ISSN: 2469-9756

**Open Access** 

# The Efficacy of the COVID-19 Vaccine against the Mutation of the Corona Virus

#### Dodi Irwan Siregar\*

Department of Immunology, Lancang Kuning University, Pekanbaru, Indonesia

#### Abstract

The delta variant (B.1.617.2) was a variant of SARS-CoV-2, the virus that causes COVID-19; it has mutations in the gene encoding the SARS-CoV-2 spike protein. When a virus replicates or makes copies of itself, it sometimes changes a little bit. These changes are called "mutations." A virus with one or several new mutations is referred to as a "variant" of the original virus. The more viruses circulate, the more they may change. These changes can occasionally result in a virus variant that is better adapted to its environment compared to the original virus. This process of changing and selection of successful variants is called "virus evolution." Some mutations can lead to changes in a virus's characteristics, such as altered transmission A COVID-19 vaccine is a vaccine intended to provide acquired immunity against Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), the virus that causes Coronavirus disease 2019 (COVID-19). Correlation is one of the analytical techniques in statistics that is used to find the relationship of how strong the relationship between two or more variables is quantitative. By using a linearity test where F arithmetic>F Tabel is 28, 9857462> 3.42, and then Ho is accepted. This means that multiple linear regression analysis can be used to predict complete vaccination for COVID-19 by analyzing COVID-19 mortality against and data confirmed COVID-19. Obtained the multiple linear regression equation is Y=4858167192- 10004, 1797X1+5, 866348716X2, the relationship between the variables above is 0,825982 is the superior correlation. Where  $t_1$  arithmetic  $<t_1$  Table=-7, 5828144<2.069, then H<sub>0</sub> is accepted meaning, there is no significant effect partially between data confirmed COVID-19 of complete vaccination for COVID-19.

Keywords: Complete vaccination for COVID-19 • Confirmed COVID-19 • COVID-19 mortality • Virus evolution • Multiple linear regression equation • T-test

# Introduction

Coronaviruses are a group of related RNA viruses that cause diseases in mammals and birds. In humans and birds, they cause respiratory tract infections that can range from mild to lethal. Mild illnesses in humans include some cases of the common cold (which is also caused by other viruses, predominantly rhinoviruses), while more lethal varieties can cause SARS, MERS and COVID-19, which is causing the ongoing pandemic. The genome size of coronaviruses ranges from approximately 26 to 32 kilobases, one of the largest among RNA viruses. In cows and pigs they cause diarrhea, while in mice they cause hepatitis and encephalomyelitis. Coronaviruses constitute the subfamily Orthocoronavirinae, in the family Coronaviridae, order. Nidovirales and realm Riboviria. When a virus replicates or makes copies of it, it sometimes changes a little bit. These changes are called "mutations." A virus with one or several new mutations is referred to as a "variant" of the original virus. The more viruses circulate, the more they may change. These changes can occasionally result in a virus variant that is better adapted to its environment compared to the original virus. This process of changing and selection of successful variants is called "virus evolution." Some mutations can lead to changes in a virus's characteristics, such as altered transmission (for example, it may spread more easily) or severity (for example, it may cause more severe disease). Some viruses change quickly and others more slowly. SARS-CoV-2, the virus which causes COVID-19, tends to change more slowly than others such as HIV or influenza viruses. This could in part be explained by the virus's internal "proofreading mechanism" which can correct "mistakes" when it makes copies of itself. Scientists continue to study this mechanism to better understand how it works [1].

A COVID-19 vaccine is a vaccine intended to provide acquired immunity against Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), the virus that causes Coronavirus disease 2019 (COVID-19). Prior to the COVID-19 pandemic, an established body of

\*Address for Correspondence: Dodi Irwan Siregar, Department of Immunology, Lancang Kuning University, Pekanbaru, Indonesia, Tel: 082171928606; E- dodi.irwan.siregar@gmail.com

**Copyright:** © 2023 Siregar DI. This is an open-access article distributed under the terms of the creative commons attribution license which permits unrestricted use, distribution and reproduction in any medium, provided the original author and source are credited.

Received: 10 September, 2022; Manuscript No. ICOA-22-74233; Editor assigned: 13 September, 2022, PreQC No. ICOA-22-74233; Reviewed: 28 September, 2022, QC No. ICOA-22-74233; Revised: 31 December, 2022, Manuscript No. ICOA-22-74233; Published: 05 January, 2023, DOI: 10.37421/2469-9756.2023.9.153

knowledge existed about the structure and function of coronaviruses causing diseases like Severe Acute Respiratory Syndrome (SARS) and Middle East Respiratory Syndrome (MERS). This knowledge accelerated the development of various vaccine platforms during early 2020. The initial focus of SARS-CoV-2 vaccines was on preventing symptomatic, often severe illness [2]. During the last decade, the increased awareness of the complexity of the immune system and its determinants, including at the host genetic level, indicated that using system biology approaches to assess how various processes and networks interact in response to immunization could prove more illustrative than trying to isolate and characterize a few components of vaccine responses. Delineating the specific molecular signatures of vaccine immunogenicity is beginning to highlight novel correlates of protective immunity and better explain the heterogeneity of vaccine responses in a population [3].

# **Materials and Methods**

#### Simple linear regression analysis

Simple linear regression analysis can be used to predict changes in the value of certain variables when other variables change. It is said simple regression, because it consists of one independent variable (independent) as a predictor, it uses a simple linear regression equation. Regression analysis is a relationship that is obtained and expressed in the form of mathematical equations which states the functional relationship between variables. According to Drapper and Smith. Regression analysis is an analytical method that can be used to analyze data and draw meaningful conclusions about the relationship of one variable's dependence on another [4]. Regression is divided into 2 namely, simple linear regression analysis and multiple linear regression. Simple linear regression analysis is used to get a mathematical relationship in the form of an equation between the dependent variable and the single independent variable. Simple linear regression analysis is a linear relationship between the independent variable (X) and the dependent variable (Y). This analysis is to determine the direction of the relationship between the independent variable with the dependent variable whether each independent variable is positively or negatively related and to predict the value of the dependent variable if the value of the independent variable has increased or decreased. The data used is usually interval or ratio scale [5].

The simple linear regression equation is as follows:  $Y=\alpha+bX$ 

Information:

Y=Dependent variable (predicted value).

X=Independent variable

 $\alpha$ =Constant (Y value is equal to  $\alpha$  if X=0)

b=Regression coefficient (increase or decrease value).

The method that can be used to estimate the parameters of a simple linear regression model or a simple linear regression model is the least squares method and the likelihood method [6].

#### Simple linear correlation

Correlation coefficient is a number that states the strength of the relationship between two or more variables, can also determine the direction of the relationship of the two variables, the correlation value is  $(r)=(-1 \le 0 \le 1)$ . Simple correlation analysis is an extension of simple correlation analysis. In a simple correlation analysis aims to find out how the degree of relationship between several independent variables (Variable X), with the dependent variable (Variable Y) together. For the strength of the relationship, the value of the correlation coefficient is between -1 to 1, while for the direction expressed in the form of positive (+) and negative (-). The Pearson product. Moment coefficient of correlation, is a measure of the strength of the linear. Relationship between two variables x and y. It is computed (for a sample of n measurements on x and y) as follows [7].

r=SSxy/√SSxx. SSyy Where; SSxy= Σ(x- x<sup>2</sup>) (y-y <sup>2</sup>) SSxx= Σ(x-x<sup>2</sup>)<sup>2</sup> SSyy = Σ(y-y<sup>2</sup>)<sup>2</sup>

Recall that a bivariate relationship describes a relationship or correlation between two variables, x and y. Scatter grams are used to graphically describe a bivariate relationship (Table 1). The concept of correlation and how it can be used to measure the linear relationship between two variables, x and y. A numerical descriptive measure of correlation is provided by the Pearson product moment coefficient of correlation, r.

The intervals for the strength of the relationship (correlation) are as follows: Simple correlation is a correlation that intends to see the relationship between variables (the dependent variable and one independent variable). Simple correlations relate to the inter isolation of independent variables as well as their correlation with the dependent variable. In addition, according to Akdon and Ridwan a simple correlation is a value that gives a strong influence of variables together with other variables. The assumptions related to the simple regression analysis are [8].

- The independent variables and the dependent variable have a linear relationship.
- All variables, both independent and dependent variables, are continuous random variables.
- Conditional distribution of values of each variable with normal distribution (multivariate normal distribution).
- For various combinations of one variable's value, the variance of the conditional distribution of each variable is homogeneous (assuming homoscedasticity applies to all variables).

For each variable, the observed values are not related. Simple correlation (single correlation) is a correlation consisting of one independent variable (X), and one dependent variable (Y). As for the relationship between variables can be described as follows: From the picture above the problem formulation consists of three or more problems, so simple linear correlation is used (Figure 1). The strength interval of a number of statistical authors makes the interval categorization of the strength of the correlation relationship Jonathan.

Sarwono, for example, makes the strength intervals of relations as follows [9].

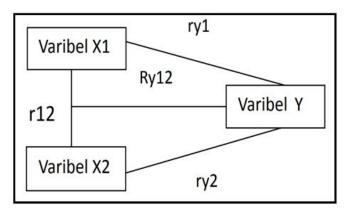


Figure 1. Multiple linear correlation.

For each variable, the value of observations from one another is not related. Multiple correlations are a correlation consisting of two independent variables  $(X_1, X_2)$  or more, and one dependent variable (Y). The relationship between variables can be described as follows. From the picture above the formulation of the problem consists of three or more problems, and then multiple linear correlations is used.

#### Research methodology

Types and research approaches: This research includes explanatory research with a quantitative approach, using multiple

linear analysis methods due to more than one independent variable. The variables that influence are called independent variables and the variables that are affected are called dependent variables (dependent variables).

**Variables in measurement:** This study consists of two independent variables, namely the complete vaccination for COVID-19 abroad  $(X_1)$  and Indonesia's gross domestic income  $(X_2)$ , while the dependent variable is the Rupiah (IDR-USD) currency exchange rate abbreviated as variable (Y).

**Data collection technique:** Data collection techniques carried out to obtain relevant data from the problems studied are through library research (Library Research), namely by reading and studying the literature contained in the library, with the intention to put a theoretical foundation on the main problems being discussed.

#### Data collection technique

Data collection techniques carried out to obtain relevant data from the problems studied are through library research (Library Research), namely by reading and studying the literature contained in the library, with the intention to put a theoretical foundation on the main problems being discussed (Table 1).

Interpretasi (R)
Doubful Correlation
Fair Correlation
Good Correlation
Superior Correlation

 Table 1. Pearson correlation value.

The virus can be spread from the mouth or nose of an infected person through tiny fluid particles when the person coughs, sneezes, talks, sings, or breathes. These particles can range from larger droplets from the respiratory tract to smaller aerosols. Corona virus disease (COVID-19) is an infectious disease caused by the SARS-CoV-2 virus. Most people who contract COVID-19 will experience mild to moderate symptoms, and will recover without special treatment. However, some people will experience severe pain and require medical assistance (Table 2).

No	Date	Confirmed COVID-19
1	22/08/2022	3457028
2	15/08/2022	5458596
3	08/08/2022	5855295
4	01/08/2022	7168081
5	25/07/2022	6834586
6	18/07/2022	7285514
7	11/07/2022	6851015
8	04/07/2022	6356880
9	27/06/2022	5542133

10	20/06/2022	4580434
11	13/06/2022	3705984
12	06/06/2022	3500081
13	30/05/2022	3279782
14	23/05/2022	3463147
15	16/05/2022	3845124
16	09/05/2022	3929558
17	02/05/2022	3707622
18	25/04/2022	4033687
19	18/04/2022	4746238
20	11/04/2022	5816094
21	04/04/2022	7488122
22	28/03/2022	9491115
23	21/03/2022	11131189
24	14/03/2022	12767035
25	07/03/2022	11676144
26	28/02/2022	10551643
27	21/02/2022	10948071
28	14/02/2022	12889417
29	07/02/2022	16294955
30	31/01/2022	20153458
Source: WHO Coronavirus (COVID-19), 2022		

Source: WHO Coronavirus (COVID-19), 2022

Table 2. Data on confirmed COVID-19 in the world.

The virus can be spread from the mouth or nose of an infected person through tiny fluid particles when the person coughs, sneezes, talks, sings, or breathes. These particles can range from larger droplets from the respiratory tract to smaller aerosols. Corona virus disease (COVID-19) is an infectious disease caused by the SARS-CoV-2 virus. Most people who contract COVID-19 will experience mild to moderate symptoms, and will recover without special treatment. However, some people will experience severe pain and require medical assistance (Table 3).

No	Date	Mortality COVID-19
1	22/08/2022	7217
2	15/08/2022	15079
3	08/08/2022	16988
4	01/08/2022	16577
5	25/07/2022	16853
6	18/07/2022	15528
7	11/07/2022	13844
8	04/07/2022	12018
9	27/06/2022	10875
10	20/06/2022	10153
11	13/06/2022	9099

12	06/06/2022	9256
13	30/05/2022	8834
14	23/05/2022	10266
15	16/05/2022	10487
16	09/05/2022	11239
17	02/05/2022	13191
18	25/04/2022	16710
19	18/04/2022	17220
20	11/04/2022	19986
21	04/04/2022	23354
22	28/03/2022	27750
23	21/03/2022	46835
24	14/03/2022	33825
25	07/03/2022	43642
26	28/02/2022	51680
27	21/02/2022	59868
28	14/02/2022	77109
29	07/02/2022	75694
30	31/01/2022	67814
Source: WHO Coronavirus (COVID-19), 2022		

Table 3. Mortality COVID-19 in the world.

You can catch it when you breathe air that contains the virus if you are near someone who is already infected with COVID-19. You can also catch it if you touch your eyes, nose, or mouth after touching a contaminated surface. Viruses are easier to spread indoors and in crowded places.

# **Results and Discussion**

This research predicts and predicts the position of Indonesia's external debt in the future by processing and analyzing past data, as

the dependent variable (bound), is the value of Indonesia's exports outside multiple linear regression analysis with dependent variable is complete vaccination for COVID-19 abbreviated as (Y), and independent variable (independent) is Indonesian COVID-19 mortality (X<sub>1</sub>), and complete vaccination for COVID-19 as (X<sub>2</sub>). Data from the variables above are as follows (Table 4).

No	Date	<b>X</b> <sub>1</sub>	<b>X</b> <sub>2</sub>	Y
1	22/08/2022	7217	3457028	4907506087
2	15/08/2022	15079	5458596	4903289817
3	08/08/2022	16988	5855295	4887555590
4	01/08/2022	16577	7168081	4872424669
5	25/07/2022	16853	6834586	4854082065
6	18/07/2022	15528	7285514	4838060651
7	11/07/2022	13844	6851015	4824130057
8	04/07/2022	12018	6356880	4808720329
9	27/06/2022	10875	5542133	4792619160

10	20/06/2022	10153	4580434	4777478756		
11	13/06/2022	9099	3705984	4753209332		
12	06/06/2022	9256	3500081	4740099304		
13	30/05/2022	8834	3279782	4752247085		
14	23/05/2022	10266	3463147	4710858723		
15	16/05/2022	10487	3845124	4694919778		
16	09/05/2022	11239	3929558	4677973745		
17	02/05/2022	13191	3707622	4662231996		
18	25/04/2022	16710	4033687	4636863951		
19	18/04/2022	17220	4746238	4621620437		
20	11/04/2022	19986	5816094	4606468303		
21	04/04/2022	23354	7488122	4577253593		
22	28/03/2022	27750	9491115	4534500003		
23	21/03/2022	46835	11131189	4503913189		
24	14/03/2022	33825	12767035	4613496584		
25	07/03/2022	43642	11676144	4436006267		
27	28/02/2022	51680	10551643	4382455875		
28	21/02/2022	77109	12889417	4269963536		
29	14/02/2022	75694	16294955	4215477416		
30	07/02/2022	67814	20153458	4164424948		
Source: WHO Coronavirus (COVID-19), 2022						

Table 4. Confirmed COVID-19 data (Y), Indonesian COVID-19 mortality (X1) and complete vaccination for COVID-19 (X2).

In a study at the stage of analyzing data, multiple linear regressions is the development of simple linear regression, which can be used to predict future demand based on past data analysis or to determine the effect of one or more independent variables on one variable dependent is used. The application of multiple methods of the number of independent variables used is more than one which influences independent non independent variables. From the table of independent and bound variable data above, we obtain multiple linear regression equations with two predictors. Start by creating a helper table as follows.

No	X1	X2	Y	X1 <sup>2</sup>	<b>X2</b> <sup>2</sup>	Υ²	X1Y	X2Y	X1X2
1	7217	3457028	4907506087	52085089	1,1951E+13	2,40836E+19	3,54175E+13	1,69654E+16	24949371076
2	15079	5458596	4903289817	227376241	2,97963E+13	2,40423E+19	7,39367E+13	2,67651E+16	82310169084
3	16988	5855295	4887555590	288592144	3,42845E+13	2,38882E+19	8,30298E+13	2,86181E+16	99469751460
4	16577	7168081	4872424669	274796929	5,13814E+13	2,37405E+19	8,07702E+13	3,49259E+16	1,18825E+11
5	16853	6834586	4854082065	284023609	4,67116E+13	2,35621E+19	8,18058E+13	3,31756E+16	1,15183E+11
6	15528	7285514	4838060651	241118784	5,30787E+13	2,34068E+19	7,51254E+13	3,52478E+16	1,13129E+11
7	13844	6851015	4824130057	191656336	4,69364E+13	2,32722E+19	6,67853E+13	3,30502E+16	94845451660
8	12018	6356880	4808720329	144432324	4,04099E+13	2,31238E+19	5,77912E+13	3,05685E+16	76396983840
9	10875	5542133	4792619160	118265625	3,07152E+13	2,29692E+19	5,21197E+13	2,65613E+16	60270696375
10	10153	4580434	4777478756	103083409	2,09804E+13	2,28243E+19	4,85057E+13	2,18829E+16	46505146402
11	9099	3705984	4753209332	82791801	1,37343E+13	2,2593E+19	4,32495E+13	1,76153E+16	33720748416

12	9256	3500081	4740099304	85673536	1,22506E+13	2,24685E+19	4,38744E+13	1,65907E+16	32396749736
13	8834	3279782	4752247085	78039556	1,0757E+13	2,25839E+19	4,19814E+13	1,55863E+16	28973594188
14	10266	3463147	4710858723	105390756	1,19934E+13	2,21922E+19	4,83617E+13	1,63144E+16	35552667102
15	10487	3845124	4694919778	109977169	1,4785E+13	2,20423E+19	4,92356E+13	1,80525E+16	40323815388
16	11239	3929558	4677973745	126315121	1,54414E+13	2,18834E+19	5,25757E+13	1,83824E+16	44164302362
17	13191	3707622	4662231996	174002481	1,37465E+13	2,17364E+19	6,14995E+13	1,72858E+16	48907241802
18	16710	4033687	4636863951	279224100	1,62706E+13	2,15005E+19	7,7482E+13	1,87037E+16	67402909770
19	17220	4746238	4621620437	296528400	2,25268E+13	2,13594E+19	7,95843E+13	2,19353E+16	81730218360
20	19986	5816094	4606468303	399440196	3,38269E+13	2,12196E+19	9,20649E+13	2,67917E+16	1,1624E+11
21	23354	7488122	4577253593	545409316	5,6072E+13	2,09513E+19	1,06897E+14	3,4275E+16	1,74878E+11
22	27750	9491115	4534500003	770062500	9,00813E+13	2,05617E+19	1,25832E+14	4,30375E+16	2,63378E+11
23	46835	11131189	4503913189	2193517225	1,23903E+14	2,02852E+19	2,10941E+14	5,01339E+16	5,21329E+11
24	33825	12767035	4613496584	1144130625	1,62997E+14	2,12844E+19	1,56052E+14	5,89007E+16	4,31845E+11
25	43642	11676144	4436006267	1904624164	1,36332E+14	1,96782E+19	1,93596E+14	5,17954E+16	5,0957E+11
27	51680	10551643	4382455875	2670822400	1,11337E+14	1,92059E+19	2,26485E+14	4,62421E+16	5,45309E+11
28	77109	12889417	4269963536	3584177424	1,1986E+14	1,88279E+19	2,59774E+14	4,75049E+16	6,55439E+11
29	75694	16294955	4215477416	5945797881	1,66137E+14	1,82326E+19	3,29253E+14	5,50373E+16	9,9389E+11
30	67814	20153458	4164424948	5729581636	2,65526E+14	1,77702E+19	3,19086E+14	6,8691E+16	1,23343E+12
Σ	1,39359E+11	3,45552E+15	1,01456E+18	8,05705E+12	32749675373	2,16999E+15	6,48632E+20	1,39359E+11	3,45552E+15
-									

Table 5. Helper data to search for multiple linear regression equations, namely the values of constants b<sub>1</sub> and b<sub>2</sub>.

#### Level correlation of multiple linear regression

The Pearson correlation coefficient can be used to express the extent of a linear relationship between two or more variables when the data is quantitative data (interval or ratio scale data) and both variables are bivariate which are normally distributed. Then the multiple linear regression correlation is obtained as follows.

 $R_{X1X2,Y} = \sqrt{(b_1 \cdot \Sigma x_1 y + b_2 \cdot \Sigma x_2 y) / \Sigma y^2}$ = 0.825982

From the analysis of the level of multiple linear regression, the equality of complete vaccination for COVID-19 by analyzing COVID-19 mortality against data confirmed COVID-19. The interpretation is superior correlation, ranging from 0.76 to 1.00.

#### Linearity Test (F-Test) multiple regression make a hypothesis

 $H_0$ : Linear regression analysis cannot be used in analyzing the influence of the complete vaccination for COVID-19 and Mortality COVID-19 on the data confirmed COVID-19.

 $H_{\alpha}$ : Linear regression analysis can be used to analyze the effect of the complete vaccination for COVID-19 and Mortality COVID-19 on the data confirmed COVID-19.

#### Determining the value of F<sub>count</sub>

Formula:  $F_{count}=(R_{x1x2,y})^2 (n-m-1)/m(1-R_{x1,x2,y}^2)$   $F_{count}=28,985746233963$ Information:  $R_{x1.x2.y}=$ Correlation of multiple linear regression n=Number of research samples

m=Number of free variables

#### Determine the value of F-table

```
Formula:
```

Ftable=F {(a) (dk denominator=n-m-1), (dk numerator=m)}

Where:

m=2, n =7, α=0.05

dk=5-2-1=2

Then;

 $F_{tabel} = F_{\{(0,05)(4,2)\}} = 3.422$ 

F count>f table namely; 28, 985746233963>3.422 So, Ho is accepted. So, multiple linear regression analysis can be used in complete vaccination for COVID-19 by analyzing COVID-19 mortality against data confirmed COVID-19.

#### Look for the value of constants

The values of constants  $b_1$  and  $b_2$  are:

 $-\Sigma x_1^2 = \Sigma X_1^2 - (\Sigma X_1)^2 / n$ 

 $-\Sigma x_2^2 = \Sigma X_2^2 - (\Sigma X_2)^2/n$ 

 $-\Sigma y^2 = \Sigma Y^2 - (\Sigma Y)^2/n$ 

- $\Sigma x_1 y = \Sigma X_1 Y - (\Sigma X_1) (\Sigma Y)/n$ 

- $\Sigma x_2 y = \Sigma X_2 Y - (\Sigma X_2) (\Sigma Y)/n$ 

 $-\Sigma x_1 x_2 = \Sigma X_1 X_2 - (\Sigma X_1) (\Sigma X_2)/n$ 

-X<sub>1</sub>= $\Sigma$ X<sub>1</sub>/n

 $-X_2 = \Sigma X_2 / n$ 

-Y=ΣY/n

Formula of constant b<sub>1</sub>;

 $b_1 = (\Sigma x_2^2)(\Sigma x_1 y) - (\Sigma x_1 x_2)(\Sigma x_2 y)$ 

 $(\Sigma x_1^2)(\Sigma x_2^2) - (\Sigma x_1 x_2)^2 = -10004, 1797$ 

Formula of constant b<sub>2</sub>;

 $b_2 = (\Sigma x_1^2)(\Sigma x_2 y) - (\Sigma x_1 x_2)(\Sigma x_1 y)$ 

 $(\Sigma x_1^2)(\Sigma x_2^2) - (\Sigma x_1 x_2)^2$ 

=5,866348716

The value of the constant  $\alpha$  is:

 $\alpha = \Sigma Y/n - b_1(\Sigma X_1/n) - b_2(\Sigma X_2/n) = 4858167192$ 

From the results of the multiple linear regression analysis the equation with the formula is obtained as follows.

 $Y = \alpha + b_1 X_1 + b_2 X_2 + ... + b_n X_n$ 

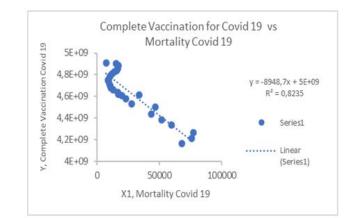
The results of multiple linear regression analysis obtained the equality of complete vaccination for COVID-19 by Analyzing COVID-19 mortality against data confirmed COVID-19. Then the obtained multiple linear regression equation is as follows.

Y=4858167192-10004,1797X1+5,866348716X2

By using the above equation, we can predict complete vaccination for COVID-19 using the multiple linear regression equation.

#### Partial effect test (t-test)

That is, determining whether there is a partial influence between the complete vaccination for COVID-19 (X<sub>1</sub>) and complete vaccination for COVID-19 (Y) and whether there is a partial data confirmed COVID-19 (X<sub>2</sub>), partial influence test (t-test) between X<sub>1</sub> and Y determine the hypothesis (Figures 2 and 3).



# Figure 2. Complete vaccination for COVID-19 vs. morility COVID-19.

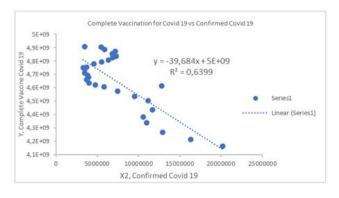


Figure 3. Complete vaccination 19 confirmed COVID-19.

 $H_0$ : There is no partial significant effect between mortality COVID-19 on complete vaccination for COVID-19.

 $H_{\alpha}$ : There is partial significant effect between mortality COVID-19 on complete vaccination for COVID-19.

Determine the value of  $t_1$  count:

$$\begin{split} &S_{X1X2}{}^2 = \Sigma y^2 - [b_2(\Sigma x_{1y}) + b_2(\Sigma x_{2y})]/n - m - 1 \\ &S_{X1X2}{} = \sqrt{S_{X1X2}}{}^2 = 90398894,53 \\ &r_{x1x2}{} = n(\Sigma X_1 X_2) - (\Sigma X_1)(\Sigma X_2)/\sqrt{\{n. \Sigma X_1^2 - (\Sigma X_1)^2\}} \{n. \Sigma X_2^2 - (\Sigma X_2)^2\} \\ &= -0,56722 \\ &S_{b1}{} = S_{X1X2}/\sqrt{[\Sigma X_1^2 - n. X_1^2]} [1 - (r_{x1x2})^2] \\ &= 1319,322766 \\ &S_{b2}{} = S_{X1X2}/\sqrt{[\Sigma X_2^2 - n. X_2^2]} [1 - (rx1x2)2] \\ &= 7,837400409 \\ &Then, t_1 _{count}{} = b_1/S b_1 {=}{} - 7,582814427 \\ &t_2 _{count}{} = b_2/S b_2 {=} 0,748506955 \\ &Menentukan nilai t_{tabel} \\ &t_{tabel}{} = t (\alpha/2)(n-2) \\ &= t (0,025) (5) \\ &= 2,069 \end{split}$$

- So, t<sub>1count</sub>>t<sub>table</sub>=-7, 582814427>2.069; then Ho is accepted meaning, there is there is no significant (significant) effect partially between COVID-19 mortality and complete vaccination for COVID 19.
- For t<sub>2count</sub> ≤ t table that is 0, 748506955 ≤ 2.069 then Ho is accepted meaning, there is no significant (significant) partial effect between data confirmed COVID-19 of complete vaccination for COVID-19.

# Conclusions

From the results of the study, it can be concluded that statistical data with the variables of complete vaccination for COVID-19 prediction by analyzing COVID-19 mortality against Mortality COVID-19 from 2003-2014 are as follows.

 F<sub>count</sub>>f<sub>table</sub> which is 28, 9857462>3.422 So, Ho is accepted. So, linear regression analysis can be used in predicting Confirmed COVID-19 by Analyzing COVID-19 mortality against mortality COVID-19's from 2003-2014.

The multiple linear regression equation is as follows

- Y=4858167192-10004, 1797X1+5,866348716X2.
- The correlation between the relationships between confirmed COVID-19 and analyzing COVID-19 mortality against data confirmed COVID-19. Shows that the results of 0,825982 with interpretation are superior, ranging from 0.76 to 0.99.
- So, t<sub>1</sub> count<t<sub>table</sub>=-7, 582814427<2.069; then Ho is accepted meaning, there is there is no significant (significant) effect partially between COVID-19 mortality and complete vaccination for COVID-19.
- For t<sub>2 count</sub> ≤ t<sub>table</sub> that is 0,748506955 ≤ 2.069 then Ho is accepted meaning, there is no partial (significant) influence between data confirmed COVID-19 of complete vaccination for COVID-19.

# References

- 1. Asundi, Archana, Leary Colin O', and Bhadelia Nahid. "Global COVID-19 vaccine inequity: The scope, the impact, and the challenges." *Cell Host Microbe* 29 (2021): 1036-1039.
- Pulendran Bali. "Systems vaccinology: probing humanity's diverse immune systems with vaccines." Proceedings of the Natl Acad Sci 111 (2014): 12300-12306.
- Werner, Steve. "Recent developments in international management research: A review of 20 top management journals." J Manag 28 (2002): 277-305.
- 4. Draper, Norman R, and Harry Smith. *Applied regression analysis*. John Wiley and Sons, (1998): 326.
- Lebedev, Pavel. "Getting insight into management accounting and control systems: a framework for survey-based research design for emerging markets context." Procedia Soc Behav Sci 213 (2015): 293-298.
- Murray ET, DA. Fitzmaurice, and Deborah McCahon. "Point of care testing for INR monitoring: where are we now?." British J haematology 127 (2004): 373-378.
- Aalen, Odd O. "A linear regression model for the analysis of life times." Stat Med 8 (1989): 907-925.
- Li, Yen Der, Yu Chi Wei, Han Su Jun, and Ferrall Louise, "Coronavirus vaccine development: from SARS and MERS to COVID-19." J Biomed Sci 27 (2020): 1-23.
- 9. Subbarao, Kanta. "The success of SARS-CoV-2 vaccines and challenges ahead." *Cell Host Microbe* 29 (2021): 1111-1123.

How to cite this article: Siregar, Dodi Irwan. "The Efficacy of the COVID-19 Vaccine against the Mutation of the Corona Virus." *Immunochem Immunopathol Open Access* 9 (2023) : 153.