ENSEMBLE CLASSIFIER FOR BREAST CANCER DETECTION

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ABSTRACT

The late discovery of breast cancer is the main reason for the low survival rate, so its early detection can lessen the risk and prevent progression, thus reducing mortality rates. Machine learning classification approaches play a significant role in predicting breast cancer in its early stages, which support the process of taking the appropriate treatment that leads to enhanced survival rates. However, selecting an adequate classifier, dataset and features are the keys to successfully improving prediction accuracy and performance. This paper has introduced an efficient ensemble classification model that is based on a stacking technique with feature selection method. The base classifiers of the proposed ensemble model are SVM, neural network, random forest, gradient boosting and KNN, while logistic regression is used as a meta classifier. An enhanced version of WBCD has been employed. WBCD is one of the most common datasets for breast cancer detection. A feature selection method has been applied and, accordingly, only 23 of the 30 features are selected. Only the features with a high influence on the prediction process are considered. Our proposed model shows a high accuracy rate that reached 98.4%. It outperforms the single classifiers and causes neglected classification errors. The proposed model has also been compared to some similar existing approaches and showed better performance.

Keywords: *Machine Learning, Deep learning, ensemble classification, stacking technique, Breast Cancer Detection.*

1. INTRODUCTION

Cancer may be treated and cured when early detection occurs; therefore, using artificial intelligence techniques has greatly contributed to the early detection of breast cancer which promotes survival rates. The late diagnosis may complicate the treatment process.

Cancer is a diverse set of diseases that attack many tissues and organs, causing their size to increase abnormally. The recent years have witnessed an increase in cancer incidence and mortality, which pose severe risks [1]. Cancer is considered the second leading cause of death worldwide. Breast cancer affects 2.1 million women each year and a large number of deaths among women are therefore reported; an estimated 627,000 women died from breast cancer in 2018 [2], so it is considered one of the most common types of cancers [3]. According to the World Health Organisation (WHO) [4] report of 2020, breast cancer is considered the leading type of cancer in terms of new cases reported, reaching 2.26 million cases; it is considered the fifth leading cause of death based on the reported number of deaths. Figures 1 and 2 show the number of newly diagnosed cases and reported deaths for the most common cancers in 2020.

Generally, the most common cancer among women is breast cancer and it is considered the second most common cancer worldwide [5]. Compared to other types of cancer, breast cancer has a high mortality rate [6]. It has been reported that early detection can improve the survival rate for small and large tumours to 98% and 73%, respectively [7]. Early detection provides the opportunity for patients to receive proper treatment [8] within an appropriate timeframe, so the success rate will therefore be increased. It is also important to help with informing subsequent treatments [9]. On the other hand, due to the absence of breast cancer symptoms in the early stages, early detection will not be an easy task [10]; therefore, this requires intensive analysis which is afforded through the use of artificial intelligence systems that are capable of

discovering unseen and tiny changes.

The manual detection of such diseases is a tedious matter that requires physicians with adequate experience; therefore, machine-based identification tools are urgently required to help with this matter.
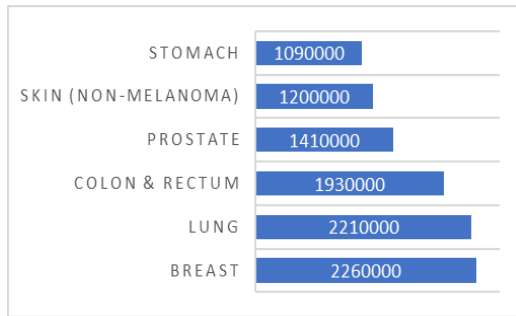

Figure 1: Number of new cases diagnosed of the most common cancers in 2020

Murtaza et.al. [11] reported that histopathological imaging (HI) is a commonly used technique for breast cancer detection compared to other technologies such as mammography, MRI, and computed tomography; however, the manual analysis of HI is time-consuming, cumbersome and requires skilled pathologists. Due to the above-mentioned limitations of HI analysis, Murtaza et al. indicated that computer-aided diagnostic systems can be considered as a second opinion for HI analysis [11].
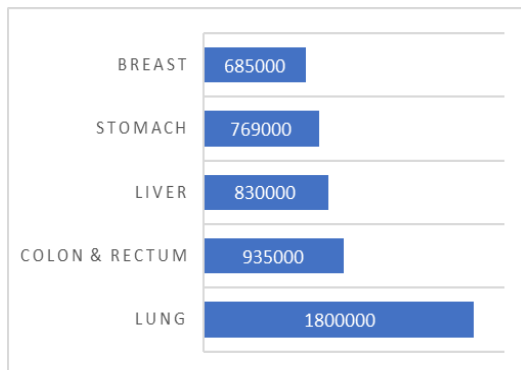

Figure 2: Number of deaths for the most common cancers in 2020

Computer-aided diagnosis (CAD) tools have shown their ability to aid physicians in diagnostic processes to detect breast cancer, especially in its early stages [12]. CAD systems are

developed as effective cost- and time-saving tools that offer highly accurate information [13]. This information leads to early detection, which can significantly reduce the mortality rate of breast cancer disease. Computer-aided diagnosis utilises machine learning (ML) models to detect whether a tumour is benign or malignant [14], and can help specialists to make swift decisions [15, 16]. Interested readers can find more information of different computer-based techniques and methods to extract information from text, images and other sources in [17, 18].

Machine learning techniques have shown their ability to define patterns in huge datasets of medical images that lead to successful classifications. However, choosing an appropriate classifier is crucial to obtain the accurate results that are required, especially in sensitive fields such as the medical and military fields, etc.

Breast cancer diagnosis is highly important as the patients' treatment and safety are directly affected by the classification results; therefore, high prediction accuracy, robustness and reliability are required, which represents a real challenge for researchers in the data mining field [19].

This paper introduces an ensemble classification model that is based on a stacking technique which combines the classifiers that are selected to construct this ensemble model. These classifiers have been selected carefully based on their reputation for reflecting good performance; they are commonly used in constructing ensemble classification models. The proposed ensemble model is expected to outperform single classification models and result in a high accuracy rate compared to the existing ensemble approaches that are based on a stacking technique. The proposed model is constructed based on a common and accurate dataset. The dataset is enhanced by applying chi-square feature selection approach. Both the original dataset and the enhanced dataset were used to train and test our model. Feature selection methods are the perfect tools to enhance datasets and promote both classification accuracy and computation time.

This section provides a brief introduction to breast cancer and addresses the rapid increase in breast cancer in recent years, especially among

women, highlighting the number of reported deaths. In addition, it sheds lights on the importance of the early detection of breast cancer which can perfectly improve the treatment process and reduce the mortality rate. Greater focus is paid to artificial intelligence techniques such as machine learning, which plays an important role in automating the classification process and providing accurate results that help physicians to identify and treat this dangerous disease in the early stages. The rest of the paper is constructed as follows: the next section discusses the relevant work that used machine learning techniques to predict breast cancer and describes the state of art technology in recently published research papers that use ensemble classification models which are expected to reflect more accurate results compared to single classification models. This motivates the authors to propose an ensemble classifier that is capable of bringing high accuracy compared to single classifiers. Section 3 illustrates the proposed ensemble classifier, while section 4 gives details on the performed experimental work, along with the associated results. It includes a thorough discussion and highlights the success of our proposed ensemble classifier to generate promising results for breast cancer detection. Subsequently, section 5 concludes the research work.

2. RELATED WORK

Every day, biological data are increasing so biologists are spending time exploring these data using various bioinformatics approaches. This flood of data is hard to manipulate manually, which is time-consuming, complex and may lead to misinterpretation; therefore, adequate analysis models are required to obtain reliable and accurate results. Machine learning techniques can meet these requirements if they are selected, implemented and validated properly. In the medical field, the misinterpretation is not accepted at all as it may lead to poor consequences; therefore, machine learning models which generate accurate results need to be presented to remove human errors in this field and enrich the diagnosis process by reflecting good performance.

Artificial intelligence contributes high performance in different fields of science. Machine learning becomes popular as it has the ability to cope with problems that are difficult to solve in conventional ways [20]. The use of machine learning models in the diagnostic process has witnessed a rapid increase. The most important issue in the diagnostic process is to have an adequate analysis of the medical data. Therefore, when this analysis is done concisely and perfectly, the results lead to proper treatment, which is the aim of any physician. Machine learning techniques can play this role by presenting accurate results, minimising errors and saving time.

On the other hand, deep learning approaches have the ability to overcome the obstacles of feature-based models and can therefore provide effective alternatives to conventional classification models [21].

Various studies feature the need to combine classification models together instead of utilising a single model. The ensemble models are expected to achieve good performance compared to single classification approaches [22]. However, the adequate selection and construction of ensemble models are important to improve the classification accuracy.

This section reviews relevant work on ensemble classification approaches while subsection A sheds light on the classifiers that are selected to form our proposed model.

The authors in [23] presented an ensemble classification model based on the stacking technique which reached an accuracy of 97.20% to detect breast cancer. They utilised the Wisconsin Diagnostic Breast Cancer (WDBC) dataset and only the top 20 features were used. The top features were selected utilising the univariate feature selection method. Their ensemble classification approach is based on combining three classifiers: support vector machine, random forest and K-nearest neighbour. Their proposed model has achieved high accuracy compared to other classifiers being investigated in their work.

Samieinasab et.al. [24] indicated that there are some gaps concerning research in breast cancer detection, including the fact that not much attention is paid to feature engineering, which increases the chance of overfitting problems and the time required for the training phase. They proposed a stacking approach in which three approaches were combined, including voting, boosting and bagging. The extra trees algorithm is used for feature selection. Their proposed approach reached an accuracy rate of 98%.

The authors in [25] proposed a heterogeneous ensemble classification approach for breast cancer detection. They used a stacking technique to build the ensemble approach which included three classifiers: KNN, SVM and DT. It achieved an accuracy of 78%.

Khuriwal et.al. [26] proposed an ensemble classification approach that is based on a voting technique. They used two classifiers: neural network and logistic regression. After applying the univariate feature selection method to the WDBC dataset, 16 features were selected for use. Their proposed approach achieved an accuracy rate of 98.5% to detect breast cancer. However, the ensemble approach was constructed using a voting approach.

The authors in [27] proposed an ensemble learning model (XGBoot classier) that accumulates the predictions of three classifiers (SVM, KNN and Logistic Regression). The dataset being used in this study were the WBCD. By applying Kendall's feature selection method, four features with lower significance were dropped, so only 26 features of the WBCD dataset were considered in their model. The model achieved an accuracy of 98.25%.

Kwon et.al [28] constructed a stacking ensemble approach that utilised four prediction models: deep neural network, distributed random forest, generalised linear model and gradient boosting machine. Each model was used as a meta-learner to aggregate the four models to form the stack classifier. Their results showed that a better prediction is achieved when using GLM as a meta learner. The accuracy reached was 97.37%.

The authors in [9] proposed a nested ensemble detection approach based on two techniques, voting and stacking, to detect breast cancer. Their experiments were conducted on the WDBC while the K-fold cross validation method was used for approach evaluation. Their approach achieved a detection accuracy of 98.07%.

Janghel et.al. [29] investigated the accuracy of 13 machine learning approaches using the WBCD dataset; their results show that three machine learning approaches have outperformed others by achieving an accuracy of 98%.

2.1 The Model Classifiers

This subsection sheds lights on the classifiers that are selected to form our proposed model: SVM, KNN, neural network, gradient boosting and random forest as the base classifiers while logistic regression was used as a meta classifier.

SVMs are extensively adopted to construct ensemble classification approaches and have many advantages (e.g., avoiding overfitting, fit to use with high dimensional data, etc.) [24] and are widely used for breast cancer detection [30]. The frequently used classification models to construct ensemble classification approaches includes SWMs, trees, and artificial neural networks [31]. It has been reported that support vector machine classification models have superior accurate diagnosis ability [32]. SVMs reflect the performance in medical diagnosis applications well and perform better in cases where relatively small training datasets are used. Moreover, SVMs have shown good performance with high dimensional data [33].

ANNs have the ability to deal with noisy data and classify untrained data patterns [34]; therefore, they are fit to use with complex datasets. ANN becomes a useful classifier for breast cancer classification [30]. Moreover, Alshayeji et al. indicate that ANN is one of the most commonly used classifiers to predict breast cancer using WBCD [13].

The authors in [35] have reported that artificial neural network and logistic regression are the two classifiers that are most commonly used in the estimation of clinical risk. When statistical inferences need to be drawn from outputs, LG is recommended, while ANN is suitable when the data involve implicit interactions and complex relationships. Both ANN and LR can be used to work together to assist in the decision-making process [35]. The efficiency of LR to draw statistical inferences from outputs is one of the reasons that motivated us to use this classifier as a meta classifier in our developed ensemble approach.

Kathija et.al indicated that the MLP classifier (neural network classifier) has achieved a better accuracy and performance. They recommend using this classifier for breast cancer prediction [36].

Random forest is an ensemble classification model that is capable of working proficiently with large databases. It is a combination of tree classifiers [37].

The authors in [38] presented a classification mode based on random forest which achieved promising results to detect breast cancer. It showed a high classification accuracy.

KNN is widely used for classification [27] and has been incorporated with other classifiers to form ensemble approaches in many studies [25, 39, 40].

The gradient boosting (GB) classifier is an ensemble tree-based method which uses the gradient descent principle [24]. Decision tree-based algorithms are known to produce excellent classification performances [27].

Based on this state-of-art review which includes recent research on some ensemble classification models with more focus on ones that are based on stacking technique, the author has selected five classifiers to work with as the base classifiers of our proposed model and one classifier to work with as a meta classifier that aggregates the outputs of the base classifiers in order to form the proposed ensemble classification model.

3. METHOD

This work proposes an ensemble classifier model. The base classifiers of the proposed model have been selected carefully and based on their good reputation; the previous section reflects this claim. These classifiers include SVM, neural network, random forest, gradient boosting and KNN. Logistic regression has shown its ability to effectively draw statistical inferences from outputs and has been used in many studies as a meta classifier to aggregate the outputs of the base classifiers. Therefore, the author has been motivated to select the logistic regression model to act as a meta classifier for our proposed ensemble model.

3.1 Dataset

This The dataset employed by this paper is the Wisconsin Breast Cancer dataset (WBCD) dataset which is publicly available via the UCI Machine Learning Repository [41]. It is one of the most commonly used datasets to train and test classification models in the prediction of breast cancer. This dataset was selected due to its reputation as one of the most commonly used datasets for ensemble classifiers [31]. It consists of 30 features and 569 instances, including malignant and benign instances. An enhanced version of this dataset is also being used to construct our proposed model. The enhanced version has been developed by applying a feature selection method to select the weighted features that have a high impact in the prediction process and neglect the others. Accordingly, 23 features were selected and the other 7 features with low influence were dropped. Both datasets, the original and the enhanced one, are split into two parts: 80% for training and 20% for testing. Then, the classifiers were trained, tested and evaluated. Accordingly, the drawn results are analysed and reported.

3.2 The Chi-square Feature Selection Method:

Applying the feature selection method has a significant impact on classification performance. Lessening the number of features by considering only those have high influence in the classification process and ignoring others that are redundant or have low impact will greatly promote the accuracy rate and decrease the computation time. Both aspects have positive impact to the performance of the classifiers.

The feature selection method that has been used in this study is the chi-square feature selection method, which measures the dependence between the class and the given feature. It aims to pick the features that are highly dependent on the response. The feature scores have been computed, and 23 features with high scores have been selected. A feature with a high chi-square value (score) means that this feature is more dependent on the response and will therefore be selected to train the proposed model.

3.3 Validation:

Many validation methods are being used in this study in order to reflect trusted, reliable and accurate findings. The random sampling validation method has been applied and repeated many times for greater validation. The performance of the proposed classifier is evaluated by computing the accuracy formula shown in equation 1, while the confusing matrix (error matrix) is utilised to calculate the classifier errors, such as false negatives and positives. False negative (FN) indicates the number of malignant cases that are classified as benign while false positive (FP) indicates the number of benign cases that are classified as malignant. A classifier with a lower

FN reflects a better performance. In addition, other methods for validation such as pression and recall are also computed and then the ROC curves are presented.

$$Accuracy = \frac{(TP + TN)}{(TP + TN + FP + FN)} \quad (1)$$

Where:

True positives (TP): Number of malignant cases that are classified as malignant.

True negatives (TN): Number of benign cases that are classified as benign.

False positives (FP): Number of benign cases that are classified as malignant.

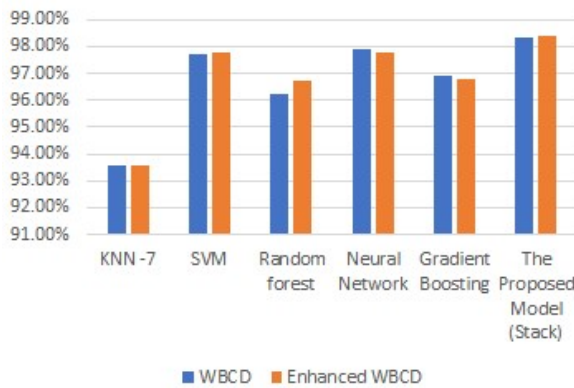False negatives (FN): Number of malignant cases that are classified as benign.

Figure 3: Classifiers Accuracy over the Two Datasets

4. RESULTS AND DISCUSSIONS

Ensemble classification approaches are expected to achieve better accuracy compared to single classification approaches. There are many techniques to construct ensemble approaches such as stacking, boosting bagging, etc. This paper has proposed, built and validated a new ensemble model based on a stacking technique in which five classifiers are selected to form the base classifiers of the model and LR has been employed as a meta classifier for the purpose of aggregating the outputs of base classifiers and generating classification prediction results of our ensemble models. Based on two different datasets (WBCD, the enhanced version of WBCD after applying feature selection), all classifiers have been trained and tested. In total, 80% of both datasets have been used to train the

classifiers and 20% for testing. The random sampling validation method was applied and repeated twenty times for all conducted experimental work to ensure the validity of the results. All experiments were performed using orange software which is an effective data mining tool that helps to construct machine learning classification models. Then, the classification accuracy, presession, recall and error matrix were computed to examine the performance of the proposed model.

Table 1-A: Classifiers Accuracy with Dataset of 30 Features (WBCD)

Classifiers	The original dataset (30 features)		
	Accuracy	Precision	recall
KNN -7	93.60%	93.70%	93.60%
SVM	97.70%	97.70%	97.70%
Random forest	96.20%	96.20%	96.20%
Neural network	97.90%	97.80%	97.90%
Gradient Boosting	96.90%	96.90%	96.90%
The Proposed model (Stack)	98.30%	98.30%	98.30%

Table 1-B: Classifiers Accuracy with Dataset of 23 Features (Enhanced WBCD)

Classifiers	The enhanced dataset (23 features)		
	Accuracy	Precision	recall
KNN -7	93.60%	93.70%	93.60%
SVM	97.80%	97.80%	97.80%
Random forest	96.70%	96.70%	96.70%
Neural network	97.80%	97.80%	97.80%
Gradient Boosting	96.80%	96.80%	96.80%
The Proposed model (Stack)	98.40%	98.40%	98.40%

Table 2: The Accuracy of the Proposed Classifier Compared to Some Similar Existing Approaches

Approach	Accuracy
Meta-Health Stack [24], 2022	98%
Ensemble based stacking technique [23], 2020	97.20%
Hybrid Ensemble [27], 2021	98.25
stacking ensemble approach [28], 2019	97.37%.
Our proposed ensemble classifier	**98.40%**

The results for all classifiers including our proposed model are shown in Table 1, which includes the accuracy, precision and recall. Our

proposed model outperformed all single classifiers, both when applying the original dataset and the enhanced dataset. It achieved the highest accuracy compared to the single classification approaches. When applying the enhanced dataset, our proposed model achieved better accuracy than when using the original dataset. This shows that our enhanced dataset has improved the classification accuracy of the proposed model. It achieved an accuracy of 98.40%, which is considered a promising result, even when compared with most of the existing ensemble classification models based on a similar technique (stacking approach). Table 2 shows the accuracy of the proposed ensemble model compared to the accuracy of some existing models, while Figure 3 showed the accuracy of our proposed ensemble model compared to the accuracy of other single classifiers in graph format

In terms of classification errors, the error matrix (confusion matrix) has been computed for all classifiers (single classification models and our prosed ensemble model). Table 3 shows the error caused by each classifier in terms of false positive and false negative errors. It can be clearly seen that our proposed model is performing well in terms of errors. This supports our findings that the proposed model has outperformed other single classification models using both datasets.

Table 3: Classification Errors

	23 Features		30 Features	
	FN	FP	FP	FN
SVM	0.034038	0.014706	0.01331	0.038732
RF	0.058685	0.018207	0.02171	0.064554
NN	0.03169	0.016106	0.01261	0.036385
GB	0.056338	0.016807	0.01541	0.057512
KNN	0.126761	0.026611	0.02661	0.126761
The proposed model	**0.032864**	0.005602	0.0077	0.032864

The Receiver Operating Characteristic (ROC) curve as a graphical presentation of our findings is presented in Figures 4 to 7. Figures 4 and 5 showed the ROC curves of our proposed ensemble classifier when constructed based on the original dataset and enhanced dataset, respectively. They reflected a good performance in both cases while the performance is better in cases using the enhanced dataset. Figures 6 and 7 showed the ROC curves of all classifiers together when using the original dataset and enhanced dataset, respectively.

Regarding sensitivity and specificity, the ROC curves show that the proposed ensemble classifier performs better compared to the other single classifiers.
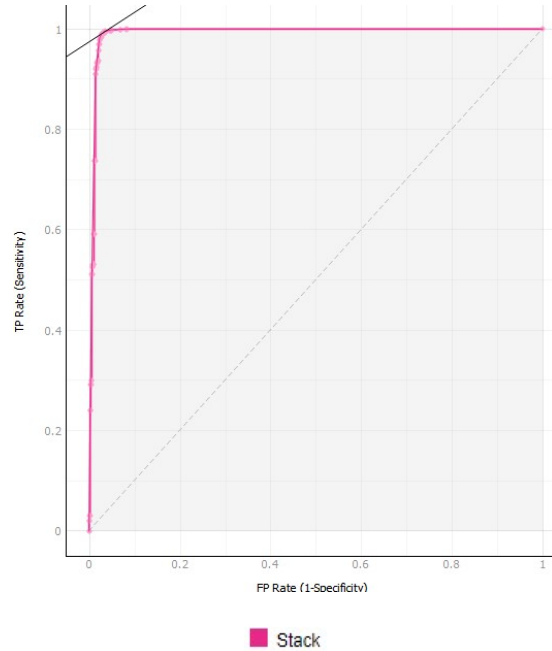

Figure 4: ROC curve our proposed mode (Original Dataset)
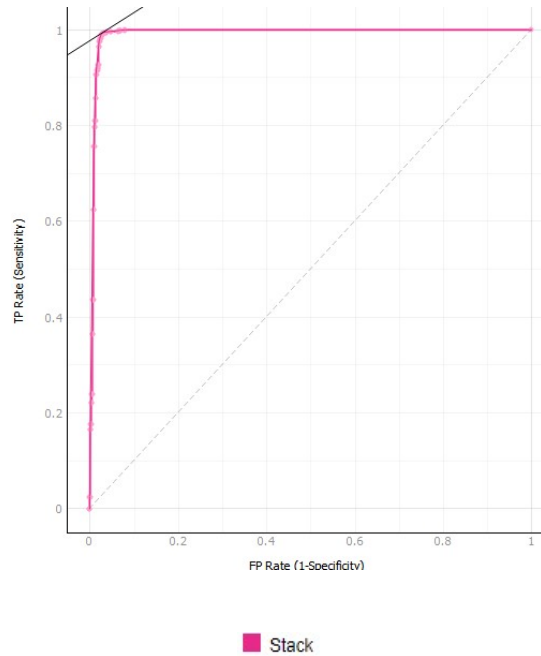

Figure 5: ROC curve our proposed mode (Enhanced Dataset)

All of these findings ensured that our proposed model is capable of achieving high

accuracy and neglected classification errors.

Figure 6: ROC curve for all classifiers (Original Dataset)
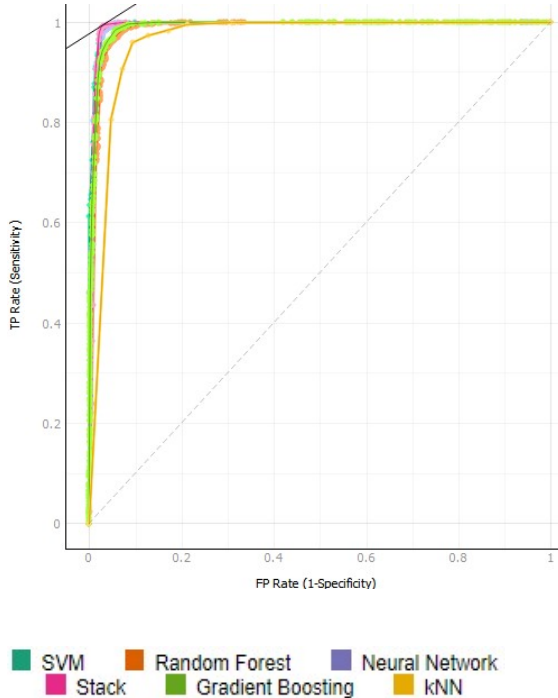
Figure 7: ROC curve for all classifiers (Enhanced Dataset

5. CONCLUSION

The incidence of breast cancer is obviously increased. The cause of this increase is not fully identified and a technique to thwart its occurrence has not yet been introduced. Therefore, its early detection is highly important to facilitate early treatment, which can lessen the risk. This paper has proposed a multi-classification model based on stacking techniques to detect breast cancer. The results indicate that the proposed model has achieved a considerable accuracy of 98.4%. It outperformed all other single classification methods and caused unweighted classification errors. In addition, the proposed classifier has outperformed most of the existing ensemble models. Therefore, this research paper reflects the usefulness of multiclassification approaches to detect breast cancer. The chi-square feature selection method has enhanced the employed dataset and thus the model's accuracy and performance have been improved. In addition, the paper has compared and evaluated different classification models.
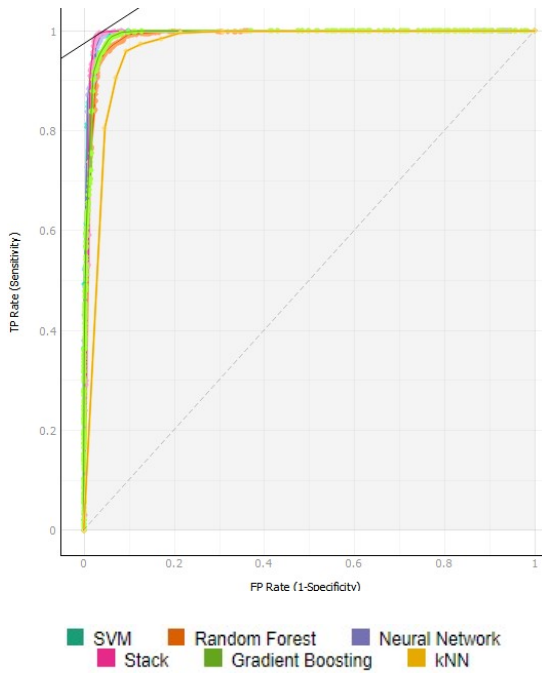
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