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HYPERPARAMETER TUNING ON RANDOM FOREST FOR DIAGNOSE COVID-19

Anna Baita^{1*}, Inggar Adi Prasetyo², Nuri Cahyono³

1,2,3 Faculty of Computer Science, Universitas Amikom Yogyakarta *Email: ¹anna@amikom.ac.id, ²inggar.25@students.amikom.ac.id, ³nuricahyono@amikom.ac.id

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Abstract

Diagnosis of Covid using the RT-PCR (Reverse Transcription Polymerase Chain Reaction) test requires high costs and takes a long time. For this reason, another method is needed that can be used to diagnose Covid-19 quickly and accurately. Random Forest is one of the popular classification algorithms for making predictive models. Random forest involves many hyperparameters that control the structure of each tree, the forest, and its randomness. Random Forest is a method which very sensitive to hyperparameter values, as their prediction accuracy can increase significantly when optimized hyperparameters are predefined and then adjusted according to the procedure. The purpose of doing hyperparameter tuning on the random forest algorithm is to increase accuracy in the diagnosis of covid-19. Searching for optimal values of hyperparameters is done by the Grid Search method and Random Search. The result explains that the Random Forest can be used to diagnose Covid-19 with an accuracy of 94%, and with hyperparameter tuning, it can increase the accuracy of the random forest by 2%.

Keywords: Hyperparameter Tuning, Random Forest, Covid-19, Accuracy, Classification

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*Corresponding Author: Anna Baita

1. INTRODUCTION (UPPERCASE, 10pt, bold)

Corona Virus Disease 2019 (Covid 19) is a global pandemic that has hit various countries. Even though the pandemic has been going on for more than 2 years, there are still 794,000 new cases of Covid-19 and more than 4,800 deaths reported in the last 28 days (12 June to 9 July 2023) [1]. Diagnosis of Covid-19 disease is generally carried out using the RT-PCR (Reverse Transcription Polymerase Chain Reaction) test [2]. The RT-PCR test can diagnose Covid disease fairly accurately [3]. However, the RT-PCR test requires quite a high cost [4] and is time-consuming [5]. Therefore, many studies have been developed to diagnose Covid disease quickly and accurately.

Machine learning is widely used in the health sector, including diagnosing covid[6]. Random Forest is a machine learning algorithm widely used to research Covid-19. Gupta's research[7] discusses predicting confirmed cases, deaths, and recoveries from Covid-19 using the Random Forest algorithm. Predictions are made based on the observation date, time, and region in India. According to this study, the random forest algorithm has better accuracy results

when compared to the Decision Tree, Multinomial Logistic Regression, Neural network, and SVM algorithms. Rostami's research [8] discusses feature selection using random forests to diagnose Covid-19. The diagnosis of COVID-19 is made based on the results of routine blood tests. Aser's research [9] conducted a classification using the KNN and Random Forest algorithms to predict Covid 19. This research was conducted to predict the number of daily cases. Several deep learning techniques have also been implemented to diagnose Covid-19 based on chest Xray images and lungs [10]–[12].

In Gupta and Aser's study, predictions of COVID-19 were not used for diagnosis but to predict the number of cases. Previous research which use images and test blood approaches to diagnose Covid-19 requires expensive fees, specialist staff, and a certified laboratory. Therefore, in this study, we proposed diagnosing Covid using symptoms and parameters everyone can check independently.

Random forest involves many hyperparameters that control the structure of each tree, the forest, and its randomness[13].

Random Forest is a method which very sensitive to hyperparameter values, as their prediction accuracy significantly increase when optimized hyperparameters are predefined and then adjusted according to the procedure[14].

Imbalanced class allocation affects training classification process, leading to an unfavorable bias for majority class [15]. Smote is a method commonly used to overcome distribution inequality imbalanced data [16], [17].

Therefore we will perform hyperparameter tuning on the random forest classifier to improve the accuracy of the random forest classifier in this Covid-19 diagnosis.

RESEARCH METHOD

The research flow is illustrated in Figure 1 below:

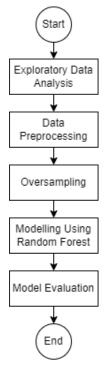


Figure 1. Research Flow

2.1 Exploratory Data Analysis

Exploratory Data Analysis (EDA) examines available datasets to find patterns, find anomalies, test hypotheses and check assumptions using statistical measures [18]. EDA is used to determine the important characteristics of the dataset used.

2.2 Data Preprocessing

Data preprocessing is the process of preparing data for analysis. The dataset is preprocessed to check missing values before executing it to the algorithm. Data transformation ensures the data's compatibility with the algorithm used in the mining process. Feature selection is selecting features to be used in model building. In this research, the feature selection process is carried out by looking for the value of Pearson's Correlation. Pearson's Correlation is the most popular

method for measuring the direction and strength of a linear relationship between two variables [19].

2.3 Oversampling

Synthetic Minority Oversampling Technique (SMOTE) [20] is one of the oversampling methods in dealing with imbalanced datasets. SMOTE generates a new sample from the minority class without repetition. SMOTE generates synthetic minority examples using the k nearest neighbors of the allowed minority examples, as the following figure 2 shows

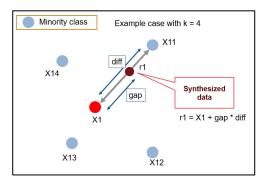


Figure 2. The principle of the synthetic minority oversampling technique (SMOTE) [21]

SMOTE can improve accuracy results compared to classifications without balancing the dataset [22].

2.4 Modelling Using Random Forest

2.4.1 Random Forest

A Random Forest model contains many decision trees[23]. A Random Forest is an effective tool in prediction. Random forest was first introduced by Breinman [24]. Determination of the classification with Random Forest is done based on the results of voting from the formed decision tree. The way Random Forest works is shown in the following figure 3:

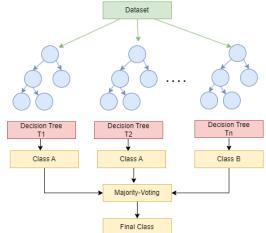


Figure 3. Random Forest Classifier

2.4.1 Tuning Random Forest

Random Forest algorithm hyperparameters that can affect its performance [13]. Tuning is finding the optimal hyperparameters of an algorithm during the learning process. Hypermeter tuning is done by training and evaluating the model using different hyperparameter combinations using kfold validation and selecting a set of hyperparameters that produce low error values [25]. There are 2 methods commonly used in hyperparameter tuning, namely grid search and random search [26]. Grid search is a method in hyperparameter tuning by trying all combinations of parameters in the search space. The combination of parameters that is want to try is stored in the grid. Grid Search will look for the parameter combination that has the smallest error [27]. Random Search exploration parameters are taken randomly from a combination of parameters in the search space [28].

2.5 Model Evaluation

A confusion matrix is used to evaluate the model that has been built. True positives are the number of predicted values worth true that identify those affected by Covid 19. True negatives are the predicted values that are true for data that are not affected by Covid 19. False positives are predictions that are false for data affected by Covid 19. Furthermore, False negatives are predictions with a false value for data unaffected by Covid 19. The analysis is carried out with accuracy, precision, recall, f1-score, and ROC-AUC value metrics.

Result And Discussion

The data used in this study comes from Kaggle[29]. In the Exploratory data analysis process, information was obtained that the dataset consisted of 5,434 data. The dataset has 20 features, namely: Breathing Problems, Fever, Dry Cough, Sore throat, Running Nose, Asthma, Chronic Lung Disease, Headache, Heart Disease, Diabetes, HyperTension, Fatigue, Gastrointestinal, Abroad travel, Contact with COVID Patient, Attended Large Gathering, Visited Public Exposed Places, Family working in Public Exposed Places, Wearing Masks, Sanitization from Market. All features of the dataset are of type object (data categorical). The target label/variable from the dataset is Covid-19 which has the values 'Yes' and 'No'. The covid-19 dataset is imbalanced dataset as shown in Figure 4 below:

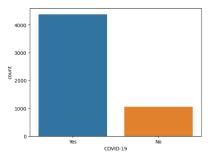


Figure 4. Target Classess

Class 'No' consists of 1051 data, while class 'Yes' consists of 4383 data.

3. 1 Data Preprocessing

3.1.1 Data Cleaning

First, we check for empty data. The results of checking the empty data are shown in the following figure:

Data	columns (total 21 columns):		
#	Column	Non-Null Count	Dtype
0	Breathing Problem	5434 non-null	
1	Fever	5434 non-null	object
2	Dry Cough	5434 non-null	object
3	Sore throat	5434 non-null	object
4	Running Nose	5434 non-null	
5	Asthma	5434 non-null	object
6	Chronic Lung Disease	5434 non-null	object
7	Headache	5434 non-null	object
8	Heart Disease	5434 non-null	object
9	Diabetes	5434 non-null	object
10	Hyper Tension	5434 non-null	object
11	Fatigue	5434 non-null	object
12	Gastrointestinal	5434 non-null	object
13	Abroad travel	5434 non-null	object
14	Contact with COVID Patient	5434 non-null	object
15	Attended Large Gathering	5434 non-null	object
16	Visited Public Exposed Places	5434 non-null	object
17	Family working in Public Exposed Places	5434 non-null	object
18	Wearing Masks	5434 non-null	object
19	Sanitization from Market	5434 non-null	object
20	COVID-19	5434 non-null	object

Figure 5. Dataset Information

From Figure 5, it can be seen that the Covid-19 dataset does not have a missing value.

3.1.2 Data Transformation

In this step, all variables from the dataset are converted into numeric types using encoder labels. The process and results of data transformation are shown in Figure 6 below:

```
In [10]: label_encoder = LabelEncoder()
for col in df.columns:
    df[col] = label_encoder.fit_transform(df[col])
In [11]: num_cols = df.select_dtypes(include=np.number).columns.tolist()
    print("Numerical Variables:")
    print(num_cols)
                              Numerical Variables:
                                 umerical Variables:
"Breathing Problem", 'Fever', 'Dry Cough', 'Sore throat', 'Runnin
(Nose', 'Asthma', 'Chronic Lung Disease', 'Headache', 'Heart Dise
se', 'Diabetes', 'Hyper Tension', 'Fatigue', 'Gastrointestinal
, 'Abroad travel', 'Contact with COVID Patient', 'Attended Large
jathering', 'Visited Public Exposed Places', 'Family working in Pu
lic Exposed Places', 'Wearing Masks', 'Sanitization from Market',
Comp. 10-12.
```

Figure 6. Data Transformation

3.1.3 Feature Selection

Feature selection is done by looking at the correlation of each feature to the target variable. Features used in the classification process have a correlation value > 0.1. From the feature selection process, 10 features were obtained with a high correlation with the target variable. These features include Respiratory Problems, Fever, Dry Cough, Sore Throat, Hypertension, Travel Overseas, Contact with COVID Patients, Attending Large Meetings, Visiting Public Exposed Places, and Families Work in Public Exposed Places. The process and results of feature selection are shown in Figure 7 below:

```
In [16]: #Correlation with output variable cor_target = abs(cor['COVID-19']) #Selecting highly correlated features relevant_features = cor_target[cor_target>0.1]
                relevant_features
Out[16]: Breathing Problem
                 Prever Dry Cough Sore throat Hyper Tension Abroad travel Contact with COVID Patient
                                                                                               0.443764
0.352891
0.464292
0.502848
0.102575
0.443875
                                                                                                0.357122
                  Attended Large Gathering
Visited Public Exposed Places
                                                                                                0.390145
                                                                                                0.119755
                  Family working in Public Exposed Places
                                                                                                0.160208
                  COVID-19
                                                                                                1.000000
                  Name: COVID-19, dtype: float64
```

Figure 7. Feature Selection

3.1.4 Oversampling

```
from collections import Counter
from imblearn.over_sampling import BorderlineSMOTE
from imblearn.over_sampling import SMOTE
print('Original dataset shape %s' % Counter(y))
Original dataset shape Counter({1: 4383, 0: 1051})
sm = SMOTE(random_state=42)
X res, v res = sm.fit resample(X, v)
print('Resampled dataset shape %s' % Counter(y res))
Resampled dataset shape Counter({1: 4383, 0: 4383})
```

Figure 8. Oversampling

In Figure 8, the SMOTE method generates samples in class 0 (No), so there are 4383 data. Thus, classes 0 and 1 are now balanced.

3. 2 Modelling

After the data is oversampled, the data is used to build a model using the Random Forest algorithm. To improve the results of the accuracy of the hyperparameter tuning process is carried out. The list of search spaces used in hyperparameter tuning is shown in Table 1 below:

Table 1. Search Space

No	Parameter	Value
1	N_estimator	[200,300,400,500]
2	Max_features	['auto','sqrt','log2']
3	Max_depth	[4,5,6,7,8]
4	Min_samples_split	[2,3,4,5]
_5	Min_samples_leaf	[1,2,3,4,5]

RandomSearchCV and GridSearchCV carry out the optimal parameter search process. The Cross Validation (CV) used in this study is 10-fold. CV RandomSearch process is faster GridSearchCV. GridSearch CV will build a model combining each value parameter in the search space. The total number of models built during the grid search process is 12,000 models. Therefore, the computational process of Gridsearch is very long. The optimal parameter results from the GridsearchCV and RandomSearchCV processes are shown in Table 2 below:

Table 2. Best Parameter

No	Parameter	Grid	Random
		Search	Search
1	N_estimator	300	300
2	Max_features	auto	auto
3	Max_depth	8	8
4	Min_samples_split	-	3
5	Min_samples_leaf	-	-

N estimator represents the number of trees in a random forest. Usually, more trees will be able to study the data pattern better. In Random Forest, a random subset of features is considered to find the best split. Max features help determine how many features should be included in the split. It can take four values: "auto", "sqrt", "log2", and "none".

Max_depth is one of the most important hyperparameters in improving model accuracy. Increasing the tree depth increases the model accuracy up to a certain limit, after which it gradually decreases due to model overfitting. Specifies the minimum number of samples an inner node must contain to split into other nodes. In this case if the value of min samples splits is very low, the tree will continue to grow, and overfitting will begin.

Min_samples_leaf specifies the minimum number of samples a node should contain after splitting. It also helps reduce overfitting when there are many

The modeling results obtained without parameter tuning and with hyperparameter tuning are shown in table 3 below:

Table 3.	Experime	nt Result
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No	Metric (mean)	Without Hyper parameter Tuning	Grid Search	Random Search	
1	Accuracy	0.94	0.96	0.96	
2	Precision	1	0.98	0.98	
3	Recall	0.93	0.93	0.93	
4	F1-Score	0.96	0.95	0.95	
5	ROC-AUC	0.99	0.99	0.99	

Hyperparameter tuning using grid search and random search can increase system accuracy by 2%. Hyperparameter tuning with grid search and random search has no difference in results. However, the computational process of grid search requires more time when compared to random search.

The default value of the random forest parameter using the Scikit learn library can produce an optimal model. Hyperparameter tuning is effective in increasing accuracy but not for other metrics.

4. CONCLUSION

Based on the above reviews, Hyperparameter tuning in random forest can increase the accuracy value but not necessarily improve Precision, Recall or F1-Score. Determining the value of the search space will affect the results of hyperparameter tuning.

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