

Deep Learning Strategies for Survival Prediction in Prophylactic Resection Patients

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Abstract. Human race is looking forward to an era where science and technology can wipeout the threats laid by lethal diseases. Major statistics shows that about 10 million people die from various forms of cancer annually. Every sixth death in the world is caused by cancer. Treatment to cancer always depend on its type and spread. Treatment includes single or combination of surgery, chemotherapy and radiation therapy. In this paper, survival prediction in prophylactic resection patients are carried out using various deep learning methods. Prophylactic resection has been found to be very effective in colon cancer, breast cancer and ovarian cancer. In this paper, we try to validate the results in a test environment using multi layered deep neural network. Classical Navie Bayer's algorithm has been used to classify the dataset and convolution neural network (CNN) has been used to create the survival prediction model. Results affirm better survival results in prophylactic resection patients.

Keywords: Survival prediction \cdot Naive Bayer's algorithm \cdot Classification \cdot Heath informatics \cdot Prophylactic resection \cdot Deep learning

1 Introduction

Over the years, cancer research has seen tremendous improvement. From challenging treatment scenarios to early detection of symptoms have surly given a positive sign in the treatment process. With the advancement in technology and availability of immense data, medical research community has grown to a bigger level of early screening and prediction of disease.

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Treatment of cancer always depends on the staging system. Inaccurate staging diagnosis can lead to life threatening situations. Most of the time surgery and removal of the affected part is a vital part in the treatment process. But there are various cases where such removal doesnt meet the purpose. Early detection of cancer can provide doctors insights on removing a particular part/organ which can prevent the occurrence of disease. Such surgeries are termed as prophylactic resections. For various type of cancer like colon, breast and ovary this process has been seen very effective. Accurate and robust predictions of overall survival, using automated algorithms can provide valuable guidance for diagnosis, treatment planning, and outcome prediction. It is however difficult to have the reliable and accurate attributes for the prediction process. Medical imaging, clinical data, family history, drug and other disease history always contribute to it. Hence having a perfect decision making model for prediction can help the physician. Not only prophylactic resections, survival prediction of patients after this process can also lead to have a positive impact on the treatment process.

Deep learning strategies has been used for initial detection from the medical imaging. CNN is a variation of deep neural network which is highly dependent on the correlation of neighbouring pixels. At start, it make use of randomly defined patches as input and later modifies the same during the training process. When the training is finished, the model uses the new modified patches for predicting and validating the result. From the clinical dataset, Naive Bayers algorithm helps in predicting to which class the cells need to be classified. Thus a combined model provides accurate prediction module.

2 Literature Survey

Many approaches and techniques have been proposed in the field of cancer detection and prediction. The following methods have been able to detect cancer detection at early stage with higher accuracy. In [1] A prototype of lung cancer prediction system is developed using data mining classification techniques. The system extracts hidden knowledge from a historical lung cancer disease database. The most effective model to predict patients with Lung cancer disease appears to be Naïve Bayes followed by IF-THEN rule, Decision Trees and Neural Network.

The [2] is a skin cancer diagnosis using machine learning by imputing skin cancer images are given to the sheartlet transformation module, which decomposes the given input images to obtain the sub-band coefficients. After that feature extraction stage selects the features according to their rank by t-test. Then the selected features are classified by naïve Bayes classifier as normal or abnormal.

In [3] Brest cancer is predicted using Naive Bayes classifier an inductive learning algorithms for machine learning and data mining. Navies Bayes classifier uses large quantities of data related to breast cancer characteristics, in order to obtain an optimal prediction of recurrent events.

Neural networks and related techniques have a vast contribution when it comes into health informatics. Over the past few decades, Convolution Neural Networks have been employed increasingly by more and more researchers, and become an active research area. ANNs have afforded numerous successes with great progress in Cancer classification and diagnosis in the very early stages. A typical ANN model is made up of a hierarchy of layers: input, hidden and output layers. Extensive research had been done with backpropagation artificial neural network (BP-ANN) method and its variations in breast cancer diagnosis. The technique, however, has some limitations such as no guarantee to global optima, a lot of tuning para-meters, and long training time. Single Hidden Layer Neural Networks (SFLN) was proposed by Huang and Babri to tackle the mentioned problems with tree steps learning process that called extreme learning machine (ELM). Standard and best parameterised ELM model were proposed for breast cancer early prediction. Results showed that it generally gave better accuracy, specificity, and sensitivity compared to BP ANN. However, most existing works focus on prediction performance with limited attention with medical professional as end user and applicability aspect in real medical setting.

3 Methodology

Symptoms leads to treatment. When ever a patient approaches the doctor, the initial step is to get the vital and other relevant clinical information. From such data and results of primary investigation, physician can generally conclude his initial diagnosis. He thus classifies the patient who can possibly affected by the disease. Those who are more prone to be affected will be reviewed frequently and treatments as and when needed will be suggested. This can be medicine intake or even surgery/removal of organs/parts etc.

Initial phase is to find the apt classifier which classifies the cells into malignant or benign. In this study we are selecting support vector machine (SVM), C4.5, Naive Bayers and K-Nearest Neighbourhood algorithm. Sien Luei dataset for classification is used for the study. It has 700 instances, with two classes benign and malignant. 10 fold cross validation is done, which means in evaluating predictive models the original set is split into a training sample to train the model, and a test set to evaluate it. The following table provides the results obtained while performing the test process in the 700 instance. Time taken to build the model and accurate classification are the attributes considered for the performance. Table 1 shows the detailed data obtained during the classification.

Perfomance indicators	Algorithms used			
	SVM	C4.5	Naive Bayers	Nearest neighbourhood
Time to build the model	0.091	0.085	0.035	0.027
Correctly classified instances	677	669	688	671
Accuracy	96.71	95.57	98.28	95.85

Table 1. Perfomance measures.

For more accurate learning; Kappa statistics, Mean absolute error, Root mean squared error has also been calculated. These values provide how accurate the instances were classified and also forecasts and predicts the eventual outcome. Table 2 shows the error measures and deviations.

Perfomance measures	Algorithms used			
	SVM	C4.5	Naive Bayers	Nearest neighbourhood
Kappa statistic	0.95	0.85	0.93	0.84
Mean absolute error	0.026	0.073	0.035	0.042
Root mean square error	0.14	0.25	0.17	0.24

Table 2. Perfomance measures.

The result statistics have been well analysed and for classification to benign and malignant cells, Naive Bayers classifier has been selected.

Once the classifier is build, a CNN model need to be build for predicting the survival of patients who are under going prophylactic resection. Our CNN model contains 3 convolutional layers which is followed by 2 fully connected layers and an output layer and is implemented over the AlexNet platform. Figure 1 shows the basic architecture of the model designed.

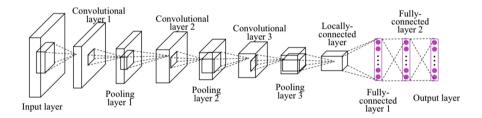


Fig. 1. Architecture details.

Standard survival regression models like Cox proportional hazards model is compared to the Deep neural network. Negative log of Cox partial likelihood was used as a loss function to train the network, and Rectified linear unit (ReLu) was used as the nonlinear activation function in the convolutional and fully connected layers. The deep learning model was trained with out Sien Luei dataset. The survival regression models were validated using 10-fold cross validation, and concordance index was used to evaluate the survival regression results. The C-Index obtained by the deep CNN model was 0.673 while the CPH model had a C- index of 0.592.

3.1 Dataset

Sien Luei survival dataset has been used for the prediction. Data consist of 4327 instances of 8 attributes. Age of the patient, operation date, number of positive auxiliary nodes detected, family history, drug used, survival in years were the top attributes used. Dataset has been specific for each analysis. For the prediction of breast cancer - the attributes used are mean radius, mean perimeter, mean compactness, smoothness, concave points, symmetry etc. Figure 2 shows the basic classification on the entire dataset with respect to each attributes. This dataset is used for the entire prediction model building.

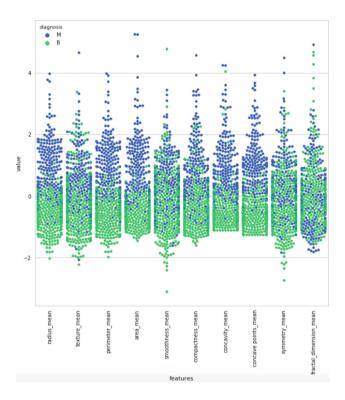


Fig. 2. Seaborn plot of attributes.

4 Results and Discussion

Setting and evaluating the various performance measure is a serious task which evaluates the entire model. Four different algorithms have been used for the classification. Table 3 shows the accuracy, precision, specificity and recall.

From Table 1 we can see that Naive Bayers takes 0.035 second to build the model. Even though time taken is higher than k-NN which about 0.027 second

Algorithm	Perfomance measure			
	Accuracy	Precision	Specificity	Recall
SVM	96.71	0.961	0.692	0.966
C4.5	95.57	0.949	0.827	0.985
Naive Bayers	98.28	0.983	0.916	0.990
K-nearest neighbour	95.85	0.952	0.875	0.882

Table 3. Perfomance measures.

we prefer NB by the fact that K-NN is a lazy learner algorithm which doesn't gets much learning during the training phase. Other than the time to build the model, accuracy obtained for Naive Bayes tops the list by 98.28% and have the highest number of correctly classified instance. Error rates can be studied from Table 2, which clearly indicates the variation from the correct classification. Naive Bayer and SVM shows the least deviation which makes them more preferred for the classification. But Naive Bayers has the best compatibility between the reliability of the data collected and their validity.

Algorithm	Benign	Malignant	Class
SVM	438	20	Benign
	15	227	Malignant
C4.5	436	22	Benign
	12	230	Malignant
Naive Bayers	446	7	Benign
	5	242	Malignant
K-nearest neighbour	439	20	Benign
	22	219	Malignant

Table 4. Confusion matrix values.

Once the model is created the efficiency of the algorithm need to be measured. Table 4 shows confusion matrix, which states the true positive and true negative split while using the four algorithms. The results affirm the use of Bayers algorithm to be more efficient when compared to others. Out of the 700 instances, 446 benign and 242 malignant has been correctly classified.

That is why the accuracy of Bayers was high when compared to other classification techniques. It outperforms with clear distinction other classifiers in accuracy, sensitivity, specificity and precision and in this work Naive Bayers was the best one which had the distinct split ratio. Figure 3 shows the box plot analysis of performance measure.

As the classification part was successful, next focus need to be given for building the CNN for survival prediction. Patients under scanner are underdone

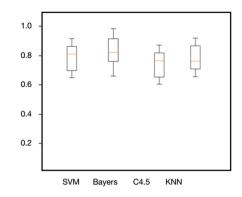


Fig. 3. Boxplot representation of performance

routine checkups and their vitals are used to create the survival models. Prophylactic resection will be suggested by doctors if they see any major changes during the checkup. System will have a close monitor on such details and creates a background knowledge from such information. This knowledge acts as the inductive logic base for prediction activities. Figure 4 shows the survival prediction curves with respect to the vital attributes.

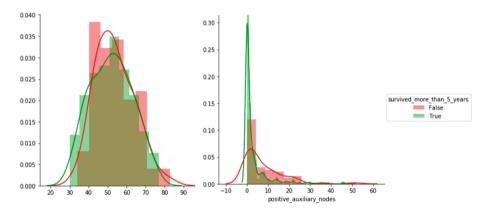


Fig. 4. Survival prediction

Experimental results on patients with ovarian, breast and colon cancer have demonstrated that the deep CNN survival analysis method could correctly predict the recurrence/risk better than state-of-the-art methods. Thus the resurrection procedure predicted by the model was found to be accurate. Experimental results demonstrate an accuracy of 98.6% and the classification model delivered an accuracy of 97.6%. A combined model of classification and survival prediction using Naive Bayers and Convolution neural network thus can be used effectively in Prophylactic Resection Patients.

5 Conclusion

Emergence of machine learning and usage of data mining techniques have helped to analyse and develop various medical related applications. An important challenge in data mining and machine learning areas is to build accurate and computationally efficient classifiers. Classifiers are always dependent to application and datasets, here even with very strong dataset Bayers classifier provided efficient classification when compared with SVM and KNN. The survival prediction model also when built showed perfectly aligned prediction results. Deep neural networks with a feedback loops are always efficient in the prediction strategies. Survival rates have been increased tremendously with the addiction of every single data record.

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