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Max Depth Impact on Heart Disease Classification: Decision Tree and Random Forest

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Abstract

Heart disease classification is an important aspect of prevention and early treatment. Heart disease classification results that are inaccurate and have low accuracy can endanger the patient's life. Several classification techniques using machine learning for heart disease have been carried out. However, there are still few studies that analyze the parameters in the algorithm model. Using inappropriate parameters can result in low accuracy. This study compares Decision Tree and Random Forest algorithms for heart disease. The max depth parameter is the parameter analyzed in this study. If the max depth is not set properly, the classification results can be inaccurate and lead to incorrect diagnoses. This study uses a holdout validation scheme for data sharing and tests different max depth parameters, namely max depth = 3, 4, 5, 6, and 7. The analysis results show that the max depth parameter that produces the best accuracy is max depth = 7 with the best accuracy result by Random Forest which is 99.29% while the Decision Tree accuracy is 98.05%. In future research, research can be conducted on the effect of other parameters by testing using several data sets.

Keywords: classification; heart disease; Decision Tree; Random Forest; machine learning

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1. Introduction

One of the most prevalent diseases in the world today is heart disease [1], [2]. According to the World Health Organization (WHO), heart disease is the number one cause of death in the world [3]. In Indonesia, heart disease ranks second in terms of causes of death, after cancer [4]. Therefore, to save lives and improve the quality of life of patients, early detection and treatment of heart disease is essential.

The use of classification systems is one method to detect heart disease [5]. The classification of heart disease is one of the important aspects of efforts to prevent and treat this disease [6], [7]. Some classification techniques that are often used in data processing are Decision Tree (DT) and Random Forest (RF) [8], [9]. In addition to heart disease classification, Decision Trees and Random Forest are used for kidney transplant prediction [10] brain stroke classification [11] and various other classifications in medicine.

In the classification of heart disease, it is important to choose the right parameters so that the classification results can be accurate [12]. One of the parameters that can affect classification is max depth, which is a parameter that sets the maximum depth of the Decision Tree or tree in a Random Forest [13].

The parameters in Decision Tree and Random Forest are max depth, max-leaf, max features, and min samples split [14], [15], [16]. The impact of the max depth parameter on Decision Tree and Random Forest in classification has been investigated in several previous studies. Research [17] shows that using the right max depth can improve the classification accuracy of the Decision Tree. While research [18], [19] shows in other studies that if the max depth in Random Forest, is properly optimized, it can produce a classification model that outperforms Decision Tree. Research [20] states that the greater the max depth value can increase the accuracy. However, no research specifically examines the effect of max depth on the classification of heart disease using the Decision Tree and Random Forest methods. The influence of max depth on heart disease classification has significant implications. If the max depth is not set properly, the classification results

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can be inaccurate and lead to incorrect diagnoses. This research can improve the accuracy of heart disease classification through optimal max depth selection.

Research [21] classifies cardiovascular datasets using several supervised machine learning algorithms such as Naive Bayes (NB), Logistic Regression, Random Forest, SVM and KNN-based approaches. Decision Tree gave the best result with 73% accuracy. Research [22] To determine whether a patient will experience coronary heart disease in the next 10 years and to assess the effectiveness of the Naïve Bayes algorithm, this study will analyze data related to coronary heart disease. The causes of coronary heart disease include the following 16 factors: total cholesterol, systolic, diastolic, diastolic, BMI, heart rate, glucose; current smoking, age, education; the number of cigarettes smoked daily; blood pressure medication; and prevalence of stroke, hypertension, and diabetes. The results show that coronary heart disease data can be classified with the Naïve Bayes algorithm, resulting in 79.10% accuracy in the moderately accurate category. Furthermore, research [23] used DT, RF and NB classification models and the grid search results showed a score of 0.84, while the Decision Tree model with random search evaluation obtained an average of 0.844. Evaluation of the naïve Bayes model showed a similarity between grid search and random search, with a difference of 0.85. The Random Forest classifier, with both grid search (0.852) and random search (0.868) evaluations, stood out as the best model in classifying heart disease after a hyperparameter setting.

Several studies have conducted research related to Random Forest and Decision Tree optimization. Research [24] analyzes Random Forest optimization, a learning model for classification and regression, by applying unequal weight voting techniques based on the performance of each tree. While research [25], performs Decision Tree optimization by discretizing continuous attributes into several data intervals. Furthermore, research [26] analyzes Random Forest optimization, with learning models for classification and regression, which applies unequal weight voting techniques based on the performance of each tree. This study compares Ranger MMCE tune, Ranger AUC tune, tuneRangerBrier, tuneRangerLogloss, hyperopt, caret, tuneRF, and default ranger. The results show that tuning the node size and sample size samples provides valuable average improvements. The average error rate (MMCE) increased by 0.004, AUC by 0.002, Brier score by 0.010, and logarithmic loss by 0.014 when setting all three parameters. Research [20] The optimized RF parameters are max_depth, max_features, n_estimator, min_sample_leaf, and min_sample_leaf. Experiments were conducted on RF using default, random search, and grid search parameters. Overall, the accuracy obtained for each experiment is 82.5% default parameters, 82% random search, and 83% grid search. The performance of the RF+Genetic Algorithm is 85.83%.

Based on the research [27], [28], the Decision Tree has advantages in ease of interpretation, and visualization, and is suitable for small and medium datasets with little data pre-processing. However, its drawbacks include susceptibility to overfitting and not always producing the optimal model. Meanwhile, Random Forest, as an ensemble method, overcomes the shortcomings of Decision Tree by reducing overfitting, improving accuracy, and being able to handle large datasets with many features as well as missing resources or outliers. However, Random Forest is difficult to interpret and requires greater computational resources.

Several previous studies have examined the classification of heart disease using Decision Tree and Random Forest. However, the results of these studies are still limited and have not discussed in detail the effect of max depth Decision Tree and Random Forest parameters.

The purpose of this research is to analyse the effect of max depth on heart disease classification using a Decision Tree and Random Forest. This research will compare the performance of both methods and determine the optimal max depth to achieve high classification accuracy. In addition, this research also measures the computational time comparison of using max depth between Decision Tree and Random Forest. The results of the information from the research are expected to help in improving the accuracy of heart disease classification.

2. Research Methods

This study used the dataset UCI Machine Learning to research heart disease data. To produce results of the highest calibre, research needs to be well-planned and structured throughout the many stages. As a result, the study's research phases are set up in a way that aligns with the goals of the research, as illustrated in Figure 1.

The research steps that will be completed in Figure 1 are problem identification, literature review, data collection, data pre-processing, data modelling using Decision Trees and Random Forests while taking max depth testing 3 to 7 into consideration, and model performance evaluation using a confusion matrix.

2.1 Identification Problem

This process is a process of identifying the problems that occur regarding the classification of heart disease and the implications that occur if these problems are not addressed. This research highlights the importance of understanding the impact of setting the max depth parameter on heart disease classification using Decision Tree and Random Forest.

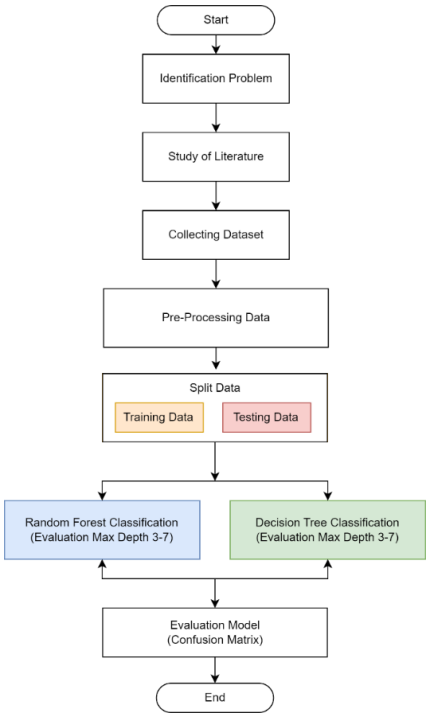

Figure 1. Phases in Conducting Research

This research identified two main problems. First, determining the right max depth is crucial to maintaining a balance between accuracy and model complexity. Max depth that is too large or too small can lead to overfitting or a model that is too simple. Secondly, a comparison between Decision Tree and Random Forest provides insight into their strengths and weaknesses in the context of heart disease classification, opening up the potential for a more thorough and effective solution. In this research, the formulation of the problem to be solved is how to classify heart disease using Decision Tree and Random Forest by considering the influence of the max depth parameter.

2.2 Study of Literature

The next step was to conduct a literature review, where information from theses, books, and journals published in the last five years were collected as references. The main focus is to understand the theories related to heart disease classification, and machine learning, as well as the Decision Tree algorithm, Random Forest, and Max Depth parameters. Through the literature review, this research will identify key findings from previous studies related to heart disease classification using Decision Tree and Random Forest. This literature review highlights that performance comparisons between these two algorithms can offer a deeper understanding of how they adapt to the complexity of medical datasets, especially in the case of heart disease classification. An in-depth understanding of how the determination of max depth affects model performance and the comparison between these two algorithms is an important foundation for developing experimental methodologies and designing informative tests. By detailing key findings in the literature, this research can gain deeper and more relevant insights, paving the way for an improved understanding of the complexities of heart disease classification. Therefore, by understanding the theoretical foundation and findings of previous literature studies, this subchapter will provide a solid foundation for the research to investigate the impact of max depth on heart disease classification using Decision Tree and Random Forest.

2.3. Collecting Dataset

Table 1 describes the variables in the dataset, where the dataset has 14 variables.

Table 1. Variable and Description Dataset

Variable	Role	Type	Description
Restecg	Feature	Categorical	Value 2: showing probable or definite left ventricular hypertrophy by Estes' criteria
Thalach	Feature	Integer	maximum heart rate achieved
Exang	Feature	Integer	exercise-induced angina
Oldpeak	Feature	Integer	ST depression induced by exercise relative to rest
Slope	Feature	Categorical	the slope of the peak exercise ST segment 1: upsloping, 2: flat, 3: downsloping
Ca	Feature	Integer	Number of major vessels (0-3) coloured by fluoroscopy
Thal	Feature	Categorical	refers to the condition of thalassemia, which can affect the production of red blood cells. 3 = normal; 6 = fixed defect; 7 = reversible defect
Target	Target	Integer	Diagnosis of heart disease (1= defective heart: 0 = healthy heart)
Sex	Feature	Categorical	Gender (1 = male; 0 = female)
Cp	Feature	Categorical	type of chest pain (1: typical angina, 2: atypical angina, 3: non-angina, 4: asymptomatic)
Trestbps	Feature	Integer	resting blood pressure (on admission to the hospital)
Chol	Feature	Integer	serum cholesterol
Fbs	Feature	Categorical	fasting blood sugar > 120 mg/dl (1 = true; 0 = false)
Restecg	Feature	Categorical	resting electro-cardiography results, 0:normal, 1:abnormal

This Research used a dataset the "Heart Disease Dataset" from UCI Machine Learning [29], which has 1025 entries and 14 attributes, from the heart disease database at Cleveland, Hungarian, Swiss, and Long Beach V. is the dataset used in this study. The patient's heart condition is indicated in the "target" field. 0 indicates no disease, whereas 1 indicates disease.

2.4 Pre-Processing Data

Data preprocessing or transforming raw data so that it may be used as needed. Preprocessing is a crucial step in the data classification process. Data that will be used in the data mining process won't always be in the best possible condition to be processed [30].

Various problems arise from data that has not undergone preprocessing; among them are numerous attributes, data that is located in an extremely narrow range, missing values, and inconsistent data formats [31]. Preprocessing involves removing obsolete or superfluous elements that could affect the data extraction process's results [32]. Preprocessing is carried out on research checking for missing values, outlier data and data encoding, which is to change the format of categorical data to numeric.

2.5 Split Data

Partitioning a dataset using split data is one of the many factors that affect the performance of classification models in machine learning algorithms [33]. The process of separating test data and training data is known as split data [34]. Training and testing data can be separated using k-fold cross-validation and holdout validation techniques. This validation process is very important to do, to give each data an equal chance to be used as test and training data [35]. The holdout validation method was applied to separate the data in this study. as shown in Formula 1.

$$X = \frac{Testing\ A + Testing\ B}{2} \quad (1)$$

The accuracy of each test that results from adding tests A and B and dividing the result by two is represented by the letter X in Equation (1). testing A and B combined, then divided into two.

Table 2. Split Data Schema

Percentage (Training Data: Test Data)	Training Data	Test Data
60:40	615	410
70:30	717	308
75:25	768	257
80:20	820	205
90:10	922	103

This research uses 5 data split schemes using holdout validation, which can be seen in Table 2.

2.6 Decision Tree Classification

The data is grouped and analyzed using the Decision Tree method to form a more structured data model, by describing the data in the form of a hierarchical tree to facilitate decision-making by determining the root or root of the appropriate attribute tree [36]. The steps in a Decision Tree are [37]:

The first step in the Decision Tree is to calculate the entropy value of each attribute, Formula 2 is for calculating entropy.

$$Entropy(S) = \sum_{i=1}^{n} - pi \times \log_2 pi \quad (2)$$

Entropy formula (Entropy(S)) measures the degree of disorder or unstructuredness in a dataset S and is calculated by summing the product of the probability of each class (pi) with the base 2 logarithm of that probability, for each class i. The lower the Entropy value, the more homogeneous or organized the dataset S.

The second step is calculating information Gain, with Formula 3.

$$InfoGain(S, A) = Ent(S) - \sum_{i=1}^{n} \frac{|S_i|}{|S|} \times Ent\ (S_i) \quad (3)$$

The Information Gain formula (Info Gain(S, A)) measures how much information is gained by dividing the data set S by the sum of the Ent (entropy) of each subset (Si) based on attribute A.

Step three is calculating Split Information, with Formula 4.

$$Split\ Info_A(D) = -\sum_{j=1}^{v} \frac{|D_j|}{|D|} \times \log_2 \left(\frac{D_j}{D}\right) \quad (4)$$

The Split Information formula (Split InfoA(D)) measures the level of diversity in the dataset D after being split by attribute A

Step four is calculating the Gain Ratio for each attribute. Formula 5 is for calculating the gain ratio.

$$GainRatio(A) = \frac{infoGain(A)}{SplitInfo(A)} \quad (5)$$

The Gain Ratio formula (Gain Ratio(A)) measures the effectiveness of splitting based on attribute A by considering Information Gain and Split Information. A higher Gain Ratio value indicates a more effective split.

Then, select the attribute with the highest Gain Ratio as the root (splitting attribute) and the attribute with the lower Gain Ratio value as the branch. After that, recalculate the Gain Ratio value of each attribute without taking into account the attribute that has been selected as the root in the previous step. Continue doing steps d and e until all remaining attributes have a Gain value = 0.

2.7 Random Forest Classification

Random Forest is Supervised Learning from Leo Breme. The Random Forest algorithm is a type of classification that uses multiple decision trees, each formed based on identically distributed random vector values that are sampled independently for each tree [38]. Random Forest, a bagging ensemble of Decision

Trees, is used for predictive modelling with each tree selecting a class, and the final classification is determined by the majority of the trees, reduces model variance by bagging techniques, and can avoid overfitting due to the use of random features for each tree [39].

The steps in Random Forest are [37], the first step is to choose *k* trees, where *k* is less than *m* out of all the features (m). Take *N* random samples from the dataset for each tree. Then, randomly select a subset of predictors, up to a maximum of $m<p$ predictor variables, for each tree. Repeat the second and third steps of the procedure *k tree.* The prediction for each tree is determined by the majority class of the classification results, repeated *k tree*. The overall prediction is derived from the majority class among the classification results of all the trees.

2.8 Evaluation Model

To ascertain whether the suggested approach is reliable, an evaluation is conducted [40]. In this research, we used a confusion matrix for the evaluation model. A confusion matrix is a method for interpreting data, including both actual data and predictions from classification results. In classification, the goal is accurate categorization with minimal errors, and the confusion matrix aids in assessing the effectiveness of the categorization process [41]. To assess the model constructed with the confusion matrix by calculating the accuracy, recall, and precision values are shown in Formulas 6, 7 and 8 [42].

$$Precision = \frac{TP}{TP+FP} \quad (6)$$

$$Recall = \frac{TP}{TP+FN} \quad (7)$$

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN} \quad (8)$$

In this context, TP (True Positive) denotes correctly classified positive data, TN (True Negative) denotes correctly classified negative data, FP (False Positive) denotes correctly classified negative data with positive results, and FN (False Negative) denotes correctly classified positive data with negative results.

3. Results and Discussions

3.1 Collecting and Pre-processing Dataset

The data used in this study is the UCI Machine Learning Heart Disease Dataset which amounts to 1025 data with 14 attributes. During the data preprocessing process, irrelevant columns and rows are removed, identifying and correcting empty values and identifying outlier data. When checking for missing values, there are some empty data such as treetops 58 data, chol 30 data, restecg 1 data, exang 55 and thalach 55 data, then to handle the missing value using the average or mean value in the dataset. After that label encoding is done for categorical data as in Table 1. The following in Table 3 is clean data after preprocessing.

Table 3. Data After Pre-processing

No	Column	Non-null count	Dtype
0	Age	1025 non-null	Int64
1	Sex	1025 non-null	Int64
2	Cp	1025 non-null	Int64
3	Trestbps	1025 non-null	Int64
4	Chol	1025 non-null	Int64
5	Fbs	1025 non-null	Int64
6	Restecg	1025 non-null	Int64
7	Thalach	1025 non-null	Int64
8	Exang	1025 non-null	Int64
9	Oldpeak	1025 non-null	Float64
10	Slope	1025 non-null	Int64
11	Ca	1025 non-null	Int64
12	Thal	1025 non-null	Int64
13	Target	1025 non-null	Int64

Table 3 is a description of datasets and dataset attributes that have been cleaned and will be used in this study with a total of 1025 datasets with 1 label, namely the target variable with 2 classes, namely "1" for patients with heart disease and "0" for patients without heart disease. There are 526 data with class 1 or patients with heart disease, and 499 data with class 0 or patients without heart disease.

Table 4. Sample Dataset

Age	Sex	Trestbps	Chol	…	Target
52	1	125	212	…	0
53	1	140	203	…	0
70	1	145	174	…	0
61	1	148	203	…	0
59	1	140	221	…	1

Table 4 is a sample of the heart disease dataset, the data used amounted to 1025 data.

3.2 Split Data

After pre-processing, the data split process is then carried out using the holdout validation scheme. There are 5 percentage split schemes for training data and after determining the split scheme of training data and testing data, a data processing process is carried out using Google Colab and Python programming language with a classification model classification model using the Decision Tree and Random Forest algorithms.

3.3 Modeling and Evaluation

The classification model used in this study uses the Decision Tree and Random Forest algorithms, with a predetermined data split scheme, in table 5 are the test results using Decision Tree and Random Forest by considering max depth 3, 4, 5, 6 and 7 tests.

Based on Table 5, the classification of heart disease using the Decision Tree algorithm and Random Forest using the analysis of the influence of the max depth parameter (3,4,5,6,7) produces the best accuracy of 99.29% in the Random Forest algorithm with max depth = 7, and Decision Tree 98.05% with max depth = 7 on split training and testing data 90:10.

Table 5. Test Results Using The Holdout Validation Scheme

No	Split Data	Max Depth	Accuracy (%)	
			Decision Tree	Random Forest
1	60:40	3	82.68	84.63
		4	82.19	86.09
		5	89.02	90.34
		6	91.46	93.17
		7	**94.87**	**95.85**
2	70:30	3	81.16	83.44
		4	82.79	84.74
		5	88.96	89.28
		6	92.20	91.23
		7	**94.80**	**95.77**
3	75:25	3	81.32	84.82
		4	83.26	85.60
		5	87.15	89.10
		6	91.43	93.77
		7	**94.94**	**95.71**
4	80:20	3	81.95	86.13
		4	85.85	86.34
		5	88.29	91.70
		6	92.68	97.07
		7	**96.09**	**98.53**
5	90:10	3	81.55	79.61
		4	82.52	85.45
		5	88.34	92.23
		6	93.20	95.14
		7	**98.05**	**99.29**

The higher the max depth value in research [20], [28] states that it can increase accuracy, but other factors such as split data also affect accuracy results, such as in split data 60:40, the accuracy on Decision Tree testing data max depth = 3 produces 82.68% accuracy, but at max depth = 4, the accuracy decreases to 82.19%.

After getting the best data split scheme, namely the 90%: 10% scheme, further testing was carried out regarding the value of precision and recall along with the difference in computation time between the Decision Tree algorithm and Random Forest.

Table 6. Result of Accuracy, Precision and Recall

Max Depth	Accuracy %		Precision %		Recall %	
	DT	RF	DT	RF	DT	RF
3	81.55	79.61	**84**	81	**81**	79
4	82.52	85.45	83	87	82	85
5	88.34	92.23	89	93	88	92
6	93.20	95.14	93	95	93	95
7	98.05	**99.29**	98	**99**	98	**99**

Based on Table 6, there is an increase in the accuracy value when using max depth = 3 to 7. The best accuracy results are at max depth = 7, using the Random Forest algorithm with an accuracy of 99.29%, while the Decision Tree algorithm produces the best accuracy of 98.05%. In addition to affecting accuracy, max depth also affects the precision and recall values which have increased. However, at max depth = 3, the precision value of DT is 3% higher than RF, while the recall value of DT is 2% higher than RF. Figures 2, 3 and 4 will illustrate the results of accuracy, precision and recall for heart disease classification.

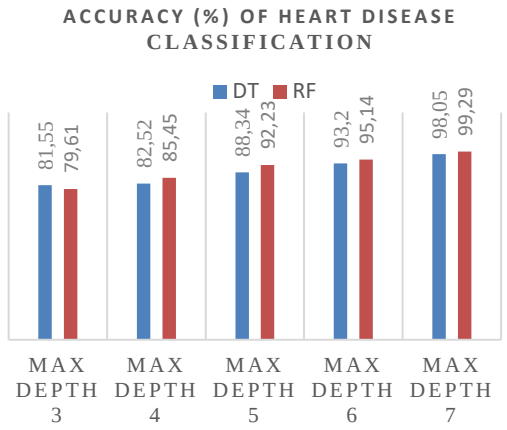

Figure 2. Accuracy of Heart Disease Classification

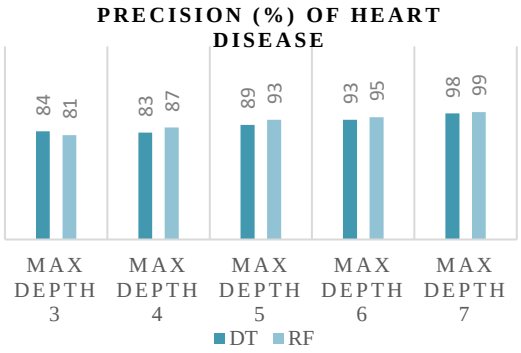

Figure 3. Precision of Heart Disease Classification

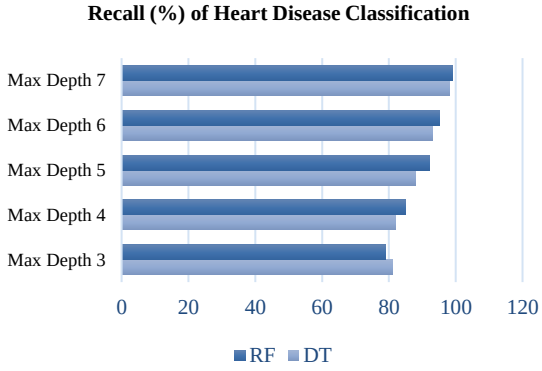

Figure 4. Recall of Heart Disease Classification

Table 7. Times Computation

Max Depth	DT		RF	
	Training Time	Time Testing	Training Time	Time Testing
3	0.0224	0.0224	0.6336	0.6336
4	0.0166	0.0166	0.3182	0.3182
5	0.0371	0.0371	0.3021	0.3021
6	0.0099	0.0099	0.5464	0.5464
7	0.0075	0.4354	0.2190	0.2190

In addition to testing evaluation using accuracy, precision and recall values, this study also tested the speed of processing time between Decision Tree and Random Forest.

Table 7 is the result of testing computing time when training and testing using Decision Tree and Random Forest algorithms.

Based on Table 7, the computation time using a Decision Tree is faster than using a Random Forest with a computation time for training data of 0.0075 seconds, while testing data is 0.009 seconds.

3.4 Discussion

This study uses five data split schemes namely 60%: 40%, 70%: 30%, 75%: 25%, 80%: 20%, 90%: 10% and tested with different max depth parameters, namely max depth = 3, 4, 5, 6, and 7. resulting in the best accuracy using the 90%: 10% scheme and max depth = 7 with the best accuracy results by the Random Forest algorithm of 99.29% while the Decision Tree algorithm is 98.05%. as well as the precision and recall values that increase according to the change in max depth, although at max depth = 3 the precision value of DT is 3% higher than RF, while the recall value of DT is 2% higher than RF.

Max_depth controls the depth of Decision Tree and Random Forest models, affecting their complexity [43], [44]. A max depth value that is too high can lead to overfitting, where the model memorizes the training data and does not generalize to new data [45]. Conversely, values that are too low can lead to underfitting, where the model does not capture the pattern well [46]. Overfitting can result in high accuracy on training but poor on tests, and underfitting can result in low performance overall [47]. Model complexity also affects precision and recall, especially with unbalanced data [48].

In addition, in this study, computation time testing was carried out and the results of computation time using Decision Tree were obtained faster than using Random Forest with computation time for training data 0.0075 seconds, while data testing 0.0099 seconds while Random Forest training and testing time 0.2190 seconds. This is because Random Forest as an ensemble of many Decision Trees, involves the formation of several trees in parallel or sequentially [49]. In addition, Random Forest involves a bootstrapping process, which is random sampling with returns from the training dataset for each tree, therefore it requires additional time to generate different samples for each tree [50]. Decision Tree only involves the formation of a single Decision Tree and Decision Tree does not involve a bootstrapping process as it only uses the given training dataset [51].

Based on the comparisons carried out, the accuracy produced in this study is better than research by [51], [52], [53], [54] which used the same dataset. In research [51] using various machine learning algorithms including Naïve Bayes, K-Nearest Neighbor (KNN), Decision Tree, Random Forest, Backpropagation, Logistic Regression and Support Vector Machine (SVM), Logistic Regression got the highest accuracy, namely 81%, while Decision Tree 66% and Random Forest 77%. The difference with the proposed research is that research [51] only uses 8 attributes and when using Decision Tree it uses a max depth of 5 and the max depth of Random Forest is 10 with a data split of 75%:25%. In the research, max depth and split data trials were not carried out.

Research [52] carried out classification using 8 machine learning methods for the classification of heart disease, with the highest accuracy results of 98.7% using Learning Vector Quantization. In the research, no consideration was made of the algorithm parameters used. Then research [53] used feature selection for heart disease classification, using 8 machine learning algorithms. The research used hyperparameters and the k-fold cross-validation method with the highest accuracy results by the Gaussian Process algorithm, namely 84.24%. Research [53] has limitations because it does not train the entire data set or perform feature selection. Research by [54] used Decision Tree and Logistic Regression, but in this study, no max depth settings and trials were carried out so this study produced an accuracy of 75%. In comparison, Logistic Regression produced an accuracy of 87%.

Overall, due to its impact on the model, variations in max depth values can affect different values of accuracy, precision, and recall. For optimal model performance, it is important to set the maximum depth value appropriately. Apart from setting the max depth, research also needs to pay attention to other parameters and factors such as the split data model or data validation, as well as the algorithm used to obtain optimal research results.

4. Conclusions

This research aims to analyse the influence of max depth on the classification of heart disease using a Decision Tree and Random Forest in the UCI Machine Learning Dataset. Based on the conducted research, it can be concluded that the max depth parameter can affect the accuracy of heart disease classification. Among the tested max depth parameters (3, 4, 5, 6, 7), the best accuracy was achieved at 99.29% with Random Forest using max depth=7, and Decision Tree achieved 98.05% with max depth=7 in the 90:10 split of training and testing data. Max depth also affects precision and recall results in Random Forest (99%) and Decision Tree (98%). However, the results also indicate that other factors, such as data split, significantly impact accuracy. For example, in a 60:40 data split, the accuracy of the Decision Tree with max depth=3 reached 82.68%, but decreased to 82.19% at max depth =4. This research also tested computation time, where the Decision Tree is faster compared to using a Random Forest with computation time for training data at 0.0075 seconds while testing data at 0.009 seconds. This is because the Decision Tree model is simpler and not as

complex as the Random Forest. Therefore, it can be concluded that while max depth has an impact, other factors need to be considered to achieve optimal classification results. This research has limitations as it only uses one dataset and compares max depth in Decision Tree and Random Forest algorithms. Subsequent research can explore the influence of other parameters by testing multiple datasets. The findings from this research are expected to serve as a reference for improving classification in data mining algorithms, especially in the medical field, regarding the classification of heart diseases and other illnesses.

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