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**Improving software defect prediction using a combination of ant colony optimization-based feature selection and ensemble technique**

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#### **1. Introduction**

Software defect prediction plays a vital role in enhancing software quality and minimizing maintenance costs. This study aims to improve software defect prediction by employing a combination of Ant Colony Optimization (ACO) for feature selection and ensemble techniques, particularly Gradient Boosting. This research utilized three NASA MDP datasets: MC1, KC1, and PC2, to evaluate the performance of four machine learning algorithms: Random Forest, Support Vector Machine (SVM), Decision Tree, and Naïve Bayes. The data preprocessing comprised handling class imbalance using SMOTE and converting categorical data into numerical representations. The results indicate that the integration of ACO and Gradient Boosting significantly enhances the accuracy of all four algorithms. Notably, the Random Forest algorithm achieved the highest accuracy of 99% on the MC1 dataset. The findings suggest that combining ACO-based feature selection with ensemble techniques can effectively boost the performance of software defect prediction models, offering a robust approach for early detection of potential software defects and contributing to improved software reliability and efficiency.

According to the National Institute of Standards and Technology, system losses in software defects amount to \$60 billion. The cost of repairing software defects during design stage can reach 60 times the software development cost, and 100 times if the software defects are found after the release [1]. In general, software defect prediction is also a cost-sensitive problem [2]. Predictions on software defects are carried out using data sets from previous software [3]. The NASA dataset is one of the publicly available datasets, which is very popular and has been widely used in developing software defect prediction models, because obtaining NASA dataset is very easy [4]. The NASA dataset shows that there is more non-defective data than defective data, causing data imbalance and noise. This is a problem frequently found in software defect predictions, so that the prediction results tend to produce many classes, namely no defect class. To overcome this problem, it is necessary to modify the prediction technique by adding other techniques or combining other algorithms [5].

Software quality can be improved in various ways, but the most effective method is to prevent defects by predicting the probability of defects [6]. The most commonly used method for predicting software defects is the Prediction method [5]. The majority of current software defect predictions use supervised machine learning algorithms to predict defects in software applications [7].

Four previous studies discussed how machine learning algorithms work in predicting software defects in NASA datasets. This research uses an ensemble technique classified as a boosting method, namely Gradient boosting, because it takes shorter time and has good performance [8], and confirms that Support Vector Machine algorithm can be used to predict software defects in NASA dataset [9]. A study [10] found that Random Forest algorithm has a good accuracy in measuring model performance. Apart from that, [11] stated that one of the feature selection techniques, namely Ant Colony Optimization, can be used to select good features to improve the performance of the algorithm model. Ant Colony Optimization utilizes a probability-based decision-making process, in which each ant constructs a solution by iteratively selecting the next step based on the combination of the desirability of the solution and the amount of pheromone present[12]. Meanwhile, according to research by [2] the Naïve Bayes algorithm and Decision Tree are the algorithms that can be used to compare several other algorithms.

Support Vector machine is a binary classification of datasets, where the decision boundaries to solve the learning sample is the maximum margin hyperplane in svm, which is very good in terms of robustness [13]. Different from other algorithm that usually find the best single line between classes to classify the data [14], SVM separates the classes by using three separating lines, one for main separating line and two other lines are the support line [15]. Decision Tree is a machine learning algorithm with the simplest modeling techniques to classify data by using graphs, such as trees that

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Kinetik: Game Technology, Information System, Computer Network, Computing, Electronics, and Control 390 show leaf structure and node [16]. Naive Bayes is a probability classification based on Bayes' theorem and considering the impact of attribute values on certain classes. The goal of Naïve Bayes is to simplify the calculations [17]. Random Forest is an ensemble bagging-based classifier as basic learner, this model divides the training data into several trees' decision [11]. Random Forest is a parallel ensemble Machine Learning classifying algorithm based on the bagging technique [18].

Different from the results of the previous researches, this research focused on comparing four machine learning algorithms with an innovative approach by combining Ant Colony Optimization-based feature selection and ensemble technique. While previous studies have highlighted the strengths of each algorithm in predicting software defects, a comprehensive comparison incorporating these advanced methods remains unexplored. By integrating Ant Colony Optimization for feature selection, this study can enhance the performance of each algorithm by selecting the most relevant features, thereby improving the prediction accuracy. Additionally, employing an ensemble technique, such as Gradient Boosting, can improve model performance by combining the strengths of each model and reducing the prediction errors. This approach can also address data imbalance issues, frequently overlooked in current research, by ensuring that the ensemble method can effectively handle varied data distributions.

### **2. Research Method**

This research employs the following methods to compare the Random Forest, Support Vector Machine (SVM), Decision Tree, and Naïve Bayes algorithms in predicting software defect using a combination of ensemble and Ant Colony Optimization. Figure 1 illustrates the research stages throughout the study.



*Figure 1. Research Stages*

The data is obtained from the NASA MDP Software Defect Datasets website in arff format, which is a file that describes a list of data containing defect and no defect data [19]. In the data collection process, researchers used three NASA MDP (Metric Data Program) datasets, namely MC1, KC1 and PC2, because these data have better accuracy than several other datasets. The NASA MDP (Metric Data Program), MC1, KC1 and PC2 datasets, each has a different amount of data, namely the MC1 dataset has a total of 39 attributes with 2031 data, the KC1 dataset has a total of 22 attributes with 1183 data, the PC2 has a total of 36 attributes with 786 records. Detailed information regarding the dataset used in this study is provided in Table 1.



Data preprocessing techniques were employed to enhance the datasets quality and suitability for classification analysis. These techniques aimed to refine and standardize the dataset by addressing missing values and irrelevant attributes. The preprocessing steps included in-depth procedures to handle missing data, ensuring the dataset remained

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robust and suitable for subsequent analysis [20]. The problem and dataset in question determine the technique used. One of which is oversampling techniques, such as SMOTE (Synthetic Minority Over-sampling Technique) [21]. SMOTE is able to reach better performance than the modified version in certain dataset and classification algorithm. Therefore, this research used SMOTE, which is the benchmark of oversampling method that has been successfully applied in many cases to improve the generalization performance of classifier in minority class. SMOTE even still has good performance when the number of the samples in the minority class is quite small [22]. Table 2 comprehensively explains the specific preprocessing techniques utilized in this study.

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Data splitting is the process of separating a dataset into subsets for building a good machine learning model [23]. At this stage, testing data and training data were generated and tested in the next stage. At this stage, scikit-learn library 'train test split()' is used to divide the dataset into two subsets, namely testing and training [24]. Data splitting is needed to separate the dataset and produce training data and testing data that can be used in training machine learning models and validating models. As previously discussed, the dataset used this time has an imbalance in the type of classification results, where the classification of safe programs is more dominant than the classification of programs labeled as malware. Therefore, a data balancing method must be applied [25]

The model employed in this study included four machine-learning algorithms, namely Random Forest, Support Vector Machine, Decision Tree, and Naïve Bayes. These algorithms were selected based on a comprehensive review of prior studies, which highlighted their superior accuracy and diverse advantages. The model was constructed by utilizing functions accessible from the Sklearn library in Python, coupled with hyperparameter optimization techniques to enhance each classifier's performance [26]. Table 3 outlines the specific parameter scenarios employed in the modelbuilding process.



Ensemble technique, specifically Gradient Boosting, is selected because it is a good technique for increasing the accuracy of four algorithms being used, namely Random Forest, Decision Tree, Support Vector Machine and Naïve Bayes. From several techniques, Gradient Boosting succeeded in obtaining good accuracy in every algorithm with good accuracy.

Model evaluation was used to measure the performance of the algorithms being used, consisting of confusion matrix, accuracy, precision and recall. This research also compared the results of the original algorithm with the combined algorithms, namely Ant Colony Optimization and ensemble technique, particularly Gradient Boosting.

## **3. Results and Discussion**

Before starting the model building phase using the NASA dataset, a comprehensive data preprocessing is necessary to optimize the suitability of datasets analysis. This preprocessing phase included several important steps to improve data integrity and facilitate practical model construction. First, a transformation stage was carried out on the categorical column, namely the Defective attribute, and it is converted into a numerical representation using the LabelEncoder() function from Sklearn. Table 4 provides an overview of the post-transformation dataset, illustrating the results of this preprocessing procedure.

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Kinetik: Game Technology, Information System, Computer Network, Computing, Electronics, and Control 392 *Table 4. Data Transformation Results*

Table 4. Data Transformation Results						
Loc Blank	Branch Count	$\cdots$	Num_Unique_Operators	Loc Total	Defective	
9.0	11.0	.	21.0	41.0		
0.0	1.0	.	6.0	7.0		
18.0	31.0	$\cdots$	28.0	184.0		
1.0	5.0	$\cdots$	12.0	23.0		
5.0	17.0	$\cdots$	15.0	96.0		
$\cdots$	$\cdots$	.	$\cdots$	$\cdots$	$\cdots$	
2.0	5.0	.	12.0	9.0		

This stage used SMOTE (Synthetic Minority Over-Sampling Technique) as a resampling technique commonly used in machine learning to handle class imbalance problems in datasets. SMOTE is useful for improving performance so as to produce a good model that increases the accuracy. SMOTE handles class imbalance, prevents overfitting, and improves model performance. Figure 2 shows the results of one of the datasets before and after SMOTE.



*Figure 2. SMOTE Results (a) before SMOTE; (b) after SMOTE*

This stage is the process of selecting the most relevant features from the dataset or features that will be used in building a prediction model which aims to improve model performance by reducing unused features. The Ant Colony Optimization (ACO) algorithm begins with initializing variables that are important for the next process, such as the number of ants (num\_ants), as well as variables to track the best features and best accuracy. Figure 3 shows an example of a flowchart in the feature selection process, and Table 5 shows the results of selecting the best features from each dataset.



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Table 5. Result the Best feature				
No	Dataset	<b>Best Feature</b>		
		Halstead effort		
		Halstead content		
	KC <sub>1</sub>	Halstead_length		
		Halstead_difficulty		
1		Num_unique_operands		
		Halstead volume		
		Loc comments		
		Loc blank		
		Branch count		
		Halstead error_est		
		Call_pairs		
		Num operands		
		Normalized_cylomatic_complexity		
	MC <sub>1</sub>	Num_operators		
$\overline{2}$		Branch count		
		Halstead effort		
		Halstead_prog_time		
		Global_data_complexity		
		Halstead level		
		Condition_count		
		Multiple_condition_count		
		Edge_count		
	PC <sub>2</sub>	Halstead volume		
		Parameter count		
3		Halstead_effort		
		Loc executable		
		Halstead error est		
		Condition_count		
		Num_unique_operators		
		Cyclomatic_density		

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This study combined four different algorithms, namely Random Forest, Support Vector Machines, Decision Trees and Naive Bayes. This study employed various evaluation methods to assess the algorithm performance, including confusion matrix, accuracy, precision, and recall.

At this stage, ensemble technique was used, namely Gradient Boosting, because it is a good technique for increasing the accuracy of the four algorithms being used, namely Random Forest, Decision Tree, Support Vector Machine and Naïve Bayes. From several techniques, Gradient Boosting succeeded in obtaining good accuracy in every algorithm with good accuracy. Figure 4 shows an example diagram of the ensemble technique process using gradient boosting. The results of the gradient boosting can be seen in Table 6.



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No	Algorithm	Dataset	Accuracy
		KC <sub>1</sub>	0,65
	<b>Support Vector</b> Machine	MC <sub>1</sub>	0,88
		rable 6. Ensemble Technique Results PC <sub>2</sub> KC <sub>1</sub> MC1 PC <sub>2</sub> KC <sub>1</sub> MC <sub>1</sub> PC <sub>2</sub> KC <sub>1</sub> MC <sub>1</sub>	0,91
			0,84
2	Random Forest		0,99
			0,97
			0,76
3	Decision Tree		0,98
		PC <sub>2</sub>	0,97
			0,59
	Naïve Bayes		0,72
			0,83

Kinetik: Game Technology, Information System, Computer Network, Computing, Electronics, and Control 394 *Table 6. Ensemble Technique Results*

The final stage of this research was the model evaluation stage, where the model evaluation was used to measure the performance of the algorithms being used, namely confusion matrix, accuracy, precision and recall. This research also compared the results of the original algorithm with the combined algorithms, namely Ant Colony Optimization and ensemble technique, particularly Gradient Boosting. Table 7 shows the comparative results of the model evaluation.

rable 7. Comparative Moder Evaluation Results							
		<b>Model Evaluation</b>					
Algorithm	Dataset	Original algorithm		Combined algorithms			
		Accuracy	Precision	Recall	Accuracy	Precision	Recall
Decision Tree	KC <sub>1</sub>	0,73	0,73	0,69	0,76	0,78	0,73
	MC <sub>1</sub>	0.94	0.91	0.97	0.98	0,97	0,98
	PC <sub>2</sub>	0.95	0.94	0.97	0.96	0.97	0,96
Random Forest	KC <sub>1</sub>	0.83	0,85	0,78	0.84	0.85	0,82
	MC <sub>1</sub>	0.99	0,98	0.99	0.99	0,98	1,00
	PC <sub>2</sub>	0.98	0,97	0.99	0,97	0,97	0,98
Support Vector Machine	KC <sub>1</sub>	0,61	0,64	0,44	0,65	0,75	0,47
	MC <sub>1</sub>	0,79	0,77	0,81	0,88	0,84	0,93
	PC <sub>2</sub>	0.85	0,78	1.00	0.91	0.84	1,00
Naïve <b>Bayes</b>	KC <sub>1</sub>	0.60	0.67	0,35	0,59	0,71	0.31
	MC <sub>1</sub>	0.62	0,73	0,32	0.72	0,68	0,81
	PC <sub>2</sub>	0.81	0,84	0,77	0.83	0,83	0,83

*Table 7. Comparative Model Evaluation Results*

From Table 7, it can be concluded that the four algorithms obtained good accuracy after being combined with Ant Colony Optimization and ensemble technique. By using Ant Colony Optimization and ensemble techniques, the four algorithms showed a significant increase in accuracy. Random Forest algorithm achieved the highest accuracy of 0.99 on the MC1 dataset both before and after the combination, showing its stable performance. After the combination, Decision Tree also showed a significant increase in accuracy, from 0.94 to 0.98 on dataset MC1, and from 0.95 to 0.96 on dataset PC2. The Support Vector Machine algorithm experienced an increase in accuracy from 0.79 to 0.88 on the MC1 dataset. These results show that the combination of Ant Colony Optimization and ensemble techniques can improve the accuracy of the algorithms, especially on the Decision Tree algorithm with an accuracy of 0.98 on dataset MC1. In addition, Random Forest algorithm is declared stable because it obtained good accuracy.

## **4. Conclusion**

The evaluation of the defect software prediction model using Random Forest, Decision Tree, Support Vector Machine, and Naive Bayes algorithms after being combined with Ant Colony Optimization-based feature selection and ensemble technique, namely Gradient Boosting, shows that the accuracy of the four algorithm models had successfully increased by an average of 2% to 10%. Therefore, it can be concluded that the Feature Selection and Ensemble technique can increase the accuracy of the four algorithms being used.

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