPPC) as a part of the wrapper method. In our previous research work, we have proposed NPPC for binary data classification that provides comparable accuracy with that of SVM classifiers with a lower computational cost.

We have discussed the various steps of formulation of NPPC ensemble. As we have pointed out earlier that the computer-aided diagnosis of cancer or cancer category discrimination should be bias-free, we have preceded the formulation of NPPC ensemble by separate training, validation, and testing set. The validation and testing set is normalized by subtracting the mean and dividing the standard deviation of the training data. It is to be noted that the NPPC ensemble does not address the small sample problem of data sets. It only offers improved classification performance on noisy microarray data sets.

#### Disadvantages

However, often turns out to be difficult to analyze. The most important application of the microarray technique is to classify unknown samples according to their expression profile

Here, feature and parameter selection technique can select the best combination of gene subset that retains the separability of the testing data.

And multiple learning algorithms are not used for the purpose of improving the classification accuracy by combination or averaging but the same algorithm is used to develop best expert models indifferent subspaces.

#### 2.2 PROPOSED SYSTEM

There are variety of options available for lung cancer treatment. The type of treatment recommended for an individual is influenced by various factors such as lung cancer-type, the severity of cancer (stage) and most important the genetic heterogeneity. In such a complex environment, the targeted drug treatments are likely to be irresponsive or respond differently. To study anticancer drug response, we need to understand cancerous profiles. These lung cancerous profiles carry information which can reveal the underlying factors responsible for cancer growth. Hence, there is need to analyse cancer data for predicting optimal treatment options. Analysis of such profiles can help to predict and discover potential drug targets and drugs. In this paper the main aim is to provide machine learning based classification technique for lung cancerous detection.

Lung Cancer patients often show heterogeneous drug responses such that only a small subset of patients is sensitive to a given anticancer drug. With the advent of next generation sequencing, huge amount of genome profiling data has driven the research on uncovering the genetic mutations and expressed genes of individual patients. These genetic mutations and expression are responsible for such a wide spread heterogeneity in drug responses. Drug related sensitivity is determined by evaluating the changes at genetic level for each specific drug. Optimal drug prediction is a key component for oncology precision medication.

Traditionally all cancers are classified based on their anatomical origin. But recent research shows that cancer patients of same type can show heterogeneous behaviour towards target drug therapy. It has been seen those computational approaches such as machine learning can help to predict the potential drugs and their targets. Machine learning algorithms facilitates adaptive learning and hence helps in predicting anti-cancer drug treatment and classifying cancer patients. So, this paper will review how machine learning algorithms are effective in classification of cancerous profiles. We are classifying cancer cell-lines based on their genetic similarity and the type of cancer.

#### Advantages

The proposed technique is an attempt to solve classification problem for cancerous genomic profiles. Our technique is based on concept of utilizing SVM and KNN machine learning algorithm.

Result provides comparative analysis of model performance when the sample size is varied.

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Volume 11, Issue 7, July 2022

#### DOI:10.15680/IJIRSET.2022.1107168

As the sample size increase model performance also increases, which shows positive aspect towards the robustness and adaptively of the model.

#### 4.3 MODULE DESCRIPTION



#### 4.3.1 Data Collection

The Datasets used in this study are taken from the UCI Machine Learning Repository and

data.world. UCI Machine Learning Repository: https://archive.ics.uci.edu/ml/datasets/lung+cancer In this dataset: Number of Instances: 32 ,Number of Attributes: 57 (1 class attribute, 56 predictive) Attribute Information: attribute 1 is the class label data.world: https://data.world/cancerdatahp/lung-cancer data. In this dataset: Number of Instances:1000 Number of Attributes:25(1 class attribute,24 predictive) Attribute Information: attribute 25 is the class label

#### 4.3.2 Importing Packages

For this project, our primary packages are going to be Pandas to work with data, NumPy to work with arrays, scikit-learn for data split, building and evaluating the classification models. Let's import all of our primary packages into our python environment.

#### 4.3.3 Data Pre-processing

Normalization is a very common technique used in data preprocessing. In this method, we assume our data is not normally distributed. In order to scaled data, we calculate the min and max of each column. normalize each value of a column, we subtract min value from each value and divided by max-min value.

Normalization = value- min/ max-min

Standardization: if we choose to do the standardization of data. then we are assuming that our input data are normally distributed. and we are calculating the means and standard deviation of each column.

SD = sqrt[(value-mean) \*\*2/ count(value-1)]

standardize of data = value- mean/SD.

Standardization of a dataset is a common requirement for many machine learning estimators: they might behave badly if the individual features do not more or less look like standard normally distributed data (e.g., Gaussian with 0 mean and unit variance).

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	age	sex	ср	restbp	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	
count	299.000000	299.00000	299.000000	299.000000	299.000000	299.000000	299.000000	299.000000	299.000000	299.000000	299.000000	299.000000	299.000
mean	54.521739	0.67893	3.163880	131.715719	246.785953	0.143813	0.989967	149.327759	0.331104	1.058528	1.605351	0.672241	4.74
std	9.030264	0.46767	0.964069	17.747751	52.532582	0.351488	0.994903	23.121062	0.471399	1.162769	0.616962	0.937438	1.940
min	29.000000	0.00000	1.000000	94.000000	100.000000	0.000000	0.000000	71.000000	0.000000	0.000000	1.000000	0.000000	3.000
25%	48.000000	0.00000	3.000000	120.000000	211.000000	0.000000	0.000000	132.500000	0.000000	0.000000	1.000000	0.000000	3.000
50%	56.000000	1.00000	3.000000	130.000000	242.000000	0.000000	1.000000	152.000000	0.000000	0.800000	2.000000	0.000000	3.000
75%	61.000000	1.00000	4.000000	140.000000	275.500000	0.000000	2.000000	165.500000	1.000000	1.600000	2.000000	1.000000	7.000
max	77.000000	1.00000	4.000000	200.000000	564.000000	1.000000	2.000000	202.000000	1.000000	6.200000	3.000000	3.000000	7.000
4													۱.

Figure 4.1 Preprocessing of data

#### 4.3.4 Splitting of data

In this process, we are going to define the independent (X) and the dependent variables (Y). Using the defined variables, we will split the data into a training set and testing set which is further used for modeling and evaluating. We can split the data easily using the 'train\_test\_split' algorithm in python.

#### 4.3.5 Modeling of data

In this step, we will be building two different types of classification models namely Decision Tree and Logistic Regression. Even though there are many more models which we can use, these are the most popular models used for solving classification problems. All these models can be built feasibly using the algorithms provided by the scikit-learn package.

#### 4.3.6 Classification using Decision Tree Classifier.

A decision tree is a supervised machine learning algorithm. A decision tree shape is just a tree where every node is a leaf node or decision node. The techniques of the decision tree are simple and easily understandable for how to take the decision. A decision tree contained internal and external nodes linked with each other. The internal nodes are the decision-making part that makes a decision and the child node to visit the next nodes. The leaf node on the other hand has no child nodes and is associated with a label.

#### 4.3.7 Classification using Logistic Regression

Logistic Regression is a Machine Learning algorithm which is used for the classification problems, it is a predictive analysis algorithm and based on the concept of probability. Logistic regression is a classification algorithm used to assign observations to a discrete set of classes. Some of the examples of classification problems are Email spam or not spam, Online transactions Fraud or not Fraud, Tumor Malignant or Benign. Logistic regression transforms its output using the logistic sigmoid function to return a probability value. We can call a Logistic Regression a Linear Regression model but the Logistic Regression uses a more complex cost function, this cost function can be defined as the 'Sigmoid function' or also known as the 'logistic function' instead of a linear functions fail to represent it as it can have a value greater than 1 or less than 0 which is not possible as per the hypothesis of logistic regression. The logistic function, also called the sigmoid function was developed by statisticians to describe properties of population growth in ecology, rising quickly and maxing out at the carrying capacity of the environment. It's an S-shaped curve that can take any real-valued number and map it into a value between 0 and 1, but never exactly at those limits.

Logistic regression models the probability of the default class (e.g., the first class). For example, if we are modeling people's sex as male or female from their height, then the first class could be male and the logistic regression model could be written as the probability of male given a person's height, or more formally:

#### P (sex=male height)

Written another way, we are modeling the probability that an input (X) belongs to the default class (Y=1), we can write this formally as:

P(X) = P(Y=1|X)

Note that the probability prediction must be transformed into a binary value (0 or 1) in order to actually make a probability prediction. More on this later when we talk about making predictions.

Logistic regression is a linear method, but the predictions are transformed using the logistic function. The impact of this is that we can no longer understand the predictions as a linear combination of the inputs as we can with linear regression, for example, continuing on from above, the model can be stated as:

 $p(X) = e^{(b0 + b1*X)} / (1 + e^{(b0 + b1*X)})$ 

I don't want to dive into the math too much, but we can turn around the above equation as follows (remember we can remove the e from one side by adding a natural logarithm (ln) to the other):

 $\ln(p(X) / 1 - p(X)) = b0 + b1 * X$ 

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Volume 11, Issue 7, July 2022

#### DOI:10.15680/IJIRSET.2022.1107168

This is useful because we can see that the calculation of the output on the right is linear again (just like linear regression), and the input on the left is a log of the probability of the default class.

This ratio on the left is called the odds of the default class (it's historical that we use odds, for example, odds are used in horse racing rather than probabilities). Odds are calculated as a ratio of the probability of the event divided by the probability of not the event, e.g., 0.8/(1-0.8) which has the odds of 4. So, we could instead write:

 $\ln(\text{odds}) = b0 + b1 * X$ 

Because the odds are log transformed, we call this left-hand side the log-odds or the probity. It is possible to use other types of functions for the transform (which is out of scope\_, but as such it is common to refer to the transform that relates the linear regression equation to the probabilities as the link function, e.g., the probity link function.

We can move the exponent back to the right and write it as:

 $odds = e^{(b0 + b1 * X)}$ 

All of this helps us understand that indeed the model is still a linear combination of the inputs, but that this linear combination relates to the log-odds of the default class.

#### V. METHODOLOGIES

#### 5.2.1 Pre-processing

The fourth column of each dataset is the tissue on the basis of which pre-processing has to be performed. The Pseudo-Code description of the pre-processing is given above.

At this stage we will explore whether or not the performance of some algorithms is affected by the type of features. The algorithms that are calculating distances, such as they may be affected more by normalization, while other algorithms, like decision trees, will not be affected because of their nature to create groups of examples depending in some range of values. In other cases, the normalization may not have great affect in the performance but it may significantly reduce the training time.

#### 5.2.2 KNN Classification

The K-Nearest Neighbour (KNN) algorithm is one of the simplest classification approaches in machine learning methods. It has been used in many applications in the field of data mining. By this algorithm, the classifying object assigns to the label of its k-nearest neighbour or neighbours according to the feature vector from reference space (training data). It is classified according to the distance and the determined number of k, Sothis algorithm is named as k-nearest neighbour algorithm.

The KNN algorithm is one of the best and commonly used for clustering and classification. In this method, each sample value fit to the test dataset and itis classified according to the nearest k sample based on the training data. The class numbers values obtained from k sample values; the maximum number is determined from class samples.

K-Nearest Neighbour Classifier KNN is simple clustering algorithm which classifies data set based on their similarity with neighbours. K stands for number of data set items that are considered for the classification. The closest match among the k nearest neighbour decides the label of the test sample. In this system, Euclidean Distances (ED) are used to find the distances between test sample and database samples.

#### Algorithm

A case is classified by a majority vote of its neighbours, with the case being assigned to the class most common amongst its K nearest neighbours measured by a distance function. If K = 1, then the case is simply assigned to the class of its nearest neighbour.



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Volume 11, Issue 7, July 2022

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It should also be noted that all three distance measures are only valid for continuous variables. In the instance of categorical variables, the Hamming distance must be used. It also brings up the issue of standardization of the numerical variables between 0 and 1 when there is a mixture of numerical and categorical variables in the dataset.

#### Hamming Distance

$D_{H}$	$=\sum_{i=1}^{k}  x $	$ x_i - y_i $		
$x = x \neq x$	$y \Rightarrow L$ $y \Rightarrow L$	$\mathbf{P} = 0$ $\mathbf{P} = 1$		
х	Y	Distance		
Male	Male	0		
Male	Female	1		

Choosing the optimal value for K is best done by first inspecting the data. In general, a large K value is more precise as it reduces the overall noise but there is no guarantee. Cross-validation is another way to retrospectively determine a good K value by using an independent dataset to validate the K value. Historically, the optimal K for most datasets has been between 3-10. That produces much better results than 1NN.

#### 5.2.3 Support Vector Machine algorithm

Support Vector Machine (SVM) method was introduced. Create a model by using training data and according to this model our test data is included in a certain class. To separate these classes, hyper plane is determined in the model building process.

SVM is one of the strongest algorithms for machine learning and especially in multi-class problems. SVM constructs hyper planes linearly and have to find the optimal hyper plane by maximizing the wideness between support vector points and minimize the risk of misclassification examples of the test dataset. Fig. 2 shows the structure of SVM.

Support vector machine (SVM) is a binary classification which can identify objects in two categories, first is by itself and secondly, by others. The SVM in the proposed algorithm is utilized by the target classification. Statistical Learning Theory forms the basis of support vector machine. It helps to learn patterns, predict labels and cluster data points. The mapping is written as below:

$$X \rightarrow Y$$
,  
where  $x \in X$  is some object and  $y \in Y$  is a class label.

#### 5.2.4 The Classification Process

The classification process utilized the trained set for both SVM by utilizing the output of Neural Network. First of all, SVM will be utilized for the target classification of tissues. The SVM Classification uses the following attributes:

a) SVM train set

b) Classified Kernel vector



Fig. 7. 2 Classified sample series

Above Figure. represents the classified sample series. At the end of all training, a rule set will be created to predict the drug for the target.

e-ISSN: 2319-8753, p-ISSN: 2347-6710 www.ijirset.com | Impact Factor: 7.569



Volume 11, Issue 7, July 2022

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- SVM Classification
- 1. import elefant. kernels. Vector
- 2. # linear kernel
- 3. k = elefant. kernels. vector. CLinearKernel ()
- 4. # Gaussian RBF kernel
- 5. k = elefant. kernels. vector.CGaussKernel(rbf)
- 6. import elefant.estimation.svm. svmclass as
- 7. svmclass
- 8. svm = svmclass.SVC(C, kernel=k)
- 9. alpha, b = svm.Train(x, y)
- 10. ytest = svm. Test(xtest)

#### VI. CONCLUSION

In this research, an intelligent machine-learning based predictive system was proposed for the prediction of lung cancer disease. The K-fold cross-validation method was used in the system for validation. In order to check the performance of classifiers different evaluation metrics were also adopted. The Decision tree and KNN classifier algorithms select important fields that improve the performance of classifiers in terms of classification accuracy. Due to the good performance of classifiers with Relief, it is a better predictive system in terms of accuracy.

Designing a decision support system through machine-learning-based method will be more suitable for diagnosis of heart disease. Additionally, some irrelevant features reduced the performance of the diagnosis system and increased the computation time. So, another innovative dimension of this study was the usage of feature selection algorithms to choose best features that improve the classification accuracy as well as reduce the execution time of the diagnosis system. In the future, we will perform more experiments to increase the performance of these predictive classifiers for lung cancer prediction by using others feature selection algorithms and optimization techniques.

#### **VII. FUTURE WORKS**

Designing a decision support system through machine-learning-based method will be more suitable for diagnosis of lung disease. Additionally, some irrelevant features reduced the performance of the diagnosis system and increased the computation time. So, another innovative dimension of this study was the usage of feature selection algorithms to choose best features that improve the classification accuracy as well as reduce the execution time of the diagnosis system. In the future, we will perform more experiments to increase the performance of these predictive classifiers for lung cancer prediction by using others feature selection algorithms and optimization techniques

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| e-ISSN: 2319-8753, p-ISSN: 2347-6710| <u>www.ijirset.com</u> | Impact Factor: 7.569|



Volume 11, Issue 7, July 2022

#### DOI:10.15680/IJIRSET.2022.1107168

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