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The Empowerment of Industry 4.0
for Healthcare and Welfare Improvement

October 23rd-24th 2019

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Performance Evaluation of Ensembles Algorithms in Prediction of Breast Cancer

Gilbert Gutabaga Hungilo
Magister Teknik Informatika
Universitas Atma Jaya Yogyakarta
Yogyakarta, Indonesia
gutabagaonline@gmail.com

Gahizi Emmanuel
Magister Teknik Informatika
Universitas Atma Jaya Yogyakarta
Yogyakarta, Indonesia
thegammy2008@gmail.com

Andi W.R. Emanuel
Magister Teknik Informatika
Universitas Atma Jaya Yogyakarta
Yogyakarta, Indonesia
andi.emanuel@uajy.ac.id

***Abstract*—Breast Cancer is the most dominant cause of mortality in women. Early diagnosis and treatment of the disease can stop the spreading of cancer in the breast. Due to this nature of the problem, accurate prediction is the most important measure of the predictive model. This paper proposes the comparison of ensemble learning techniques in predicting breast cancer. Ensemble learning is widely used for performance improvement of the predictive task. The ensembles algorithms used in this research study are AdaBoost, Random Forest, and XGBoost with data from Wisconsin hospitals. The result indicates that the random forest is the best predictive model for this dataset. The model has the following performance measure, accuracy 97%, sensitivity 96%, and specificity 96%. The experiment is executed using scikit-learn machine learning library. With this high level of accuracy offered by the model, the model can help the doctor to identify whether the patient has malignant or benign tumor cancer cells with high precision.**

Keywords*—Predictive Model; Breast Cancer; Ensemble Learning; Machine Learning.*

I. INTRODUCTION

Cancer has become the top second cause of mortality rate worldwide and is accountable for 9.6 million mortality in 2018. Global trends and patterns continue to show that there is an estimate of 11.6% diagnosed cases of breast cancer and breast cancer is shown to be the second dominant type of cancer which causes deaths to 627,000 people worldwide [1,2]. In Indonesia itself, breast cancer has 40.3% incidence rate and causes deaths by 16.6% out of 100,000 people [3, 4]. Changing lifestyle is important to prevent breast cancer. The factor that influences the risk of breast cancer in women is the lack of diet and exercise also high consumption of alcohol and smoking. Breast cancer is estimated to increase by 2% in the year 2030 [5].

The economic burden of breast cancer Worldwide in 2009 was estimated to be $ 24 billion [6]. While in Indonesia, breast cancer economic output loss of $0.70 trillion was estimated from the GDP for the year 2010 – 2030 [7]. This burden will continue to increase due to the lifestyle changes of the people. The survey done in Indonesia shows poor awareness of breast cancer risk among women [8]. This problem leads to cancer be diagnosed in the advanced stages. The early-stage detection of breast tumors and start of the screening can reduce the mortality caused by breast cancer [9, 10].

Machine learning becomes very useful and accurately used in the identification of breast cancer. Data mining and big data analytics can be used to help the doctor to make a smart decision regarding the health of the patients by using previous medical data of other patients with a similar problem [11]. This paper aims to create the machine learning model which can help doctors in making decisions on whether a patient has a benign or malignant tumor. The model helps patients to receive early diagnosis and treatment before cancer starts to spread in the breast. Since the study involves prediction of health-related issue, accuracy of prediction is the most important performance measure. To ensure better performance the study uses ensemble learning algorithms that use bagging and boost. Based on previous research which used ensemble learning, the results show that the algorithm tends to give a high level of accuracy [12, 13]. Ensemble learning combines weak learners to make one strong learner. The study used data from the University of Wisconsin hospitals.

Paper organization: part number 1 introduces the study, part number 2 describes works which relate with this study, part number 3 describes in detail the source of data, methods, and algorithm used in this research. While part number 4 describes results and discussion from the study and the last part number 5 presents conclusions of this study.

II. RELATED WORK

Several researchers have used machine learning in creating a predictive model in health sector which helps to save the lives of the patients. For the case of breast cancer, some studies have been conducted to create a machine learning model that will accurately classify patients with a benign or malignant tumor. The work is done by Hongya Lu *et al.* [13] which creates incremental learning model for breast cancer survivability forecast using dynamic gradients boosting machine learning algorithm. This approach increases real-time prognosis accuracy and reduces redundancy during retraining of new data received.

Other researchers tend to compare machine-learning algorithm to check which one has good performance on the classification of breast cancer. Haifeng wang *et al.* [14] compared four machine learning algorithms which are artificial neural network classifier, support vector machine classifier, Naïve Bayers and AdaBoost tree using 10 fold rotation estimation method. The same method was used by Hiba Asri [15], Meriem Amrene [16] and Vikas Chaurasi [17]. The parameter used to select the best model is Accuracy, Specificity, Sensitivity, Precision, and AUC.

Breast cancer can be detected and classified by using image data. An example can be taken from the study by Zobia Suhail [18] which used a mammogram image to classify three states of breast cancer namely normal, abnormal and breast cancer. The machine learning model is created after features have been extracted from image data and use fisher linear discriminant analysis (LDA) together with a support vector machine classifier. The average accuracy of the two models is 96%.

This research study is doing a comparative analysis of the performance of three ensemble learning algorithms on the predictions of tumor cancer cells in the breast. Ensemble learning is a technique in which weak classifiers are combined to form strong classifiers using bagging, boosting and stacking. The approach aims to reduce variance, noise, and bias of the single model. This technique increases the stability and generalization power of machine learning model [19]. The ensembles learning algorithms used in this study are Ada boosting, XGBoost and random forests. These algorithms were selected because they win in most machine learning compitations and hackathons.Top machine learning compitations are Kaggle, DriveData, CrowdAnalytix, and Innocentive. To select best machine learning model for this study we are going to calculate/obtaining the following performance measures namely classification accuracy, logarithmic loss, area under ROC curve, confusion matrix, and classification report.

III. MATERIALS AND METHOD

This section is going to describe in detail the source of data, methodology, and machine learning algorithms used in this study implementation.

A. Materials

The data was downloaded from the website of UCI Machine Learning Repository [20], and the source of this data is from the University of Wisconsin hospitals. The dataset consists of 699 patients' record with 11 attributes as shown in the table number 1 below

Table 1: Shows the features in the dataset

No	Features Name	Value Type
1.	Sample code number	Id number
2.	Clump Thickness	1-10
3.	Uniformity of cell size	1-10
4.	Uniformity of Cell Shape	1 - 10
5.	Marginal Adhesion	1 -10
6.	Single Epithelial Cell Size	1 -10
7.	Bare Nuclei	1 - 10
8.	Bland Chromatin	1 - 10
9.	Normal Nucleoli	1 - 10
10	Mitoses	1 - 10
11	Class	2 for benign, 4 for malignant

From the table row, number one shows the sample code number which acts like id number of the sample. For row number two up to row number 10 shows attributes of the information in integer starting from 1 to 10 scale interval which represents shape, size and thickness attributes of the cell. Row number eleven shows the class attribute with number 2 shows the benign tumors cells, and number 4 shows the malignant tumors.

B. Method

To gain insight from data and create a machine learning model, the study uses the **CRISP-DM** methodology. The acronym **CRISP-DM** stands for **Cross-Industry Standard Process for Data Mining** [21, 22]. Data mining is a leading technology in health care predictive analytics and is mostly used with machine learning. The CRISP-DM offers a structured way of planning data mining project execution. The methodology of CRISP-DM involves six stages as shown in figure number 1 below.

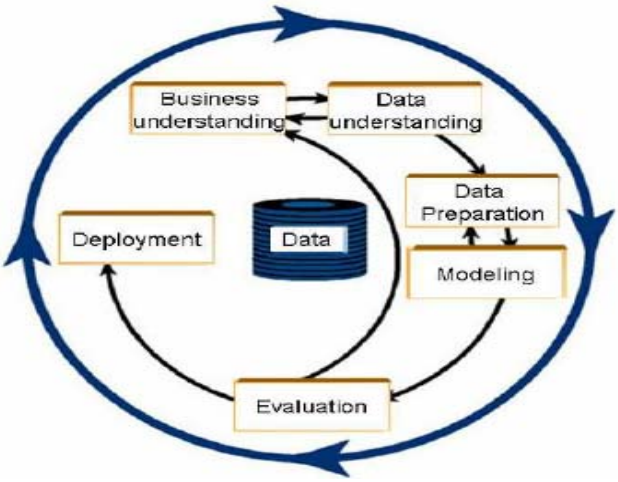

Figure 1: Shows the stages of CRISP-DM

The six stages shown in figure 1 above are Business understanding, Data understanding, Data preparation, modeling, evaluation, and deployment. The detailed explanation of what is happening at each stage is described in the sections below.

1) Business Understanding

At this stage of CRISP-DM, the main aim of this stage is to understand the business objective of conducting a data mining project. For the case of this study, the aim is to create the machine learning model for predicting the presence of a benign or malignant tumor on the patient's breast. The prediction is based on the patient's medical records and previous medical records of other patients. The predictive model helps the patients to know the health status of the breast in order to receive an early diagnosis to prevent the tumor from spreading in the breast.

2) Data Understanding

The second stage involves data collection and explanatory data analysis. This is the most important part of a machine learning model in which building it, takes around 92% of project time. In this project we use Pandas Python library to get insight from the data. The summary of insight gained from the data are:

- The dataset consists of 699 instances.
- Several features nine plus one class = 10.
- The dataset has missing values.

- The distribution of the class is 66% benign and 34% malignant class.
- Dataset has imbalance class distribution.

In this study, we didn't deal with imbalance distribution of the class variable because ensemble classifiers are more effective in dealing with imbalance dataset classification and enhance the performance [23].

3) Data Preparation

This phase involves the process of cleaning, transforming and normalizing the data before being used in the model creation process. In this study, we clean the data by replacing the misspelling value of the bare_nuclei column to -99999 value because most of machine learning algorithms understand it as the outlier. Then changing the data type of bare_nuclei to a numeric value. According to the description of the dataset, every column value is an integer. Finally is removing the sample code number column because it is just used to identify the sample and has no contribution to machine learning model creation process.

4) Modeling

This phase is a model creation stage. In this study, the model created uses Ensemble learning algorithm which uses bagging [24] random forest and the other uses boosting [25]. AdaBoost, XGBoost, and Gradients Boosting are created using a decision tree as the estimators. Bagging use bootstrapping sampling technique to create sub-dataset from the main dataset then creates a model on each sub-dataset. The final model is obtained by the aggregation of the predictions from all models [26, 27]. This method reduces variance.

Boosting operates in a sequential way in which each sub-model created from sub-dataset tries to correct the error of the preceding model and the overall final model result is obtained by calculating the weighted mean of all weak learner models [28, 29]. This approach reduces bias and also variance.

5) Evaluation

The main aim of this research study is to compare the performance of ensemble learning models for predicting Breast cancer. To evaluate the performance of each machine learning model, the study calculates accuracy, sensitivity, specificity, precision, recall, and F1 – score. That measure was used to compare performance and get the best model

6) Deployment

This phase is the last stage of the development process, in which the model is created using scikit-learn machine learning library on anaconda distribution. The main task at this stage is to plan on how to do deployment, monitoring, and maintenance plan. Then produces the report which describes and reviews the work done.

C. Algorithm Used

The detailed explanation of the algorithms used in this study is described here.

I. Random Forest

Random Forest uses the bagging technique to combine the weak learner model. The base estimators used in this study are decision trees. It starts with bootstrapping the dataset, then each sub-dataset created is used to create decision tree models, and the final prediction results are an average of the prediction from all decision trees for regression problems. But for the classification problems predicted class is obtained by taking majority vote from each sub model created. This approach is good in avoiding overfitting of the model because it selects data point and feature in random [30]. Random Forest is simple, faster, and easy; also it has internal approximations of error, strength correlation and variable significance [31]. Figure 2 below shows a random forest flow.

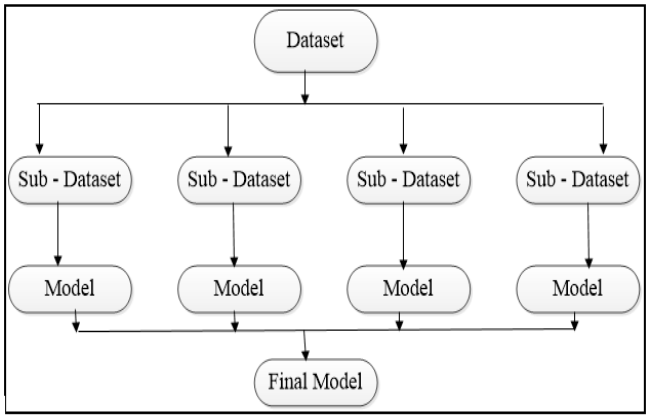

Figure 2. Shows the flow of the Random Forest

From the figure 2 above shows that Dataset is bootstrapped into sub dataset, then the decision tree classifier is created on those sub – dataset. Final model is obtained by averaging the sub model created.

II. AdaBoost

This algorithm is proposed by Freund and Shapire [32, 33] and is deeply explained by Hastie et al [34]. According to those studies, Ada boosting works as follow; multiple sequential models are formed, each trying to fix the errors made from the previous model by assigning high weights to the observations which are incorrectly predicted. The preceding model works to predict these values appropriately. The adaptive AdaBoost algorithm is described below by adapted pseudocode from the study by Haifeng Wang *et al* [14].

Initialize: $D_1(i) = \frac{1}{m}\ for\ i = 1, \ldots\ldots, m$

For $t = 1, \ldots\ldots, T$

Train decision tree using distribution D_t

Select h_t to minimize the weighted error $\epsilon_t = P(h_t(x_i \neq y_i))$

Choose $\propto_t = \frac{1}{2} \ln\left(\frac{1-\epsilon_t}{\epsilon_t}\right)$

Update for $i = 1, \ldots\ldots, m$

$$D_{t+1}(i) = \frac{D_t(i)}{Z_t}\begin{cases} e^{-\propto_t} if\ h_t(x_i) = y_i \\ e^{\propto_t} if\ h_t(x_i) \neq y_i \end{cases}$$

$$= \frac{D_t(i)\exp(-\propto_t y_i h_t(x_i))}{Z_t} \begin{cases} e^{-\propto_t} \; if \; h_t(x_i) = y_i \\ e^{\propto_t} \; if \; h_t(x_i) \neq y_i \end{cases}$$

Get final classifier

$$H(x) = sign\left(\sum_{t=1}^{T} \propto_t h_t(x)\right)$$

From the pseudocode above $D_t(i)$ show the distribution of i^{th} instance on t^{th} iterations, while h_t is the weak base classifier,ε_t is weighted error calculated from classification result, and α_t is an important factor.

III. XGBoost

XGBoost is an algorithm which uses gradients boost approach on decision tree-based ensemble learning. The XGBoost is an acronym for extreme gradient boosting. XGBoost is faster and has high predictive power. That is why it is mostly used in machine learning competitions [35]. The approach uses a variety of regularization techniques to reduce overfitting, and it operates in parallel to speed up tree contraction process and reduce lookup time. The main competitive characteristics of this machine learning algorithm are its portability, flexibility, and efficiency

IV. RESULT AND DISCUSSION

After following each step of CRISP-DM methodology, the data preprocessing stage goes by replacing the mistyped value on the bare_nuclei column by putting -9999 because most of the algorithms take it as the outlier. Then we examine the data visually to check the distribution of the data; most of the features were normally distributed and correlated with the class variable. The final data preparation was to map class 2 which denotes benign cancer with 0 and 4 which denotes malignant with 1. The following classification metrics classification accuracy, logarithmic loss, area under ROC curve, confusion matrix, and classification report were used to evaluate effectiveness and efficiency of algorithm on breast cancer dataset.

The experiment was carried out using two statistical techniques for estimation of performance. 10 – Fold cross-validation on all dataset to estimate cross-validation accuracy, logarithmic loss, and area under ROC curve. Meanwhile, train test split with 20% test size and 33% of test size to estimate test accuracy, confusion matrix, and classification report. Using scikit-learn machine learning library, we manage to create three classifiers which are AdaBoost Classifier (ADB), Random Forest Classifier (RF) and XGBoost Classifier (XGB). All algorithms were based on the decision tree classifier, so, no data standardization used because the decision tree is less sensitive to data distribution. All the classifiers were having the same setup number of estimator 500, random state 1, learning rate 0.1 and maximum depth 4.

After the successful building of all classifiers, we managed to measure the effectiveness of the classifier by looking at test accuracy (TA), collect classified instance (CC) and misclassified instance (MC) from train test split with 20% and 33% of test size (TZ). Also, the classification accuracy (VA) was checked on 10 fold cross-validation. Since classification accuracy presents several correctly classified instances made from ratio of all predictions made, so, in all the cases above, the one with high accuracy presents the best classifier. While from confusion matrix we were able to get number of correctly classified instances and misclassified instance. The result is presented in table 2 below.

Table 2: show Classifier Performance

	TZ	TA	VA	CC	MC
ADB	0.20	0.96	0.95	135	5
	0.33	0.95	0.95	220	11
XGB	0.20	0.95	0.96	133	7
	0.33	0.95	0.96	219	12
RF	0.20	0.96	0.97	134	6
	0.33	0.96	0.97	221	10

From the result, the table above shows that Random forest was having high classification accuracy of 97% on 10 – fold cross-validation setup but same accuracy of 96% with Adaboost classifier on train test split method. To know the better algorithm, logarithmic loss was used to measure the prediction confidence of the model. This was calculated using 10 – fold cross-validation and Random forest archive 0.11, XGBoost classifier archive 0.15 and AdaBoost classifier archive 0.25. With this measure, smaller is better, so, Random Forest is the best model. All classifiers achieve area under ROC curve of 0.99 which is near 1 and indicates the predictive power of the model, based on this measure we can say all classifiers are good.

To compare the efficiency of the algorithm, we calculated the sensitivity, specificity precision, recall, and F1 – score of each class as presented in table number 3 below.

Table 3: shows the efficiency measure of models.

Model	SE	SP	Precision	Recall	F1-score	Class
ADB	0.95	0.94	0.95	0.95	0.93	0
			0.97	0.95	0.96	1
XGB	0.95	0.95	0.90	0.95	0.93	0
			0.97	0.95	0.96	1
RF	0.96	0.96	0.92	0.96	0.94	0
			0.98	0.95	0.97	1

On the class column, 0 stands for benign cancer and 1 stands for malignant. But on the row header, SE stands for sensitivity and SP for Specificity. The sensitivity indicates the number of benign class which is collect classified and specificity indicate number of malignant class which is correctly classified. Based on that, Radom forest is the best model because it has the highest number of correct classified instances in all classes. From sensitivity and specificity we were able to calculate false-negative rates and false-positive rates respectively. False-negative rate (FNR) indicate rate of misclassifying benign class and False positive rate (FPR) is also indicate rate of misclassifying malignant class. Both go by formula (1) and (2) below.

$$FNR = 1 - Sensitivity \quad \ldots\ldots\ldots\ldots\ldots\ldots \quad (1)$$

$$FPR = 1 - Specificity \quad \ldots\ldots\ldots\ldots\ldots\ldots \quad (2)$$

After calculating FNR and FPR from the table above, AdaBoost classifier has FNR of 0.05 and FPR of 0.06, XGBoost classifier has FNR of 0.05 and FPR of 0.05 while

Random forest has FNR of 0.04 and FPR of 0.04 which is very small compared to other two classifiers hence is good classifier. Random forest achieves higher on other measures that is Precision, Recall, and F1 – score. In general, by looking at effectiveness and efficiency result of all classifiers, we conclude that Random Forest is the best model for this data set with accuracy of 97%, specificity of 96% and sensitivity of 96%.

V. CONCLUSION

The aim of breast cancer prediction in this context of data mining processing and machine learning model development is to develop an effective model that has high prediction accuracy and low error rate. This is specifically done because of the fact that this process involves someone's life. Ensemble learning using bagging and boosting tend to improve the predictive model performance in terms of the accuracy of the model. The study compares the performance of three ensemble learning classifier algorithm which is AdaBoost, Random Forest, and XGBoost. The data used in this study of breast cancer were obtained from the University of Wisconsin Hospitals and the dataset is published in the UCI machine learning repository. The result indicates that random forest classifier performs better than the other two with the following classification measures, accuracy 97%, Sensitivity 96% and Specificity 96%. To measure the performance we use classification accuracy, logarithmic loss, area under ROC curve and classification report to obtained Sensitivity, Specificity, Precision, Recall, and F1 – score. The study gives an overview of applying data mining technique in the healthcare field to help the doctor to prescribe patients with breast cancer.

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