

An Application of Genetic Algorithm Approach and Cobb-Douglas Model for Predicting the Gross Regional Domestic Product by Expenditure-Based in Indonesia

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Abstract—This paper empirically investigates the modeling of Gross Regional Domestic Product (GRDP) prediction using a genetic algorithm approach and Cobb-Douglas model and also studied the variables that influence it. The genetic algorithm approach used to estimate the Cobb-Douglas model parameters. Meanwhile, the Cobb-Douglas model utilized for predicting the model of GRDP that measured using the value of expenditure (expenditure-based). Further, we also discussed the comparison of the level of prediction errors using the genetic algorithm and ordinary least square (OLS) approaches. The results of the analysis show the level of prediction errors in the sample assessed by using Mean Absolute Percentage Error (MAPE) that obtained from the estimator using genetic algorithms approach is 0.177, while by using the OLS approach is 0.190. It shows that the prediction value of errors from a genetic algorithms approach is smaller when compared to the OLS approach. Of these, we found that the genetic algorithm is the best approach used to estimate the model of GRDP that measured using the value of expenditure in Garut Regency, Indonesia. Also, by using a genetic algorithm approach, this study also found that the variables of government consumption expenditure, gross domestic fixed capital formation, and net export, and determined inventory changes, the GRDP prediction for the next two periods is IDR 44,449,327 and IDR 45,457,805. Therefore, the model of GRDP prediction using expenditure-based values can be used as a consideration in making the budget plan by the local government in Garut Regency, Indonesia.

Keywords : GRDP; Cobb-Douglas model; Genetic algorithm and MAPE.

I. INTRODUCTION

GROSS Regional Domestic Product (GRDP) at the regional level (province / regency) is an indicator to measure the ability of a region to create output (value added)

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at a certain period [1]. GRDP is the amount of added value generated by all business units in a in a particular region or the sum of the value of end goods and services produced by all economic units in a region [2]. GRDP based on expenditures are all components of final demand consisting of: household consumption expenditure and private non-profit entities, government consumption, gross domestic fixed capital formation, inventory change, and net exports (representing exports minus imports). GRDP describes the economic development of a region and can also be used as a reference in evaluating and planning regional development [3]. Therefore, it is crucial to predict GRDP by using an appropriate method.

There are several studies relevant to GRDP prediction modeling referenced, in this study. For example, analyzed the effect of foreign direct investment net entry on GDP in Poland between 1994-2012, using the Cobb-Douglas production function was presented in [4]-[5]. In such an analysis defined conditions necessary for the positive influence of foreign direct investment in Poland. Also assumed the assumptions are the Cobb-Douglas production function and predicted changes in GDP value in Poland. I also identify the factors that significantly affected economic growth in Poland. Based on the analysis, it is shown that gross fixed capital formation, employment, foreign direct investment, exports, and research & development affected the change of GDP value in Poland. Similar research using Cobb-Douglas production function for GDP prediction can be seen in [6]-[9]. In 2004, Junoh described a comparative case study between neural network and econometric approaches to predict GDP growth in Malaysia using knowledge-based economy indicators based on time series data collected from 1995-2000. The results show that the neural network technique has an increased potential to predict GDP growth based on knowledge-based economy indicators [10]. In 2013, Nigar and Saxena presented a new genetic algorithm-based system for inductive machine learning [11]. The system presented can be used for economic prediction, especially to predict a country's GDP. They present a genetic algorithm-based system that can be used to predict a country's GDP, with adaptive genetic algorithm learning techniques. The system presented provides all the necessary input facilities, in order to make predictions with the best results. In 2016, Gaffar developed a genetic algorithm for the analysis and forecast of regional economic growth, in which agricultural and industrial sectors as independent variables [1]. The research

was conducted in East Kalimantan Province between 2002-2012. Based on the results of the study, it is suggested to use genetic algorithms in order to improve the accuracy of regional economic growth predictions. Similar studies have also been carried out on [12]-[13].

Motivated by a considerable in GRDP, this work makes a contribution to the predictive modeling of GRDP based on expenditure by using Cobb-Douglas production function, and parameter estimation by using a genetic algorithm approach. In the last focus section, the Cobb-Douglas model and genetic algorithm are used for predictive modeling of GRDP based on expenditure in Garut regency of Indonesia.

II. MATERIALS AND METHODS

In this section, the discussion covers materials and methods. The material is to describe the data used in the research following the source while the method is to explain the models and approaches used to analyze the data.

A. Material

The data analyzed in this research is the economy of Garut Regency, namely Gross Regional Domestic Product (GRDP), especially those based on expenditure. Related data obtained from the Central Bureau of Statistics (CBS) Garut regency, between 2010 and 2016. The model used in this study is the Cobb-Douglas production function, which is estimated using a genetic algorithm. The data were analyzed using Microsoft Excel and Eviews 9.0 software applications, as well as Matlab R2013a.

B. Method

In this section, we discussed the models and the algorithm approach used in data analysis, for predictions modeling of GRDP based on expenditure.

Cobb-Douglas production function

The production function is defined as the relationship between the factors of production (input) used with the resulting output [14]-[15]. In 1928, Charles Cobb and Paul Douglas developed a model of the relationship between factors of production and output, after this referred to as the Cobb-Douglas production function [16]. In economics, the Cobb-Douglas production function is widely used to describe the relationship between output and input.

The Cobb-Douglas production function with more than two independent variables can be described as follows [17]:

$$Y = bX_1^{\beta_1} X_2^{\beta_2} X_3^{\beta_3} \dots X_n^{\beta_n} e^\varepsilon \quad (1)$$

Where Y is the dependent variable (output); b constant intercept; $X_1, X_2, X_3, \dots, X_n$ independent variable (input); $\beta_1, \beta_2, \beta_3, \dots, \beta_n$ elasticity of the independent variable; $e = 2.7182818285$ natural numbers; and ε error (residual).

The sum of elasticities is a measure of returns to scale. Thus, there are three possible alternatives [18]-[19]:

- Decreasing returns to scale, if $\sum_{i=1}^n \beta_i < 1$

It is an increasingly decreasing yield on the scale of production, where output increases with a smaller proportion of inputs.

- Constant returns to scale, if $\sum_{i=1}^n \beta_i = 1$

It is an addition that has a constant result on the scale of production, when all inputs increase in certain proportions, and the output produced in the same proportion equals the proportion of the input.

- Increasing returns to scale, if $\sum_{i=1}^n \beta_i > 1$

It is an increasing addition to the production scale, where output increases with a greater proportion of inputs.

Equation (1) can be transformed natural logarithm into equation (2), thus yielding the following linear equation:

$$\ln Y = \ln b + \beta_1 \ln X_1 + \beta_2 \ln X_2 + \beta_3 \ln X_3 + \dots + \beta_n \ln X_n + \varepsilon \quad (2)$$

If we let $A = \ln Y, \beta_0 = \ln b, D_1 = \ln X_1, D_2 = \ln X_2, D_3 = \ln X_3, \dots, D_n = \ln X_n$, then equation (2) can be expressed as a linear regression equation:

$$A = \beta_0 + \beta_1 D_1 + \beta_2 D_2 + \beta_3 D_3 + \dots + \beta_n D_n + \varepsilon \quad (3)$$

The estimator of equation (3) is:

$$\hat{A} = \beta_0 + \beta_1 D_1 + \beta_2 D_2 + \beta_3 D_3 + \dots + \beta_n D_n \quad (4)$$

The following equation gives the sum of the residual squares of equation (3):

$$\sum \varepsilon^2 = \sum (A - \beta_0 - \beta_1 D_1 - \beta_2 D_2 - \beta_3 D_3 - \dots - \beta_n D_n)^2, \quad (5)$$

where is the residual $\varepsilon = A - \hat{A}$.

Genetic algorithm

A genetic algorithm is a heuristic method developed based on genetic principles and the natural selection process of Darwin's Evolutionary Theory [20]. A genetic algorithm was invented by John Holland around the 1960s and was developed by his student David Goldberg in the 1980s. The search process of a settlement in a genetic algorithm takes place the same as the election of an individual to survive in the evolutionary process [21-22]. In the process of evolution will be obtained individuals who can survive, which these individuals have repeatedly experienced gene changes to adjust to the environment. These gene changes occur through breeding, which in the genetic algorithm this breeding process is the rationale in getting better children.

The general structure of the genetic algorithm is the following steps [23-25]:

- Initial population generation, this initial population was generated randomly to obtain an initial solution;
- The population consists of some chromosomes that indicate the solution achieved;
- The formation of a new generation, to form a new generation three operators are involved, namely reproduction / selection, cross over and mutation;

- Evaluation of the solution, the process of each population is evaluated by determining the fitness value of each chromosome, and the evaluation is carried out until the criteria of discontinuation are met. If the termination criterion has not been met, a new generation is re-established by repeating step b).

Based on the structure of the genetic algorithm, to minimize the objective function as the sum of residual squares (5), the following genetic algorithms can be prepared [26]:

- 1) Determination of the initial population, the initial population is determined as much J , which generated randomly. This initial random population number is then transformed into the form of decimal values θ_j , with $j = 1, \dots, J$;
- 2) Evaluation of the chromosome, the fitness value of the chromosome is the objective function as the sum of the residual quadratic equations (5). The fitness values are chosen the smallest, for the minimization program.
- 3) Determination of population convergent percentage, percentage convergent population p_c , is a percentage of the number of individuals who generate the same fitness score and the most. The value of population convergence p_c this is calculated based on the following equation:

$$p_c = \frac{n}{pop} \times 100\%, \quad (6)$$

Where n the number of individuals that can produce the same fitness and the most, and pop population number. Item Evaluation of dismissal conditions is the genetic algorithm process will be dismissed when the generation counter has reached the number of generations c_g , which is specified as big as $c_g = 1000$, or a convergent percentage population p_c has reached the threshold limit specified i.e. $\tau = 90\%$.

- 4) Chromosome selection is the selection process based on roulette wheel selection. For the minimization program, evaluate the fitness value $eval(v_i), i = 1, \dots, n$, do refer to equation (5), using equations:

$$eval(v_i) = \frac{1}{1 + f(\theta)} \quad (7)$$

with $f(\theta)$ the fitness values based on equations (5), and $\theta' = (\beta_0, \beta_1, \beta_2, \beta_3, \dots, \beta_n)$.

- 5) Cross-breeding is a new population of selection is conducted by cross-breeding, based on the Single-Point Crossover (SPX).
- 6) Mutations; the mutation of each generation is done by calculation $m \times pop_size \times p_m$, where is the number of mutations, pop_size population size, and p_m probability of mutation (probability value is determined randomly).
- 7) Decoding, is the process of coding the genes in the chromosome to return its original value, i.e. transforming coding into decimal values.

Test statistic for model evaluations

- **Multicollinearity test statistic**

On the assumption of multiple linear regression model is the absence of multicollinearity on independent variables. The multicollinearity test was performed to test the strong linear relationship between the

independent variables in multiple regression equations. There are several testing methods that can be used for multicollinearity test, i.e. by looking at the value of Variance Inflation Factor (VIF) in the regression model. If the value of Variance Inflation Factor (VIF) > 10 on each independent variable, it can be concluded that the model is multicollinearity [27-28].

Some alternative ways to solve the problem if there is multicollinearity are as follows: (i) replacing or removing variables that have high correlation; (ii) Increasing the number of observations; and (iii) Transforming data into other forms, such as natural logarithms, square roots, or first difference delta form.

- **Heteroscedasticity test statistic**

The linear model of multiple regression has the assumption that the equation is the same, or in other words homogeneous so that heteroscedasticity should not occur. Heteroscedasticity occurs at the time of residual and the predicted value has a correlation or relationship pattern. Heteroscedasticity test is performed to determine the equal or not variant, from residual observation one with other observation on regression model [29]. Spearman correlation rank test is one way to determine the occurrence of heteroscedasticity.

In Spearman's rank correlation test statistic, the hypothesis used is H_0 : no heteroscedasticity occurs, and H_1 : heteroscedasticity occurs. The test is done by determining the sequence value of $|\varepsilon_t|$ and D_{it} , determined rank $r_{i.s}$ using equations:

$$r_{i.s} = 1 - 6 \left[\frac{\sum_{i=1}^n d_i^2}{n(n^2 - 1)} \right] \quad (8)$$

where $r_{i.s}$ is Spearman's correlation rank coefficient, and d_i deviation, which can be determined by using the equation $d_i = rank(D_{i,t}) - rank|\varepsilon_t|$. Next, specify a statistical value $t_{i.stat}$ with equations:

$$t_{i.stat} = \frac{r_s \sqrt{n-2}}{\sqrt{1-r_s^2}} \quad (9)$$

Determining the value of $t_{(\frac{\alpha}{2}, v)}$ with a significance level $\alpha = 0.05$ and degrees of freedom $v = n - 2$. Testing criterion is rejected H_0 , if $t_{i.stat} < -t_{(\frac{\alpha}{2}, v)}$ or $t_{i.stat} > t_{(1-\frac{\alpha}{2}, v)}$

- **Autocorrelation test statistics**

Autocorrelation tests are used to determine whether the residuals of an observation are related to each other. Autocorrelation occurs when there is a high correlation between error values [30]. The assumption of multiple linear regression model is no autocorrelation. How to detect the existence of autocorrelation can be done by using Durbin-Watson test statistic (DW).

The hypothesis used is H_0 : no autocorrelation occurs, and H_1 : autocorrelation occurs. The DW statistical test, done by calculating the statistical value d_{stat} using

equations:

$$d_{stat} = \frac{\sum_{t=1}^T (\varepsilon_t - \varepsilon_{t-1})^2}{\sum_{t=1}^T \varepsilon_t^2} \quad (10)$$

where T the number of data, and ε_t residual at time t . Next, determine the value d_L and d_U from the Durbin-Watson (DW) table. Testing criterion is rejected H_0 if $d_{stat} < d_L$ or $d_{stat} > 4 - d_L$, and accept if $d_L \leq d_{stat} \leq 4 - d_U$. If in other conditions, it cannot be concluded [31].

- **Normality test statistic**

The normality test is used to determine the distribution of residual data to spread normally or not. Normality can be detected by testing Kolmogorov-Smirnov (KS). The hypothesis used is H_0 : data is normally distributed, and H_1 : data is not normally distributed. The test is done by determining the residual deviation, ie by using the equation:

$$s_{\varepsilon_t} = \sqrt{\frac{\sum_{t=1}^T (\varepsilon_t - \bar{\varepsilon})^2}{T - 1}} \quad (11)$$

Transform value ε_t become z_t with equations $z_t = (\varepsilon_t - \bar{\varepsilon})/s_{\varepsilon_t}$. Determine the probability value $P(z_i)$ based on standard normal distribution table. While the chances are proportional $S(z_t)$ determined using the equation $S(z_t) = randl(z_t)/n$.

Next, calculated the value of the absolute difference $|S(z_t) - P(z_t)|$. Statistics of Kolmogorov-Smirnov KS_{stat} determined using the equation:

$$KS_{stat} = \max \{ |S(z_t) - P(z_t)| \} \quad (12)$$

Determine the critical value of statistic $KS_{(\alpha, T-1)}$, with significant levels $\alpha = 0.05$. The testing criteria are rejected H_0 if $KS_{stat} > KS_{(\alpha, T-1)}$.

- **Goodness of fit test**

Goodness of fit test is conducted to know whether a variable can be approached by using a theoretical model or not [32]. In this research the goodness of fit test performed include: partial parameter significance test, simmer synthesis significance test, and correlation test between independent variable with dependent variable.

- **Partial significance test statistic**

This partial significance test, intended to test the significance of each parameter $\theta_i (i = 0, 1, 2, 3, \dots, n)$, where $\theta_i \in \{\beta_0, \beta_1, \beta_2, \beta_3, \dots, \beta_n\}$ of equation (4), in affecting the dependent variable. For parameter test θ_i , the hypothesis used is $H_0 : \theta_i = 0$ and $H_1 : \theta_i \neq 0$. The test is conducted by using statistic t_{stat} , where the equation is:

$$t_{stat} = \frac{\theta_i}{SE(\theta_i)}, \quad (13)$$

where $SE(\theta_i)$ is the standard error of parameter θ_i .

Reject the hypothesis H_0 if $|t_{stat}| > |t_{(T-2, \frac{1}{2}\alpha)}|$, or $Pr[t_{stat}] < \alpha$, where $t_{(T-2, \frac{1}{2}\alpha)}$ the critical value of the distribution- t at a level of significance of $100(1 - c)\%$, and T the number of data.

- **Test statistics for parameters simultaneously**

This simultaneous significance test, intended to test the significance of the parameters simultaneously $\theta_i (i = 0, 1, 2, 3, \dots, n)$, where $\theta_i \in \{\beta_0, \beta_1, \beta_2, \beta_3, \dots, \beta_n\}$ of equation (4), in affecting the dependent variable. The hypothesis used is $H_0 : \theta_1 = \theta_2 = \theta_3 = 0$ and $H_1 : \theta_1 \neq \theta_2 \neq \theta_3 \neq 0$. Testing is done by using statistic F , where the equation is:

$$F_{stat} = \frac{MS_{reg}}{s^2}, \quad (14)$$

Where MS_{reg} mean square due to regression, and s^2 mean square due to residual variation.

Reject the hypothesis H_0 if $F_{stat} > F_{(1, T-2, 1-\alpha)}$, or $Pr[F_{stat}] < \alpha$, where $F_{(1, T-2, 1-\alpha)}$ the critical value of the distribution F at the level of significance $100(1 - \alpha)\%$, and T the number of data.

- **Test statistic of coefficient of determination R^2**

The coefficient of determination R^2 measure how large the diversity of independent variables to the dependent variable, based on the level of strength of the relationship. So the coefficient of determination is the ability or influence of independent variables $D_i (i = 1, 2, 3, \dots, n)$ to affect the dependent variable A . The equation of R^2 are as follows:

$$R^2 = \frac{\sum_{t=1}^T (\hat{A}_t - \bar{A})^2}{\sum_{t=1}^T (A_t - \bar{A})^2} \quad (15)$$

The value of the coefficient of determination is between 0 and 1. Values R^2 a small close to 0 means that the variation of the independent variable is very limited, and a value close to 1 means the variation of the independent variable can provide all the information needed to predict the dependent variable.

- **Prediction(Forecasting)**

Forecasting is done because of the complexity and uncertainty faced by the forecasting model [33]. There are many methods that can be used to measure the accuracy of a forecasting model, including the Mean Absolute Percentage Error (MAPE). MAPE can be determined using the following equation [34-35]:

$$MAPE = \left(\frac{1}{T} \sum_{t=1}^T \left| \frac{A_t - \hat{A}_t}{A_t} \right| \right) \times 100\% \quad (16)$$

The smaller the MAPE values, the smaller the value of error, and the greater the degree of accuracy.

III. RESULTS AND ANALYSIS

In this section we discuss the result and analysis which includes: natural logarithm transformation data; estimating parameters; test classical assumptions; estimating parameters using genetic algorithm; test the goodness of fit; and predict GRDP based on expenditure.

- **A. Data of natural logarithm transformation**

Referring to equation (5), for the purpose of estimating Cobb-Douglas model parameters, the GDP data based on expenditure is done by natural logarithm transformation. The data of natural logarithm transformation is given in

TABLE I
TRANSFORMATION DATA OF GRDP BASED ON EXPENDITURE

ln Y	ln X ₁	ln X ₂	ln X ₃	ln X ₄	ln X ₅
17.053	16.833	11.860	14.489	14.347	14.014
17.125	16.917	11.913	14.571	14.716	13.950
17.229	17.013	11.988	14.727	14.055	14.501
17.333	17.106	12.208	14.785	14.674	14.301
17.429	17.199	12.283	14.843	14.708	14.577
17.521	17.303	12.247	15.031	14.586	14.612
17.609	17.393	12.308	15.161	14.694	14.605

Table I.

Where Y is GRDP based on expenditure; X₁ household consumption expenditure; X₂ consumption expenditures of non-profit households; X₃ government consumption expenditure; X₄ gross domestic fixed capital formation and net exports (exports minus imports); and X₅ inventory changes.

B. Estimating parameters

Parameter estimation on equation (2) is done by analytical method and genetic algorithm. Referring equation (5), analytical parameter estimation can be done by using Ordinary Least Square (OLS) method with Eviews 9.0 software, obtained by estimator of coefficient parameter and standard error as given in Table II.

TABLE II
ESTIMATOR OF COEFFICIENT PARAMETERS

Variable	Coefficient	Std. Error
D ₁	0.305366	0.125006
D ₂	-0.022354	0.011528
D ₃	0.378964	0.075314
D ₄	0.144172	0.019291
D ₅	0.155369	0.023682
C	2.44177	0.420262

Based on the parameter estimators in Table II, with rounding up to two decimal places, a linear regression equation can be composed as follows:

$$\hat{A} = 2.44 + 0.31D_1 - 0.02D_2 + 0.38D_3 + 0.14D_4 + 0.16D_5 \quad (17)$$

C. Testing the classical assumptions

Testing the classical assumptions made here include: multicollinearity test, heteroscedcedity test, autocorrelation test, and normality test.

Testing the multicollinearity

The multicollinearity test was performed on the parameter of the estimated regression equation presented in Table II and equation (18). The tests were performed using the help of Eviews 9.0 software, and the results are given in Table III.

The VIF value can be seen in the fourth column of the centered VIF column. Based on Table III, the VIF value of all independent variables is higher than 10, so it can be concluded that multicollinearity occurs. Because multicollinearity occurs, it must issue the independent variable that has the most substantial VIF value is variable D₁. After that, re-estimation is done. The re-estimate is also done using

the help of Eviews 9.0 software, and the results presented in Table IV.

TABLE III
MULTICOLLINEARITY TEST RESULTS

Variable	Coefficient Variance	Uncentered VIF	Centered VIF
D ₁	0.015626	28345386	3445.415
D ₂	0.000133	120879.8	25.06571
D ₃	0.005672	7700851	1708.662
D ₄	0.000372	487596.1	123.5563
D ₅	0.000561	717401.0	238.9366
C	0.176620	1094326	NA

TABLE IV
FIRST RE-ESTIMATE RESULTS

Variable	Coefficient	Std. Error
D ₂	-0.019624	0.021415
D ₃	0.562562	0.009044
D ₄	0.189614	0.009539
D ₅	0.210421	0.013583
C	3.463677	0.070204

Based on the parameter estimators in Table IV, with rounding up to two decimal places, a linear regression equation can be prepared as follows:

$$\hat{A} = 3.46 - 0.02D_2 + 0.56D_3 + 0.19D_4 + 0.21D_5 \quad (18)$$

Multicollinearity test results after removing the variable D₁ shown in Table V.

TABLE V
MULTICOLLINEARITY TEST RESULTS FIRST RESET

Variable	Coefficient Variance	Uncentered VIF	Centered VIF
D ₂	0.000459	119743.6	24.83010
D ₃	8.18E-05	31877.57	7.072986
D ₄	9.10E-05	34218.84	8.671015
D ₅	0.000185	67747.23	22.56380
C	0.004929	8765.936	NA

Based on Table V, there is still a VIF value greater than 10 i.e. $VIF_{D_2} = 24.83010$, so that will be released again independent variable that cause multicollinearities that have the biggest VIF value that is variable D₂. Repeat the second, also using the Eviews 9.0 software. The re-estimation results are presented in Table VI.

TABLE VI
SECOND RE-ESTIMATE RESULTS

Variable	Coefficient	Std. Error
D ₃	0.562406	0.008798
D ₄	0.181856	0.004277
D ₅	0.199818	0.006923
C	3.493336	0.060612

Based on the parameter estimators in Table VI, with rounding up to two decimal places, a linear regression equation can be composed as follows:

$$\hat{A} = 3.50 + 0.56D_3 + 0.18D_4 + 0.20D_5 \quad (19)$$

The second multicollinearity test results after removing the variable D₁ and D₂ given in Table VII.

TABLE VII
MULTICOLLINEARITY TEST RESULTS SECOND RESET

Variable	Coefficient Variance	Uncentered VIF	Centered VIF
D_3	7.74E-05	31866.39	7.070505
D_4	1.83E-05	7266.674	1.841367
D_5	4.79E-05	18591.80	6.192159
C	0.003674	6902.868	NA

Based on Table VII, the VIF value of all independent variables is smaller than 10, so it can be concluded that there is no multicollinearity to the independent variable D_3 , D_4 and D_5 . Therefore, the next stage is to test heteroscedasticity.

Testing the heteroscedasticity

Heteroscedasticity test was performed by Spearman’s rank correlation test statistic referring to equations (8) and (9). From the calculation results obtained respectively are as follows: for independent variable D_3 value of $r_{3.s} = 0.57$ and $t_{3.stat} = 1.55$; for independent variable D_4 value of $r_{4.s} = 0.29$ and $t_{4.stat} = 0.68$; and for independent variable D_5 value of $r_{5.s} = 0.64$ and $t_{5.stat} = 1.68$.

While at the level of significance $\alpha = 0.05$, of the distribution- t standard table and with degrees of freedom $v = 5$, obtained statistical critical value $t_{(0.025;5)} = -2.5706$ or $t_{(1-0.025;5)} = 2.5706$. So it happens that $t_{(0.025;5)} \leq r_{3.s}, r_{4.s}, r_{5.s} \leq t_{(1-0.025;5)}$, thus if the hypothesis refers to the Spearman rank correlation test, then the hypothesis H_0 be accepted. Means there is no heteroscedasticities on each independent variables D_3 , D_4 , and D_5 .

Testing the autocorrelation

The autocorrelation test conducted to identify the existence of correlation on the residual data of ε_t . The autocorrelation test was performed using the Durbin-Watson statistic test. The test is performed concerning (11), using the help of Eviews 9.0 software, the results are shown in Table VIII.

TABLE VIII
AUTOCORRELATION DETECTION RESULTS

R-squared	0.986106	Mean dependent var	4.57E-15
Adjusted R-squared	0.916635	S.D dependent var	0.001365
S.E. of regression	0.000394	Akaike info criterion	-13.07173
Sum squared resid	1.55E-07	Schwarz criterion	-13.11809
Log-likelihood	51.75104	Hannan-Quinn Criter	-13.64476
F-Statistic	14.19448	Durbin-Watson Stat	2.089043

Based on Table VIII, the Durbin-Watson statistical value $d_{stat} = 2.089043$. While with a significant level $\alpha = 0.05$, from the Durbin-Watson statistical table obtained values $d_L = 0.46723$ and $d_U = 1.896362$. To obtain the composition of values $d_L \leq d_{stat} \leq 4 - d_U$. If we refer to the Durbin-Watson statistic test, then the hypothesis H_0 is accepted. That is, there is no autocorrelation in the residual ε_t in observational data. When compared with research conducted by [36]. The results of our R-squared (98.16%) have a better performance level than the previous study, which was 95.09%.

Testing the residual normality

Normality assumption testing is performed with the aim of ensuring that residual ε_t the distribution follows a normal distribution with a mean of zero and a certain variance. Testing assumption of residual normality ε_t here is performed using the Kolmogorov-Smirnov (KS) statistical test. Testing

assumption of residual normality is done by referring to equations (12) and (13), using the help of Microsoft Excel 2010 software, and the results obtained values $KS_{stat} = 0.23741$.

While at the level of significance $\alpha = 0.05$ and with degrees of freedom $v = 7 - 1$, from the statistical table of Kolmogorov-Smirnov obtained critical value $KS_{(0.05;6)} = 0.483$. So it shows that $KS_{stat} \leq KS_{(0.05;6)}$, thus the hypothesis H_0 be accepted. Meaning that residual ε_t distribution follows normal distribution. Based on the estimation result obtained the mean value of residual ε_t is $\mu_\varepsilon = 3.5 \times 10^{-15} \approx 0$, and value of variance $\sigma_\varepsilon^2 = 1.86323 \times 10^{-16}$, thus residual $\varepsilon_t \sim N(0, 1.86323 \times 10^{-16})$.

Cobb-Douglas model estimate based on OLS

Based on the above description, the model evaluation test is met. The test results show that the data are normally distributed, free from multicollinearity, no heteroscedasticity, and no residual autocorrelation, and residual normal distribution with zero mean and variance. Therefore, indicating that the model estimator generated for GRDP is based on expenditure is the best estimator. The estimate of multiple linear regression equations for GRDP based on expenditure is given by equation (19).

Estimating the parameters by using genetic algorithms

Referring to the equation of multiple linear regression equations (19), in this section parameter estimation is used $\beta_0, \beta_3, \beta_4$, and β_5 , using a genetic algorithm approach. The goal is to get parameter estimators $\beta_0, \beta_3, \beta_4$, and β_5 , which is better than the estimator estimation parameter using OLS. Where parameter estimator results from genetic algorithm approach is expected to produce residual quantity $\sum \varepsilon_t^2$ and smaller MAPE values, as compared to the result parameter estimators of OLS.

Estimated parameters $\beta_0, \beta_3, \beta_4$, and β_5 , using a genetic algorithm approach is done by referring to the structure and stages contained in the genetic algorithm. The stages of parameter estimation $\beta_0, \beta_3, \beta_4$, and β_5 , using a genetic algorithm in this research was done with the help of Matlab R2013a software, as follows.

- Declaration of fitness function by click *file* → *new* → *function*.
- Type *optimtool* in the *command window*, then enter.
- Select *ga-Genetic Algorithm* on the solver. Enter the *fitness function* that has been stored in the *fitness function* box. In this case, the *fitness function* is the residual value equation for each sequence of periods (years).
- Enter the number of variables that the solution will look for in the number of variables box. In this study the sought is $\beta_0, \beta_3, \beta_4$, and β_5 , therefore the number of variables box is *filled 4*.
- Enter the lower limit and lower limit for parameter values $\beta_0, \beta_3, \beta_4$, and β_5 , on the bounds box. In this study, the lower limit enter [0 0 0 0] in the lower box, and [3.55 0.6 0.2 0.25] to the upper as the upper limit.
- Select *roulette* on *selection function* and *single point* on *crossover function*.
- Select *the stopping criteria*, select the stop criteria for the optimization process using genetic algorithm. In this study, the stopping criterion used is the number of generations.

- Check the *best fitness*, best individual, and *stopping options* in the plot functions.
- Click *start* to run the program and get the solution of the problems sought.

The process of parameter estimation $\beta_0, \beta_3, \beta_4$, and β_5 , using genetic algorithms done iteratively according to the sequence of years of GRDP data. In 2016 iteration sequence, in this study yields the smallest residual value. So the values of $\beta_0, \beta_3, \beta_4$, and β_5 , on the order of the year is selected for use in the formation of multiple linear regression models. The parameter estimator values obtained using the genetic algorithm are rounded to two decimal places $\beta_0 = 3.54, \beta_3 = 0.52, \beta_4 = 0.18$, and $\beta_5 = 0.24$. Using the parameter estimator by referring to equation (3), can compile multiple linear regression equations as follows:

$$A = 3.45 + 0.52D_1 + 0.18D_2 + 0.24D_5 + \varepsilon \quad (20)$$

- *Testing the goodness of fit*

To be more convincing result of estimation, in this research parameter estimator resulted from genetic algorithm approach, goodness of fit test is done. Goodness of fit test of parameter estimator is done by partial significance test, simultaneous significance test, and coefficient of determination test.

- *Testing the partial significance*

Partial testing is done with the aim to find out how significant each estimator contributes to the effect on the dependent variable. Testing of partial significance in this research is done by using statistic-*t*, refers to equation (14).

For parameter estimator $\hat{\beta}_0 = 3.54$, the hypothesis used is $H_0 : \hat{\beta}_0 = 0$ and $H_1 : \hat{\beta}_0 \neq 0$. The statistical value for $\hat{\beta}_0$ is $t_{stat(\hat{\beta}_0)}$ is determined by reference of equation (14), and values are obtained $t_{stat(\hat{\beta}_0)} = 6.35082$. While at the level of significance $\alpha = 0.05$ and degrees of freedom $v = 7 - 3 - 1$, from the distribution statistic-*t* table obtained critical value $t_{(1-0.025;3)} = 2.35366$. Therefore, $t_{stat(\hat{\beta}_0)} > t_{(1-0.025;3)}$, so hypothesis H_0 rejected. Meaning that parameter estimator $\hat{\beta}_0 = 3.54$ is a significant contribution to affect the dependent variable *A*.

Furthermore, in the same way, the test of partial significance is made against the parameter estimator $\hat{\beta}_3 = 0.52, \hat{\beta}_4 = 0.18$, and $\hat{\beta}_5 = 0.24$. The test results show that the three parameter estimators, each contributing significantly affect the dependent variable *A*.

- *Testing significance simultaneously*

Tests of simultaneous significance, conducted with the aim to find out how much the significance level of all parameter estimators together can affect the dependent variable. Significant testing simultaneously in this study was conducted by using statistical test *F*, which refers to equation (15).

In testing the simultaneous significance of the parameter estimator $\hat{\beta}_3 = 0.52, \hat{\beta}_4 = 0.18$, and $\hat{\beta}_5 = 0.24$, the hypothesis used is $H_0 : \hat{\beta}_0 = \hat{\beta}_3 = \hat{\beta}_4 = \hat{\beta}_5 = 0$, and $H_1 : \exists \hat{\beta}_0 \neq \hat{\beta}_3 \neq \hat{\beta}_4 \neq \hat{\beta}_5 \neq 0$. Statistic value of F_{stat} is determined by using equation (15), and the result is $F_{stat} = 36420643$. While at a significant level $\alpha = 0.05$, and with degrees of freedom $v_1 = 3$ and $v_2 =$

$7 - 3 - 1$, of the distribution F_{table} obtained critical value $F_{(0.05;3;3)} = 9.28$. So it shows that $F_{stat} > F_{(0.05;3;3)}$, therefore hypothesis H_0 rejected. Meaning that parameter estimators $\hat{\beta}_0 = 3.54, \hat{\beta}_3 = 0.52, \hat{\beta}_4 = 0.18$, and $\hat{\beta}_5 = 0.24$, simultaneously significantly affect the dependent variable *A*.

Determine the coefficient of determination

Determination of coefficient of determination done with purpose to know how strong correlation between independent variable with dependent variable. Determination of coefficient of determination correlation between independent variable D_3, D_4 and D_5 , with the dependent variable *A*, is determined using equation (16). The calculation results obtained coefficient of determination $R^2 = 0.973$ or $R^2 = 97.32\%$. This shows that the correlation between the independent variables D_3, D_4 and D_5 , with the dependent variable *A*, is very strong.

Cobb-Douglas model estimator based on genetic algorithm

Based on the estimation using genetic algorithm, and goodness of fit test and also very strong correlation, this shows that multiple linear regression equation (20) is the best estimator. Referring to equation (4), the multiple linear regression equation estimator of equation (20) is as follows:

$$\hat{A} = 3.54 + 0.52D_1 + 0.18D_2 + 0.24D_5 \quad (21)$$

The estimate of multiple linear regression equations for GRDP based on expenditure is given by equation (21). Referring to equations (1) and (2), equation (21) can be transformed into the Cobb-Douglas production function as follows:

$$\hat{Y} = e^{3.54} X_3^{0.52} X_4^{0.18} X_5^{0.24} \quad (22)$$

Furthermore, because of the amount of elasticity $\beta_3 + \beta_4 + \beta_5 = 0.52 + 0.18 + 0.24 = 0.94$ or $\beta_3 + \beta_4 + \beta_5 < 1$, this shows the characteristic decreasing return to scale. That is, when the expenditure is enlarged, the GRDP based on expenditure will decrease.

Determine prediction error rate

Determination of prediction error rate is done in order to know how well the estimation model is fit. The model estimate is considered suitable if it can produce a very small predictive error rate near zero. In this study to the level of error prediction is determined by using Mean Absolute Percentage Error (MAPE) in equation (17). For the purposes of determining the error rate, it is necessary to predict the sample. Predictions in the sample were performed using multiple linear regressions (21), and the results can be shown as the graph in Fig. 1.

Based on the prediction result in the sample done by using equation (21), obtained MAPE value of 0.177 or 17.7%. MAPE of 17.7% is a relatively small value, thus the estimator of multiple linear regression equation (21) or Cobb-Douglas production function (22) is suitable for modeling data of GRDP based on expenditure of Garut Regency.

For an analysis of this level of accuracy, the actual data of GRDP in Garut Regency is projected for 20 years. In the same way, actual government consumption expenditure X_3 data, gross domestic fixed capital formation, and net exports X_4 , and inventory changes X_5 are projected for 20 years. Furthermore, the projected value of variables X_3, X_4 , and

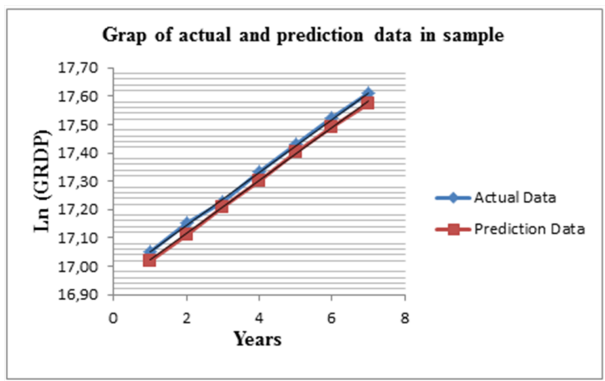


Fig. 1. Graph of predictive and actual data

X_5 , substituted in equation (21), can be obtained from the projected GRDP prediction data \hat{Y} . Graphs of actual data projection and prediction data projection are presented in Fig. 2.

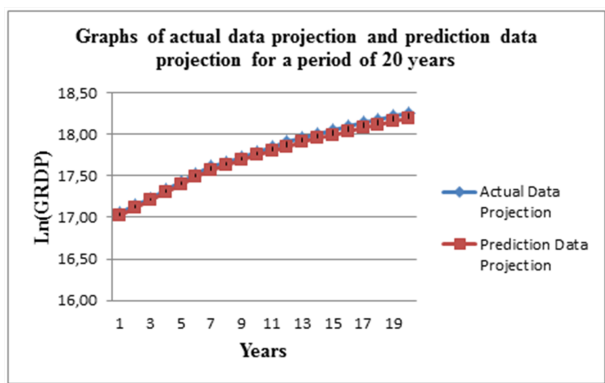


Fig. 2. Graphs of Actual Data Projection and Prediction Data Projection

Using equation (16), Prediction Data Projection for a period of 20 years has a MAPE value of 0.044902415 or 4.49%. This means that the model in equation (21) for the 20 years projected data has an accuracy rate of 95.91%. Next, if noted Fig. 2, from the period of the 1st to the 10th year, it appears that Actual Data Projection and Prediction Data Projection graphs are relatively coherent. After the 10th year period the graph began to move away between the two. This shows that the model parameter estimates in equations (21) and (22), at the latest every 10 years, need to be re-evaluated. Also using equation (16), Prediction Data Projection for up to 10 years has MAPE value of 0.032832684 or 3.28%. This means that the model in equation (21) for the 10 years projection data has an accuracy rate of 96.72%.

Furthermore, by using the Cobb-Douglas production function model (22), we can predict the out sample value of GRDP based on expenditure for the two future periods. It assumed that the value of each variable increases from the previous year and the results as given in Table IX.

Comparison of estimation results from OLS and genetic algorithm

Comparison of estimation results is done to determine the level of suitability of the model, which is obtained from the estimation by using OLS and genetic algorithm. Based on the estimation results and the prediction error rate, it is

TABLE IX
PREDICTED VALUES OF GRDP BASED ON EXPENDITURE FOR THE NEXT TWO PERIODS

Period	Y	X ₃	X ₄	X ₅
1	44,449,327	3,841,167	2,406,357	2,202,809
2	45,457,805	4,000,000	2,500,000	2,500,000

summarized in Table X.

TABLE X
COMPARISON OF MODEL ESTIMATION RESULTS

Parameters Method	$\hat{\beta}_0$	$\hat{\beta}_3$	$\hat{\beta}_4$	$\hat{\beta}_5$	$\sum \varepsilon_i^2$	MAPE
OLS	3.50	0.56	0.18	0.20	0.075	0.192
Genetic Algorithm	3.54	0.54	0.18	0.24	0.007	0.177

Based on Table X, it is shown that the residual squared sum of the genetic algorithm approach is 0.007 smaller than the ordinary least square (OLS) approach of 0.075. The predicted error rate in the sample measured using Mean Absolute Percentage Error (MAPE) obtained from the estimator using the genetic algorithm is 0.177, smaller than that of the OLS approach of 0.192. So it can be concluded that estimation using genetic algorithm is better, compared with using OLS. Therefore, furthermore to predict the value of GRDP based on expenditure in Garut Regency, conducted by using genetic algorithm approach. Also, MAPE values obtained from OLS analysis and genetic algorithms are less than 10%. This shows that the analysis obtained is very good forecasting of GRDP values.

IV. CONCLUSION

In this paper, we have analyzed the modeling of GRDP prediction based on expenditure using genetic algorithm approach and the Cobb-Douglas model as a case study of Garut Regency, Indonesia. Based on the result of analysis, we can be concluded that the GRDP based on expenditure in Garut Regency, significantly follow the Cobb-Douglas model. The estimation of parameters performed by using a genetic algorithm, obtained the estimator values are $\beta_0 = 3.54$, $\beta_3 = 0.52$, $\beta_4 = 0.18$ and $\beta_5 = 0.24$. The prediction results of GRDP based on expenditure in Garut Regency using a model estimator from the genetic algorithm approach is IDR 44,449,327 and IDR 45,457,805. This value is used for consideration in making a budget expenditure plan for the Garut Regency.

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