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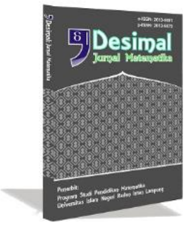

Prediction analysis of the length of time for changes in the status of positive patients for covid-19 delta and omicron variants using the markov chain model

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ABSTRACT

In this research, a Markov chain model was constructed from the conditions that might be experienced by the people during the Delta or Omicron variant of the COVID-19 pandemic. This condition is divided into 3 states; "0" indicates a healthy condition, "1" indicates the state of being infected with COVID-19, and "2" indicates the death state. Furthermore, from the model obtained, a transition probability matrix is made to determine the transition probability value and calculate the average number of steps needed to get to the death state. From the results of the analysis, the probability of transition to a state of death is 1. This shows that a person will surely die from being healthy or positive for COVID-19 within a certain time. During the Delta variant of the COVID-19 pandemic, the average time that a person reaches a death state from a healthy state is 34.02 years. Meanwhile, the average time taken for someone infected with the Delta variant of COVID-19 to death is 33.79 years. During the Omicron variant of the COVID-19 pandemic, the average time that a person reaches a death state from a healthy state is 37.63 years. Meanwhile, the average time taken for someone infected by the Omicron variant of COVID-19 to death is 37.41. This shows that the average age of a person infected with the Delta variant of COVID-19 has decreased by 2.79 months, while the average age of a person infected with the Omicron variant of COVID-19 has decreased by 2.70 months.

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INTRODUCTION

Since the end of 2019, the world has been shocked by the increasing outbreak of the Corona Virus Disease-19 (COVID-19). This disease first appeared in December 2019, in Wuhan city, China. During the COVID-19 pandemic, several variants have emerged due to mutations in the viral RNA genome. Several variants of the COVID-19 disease are detected in Indonesia, but two variants spread quickly, namely the Delta (B.1.617.2) and Omicron (B.1.1.529) variants. The Delta variant (B.1.617.2) was first identified in

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late 2020 in India (Bernal et al., 2021; Mlcochova et al., 2021). Meanwhile, the Omicron variant (B.1.1.529) was first discovered in South Africa in November 2021 (Accorsi et al., 2022).

Furthermore, the death toll from COVID-19 has become part of the daily news cycle around the world. But the high death toll does not give a clear picture of the speed and scale of the pandemic. The drop in life expectancy caused by COVID-19 deaths would provide a more intuitive measure (Heuveline, 2021).

Research using mortality tables shows that men in the US and Lithuania experienced a decrease in life expectancy ever since birth during 2020, by 2.2 and 1.7 years, respectively (Aburto et al., 2022). Meanwhile, Heuveline (2020, 2022) measured the Mean Unfulfilled Lifespan (MUL) and found that in 2020 in the cities of Lombardy, New Jersey, and Mexico, there was an increase in the difference between the average age of death and the expected age of death. This indicates a decrease in life expectancy due to COVID-19. Similar results were obtained using the Usher projection matrix model that represents the life cycle (Oshinubi et al., 2022), using the lifespan inequality (Aburto et al., 2021), using the life expectancy of the Continuous Renal Replacement Therapy (CRRT) filter (Legouis et al., 2021), using the calculation of life expectancy (Castro et al., 2021; Gibson & Olivia, 2020; Marois et al., 2020), and calculation of premature mortality or the number of years lost due to early death (years of potential life lost) (Islam et al., 2021).

Life expectancy is generally calculated using life expectancy obtained from mortality tables. Life expectancy, in terms of remaining life span, can also be predicted indirectly using the Markov chain model. A patient who is positively infected with COVID-19 within a certain time can experience a change in status (state) to be healthy or even die. The probability of changing the patient's status can be modeled using the Markov chain model (Marfak et al., 2020). From the values of the probability for status changes, the average length of time for a healthy person to death status can be predicted, which is the average remaining life span during the COVID-19 pandemic. Furthermore, with the Markov chain model, it is possible to predict the average length of time a person infected with COVID-19 (Delta or Omicron variant) reaches death, which is the average remaining life span after being infected with COVID-19 during the pandemic. This average remaining life span has a similar meaning to life expectancy. So that the comparison of the two average values will show the effect of the COVID-19 pandemic on a person's life expectancy.

This research modeled the probability of changing a person's status (healthy, infected with COVID-19, or died) during the Delta and Omicron variants of the COVID-19 pandemic using the Markov chain model. The probability value of a status change is used to predict a person's remaining life span during the COVID-19 pandemic, which is the average length of time a person changes to death status. Furthermore, a comparison will be made between a person's remaining life after being infected with the Delta variant of COVID-19 and the remaining life of a person after being infected with the Omicron variant of COVID-19.

METHOD

The method used in this research is the literature study method. The data used is secondary data sourced from the internet, the DKI Jakarta Province COVID-19 Monitoring Data (Pemerintah Provinsi DKI Jakarta, 2022), the DKI Jakarta Population and Civil Registration Office (Dinas Kependudukan dan Pencatatan Sipil DKI Jakarta, 2020), and the Central Statistics Agency (Badan Pusat Statistik Provinsi DKI Jakarta, 2020). The theory used in this research is Markov chain, n-step transition probability, Chapman-Kolmogorov equation, and first-step analysis. The steps of the research method carried out are depicted in the research flow chart in Figure 1.

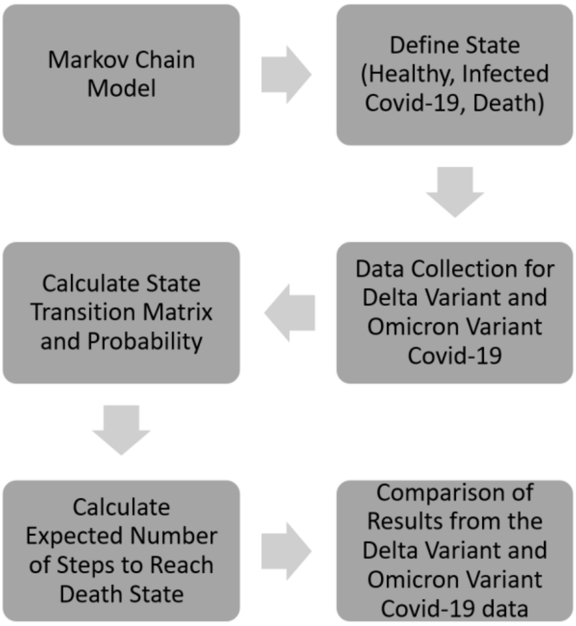

Figure 1. Research Flowchart

Markov Chain

The stochastic process $\{X_t\}$ is a set of random variables X_t where t represents the time index. Consider the random variables $X_0, X_1, \dots, X_t, X_{t+1}$ following a stochastic process. A stochastic process is said to be a Markov chain if for all states $i_0, i_1, \dots, i, j$ satisfy the following equation (Ross, 1996).

$$P(X_{t+1} = j | X_t = i, X_{t-1} = i_{t-1}, \dots, X_0 = i_0)$$

$$= P(X_{t+1} = j | X_t = i) = P_{ij} \qquad (1)$$

where P_{ij} is the probability of transition from a process in state i at time t being in state j at time $t+1$. In other words, the event X_{t+1} depends only on the event X_t and is independent of the event $X_0, X_1, \dots, X_{t-1}$.

n-Step Transition Probability

Let P_{ij}^n be the $n-$ step transition probability of a Markov chain. P_{ij}^n is defined as a conditional probability that a process will be in state j after the process has undergone n transitions, it is known that the initial process is in state i (Ross, 1996). Therefore,

$$P_{ij}^n = P(X_n = j | X_0 = i) \qquad (2)$$

where $i, j \geq 0$, and $n \geq 0$. The value $P_{ij}^1 = P_{ij}$. The value of P_{ij} states that, if a process is in state i, the next one will move to state j. Furthermore, because the probability value is non-negative, the following conditions are obtained.

(i) $P_{ij} \geq 0, \forall i, \forall j \in \{1,2, \dots\}$

(ii) $\sum_{j=0}^{\infty} P_{ij} = 1, \forall i \in \{0,1,2, \dots\}$

The Chapman-Kolmogorov Equation

Let P_{ij}^n be the probability that the $n-$ step transition of a process in state i will be in state j then

$$P_{ij}^n = P(X_{n+m} = j | X_m = i), n, i, j \geq 0 \qquad (3)$$

The Chapman-Kolmogorov equation can be used to calculate the transition probability $n+m$ steps or P_{ij}^{n+m} as follows.

$$\begin{aligned} P_{ij}^{n+m} &= P(X_{n+m} = j | X_0 = i) \\ &= \sum_{k=0}^{\infty} P(X_{n+m} = j, X_n = k | X_0 = i) \\ &= \textstyle\sum_{k=0}^{\infty} P_{ik}^n P_{kj}^m \end{aligned}$$

for every $m, n \geq 0$ and every i, j. In the above equation, $P_{ik}^n P_{kj}^m$ is the probability that a process in state i will be in state j in $n+m$ transitions, with the process passing through state k in n transitions. Let $\boldsymbol{P}^{(n)}$ be the transition probability matrix of n steps. The transition probability matrix n steps can be obtained by recursive as follows (Ross, 1996).

$$\begin{aligned}\boldsymbol{P}^{(n)} &= \boldsymbol{P}^{(1)}\boldsymbol{P}^{(n-1)}\\ &= \boldsymbol{P}\boldsymbol{P}^{(n-1)}\\ &= \boldsymbol{P}^{2}\boldsymbol{P}^{(n-2)}\\ &= \cdots\\ &= \boldsymbol{P}^{n}\end{aligned}$$

That is, the transition probability matrix in the n^{th} step is obtained from the $\boldsymbol{P}$ matrix raised to the power of n. So, $\boldsymbol{P}^{(n+m)} = \boldsymbol{P}^{n}\boldsymbol{P}^{m}$.

First Step Analysis

One of the interesting parts of a Markov chain process is knowing the probability and the average number of steps required so that the process can be absorbed into a state. Both questions can be answered using the first step analysis (Ross, 1996). Suppose the time it takes for the process to be absorbed into a state is defined as follows.

$$T = min\{n \geq 0 | X_n = i\} \tag{4}$$

Next, let u be the probability of the process getting to the absorbing state and v be the average number of steps needed to get the process to the absorbing state, then

$$u = P(X_T = k | X_0 = i) \tag{5}$$

$$v = E\{T | X_o = i\} \tag{6}$$

where i is the initial state which is not an absorbing state, and k is an absorbing state when $P_{kk} = 1$.

Research Limitation

In this research, there are several assumptions or limitations used, namely:

1. From June 2021 to August 2021, it is assumed that all people who are positive for COVID-19 are infected with the Delta variant.
2. From January 2022 to April 2022, it is assumed that all people who are positive for COVID-19 are infected with the Omicron variant.
3. The probability of a person infected with the Delta or Omicron variant of COVID-19 (state "1") remaining infected (remaining in the state "1") is the same.

RESULTS AND DISCUSSION

Markov Chain Model of COVID-19 Infected Patient Status

In this research, the status of COVID-19 patients was grouped into three, namely Healthy, Infected by COVID-19, and Death. The state of health is denoted by "0", the state of being infected with COVID-19 by "1", and the state of death by "2". Furthermore, suppose P_{00} has the value of α_i, P_{01} has the value of β_i, P_{02} has the value of γ_i, P_{10} has the value of δ_i, P_{11} has the value of ε_i, P_{12} has the value of λ_i, and P_{22} has the value of θ_i.

Index i in these probability notations state the type of COVID-19 variant that will be studied. The value of $i = 1$ means that the probability notation states the probability of the type of COVID-19 Delta variant. So, the values of $\alpha_1, \beta_1, \delta_1, \varepsilon_1, \lambda_1, \gamma_1$, and θ_1 represent the transition probabilities that may be experienced by patients infected with the Delta variant of COVID-19. The value of $i = 2$ means that the probability notation expresses the probability of the COVID-19 Omicron variant. So, the values of $\alpha_2, \beta_2, \delta_2, \varepsilon_2, \lambda_2, \gamma_2$, and θ_2 represent the transition probability that may be experienced by patients infected with the Omicron variant of COVID-19. Therefore, the Markov chain model for the status of patients infected with COVID-19 can be described as follows.

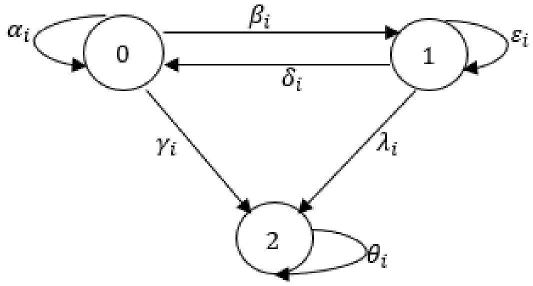

Figure 2. Markov Chain Model of COVID-19 Infected Patient Status

where $i = 1$ or $i = 2$. The transition probability matrix of the model in Figure 2 is

$$\boldsymbol{P} = \begin{pmatrix} \alpha_i & \beta_i & \gamma_i \\ \delta_i & \varepsilon_i & \lambda_i \\ 0 & 0 & \theta_i \end{pmatrix} \tag{7}$$

Note that a person who is in a state of death is unlikely to move to a healthy state or be infected with COVID-19, so state "2" is an absorbing state. So, the value of $P_{22} = \theta_i = 1$ and the transition probability matrix can be written as follows.

$$\boldsymbol{P} = \begin{pmatrix} \alpha & \beta & \gamma \\ \delta & \varepsilon & \lambda \\ 0 & 0 & 1 \end{pmatrix} \tag{8}$$

Transition Probability Markov Chain Model for the Status of COVID-19 Infected Patients in DKI Jakarta Province

From the transition probability matrix in equation (8), the transition probability value from one state to another is calculated. The transition probability values are then used to calculate the probability and predict the average number of steps required to reach death. The data used to find the value of the transition probability is generally divided into two, namely when the COVID-19 Delta variant and the Omicron variant are spreading in Indonesia.

The Delta variant of COVID-19 began to be detected in Indonesia in June 2021 (Kompas, 2021) so for the Delta variant of COVID-19 case data, daily case data was selected for 3 months from June 1, 2021, to August 31, 2021, or a total of 92 data. As for the case data for the Omicron variant of COVID-19, it was detected in Indonesia from the end of December 2021 (Kemenkes Republik Indonesia, 2021). So, for the Omicron variant of the COVID-19 case data, 92 daily case data were selected, where the data has been sorted based on the one with the highest daily positive number during the range from January 2022 to April 2022.

Transition Probability from Healthy State to Positively Infected by COVID-19 State

The transition probability from a healthy state "0" to a COVID-19 infected state "1" is denoted by $P_{01} = \beta_i$. The value of β_i can be obtained from the ratio between the number of daily positives to the number of people tested daily. The data is sourced from the COVID-19 monitoring data for the DKI Jakarta province (Pemerintah Provinsi DKI Jakarta, 2022).

$$\beta_i = \frac{the\ number\ of\ daily\ positives}{the\ number\ of\ people\ tested\ daily} \tag{9}$$

Transition Probability from Healthy State to Death State

The transition probability from a healthy state "0" to a dead state "2" is denoted by $P_{02} = \gamma_i$. The value of γ_i can be obtained through the ratio between the number of people who died during 2019 to the total population in DKI Jakarta Province in 2019.

$$\gamma_i = \frac{the\ number\ of\ people\ who\ died}{the\ total\ population} \tag{10}$$

Table 1 presents monthly data on the number of people who died throughout 2019 (Badan Pusat Statistik Provinsi DKI Jakarta, 2020). From the data, the number of deaths in DKI Jakarta throughout 2019 was 60,955. Meanwhile, according to (Badan Pusat Statistik Provinsi DKI

Jakarta, 2020), the population in DKI Jakarta Province in 2019 was 10,557,810. Note that γ_i is the transition probability from a healthy state "0" directly to a dead state "2", without going through a COVID-19 infection state "1". So, the values of γ_1 and γ_2 can be assumed to be the same, or $\gamma_1 = \gamma_2$, using data from 2019. This is because in 2019 it is assumed that there are no people who have died from COVID-19 in DKI Jakarta.

Table 1. The Number of Deaths in DKI Jakarta Province in 2019

Month	Number of Deaths
January	4997
February	4881
March	5281
April	4865
May	4681
June	4383
July	5756
August	5176
September	5170
October	5660
November	4636
December	5469

Transition Probability that Healthy State Remains in Healthy State

The transition probability from a healthy state “0” to a healthy state “0” is denoted by $P_{00} = \alpha_i$. One of the properties of the transition probability matrix is that the number of probabilities in each row is equal to one. Therefore, the value of α_i can be obtained in the following way.

$$\alpha_i = 1 - (\beta_i + \gamma_i) \tag{11}$$

Transition Probability from Positively Infected by COVID-19 State to Healthy State

The transition probability from being infected with COVID-19 “1” to a healthy state “0” is denoted by $P_{10} = \delta_i$. The value of δ_i is obtained from the ratio between the number of patients who recovered from COVID-19 to the number of daily positive people.

$$\delta_i = \frac{the\ number\ of\ patients\ who\ recovered}{the\ number\ of\ daily\ positive\ people} \tag{12}$$

Transition Probability from Positively Infected by COVID-19 State to Death State

The transition probability from being infected with COVID-19 “1” to a state of the death “2” is denoted by $P_{10} = \lambda_i$. In the case of the Delta variant of COVID-19, the value of λ_1 is obtained from the ratio between the number of people who died from the Delta variant of COVID-19 to the number of people who were daily positive for the Delta variant of COVID-19.

$$\lambda_1 = \frac{the\ number\ of\ people\ who\ died}{the\ number\ of\ daily\ positive\ people} \tag{13}$$

In the case of the Omicron variant of COVID-19, the value of λ_2 is obtained using the help of assumption number 3, namely the assumption that the probability of a person infected with the Delta or Omicron variant of COVID-19 (state "1") to remain infected (remain in state "1") is the same, or $\varepsilon_2 = \varepsilon_1$. So, if the values of δ_2 and ε_2 have been calculated, the value of λ_2 will be obtained as follows.

$$\lambda_2 = 1 - \delta_2 - \varepsilon_2 = 1 - \delta_2 - \varepsilon_2 \tag{14}$$

Transition Probability that Positively Infected by COVID-19 State Remains in Positively Infected by COVID-19 State

The transition probability from being infected with COVID-19 “1” remains infected with COVID-19 “1” is denoted by $P_{11} = \varepsilon_i$. The value of ε_1 is obtained by using the transition probability matrix, that is, each row has a probability equal to one. So that,

$$\varepsilon_1 = 1 - (\delta_1 + \lambda_1) \tag{15}$$

Meanwhile, based on assumption number 3, the value of $\varepsilon_2 = \varepsilon_1$ is obtained. The value of ε_2 is then used to calculate the value of λ_2.

Table 2. Transition Probability Value

Transition Probability	$i = 1$ Delta Variant	$i = 2$ Omicron Variant
α_i	0.76359	0.84873
β_i	0.23063	0.14550
γ_i	0.00577	0.00577
ε_i	0.00063	0.00063
δ_i	0.98520	0.98676
λ_i	0.01417	0.01262

Based on equations (9), (10), (11), (12), (13), (14), and (15), the transition probability values are obtained as in Table 2. It can be seen that the transition probability from a healthy state " 0” to the state of being infected with COVID-19 “1” in the Delta variant of COVID-19, or β_1, is greater than the similar chance of the Omicron variant of COVID-19, or β_2. This means that the Delta variant of COVID-19 is more contagious than the Omicron variant of COVID-19. This is also supported by the value of the transition probability from a healthy state "0" to a healthy state "0" which is lower in the COVID-19 Delta variant compared to the COVID-19 Omicron variant.

Then it is seen that the transition probability from being infected with COVID-19 "1" to a state of death "2" in the Delta variant of COVID-19, or λ_1, is greater than the similar probability in the Omicron variant of COVID-19, or λ_2. This means that the Delta variant of COVID-19 is more deadly than the Omicron variant of COVID-19. Even so, the chance that someone infected with the Delta variant of COVID-19 will die is small, that is 0.01417.

The Prediction of the Length of Time for Status Changes to the Death State

The process of predicting the length of time (number of steps) for status changes to the death state begins by calculating the probability of transition from state "0" or "1" to state "2" over a period of time T, where $T = min\{n \geq 0|X_n = 2\}$. Furthermore, suppose u_0 is the probability of the process reaching the absorbing state, namely the death state "2", given that the initial state is healthy state "0" and u_1 is the probability of the process reaching an absorbing state, namely the death state "2", given that the initial state is being infected with COVID-19 19 "1". Let also suppose that v_0 is the average number of steps needed until the process to the death state "2" given that the initial state is healthy state "0" and v_0 is the average number of steps needed until the process to the death state "2" given that the initial state is being infected with COVID-19 19 "1". The equations u_0, u_1, v_0, and v_1 can be defined as follows

$$u_0 = P(X_T = 2|X_0 = 0)$$

$$u_1 = P(X_T = 2|X_0 = 1)$$

$$v_0 = E\{T|X_0 = 0\}$$

$$v_1 = E\{T|X_0 = 1\}$$

To determine the value of u_0, u_1, v_0, and v_1 used the first step analysis. There are three possibilities for X_0, namely $X_0 = 0$, $X_0 = 1$, and $X_0 = 2$. The state process probabilities of the three possible values of X_0 are shown in Table 3.

Table 3. Possible Value of X_0

Possibility	n	Probability
I	0	$P(X_T = 0\|X_0 = 0)$ $P(X_T = 1\|X_0 = 0)$ $P(X_T = 2\|X_0 = 0)$
II	1	$P(X_T = 0\|X_0 = 1)$ $P(X_T = 1\|X_0 = 1)$ $P(X_T = 2\|X_0 = 1)$
III	2	$P(X_T = 0\|X_0 = 2)$ $P(X_T = 1\|X_0 = 2)$ $P(X_T = 2\|X_0 = 2)$

Note that the equation u_0 can be written as follows

$$\begin{aligned} u_0 &= P(X_T = 2|X_0 = 0) \\ &= \sum_{k=0}^{2} P(X_T = 2, X_1 = k|X_0 = 0) \\ &= u_0\alpha_i + u_1\beta_i + \gamma_i \end{aligned}$$

So, $u_0 = \frac{u_1\beta_i+\gamma_i}{1-\alpha_i}$ is obtained. Furthermore, in the same way, the equation u_1 can be written as follows

$$\begin{aligned} u_1 &= P(X_T = 2|X_0 = 1) \\ &= \textstyle\sum_{k=0}^{2} P(X_T = 2, X_1 = k|X_0 = 1) \\ &= u_0\delta_i + u_1\varepsilon_i + \lambda_i \end{aligned}$$

By using elimination and substitution, obtained the value of

$$u_1 = \frac{\gamma_i\delta_i+\lambda_i-\lambda_i\alpha_i}{(\beta_i+\gamma_i)(\delta_i+\lambda_i)-\beta_i\delta_i}$$

So, u_0 can be written in more detail, that is

$$u_0 = \frac{\lambda_i\beta_i+\gamma_i-\gamma_i\varepsilon_i}{(1-\varepsilon_i)(1-\alpha_i)-\delta_i\beta_i}.$$

Then note that the equation v_0 can be obtained using the following way

$$\begin{aligned} v_0 &= E\{T|X_0 = 0\} \\ &= 1 + \textstyle\sum_{k=0}^{2} E\{T, X_1 = k|X_0 = 0\} \\ &= \frac{1 + v_1\beta_i}{1-\alpha_i} \end{aligned}$$

Furthermore, the equation v_1 can be obtained using the following way

$$\begin{aligned} v_1 &= E\{T|X_0 = 1\} \\ &= 1 + \sum_{k=0}^{2} E\{T|X_1 = k\}\, P(X_1 = k|X_0 = 1) \\ &= \frac{\boldsymbol{1+v_0\delta_i}}{\boldsymbol{(1-\varepsilon_i)}} \end{aligned}$$

By using elimination and substitution, obtained the value of

$$\boldsymbol{v_0} = \frac{\boldsymbol{1-\varepsilon_i+\beta_i}}{\boldsymbol{((1-\varepsilon_i)(1-\alpha_i)-\beta_i\delta_i)}}$$

and

$$\boldsymbol{v_1} = \frac{\boldsymbol{1+v_0\delta_i}}{\boldsymbol{(1-\varepsilon_i)}}.$$

Based on the explanation that has been done and the equations u_0, u_1, v_0, and v_1, the values are obtained as in Table 4.

Table 4. The Value of u_0, u_1, v_0, and v_1

	$\boldsymbol{i = 1}$ **Delta Variant**	$\boldsymbol{i = 2}$ **Omicron Variant**
$\boldsymbol{u_0}$	1	1
$\boldsymbol{u_1}$	1	1
$\boldsymbol{v_0}$ (month)	408.24	451.58
$\boldsymbol{v_1}$ (month)	405.45	448.88
$\boldsymbol{v_0}$ (year)	34.02	37.63
$\boldsymbol{v_1}$ (year)	33.79	37.41
$\boldsymbol{v_0 - v_1}$ (month)	2.79	2.70

It can be seen that during the Delta variant of the COVID-19 pandemic, the average length of time a healthy person will die is 34.02 years or 408.24 months. Meanwhile, the average length of time a person infected with COVID-19 will die is 33.79 years or 405.45 months. These two values are the average remaining life span of a person during the Delta variant of the COVID-19 pandemic. This shows that the average remaining life span of someone infected with the Delta variant of COVID-19 is 2.79 months less than the average remaining life span of someone who is healthy during the COVID-19 pandemic.

Then it was seen that during the Omicron variant of the COVID-19 pandemic, the average length of time a healthy person would die was 37.63 years or 451.58 months. Meanwhile, the average length of time a person infected with COVID-19 will die is 37.41 years or 448.88 months. These two values are the average remaining life span of a person during the Omicron variant of the COVID-19 pandemic. This shows that the average remaining life span of someone infected with the Omicron variant of COVID-19 is 2.70 months less than the average remaining life span of someone who is healthy during the COVID-19 pandemic.

These results are consistent and in line with the previous research. Previous research has shown that life expectancy, in general, will decline in 2020 and 2021, during the COVID-19 pandemic, compared to previous years (Aburto et al., 2021; Aburto et al., 2022; Gibson & Olivia, 2020; Heuveline, 2021; Legouis et al., 2021; Oshinubi et al., 2022). Meanwhile, in this research, it was seen that there was a decrease in the average remaining life span of someone infected with COVID-19 compared to healthy people.

CONCLUSIONS AND SUGGESTIONS

A patient who is positively infected with COVID-19 within a certain time can experience a change in status to be healthy or even die. During the Delta variant of the COVID-19 pandemic, the average age of a person infected with COVID-19 was reduced by 2.79 months. This is because the average time taken by someone from being healthy to the death is 34.02 years and the average time taken by someone infected with COVID-19 to death is 33.79 years. During the Omicron variant of the COVID-19 pandemic, the average age of a person infected with COVID-19 was reduced by 2.7 months. This is because the average time taken by someone from being healthy to death is 37.63 years and the average time taken by someone infected with COVID-19 to death is 37.41 years. Therefore, it can be concluded that the average lifespan of a person who has been infected with the Delta or Omicron variant is shorter than that of a healthy person. Where the average life span of someone infected with the Delta variant of COVID-19 is 0.09 months shorter than someone who has the Omicron variant of COVID-19.

This research can be developed to predict the average remaining life span after the COVID-19 pandemic from people in various countries. These results can be compared with conclusions regarding the reduction in life expectancy that have been carried out by previous researchers.

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