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A Comparative Analysis on Virus Mutation with Fibonacci Numbers

Rexma Sherine V[1], Gerly TG[2], Britto Antony Xavier G [3] and Abisha M[4]

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Abstract

In our research, we have derived the fibonacci numbers from the virus mutation. For example, if a virus is first mutated, the fibonacci numbers are capable of identifying the splitting ratio between the parent and first mutant virus. Likewise, the second mutant can be predicted using the Tribonacci numbers, and so on. Here, we compare the fibonacci numbers with the virus spread of each mutant virus to get the transmission ratio for each mutation. This will help prevent the spread of the virus before it reaches a critical level.

Key words: Fibonacci, virus mutant, spreading ratio and critical level.

AMS classification: 92B05, 92D15, 92F05.

1 Introduction

The Fibonacci sequence is named for Leonardo Pisano (also known Fibonacci), an Italian mathematician who lived from 1170 to 1250. Fibonacci sequences are set of numbers based on the rule that each number is equal to the sum of the preceding two numbers; it can be also evaluated by the general formula where $F(n)$ represents the n-th Fibonacci number (n is called an index), the sum of values in pascal's triangle diagonal also demonstrates Fibonacci sequences.

The presentation and report are designed to discover the application of Fibonacci sequences in daily life. The famous Fibonacci sequence has captivated mathematicians, artists, designers, and scientists for centuries therefore it is suggested as an important fundamental characteristic in real life.

A detailed explation of generalized fibonacci numbers is provided in [6]. The author

[1]Department of Mathematics, Sacred Heart College(Autonomous), Tirupattur - 635601, Tamil Nadu, S.India. Email:rexmaprabu123@gmail.com

[2]Department of Mathematics, Sacred Heart College(Autonomous), Tirupattur - 635601, Tamil Nadu, S.India. Email:tgp.gerlyjose@yahoo.com

[3]Department of Mathematics, Sacred Heart College(Autonomous), Tirupattur - 635601, Tamil Nadu, S.India. Email:brittoshc@gmail.com

[4]Department of Mathematics, Sacred Heart College(Autonomous), Tirupattur - 635601, Tamil Nadu, S.India. Email:mabisha1996@gmail.com

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in [1] propagated the phenomenon of flow and load capacity using the generalized fibonacci sequence. In [24], the authors showed Diophantine equation has only two solutions in k-generalized Fibonacci sequences. [14] The infinite sums derived from the reciprocals of the generalized Fibonacci numbers. [22] The authors developed interpretation of $J_{t,n}$ in the generalization of Fibonacci numbers. The Fibonacci numbers have many interpretations also in graph theory [11, 18, 26]. In 2020, [10] gives a simple model for the spread of virus in terms of Fibonacci numbers. A lot of interesting facts and properties of fibonacci sequence is provided in [15]. Finding the perfect powers in some generalized Fibonacci sequences by Luca and Shorey [16]. Marques and Togbe [17] found that Fibonomial coefficients. The connections between generalized Fibonacci and Tribonacci sequences [12]. [19] This paper serves to review the observed documentation of the Fibonacci sequence in the human body. The convergence properties of Generalized Fibonacci Sequences and the series of partial sums associated with them are provided in [13]. The Fibonacci application in Extorial function and partial delay difference equations are provided in [23, 3, 5]. The higher order Infinite Fibonacci series equation is briefly given in the articles [4, 21].
There are numerous ways to find the Fibonacci numbers in various objects all around the world. In this paper, we develop the Fibonacci numbers from the virus mutantion process. This paper is structued as follows: Section 1 Introduction. Section 2 deals with some fibonacci definitions and its properties. The development of fibonacci numbers from the virus mutation process is briefly explained in section 3. The transmission ratio of virus spread from fibonacci sequence is provided in section 4. Finally section 5 is conclusion.

2 Fibonacci Approach and its Properties

Definition 2.1 Let $n \in \mathbb{N}(0)$ and $m > 1$ be a positive integers, then the generalized m-th Fibonacci sequence is defined as

$$F_{n+(m)} = \begin{cases} 1, & 0 \le n \le m-1 \\ \sum\limits_{r=1}^{m} F_{n-r}, & n > m-1 \end{cases} \tag{1}$$

Some of the sequences of equation (1) are stated as follows:

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$F_{n+(m)},\ m>1$	some of first few sequence	name of the fibonacci
$F_{n+(2)}$	$1,1,2,3,5,8,13,21,\ldots$	Fibonacci
$F_{n+(3)}$	$1,1,1,3,5,9,17,31,\ldots$	Tribonacci
$F_{n+(4)}$	$1,1,1,1,4,7,13,25,\ldots$	Tetranacci
$F_{n+(5)}$	$1,1,1,1,1,5,9,17,33,\ldots$	Pentanacci
$\vdots$	$\vdots$	$\vdots$
$F_{n+(m)}$	$\underbrace{1,1,\ldots,1}_{m\ times},m,m+\underbrace{1,1,\ldots,1}_{m-1\ times},\ldots$	m-th fibonacci

Definition 2.2 If $n+(m)$ be any positive and negative indices, then the generalized m-th Fibonacci sequence is defined as

$$F_{n+(m)} = \sum_{r=1}^{m+1} F_{n-r}, \tag{2}$$

whose initial conditions are

$F_{n+(m)}$	F_{-1}	F_{-2}	F_{-3}	F_{-4}	F_{-5}	F_{-6}	$\cdots$
$m=2$	0	1					$\cdots$
$m=3$	-1	1	1				$\cdots$
$m=4$	-2	1	1	1			$\cdots$
$m=5$	-3	1	1	1	1		$\cdots$
$m=6$	-4	1	1	1	1	1	$\cdots$
$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	

Lemma 2.3 Let $\{x_0, x_1, x_2, x_3, x_4, \ldots\}$ be any sequence of positive integers and if the sequence satisfies the condition $\frac{x_r}{x_{r-1}} = \frac{x_{r+1}}{x_r} = \frac{x_{r+2}}{x_{r+1}} = \ldots = I_r$, then for $r \in \mathbb{N}(1)$, we have

$$\lim_{r\to\infty} \frac{x_r}{x_{r+1}} = I_r. \tag{3}$$

Proof:
The proof completes by dividing the two consecutive numbers (x_r/x_{r-1}) and the value is deoted as I_r for $r \in \mathbb{N}(1)$.

Illustration 2.4 Let us take sequence as $\{1,1,2,3,5,8,13,21,\ldots\}$ in Lemma 2.3, then we have $x_0 = 1,\ x_1 = 1,\ x_2 = 2,\ x_3 = 3,\ldots$ such that $\frac{x_1}{x_0} = 1(I_1)$, $\frac{x_2}{x_1} = 2(I_2)$, $\frac{x_3}{x_2} = I_3$, $\frac{x_4}{x_3} = I_4,\ldots$. Here $I_1, I_2, I_3, \ldots$ are distinct values. Proceeding like this, we get $\frac{x_{10}}{x_9} = \frac{x_{11}}{x_{10}} = \frac{x_{12}}{x_{11}} = \ldots = 1.618$.
If we consider $x_{10} = x_r$, then $\frac{x_r}{x_{r-1}} = \frac{x_{r+1}}{x_r} = \frac{x_{r+2}}{x_{r+1}} = \ldots$ will gives the value 1.618 which implies $\lim_{r\to\infty} \frac{x_r}{x_{r+1}} = 1.618$.

Remark 2.5 If $\lim_{r\to\infty} \frac{x_r}{x_{r+1}} = I_r$, then we say that I_r is a critical value. For example, in Illustration 2.4, the value 1.618 remains constant throughout the sequence, hence we say that 1.618 is a critical value.

Theorem 2.6 Let $\{F_0, F_1, F_2, F_3, F_4, \ldots\}$ be a sequence of positive numbers that satisfies $F_n = F_{n-1} + F_{n-2} + F_{n-3}$, $r \in \mathbb{N}(0)$ with initial conditions $F_{-1} = -1$, $F_{-2} = 1$ and $F_{-3} = 1$. Then $\lim_{n\to\infty} \frac{F_{n+2}}{F_{n+1}} = I_1$, if $\lim_{n\to\infty} \frac{F_{n+1}}{F_n} = I_1$ and $\lim_{n\to\infty} \frac{F_{n+2}}{F_n} = I_2$.

Illustration 2.7 Let $\{1,1,1,3,5,9,17,31,57,\ldots\}$ be a sequence of positive numbers that satisfies the conditions given in Theorem 2.6. Prove that $\lim_{n\to\infty} \frac{F_{n+2}}{F_{n+1}} = I_1$.
Proof: From the given sequence $\{1,1,1,3,5,9,17,31,57,\ldots\}$, we have $F_0 = 1$, $F_1 = 1,\ F_2 = 1,\ F_3 = 3,\ldots$ and goes on. Taking $\frac{F_{n+1}}{F_n}$ for $n = 0,1,2,3\ldots$, we get $\{1,1,3,1.67,1.8,1.89,1.84,1.84,1.84,\ldots\}$ and which will converges to 1.84.
Similarly, by taking $\frac{F_{n+2}}{F_n}$, we obtain the sequence of the form $\{1,3,5,3,3.4,3.4,3.35,3.387,3.385,3.381,3.383,3.383,3.383,\ldots\}$, and converges to 3.383. Therefore,

$$\lim_{n\to\infty} \frac{F_{n+1}}{F_n} = 1.84(I_1). \tag{4}$$

and

$$\lim_{n\to\infty} \frac{F_{n+2}}{F_n} = 3.383(I_2). \tag{5}$$

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Hence, by dividing equation (5) by (4), we obtain $\lim_{n\to\infty}\frac{F_{n+2}}{F_{n+1}}=\frac{I_2}{I_1}=1.84=I_1$.

Remark 2.8 The sequence $\{1,1,1,3,5,9,17,31,57,\ldots\}$ is known as Tribonacci numbers and its critical values are 1.84 and 3.383.

Theorem 2.9 Let $\{F_n\}_{n=0}^{\infty}$ be a sequence of generalized fibonacci numbers and if $\lim_{n\to\infty}\frac{F_{n+1}}{F_n}=I_1$, $\lim_{n\to\infty}\frac{F_{n+2}}{F_n}=I_2$, $\lim_{n\to\infty}\frac{F_{n+3}}{F_n}=I_3,\ldots,\lim_{n\to\infty}\frac{F_{n+m}}{F_n}=I_m$. Then $\frac{I_{n+1}}{I_n}=I_1$, $\frac{I_{n+2}}{I_n}=I_2$, $\frac{I_{n+3}}{I_n}=I_3,\ldots,\frac{I_{n+m}}{I_n}=I_m$, where $n\in\mathbb{N}(0)$ and $m\in\mathbb{N}(1)$.

Proof: Let us consider the Generalized fibonacci sequence as $\{\underbrace{1,1,1,\ldots,1}_{m\ times},m,m+\underbrace{1,1,1,\ldots,1}_{m-1\ times},\ldots\}$. Now, we shall prove this theorem using the induction method.

The proof for $m=1$ is given in Lemma 2.3 and Illustration 2.4.

For $m=2$, the proof is verified in Theorem 2.6 and Illustration 2.7.

For $m=3$, we consider the sequence in the form of $\{1,1,1,1,4,7,13,25,\ldots\}$. If

$$\lim_{n\to\infty}\frac{F_{n+1}}{F_n}=I_1(say), \tag{6}$$

$$\lim_{n\to\infty}\frac{F_{n+2}}{F_n}=I_2(say) \tag{7}$$

and

$$\lim_{n\to\infty}\frac{F_{n+3}}{F_n}=I_3(say). \tag{8}$$

Now, dividing the equations (7) by (6), (8) by (7) and (8) by (6), we get

$$\lim_{n\to\infty}\frac{F_{n+2}}{F_{n+1}}=\frac{I_2}{I_1}=I_1, \tag{9}$$

$$\lim_{n\to\infty}\frac{F_{n+3}}{F_{n+2}}=\frac{I_3}{I_2}=I_1, \tag{10}$$

$$\lim_{n\to\infty}\frac{F_{n+3}}{F_{n+1}}=\frac{I_3}{I_1}=I_2. \tag{11}$$

For more understanding, one can easily verify the equations (9), (10) and (11) using the similar procedure of Illustration 2.4 and Illustration 2.7 by taking the sequence $\{1,1,1,1,4,7,13,25,\ldots\}$, where $F_n=F_{n-1}+F_{n-2}+F_{n-3}+F_{n-4}$ with initial conditions

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$F_{-1} = -2$, $F_{-2} = 1$, $F_{-3} = 1$ and $F_{-4} = 1$.
Similarly, when taking $m = m-1$, we get the sequence as the form of
$\{\underbrace{1,1,1,\ldots,1}_{m-1\ times}, m-1, m-1+\underbrace{1,1,1,\ldots,1}_{m-2\ times}, \ldots\}$.
Therefore, we have $\lim_{n\to\infty} \frac{F_{n+1}}{F_n} = I_1$, $\lim_{n\to\infty} \frac{F_{n+2}}{F_n} = I_2, \ldots, \lim_{n\to\infty} \frac{F_{n+m-1}}{F_n} = I_{m-1}$. So that, we get $\lim_{n\to\infty} \frac{F_{n+2}}{F_{n+1}} = \lim_{n\to\infty} \frac{F_{n+3}}{F_{n+2}} = \ldots = \lim_{n\to\infty} \frac{F_{n+m-1}}{F_{n+m-2}} = I_1$,
$\lim_{n\to\infty} \frac{F_{n+3}}{F_{n+1}} = \lim_{n\to\infty} \frac{F_{n+4}}{F_{n+2}} = \ldots = \lim_{n\to\infty} \frac{F_{n+m-1}}{F_{n+m-3}} = I_2, \ldots\ldots, \lim_{n\to\infty} \frac{F_{n+m-1}}{F_{n+1}} = I_{m-2}$.
Hence the proof is verified for m times.

3 Virus Mutation

It is normal for viruses to change and evolve as they spread between people over time. When these changes become significantly different from the original virus, they are known as variants. To identify variants, scientists map the genetic material of viruses (known as sequencing) and then look for differences between them to see if they have changed. Since the SARS-CoV-2 virus, the virus that causes COVID-19, has been spreading globally, variants have emerged and been identified in many countries around the world. Viruses are constantly evolving and changing. Every time a virus replicates (makes copies of itself), there is the potential for there to be changes in its structure. Each of these changes is a mutation. A virus with one or more mutations is called a variant of the original virus. Some mutations can lead to changes in important characteristics of the virus, including characteristics that affect its ability to spread and/or its ability to cause more severe illness and death. For more reference, one can refer [7, 8, 9, 25, 20, 2].

3.1 Fibonacci numbers in virus mutation

From the Figure:1, it is clear that that virus replicates and changes a little bit and produce a new form of virus called as "first mutation". This newly developed virus can be split into two forms: a parent virus and first mutant virus. Later that the parent virus replicates and develops a first mutant virus, but the first mutant virus again splits into parent virus and first mutant virus. Similarly, the parent virus replicates itself and first mutant virus splits in two forms and the process will goes on repeatedly.

Finally, we obtain the transmission of virus spread in the human population will occur in the form of $\{1,1,2,3,5,8,13,\ldots\}$, which is nothing but the fibonacci sequence

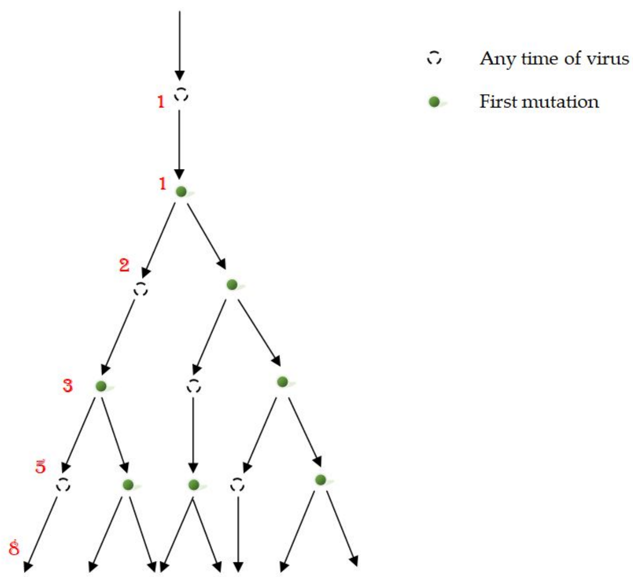

Figure 1: First mutation

$F_{n+(2)}$. The theorital proof of the fiboancci sequence is clearly explained in Theorem 2.3 and Illustration 2.4. Hence, if the spreadness does not exceed the critical value, then we can control the virus transmission. But if the spreadness exceeds the critical value, then it leads to the severe illnes and causes death to the human population. Therefore, we should take control measures before the spreadness reaches the critical. Now, if the first mutant virus replicates itself and produces a new virus called "second mutation". Here, at very first the parent virus replicates itself and turns into first mutation. After that the first mutant virus replicates itself and produce second mutant. The possiblity of this second mutant virus splitting is three forms such as parent virus, first mutant virus and second mutant virus. Again the parent virus will replicates to produce first mutant virus, the first mutant virus will replicates to produce the second mutant virus, and the second mutant virus will splits in all the three forms. Hence, this process will goes on repeatedly and which is clearly demonstarted in Figure:2. Therefore, for the second mutation, the spreadness of virus will occur in the sequence of the form $\{1,1,1,3,5,9,17,\ldots\}$ which gives $F_{n+(3)}$. The critical point of the second fibonacci sequence is clearly explained in Theorem 2.6 and Illustration 2.7. Similarly, during the third mutation, the spreadness of virus will occur in the sequence of the form $\{1,1,1,1,4,7,13,\ldots\}$ which is given in Figure:3. Hence, one can esaily find the fourth, fifth, sixth,... fibonacci sequence at

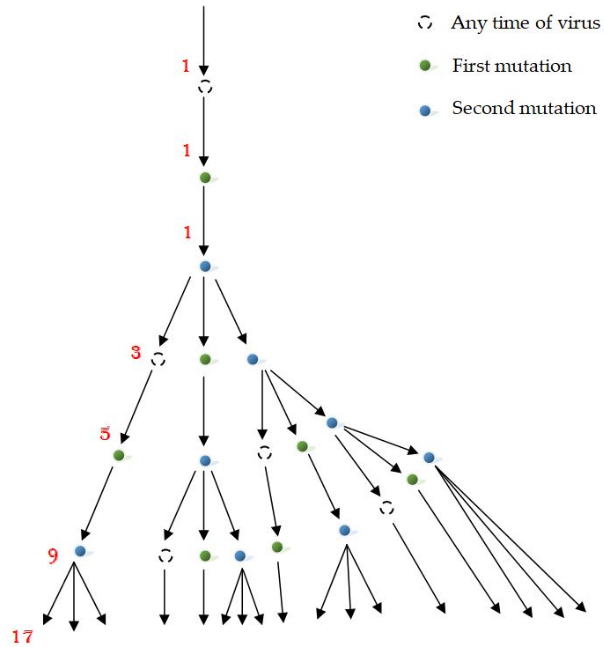

Figure 2: Second mutation

each mutation and its critical point can be identify using the Theorem 2.9.

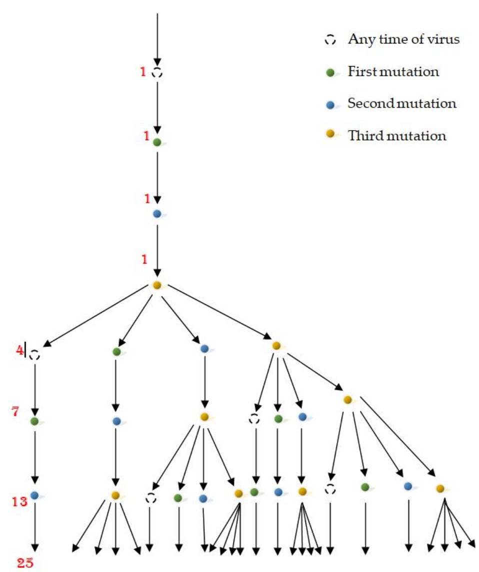

Figure 3: Third mutation

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4 Transmission ratio of virus spread from Fibonacci numbers

When comparing the first and second mutant virus, the transmission rate will obtained in the form of 1 : 1, 1 : 1, 2 : 1, 3 : 3, 5 : 5, 8 : 9, 13 : 17, ... From this transmission rate, we can say that the spreading ratio of the first mutant is large when compared to the second mutant and then both of the mutant becomes constant for some particular time. Later that the spreading ratio of the second mutant will becomes very fast when compared to the first mutant. Hence, we can say that if the virus mutant occurs at one time, the speed of virus transmission will go fast. Now, by adding the first and second fibonacci sequence, we get

$F_{n+(2)}$	1	1	2	3	5	8	13	21	34	$\cdots$
$F_{n+(3)}$	1	1	1	3	5	9	17	31	57	$\cdots$
$F_{n+(2)}+F_{n+(3)}$	2	2	3	6	10	17	30	52	91	$\cdots$

Now, comparing the $F_{n+(2)}+F_{n+(3)}$ sequence into the third fibonacci sequence, we arrive the ratio in the form of 2 : 1, 2 : 1, 3 : 1, 6 : 1, 10 : 4, 17 : 7, 30 : 13, 52 : 25, 91 : 49,...,16329 : 17905, 29329 : 34513, 53264 : 66526,... From the above ratio, the transmission of fourth fibonacci will spread fast when comparing the first and second fibonacci. Similarly, comparing the other fibonacci sequences, the rate of transmission occurs very severe at each mutation.

4.1 Finding the virus spread from Generalized Fibonacci numbers

If there exists k number of virus and the mutation occurs for m times, then the generalized fibonacci sequence are described below.

For $m>1$	some of first few sequence	name of the sequence
$k(F_{n+(2)})$	$k,k,2k,3k,5k,8k,13k,21k,34k,\ldots$	k-th fibonacci
$k(F_{n+(3)})$	$k,k,k,3k,5k,9k,17k,31k,57k,\ldots$	k-th Tribonacci
$k(F_{n+(4)})$	$k,k,k,k,4k,7k,13k,25k,49k,\ldots$	k-th Tetranacci
$k(F_{n+(5)})$	$k,k,k,k,k,5k,9k,17k,33k,\ldots$	k-th Pentanacci
$\vdots$	$\vdots$	$\vdots$
$k(F_{n+(m)})$	$\underbrace{k,k,\ldots,k}_{m\ times},mk,mk+\underbrace{k,k,\ldots,k}_{m-1\ times},\ldots$	mk-th fibonacci

If the first mutant, second mutant, third mutant,...,m-th mutants are all present in our surroundings at the same time, then the transmission of virus will occur in the form of $\{1,1,2,3,5,8,\ldots\}+\{1,1,1,3,5,9,\ldots\}+\{1,1,1,1,4,7,13,\ldots\}+\ldots+\{\underbrace{1,1,1,\ldots,1}_{m\ times},m,\ldots\}$. That is,

$$\text{Transmission rate} = F_{n+(2)} + F_{n+(3)} + F_{n+(4)} + \ldots + F_{n+(m)}.$$

Similarly, if each of the mutant virus exists k times, then the transmission rate of virus can be generated as $\{k,k,2k,3k,5k,8k,\ldots\}+\{k,k,k,3k,5k,9k,\ldots\}+\{k,k,k,k,4k,7k,13k,\ldots\}+\ldots+\{\underbrace{k,k,\ldots,k}_{m\ times},mk,mk+(\underbrace{k,k,\ldots,k}_{m-1\ times}),\ldots\}$. This generalized fibonacci sequence can be written as the linear combination of $k\{1,1,2,3,5,8,\ldots\}+k\{(1,1,1,3,5,9,\ldots\}+k\{1,1,1,1,4,7,13,\ldots\}+\ldots+k\{\underbrace{(1,1,1,\ldots,1)}_{m\ times},m,\ldots\}$. Therefore,

$$\text{Transmission rate} = k(F_{n+(2)}) + k(F_{n+(3)}) + k(F_{n+(4)}) + \ldots + k(F_{n+(m)}).$$

Hence, if the mutation occurs k times, then the rate of transmission of virus can be detected using this Linear combination method.

5 Conclusion

In our research, we developed the Fibonacci numbers while analysing the virus mutation process. The spreading ratio of each mutant virus can be easily determined by applying the Generalised Fibonacci numbers. Using this method, we might control the virus's transmission rate before it reaches a critical level.

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