

COMPARATIVE APPROACH OF BACK PROPAGATION NEURAL NETWORK AND DECISION TREE ON BREAST CANCER CLASSIFICATION

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ABSTRACT

The use of data mining methods in incorporating decision making has been increasing in the past decades. Data mining simply refers to extracting or mining knowledge from large amount of data. Over the years, medical image processing has benefited immensely from data mining techniques including breast cancer diagnosis. Sonography (also known as ultrasound) has become a great addition to mammography and magnetic resonance imaging (MRI) as imaging techniques dedicated to providing breast cancer screening. This technique is time-consuming and often characterized with low accuracy. Hence, the need to develop a robust classification model with high performance accuracy and reduced false alarm.

In this paper, the performance of back propagation neural networks (BPNN) and C4.5 decision tree (DT) for breast cancer prediction was carried out. Filter based feature selection approach using correlation filter was employed for ranking features according to their predictive power. The model was simulated using WEKA data mining tools and extensive comparative study was performed based on the standard evaluation metrics. The performance of the two classifiers was compared based on their predictive accuracy, precision, recall, kappa statistic and other relevant statistical measures.

The simulation results shows that C4.5 outperforms BPNN in terms of training time (0.16 secs) and accuracy (94.2857%) while BPNN has 46.9secs training time and accuracy of 90.9524%. However, the result also reveals that BPNN outperforms C4.5 in terms of error rate, with BPNN having mean absolute error of 0.0542 while C4.5 has mean absolute error of 0.0834.

It can therefore be deduced from the comparison that C4.5 can be a good option for prediction task considering the fast training time of the algorithm as well as the high accuracy of prediction.

Keywords: Neural Network, Decision Tree, Prediction, Data mining, Simulation

1. INTRODUCTION

Over the years, there has been a significant increase in breast cancer cases among women. “Cancer is a disease that occurs as a result of distorted or unregulated growth of cells in human body”. Consequently, the cells divide and grow uncontrollably, forming an abnormal mass of tissue known as a tumor. Tumor cells grow and invade the digestive, nervous and circulatory systems, thereby disrupting the body’s normal functioning (Aiswarya, Jelaytha and Ronak, 2015). Breast cancer is the most commonly occurring cancer in women and the second most common cancer overall. There were over 2 million new cases in 2018 according to World Health Organization.

According to Global Burden of Disease Cancer Collaboration, Cancer is a leading cause of morbidity and mortality among women globally, accounting for about 17.5 million cancer cases and 9 million deaths in 2015. Breast cancer is now ranked the most common cancer worldwide, increasing from 1.7 million incident cases in 2005 to 2.4 million cases in 2015. Recent years have seen an intense improvement in survival rates for women with breast cancer, which can be mainly attributed to an extensive screening and enhanced prediction prior to occurrence with technological improvement and use of Computers. (Vishnusri, 2014).

Computers can be used to predict the possibility of breast cancer as well as classify breast cancer type, of which these classifications result in binary values; either benign or malignant. Additionally, recent advances in data collection and storage techniques have made it possible for various medical organizations and hospitals to keep vast amount of data relating to their medical records, medication and symptoms of a diseases. These automated tools have made it possible to collect large volumes of medical data, which are made available to researchers. These results into large datasets and subsequently, running powerful algorithms on these data to extract useful information from them is called Data mining. Data mining has several tasks such as association rule mining, classification, prediction and clustering. (Aiswarya et. al., 2015). According to Eltalhi and Kutrani, (2019) Data mining algorithms can be effectively used to mine relevant information extracted from the huge amounts of data generated by healthcare services. More often, these tasks involve identify patterns and relationship among large number of variables, which make it possible to predict the outcome of the disease using preexisting datasets (Rajesh, 2013). Amongst other tasks, Prediction is an attempt to accurately forecast the

outcome of a specific situation, using the information obtained from a concrete set of variables that potentially describe the situation, (Vishnusri, 2014).

However, a major problem often faced in clinical medicine is how to reach a conclusion about the prognosis of cancer patients when presented with complex clinical and prognostic information, since specialists usually make decisions based on a simple dichotomization of variables into a favourable and unfavourable classification. This has been an open issue that calls for continuous research attention (Jiankun and Athanasios, 2016).

There are several algorithms for data classification such as Decision Tree, Support Vector Machine, Naïve Bayes classifiers, and Artificial Neural network amongst others. Several researches, including Punitha and Santhanam (2007) and Hassani and Jafarian (2016) showed that Data mining algorithms delivered good accuracy in breast cancer prediction.. ANN and C4.5 are commonly used data mining algorithms for this purpose. However, the ANN has two major limitations. First, ANN has some parameters to be tuned in the beginning of training process such as number of hidden layer and hidden nodes, learning rates, and activation function. Tuning those parameters may pose some computational challenges. Second, the training process takes long due to complex architecture and parameters update process in each iteration. Also, Yunzhi, Morteza, Seyedehnafiseh, Jing, Wei, Yuchen, and Bin, (2018) identified the effectiveness of the use of a deep convolution neural network for breast cancer prediction. It is worthy of note that uninformative features produce bad predictions. Consequently, this research seeks to carry out a comparison of the effectiveness of the prediction approach of C4.5 and BPNN. The feature vectors from the breast cancer data samples were passed differently onto C4.5 and BPNN to determine the prediction rate of the algorithms.

The rest of this paper is structured as follows; Section II discusses previous researches related to Predictive analysis in breast cancer. Section III explains the materials and methodology which includes the acquisition of dataset, preprocessing, feature ranking as well as the classification procedure. The Algorithm Evaluation and Results are also detailed in this section. The outcomes of the simulation are discussed in section IV. Section IV concludes the paper.

2. RELATED WORK

In Kamran and Kamal (2016), some metaheuristic optimization algorithms was used to find the parameters of the Fuzzy-ART. These hybrid classification techniques were tested on a training dataset provided by the Wisconsin dataset for breast cancer. Results showed that the proposed harmony search (HS) algorithm provides better result with less time and less number of steps than genetic algorithm (GA) and particle swarm optimization (PSO) in the same conditions. As seen in this research, evolutionary HS algorithm had a higher convergence ability to obtain optimal solution too. The best performance obtained from this algorithm is 97.80% for accuracy and 98.92% for specificity.

Chandra *et. al.*, (2013), propose an automated method to identify the pectoral muscle in Medio-Lateral Oblique (MLO) view mammograms. The work used a histogram based 8-neighborhood connected component labelling method for breast region extraction and removal of pectoral muscle. The proposed method was evaluated using the mean values of accuracy and error. The comparative analysis with other methods that uses histogram thresholding and hybrid wavelet decomposition shows that the method identifies the breast region more accurately.

In Menglin *et. al.*, (2015), a scalable method for retrieval and diagnosis of mammographic masses was proposed. In the research, for a specific query mammographic region of interest (ROI), scale-invariant feature transform (SIFT) features were extracted and searched in a vocabulary tree, which stores all the quantized features of previously diagnosed mammographic ROIs. In addition, to fully exert the discriminative power of SIFT features, contextual information in the vocabulary tree was employed to refine the weights of tree nodes. The retrieved ROIs were then used to determine whether the query ROI contains a mass. The presented method has excellent scalability due to the low spatial-temporal cost of vocabulary tree. The experiments were conducted on a large dataset of 11,553 ROIs extracted from the digital database for screening mammography, which demonstrate the accuracy and scalability of their approach.

In Hiba, *et. al.*, (2016), a performance comparison between different machine learning algorithms: Support Vector Machine (SVM), Decision Tree (C4.5), Naive Bayes (NB) and k Nearest Neighbors (k-NN) on the Wisconsin Breast Cancer dataset was conducted using WEKA data mining tool. The work compared the efficiency and effectiveness of those algorithms in terms of accuracy, precision, sensitivity and specificity to find the best classification accuracy. Experimental results from the research shows that SVM gives the highest accuracy (97.13%) with lowest error rate.

Yunzhi *et. al.*, (2018) develop and evaluate a new hybrid deep learning based computer aided diagnostic (CAD) approach to predict likelihood of a breast lesion detected on mammogram being malignant. In the approach, a deep Convolution Neural Network (CNN) was firstly pre-trained using the ImageNet dataset and serve as a feature extractor. A pseudo-color Region of Interest (ROI) method was used to generate ROIs with RGB channels from the mammographic images as the input to the pre-trained deep network. The transferred CNN features from different layers of the CNN were then obtained and a linear support vector machine (SVM) was trained for the prediction task. A dataset involving 301 suspicious breast lesions were tested and using a leave-one-case-out validation method, the results demonstrated feasibility and potentially improved performance of applying a new hybrid deep learning approach to develop CAD scheme using a relatively small dataset of medical images.

In Younus and Mohammad (2017), the performance of three selected machine learning algorithms in terms of accuracy and sensitivity was carried out, the intent was to select the best classifier for the early diagnosis of the Breast Cancer. The whole experiment was simulated using the WEKA tool and a corresponding evaluation of the selected algorithms was done on Breast Cancer dataset. Out of the three algorithms, Random Forest had the best performance, having accuracy of 98% and sensitivity 99% followed by Logistic Regression, with accuracy of 96% and sensitivity 98% and finally, Naive Bayes with accuracy of 91% and sensitivity 94%.

Meraryslan, Meirambek and Kamalkhan (2017), carried out an experiment on 5 modeling algorithms with Greedy Search and K-fold Cross-validation. Algorithms that were considered are Neural Networks, Decision Tree Classifier, Logistic Regression, K-nearest Neighbour and Support Vector Machines. The work also used Greedy Search algorithm to test different parameters for the models, to measure the fitness and find the best model for the dataset. The obtained results of modeling show that the SVM and KNN algorithms were both suitable for breast cancer prediction.

Shravya, Pravalika and Subhani (2019) carried out an implementation of Logistic Regression, Support Vector Machine (SVM) and K Nearest Neighbor (KNN) models for breast cancer prediction. Experimental result from the research shows that SVM outperforms the other models considered in the predictive analysis with an accuracy of 92.7%.

3. METHODOLOGY

This research employed an experimental framework of the WEKA platform with a comparative approach for breast cancer classification. It uses an intuitive platform that will initiate the loading of dataset into the system, the selection of relevant features using the correlation feature filter approach to rank the features with high predictive power, the classification of the dataset with the Back Propagation neural network and the C4.5 decision tree classifier. The system performs comparative evaluation based on this two classifiers using relevant statistical measure

3.1 Dataset Acquisition

The database used in this research is the Wisconsin breast cancer database compiled in the University of Wisconsin by Dr. William H. Wolberg (UCI Machine Learning Repository). The dataset is publicly available at. The dataset used comprises of a total of 699 samples. The dataset features used as the predictor variables was provided to the network input layer which was classified as input and target. The variables/features for the classification are; Clump Thickness, Uniformity of Cell Size, Uniformity of Cell Shape, Marginal Adhesion, Single Epithelial Cell Size, Barei Nuclei, Bland Chomatin, Normal Nucleoli and Mitosis. The dataset was grouped into the following classes arbitrarily: (1 for benign, 2 for malignant).

3.2 Data Preprocessing and Feature Ranking

The dataset was preprocessed by scaling and normalization. The preprocessed data was further passed on for ranking to select attributes with high predictive ability with respect to the class label. The correlation feature selection was used to rank the breast cancer dataset features according to their predictive power. The correlation attribute evaluation was used to evaluate the worth of an attribute by measuring the Pearson's correlation between it and the class label, afterwards the ranked data is classified. The Pearson's correlation coefficient is obtained using Equation 1. Figure 1 shows the process flow of the prediction system. The features selected were further passed on to the BPNN classifier and also represented as rules for the C4.5 classifiers.

$$r = \frac{\sum_{i=0}^n xy - (\sum x)(\sum y)}{\sqrt{(n \sum x^2 - (\sum x)^2)}} \quad (1)$$

Where $n = \text{number of pair of score}$

$x = \text{feature1}$

$y = \text{feature2}$



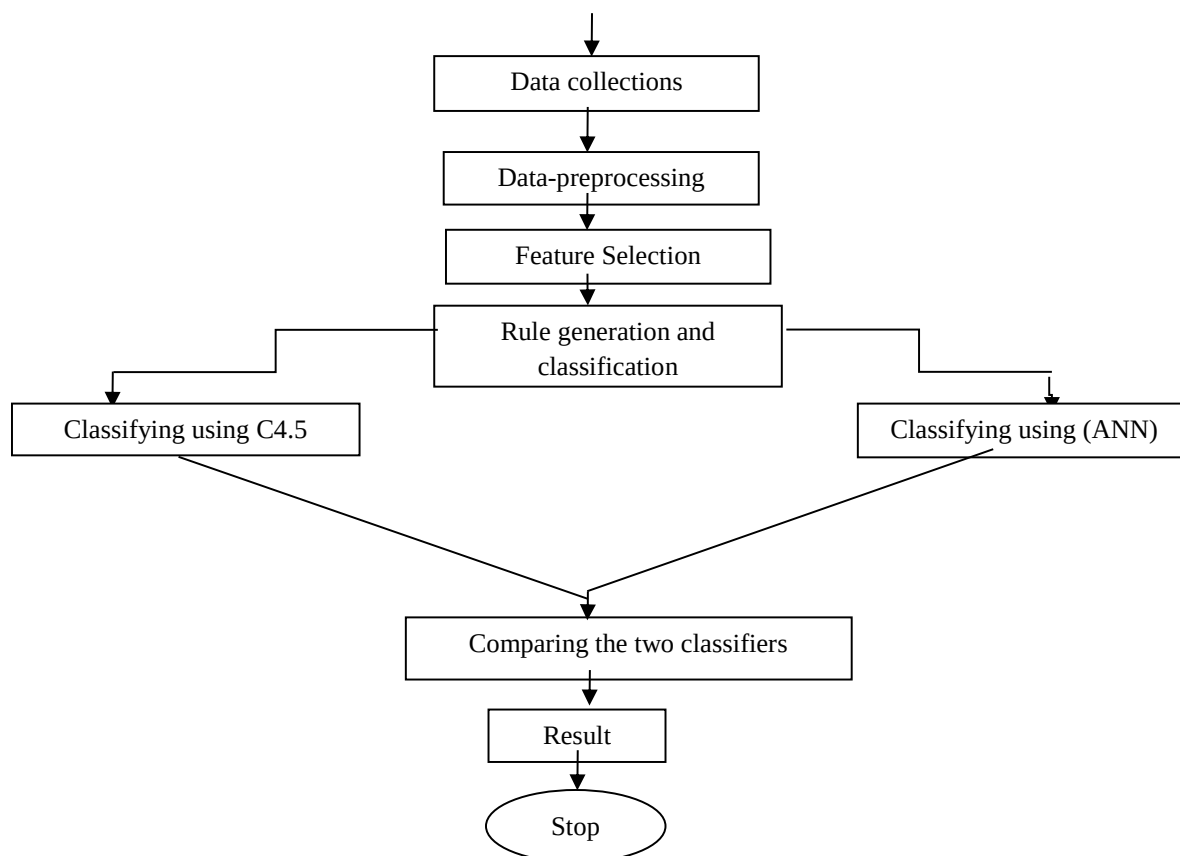


Figure 1: Process flow of the prediction model

The breast cancer dataset is loaded into the system via the open file action button. The result shown in Figure 2 highlights the dataset without normalization and filtering.

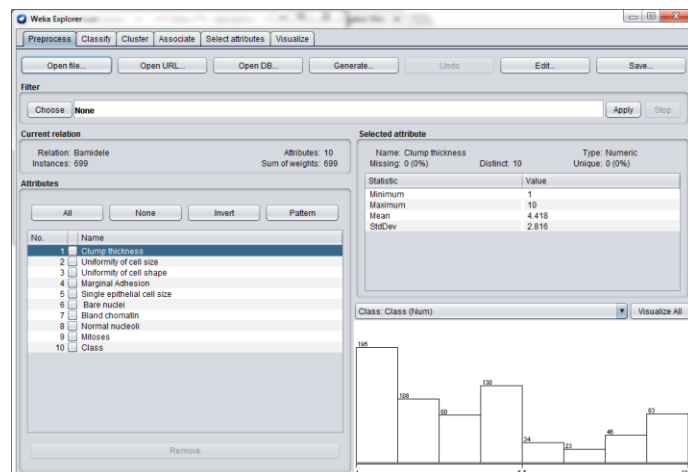


Figure 2: Loading of Dataset.

Figure 3 shows the outcome when the data was filtered by the unsupervised approach of converting the class variable from numeric to nominal using the “unsupervised numeric to nominal filter type” option in the WEKA simulator. The results of the correlation attribute evaluation which evaluates the worth of an attribute by measuring the correlation (Pearson’s) between the attribute and the class label is also shown in Table 1. It also reveals the strength of the selected attributes with their correlation factor. The Clump thickness and Bland chromatin was discarded from the further classification analysis due to their very low correlation factor.

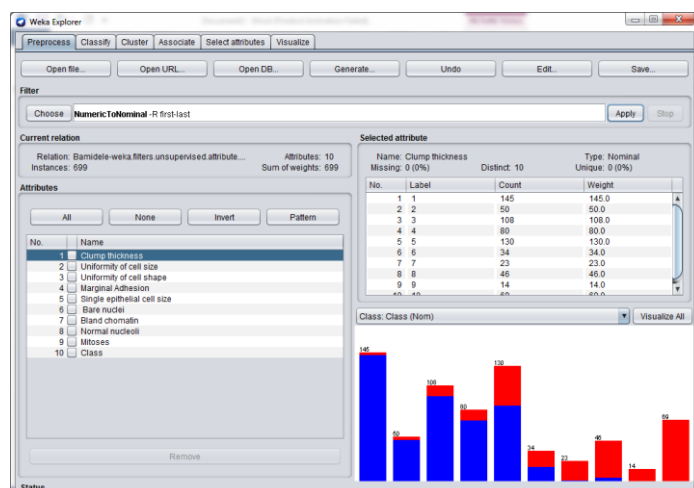


Figure 3: Filtered Class variable

Table 1: Ranked Features

No	Correlation Factor	Attributes
1	0.579	Bare nuclei
2	0.534	Uniformity of cell size
3	0.528	Normal nucleoli
4	0.473	Single epithelial cell size
5	0.473	Uniformity of cell shape
6	0.469	Mitoses
7	0.46	Marginal Adhesion
8	0.29	Bland chromatin
9	0.215	Clump thickness

Having carried out ranking and selection of highly correlated features, the selected features were loaded back into WEKA.

The performance of the BPNN and C4.5 was measured based on the common evaluation metrics which include classification accuracy, precision, recall, as well as statistical measure such as F-score (weighted harmonic mean of precision and recall), root means square error (RMSE), mean absolute error (MAE) and Kappa statistics (K), where;

$$precision = \frac{TP}{TP+FP} \quad (2)$$

$$recall = \frac{TP}{TP+FN} \quad (3)$$

$$F - score = 2 * \left(\frac{(precision \times recall)}{(precision + recall)} \right) \quad (4)$$

$$RMSE = \sqrt{\frac{\sum_{i=1}^N (predicted - actual)^2}{n}} \quad (5)$$

$$MAE = \frac{1}{n} \sum_{i=1}^N |xi - x \vee| \quad (6)$$

$$K = \frac{P_{observed} - P_{expectedchance}}{1 - P_{expectedchance}} \quad (7)$$

The results of the computation of the above metrics was obtained from the WEKA simulator

4. RESULTS AND DISCUSSION

Simulation result for BPNN and C4.5

The BPNN is the most widely used neural network for prediction purposes. The typical BPNN is shown in equation 8. The input data x_i is presented to the network through the input layer, which is then passed to the hidden layer along with the weights w_{ij} . The weighted output $x_i w_{ij}$ is then summed and added to a threshold θ_j to produce the neuron input I_j in the output layer as represented.

$$I_j = \sum_{i,j=1}^{i,j=n} w_{ij}x_i + \theta_j \quad (8)$$

The BPNN model was simulated, varying the NN parameters which include training cycle, number of neurons in input layer, hidden layer and output layer, learning rate, epoch and error tolerance. The variation was done in a bid to achieve maximum target value which is 100% hence trial and error approach was used, keeping some training parameters constant and gradually moving the other parameters over a wide range of values, as suggested in some preceding research.

On the other hand, C4.5 is widely used in Machine Learning due to its ease of understandability. It generates a decision tree from a set of training data using the concept of information entropy. As shown in Figure 4, at each node of the tree, C4.5 chooses the feature that most effectively splits its set of samples into subsets that are enriched in one class or the other. Therefore the attribute with the highest normalized information gain is chosen to make the decision, for X and C which are two random variables jointly distributed as shown in equation 9

$$H(X:C) = \sum_{i=1}^n P(C_i) \log_2 P(C_i) \quad (9)$$

The result analytics of the C4.5 classification obtained by the simulator is given in Figure 4

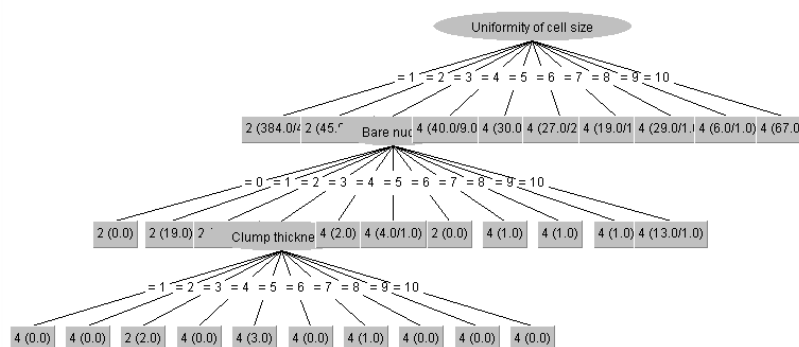


Figure 4: C4.5 Tree Viewer

Table.2 shows the summary of statistic of both the neural network classifier and C4.5 being compared. The results show that BPNN results in a classification accuracy of 90.9524%, with a training time of 46.9 seconds. While the C4.5 classifier has a classification accuracy of 94.2857% and training time of 0.16 seconds.

Table 2 Performance Comparison of result for BPNN and C4.5

Metrics	BPNN		C4.5	
Correctly Classified Instances	191	90.9524 %	198	94.2857 %
Incorrectly Classified Instances	19	9.0476 %	12	6.1905 %

Kappa statistic	0.8664		0.8756	
Mean absolute error	0.0542		0.0834	
Root mean squared error	0.2209		0.2234	
Total Number of Instances	210		210	
Training Time	46.9secs		0.16 secs	

This results shows that the C4.5 behaved generally well with low root mean square error of 0.2234, though slightly higher than that of back propagation neural networks with mean square error of 0.2209. The true positive rate, false positive rate, precision, f-score and the recall for both BPNN and C4.5 is shown in Table 3. These values were obtained from the WEKA simulator.

Table 3: Classification Results obtained for BPNN and C4.5

BPNN			C4.5	
CLASS			CLASS	
	1	2	1	2
TP Rate	0.934	0.946	0.949	0.932
FP Rate	0.054	0.066	0.068	0.051
Precision	0.969	0.886	0.963	0.908
Recall	0.934	0.932	0.949	0.946
F-Measure	0.951	0.915	0.956	0.920

The recall measures the proportion of positives that are correctly identified as such (e.g. the percentage of sick people who are correctly identified as having the condition). The C4.5 shows a higher rate of detection with recall measure for malignant cases than the BPNN.

5. CONCLUSION AND FUTURE WORK

This work presents a comparative classification case study for Breast Cancer by comparing the performance of two data mining algorithms; Back Propagation Neural Network (BPNN) and C4.5. The results shows that the C4.5 was slightly efficient in the knowledge retention rate as its classifier accuracy is higher than the BPNN, the C4.5 also gave a very low training time than the BPNN model. It can be deduced that the C4.5 model slightly outperformed the BPNN model, giving the empirical result in this study.

The system predicts cancer stage as belonging to class 1 as benign and class 2 as malignant using back propagation neural network algorithm and decision tree algorithm. The performance of the two algorithms was compared. Future direction in this regard is the experimentation of breast cancer prediction on a larger dataset, employing deepNets, an advance machine learning technique for empirical research.

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