ORIGINAL PAPER

GAUSSIAN FIBONACCI MODELS IN DISEASE SPREAD DYNAMICS

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Abstract. *In this study, a Gaussian Fibonacci framework for simulating the transmission of illness among interrelated populations is developed. A basic exponential growth model, a scaled transmission variation, and a generalised form with complex coefficients are the three main recurrence relations proposed in this study. New extensions tackle important epidemiological issues. To avoid repeated simulation, a closed-form method first computes cumulative infections directly. The second step is to determine when delayed measures reduce outbreaks by developing stability criteria for control actions with fixed latency. Third, the intake of travel-linked infections is captured by the continual migration terms. Fourth, seasonal forcing components are used to model influenza winters and other oscillatory outbreaks. Fifth, subexponential growth under poor transmission parameters is guaranteed by strict constraints. Lastly, large-scale projections can be made quickly and accurately using a golden ratio approximation. Taken together, these advances improve analytical tractability in migration, seasonality, and intervention-delay settings, offering useful tools for managing and forecasting epidemics.*

Keywords: *Gaussian Fibonacci sequence; dual population epidemic models; stability theorems; vaccination delay effects; epidemic control with complex dynamics.*

Mathematics Subject Classification: *11B39; 92D30; 39A06; 39A70; 93D20; 26D07; 41A25.*

1. INTRODUCTION

Mathematical models have become essential in understanding how diseases spread; they are like maps for epidemics. While classic models like SIR rely heavily on differential equations, there is another side to explore: discrete, recursive models. These are especially handy when we are dealing with populations that are split or otherwise networked.

In this paper, we use Gaussian Fibonacci sequences, which are essentially complex-number representations of the standard Fibonacci series, to take a new approach. We can add more depth to the model by using Gaussian integers, which are numbers of the type $a + bi$, where a and b are both integers. For instance, we may consider the imaginary part to follow the spread of illnesses in rural areas (B) and the real part to represent infections in metropolitan areas (A) ([1,2]).

The Gaussian Fibonacci number sequence [3] is defined by the recurrence relation that follows,

$$GF_n = GF_{n-1} + GF_{n-2}, n > 1, \tag{1.1}$$

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With $GF_0 = i, GF_1 = 1$. One can see that

$$GF_n = F_n + iF_{n-1} \tag{1.2}$$

where $F_n$is the *n*th Fibonacci number [4].

The first few Gaussian Fibonacci numbers are

$$\{GF_n\} = \{i, 1, 1 + i, 2 + i, 3 + 2i, 5 + 3i, \dots\}$$

2. PRELIMINARIES

2.1. GAUSSIAN FIBONACCI PROPERTIES

Let us start with a few key ideas about Gaussian Fibonacci numbers. First off, the *norm* of GF_n, which just means its squared magnitude, is given by:

$$\|GF_n\|^2 = F_n^2 + F_{n-1}^2 = F_{2n-1} \tag{2.1}$$

So, interestingly, it's directly related to a higher-index Fibonacci number. Now for the Binet-like formula for GF_n,

$$GF_n = \frac{x_1^n - x_2^n}{x_1 - x_2} + i\frac{x_1^{n-1} - x_2^{n-1}}{x_1 - x_2} \tag{2.2}$$

The characteristic equation of the recurrence relation (1) is

$$x^2 - x - 1 = 0 \tag{2.3}$$

This equation has two real roots: $x_1 = \frac{1+\sqrt{5}}{2}$ and $x_2 = \frac{1-\sqrt{5}}{2}$ $(x_1 > x_2)$, we might recognize that they are the golden ratio and its conjugate. These expressions help calculate GF_n directly, without stepping through the sequence.

2.2. EPIDEMIOLOGICAL FRAMEWORK

Let us now turn to how these fit into modelling diseases. Imagine that the total infection counts at time n is represented as a complex number:

$$Z_n = I_A(n) + iI_B(n) \tag{2.4}$$

Here, $I_A(n)$ tracks infections in one group, say, an urban population, while $I_B(n)$ represents another, maybe a rural or isolated community. The real and imaginary parts evolve together but can behave differently.

We then define the Gaussian Fibonacci model as,

$$Z_n = \mathbb{c}_1 Z_{n-1} + \mathbb{c}_2 Z_{n-2} \tag{2.5}$$

with $\mathbb{c}_1 = a_1 + ib_1$ and $\mathbb{c}_2 = a_2 + ib_2$, where each coefficient can capture different aspects, such as transmission or recovery, in each subgroup. These are complex parameters, so they provide us with greater flexibility in modelling coupled dynamics [2].

3. RESULTS AND DISCUSSION

3.1. MODEL 1: SIMPLE GAUSSIAN FIBONACCI SPREAD

Definition 1. *Let us begin with the simplest case: both coefficients equal to 1*. That gives us the recurrence,

$$Z_n = Z_{n-1} + Z_{n-2} \tag{3.1}$$

which breaks down into two independent Fibonacci sequences:

$$\begin{cases} I_A(n) = I_A(n-1) + I_A(n-2) \\ I_B(n) = I_B(n-1) + I_B(n-2) \end{cases} \tag{3.2}$$

So, each group grows independently and exponentially just like an uncontrolled outbreak would in its early stages [5].

Proposition 2. (Explicit solution for simple GF Model: [6]). If we know the first two values Z_0 and Z_1, we can write a direct formula for the nth value,

$$Z_n = \mathcal{A}x_1^n + \mathcal{B}x_2^n \tag{3.3}$$

where the constant $\mathcal{A}\ and\ \mathcal{B}$ depends on the initial data, $\mathcal{A} = \frac{Z_1 - x_2^n Z_0}{x_1 - x_2}$, $\mathcal{B} = \frac{Z_1 - x_1^n Z_0}{x_1 - x_2}$.

Corollary 3. (Growth Rate). In the long run, the dominant terms are x_1^n, so we can say

$$\lim_{n\to\infty}\left(\frac{\ln|Z_n|}{n}\right) = \ln x_1 \approx 0.481 \tag{3.4}$$

That means infections grow exponentially and fast. The golden ratio once again appears as the growth driver ([4], [6]).

Theorem 4. (Fast Simulation via Golden-Ratio approximation). *Let* $\{Z_n\}_{n\geq 0} \subset \mathbb{R}$ *satisfy the Fibonacci recurrence for* $n \geq 2$,

$$Z_n = Z_{n-1} + Z_{n-2}$$

with $Z_0, Z_1 \in \mathbb{R}$. Let $x_1 = \frac{1+\sqrt{5}}{2}$ and $x_2 = \frac{1-\sqrt{5}}{2} = -\frac{1}{x_1}$.

Then for every n ≥ 0,

$$Z_n = \frac{Z_1 - x_2 Z_0}{\sqrt{5}}\, x_1^n + \varepsilon_n \tag{3.5}$$

With the exact reminder $\varepsilon_n = \mathcal{B}x_2^n$, where $\mathcal{B} = \frac{x_1 Z_0 - Z_1}{\sqrt{5}}$. Moreover, the error admits the explicit bound

$$|\varepsilon_n| \le \frac{x_1|Z_0| + |Z_1|}{\sqrt{5}}\, x_1^{-n} = \frac{x_1^{1-n}|Z_0| + x_1^{-n}|Z_1|}{\sqrt{5}} \tag{3.6}$$

In particular $|\varepsilon_n| = O(x_1^{-n})\ as\ n \to \infty$.

Proof: Using $Z_n = \mathcal{A}x_1^n + \mathcal{B}x_2^n$, where $\mathcal{A} = \frac{Z_1 - x_2 Z_0}{x_1 - x_2}$, $\mathcal{B} = \frac{x_1 Z_0 - Z_1}{x_1 - x_2}$. Thus,

$$Z_n = \frac{Z_1 - x_2 Z_0}{\sqrt{5}} x_1^n + \frac{x_1 Z_0 - Z_1}{\sqrt{5}} x_2^n$$

holds for every *n*. Put $\varepsilon_n = \mathcal{B}x_2^n$; this yields the stated representation.

Since $x_1 x_2 = -1$ and $|x_2| = x_1^{-1}$. Hence

$$|\varepsilon_n| = |\mathcal{B}||x_2|^n = \frac{|\, x_1 Z_0 - Z_1|}{\sqrt{5}}\, x_1^{-n}$$

Therefore

$$|\varepsilon_n| \le \frac{x_1|Z_0| + |Z_1|}{\sqrt{5}}\, x_1^{-n} = \frac{x_1^{1-n}|Z_0| + x_1^{-n}|Z_1|}{\sqrt{5}}$$

3.2. MODEL 2: SCALED GAUSSIAN FIBONACCI MODEL

Definition 5. *In this model, the recurrence relation is scaled by a complex number* ℂ*, so we get*

$$Z_n = \mathbb{c}(Z_{n-1} + Z_{n-2}) \tag{3.7}$$

where $\mathbb{c} \in \mathbb{C}$ acts as a control parameter, basically tuning how the infection spreads across time. This coupling introduces some interesting dynamics between the two groups through complex multiplication. i.e.,

$$\mathbb{c}\,.\,(x + yi) = (ax - by) + i(ay + bx)\,, with\ \mathbb{c} = a + bi$$

So, the interaction between the two subpopulations (say, urban and rural) is governed by both parts of ℂ, creating a kind of dynamic coupling between them.

Proposition 6. (Stability for Scaled GF Model: [7]). We can understand how this system behaves by looking at the roots of its characteristic equation. They're given by

$$x_{1,2} = \frac{-\mathbb{c} \pm \sqrt{\mathbb{c}^2 - 4\mathbb{c}}}{2} \tag{3.8}$$

This comes from solving the equation,

$$x^2 - \mathbb{c}x - \mathbb{c} = 0$$

Now, depending on the size of those roots, one of two things happens

- If the largest root's magnitude is more than 1, i.e. $\max|x_k| > 1$, the system grows fast.
- If less than 1, i.e. $\max|x_k| < 1$, the infections eventually die out.

3.2. MODEL 3: GENERALIZED LINEAR RECURRENCE

Definition 7. In this model we generalize things a bit. Instead of using a fixed multiplier like before, we now let the system evolve using *two* complex parameters,

$$Z_n = \mathbb{c}_1 Z_{n-1} + \mathbb{c}_2 Z_{n-2}$$

Here, both $\mathbb{c}_1$ *and* $\mathbb{c}_2$ are complex numbers, so we've got more room to play with how the dynamics behave. To make things tidier, we can rewrite this in vector form,

$$V_n = \begin{bmatrix} Z_n \\ Z_{n-1} \end{bmatrix} = \underbrace{\begin{bmatrix} \mathbb{c}_1 & \mathbb{c}_2 \\ 1 & 0 \end{bmatrix}}_{L} V_{n-1} \tag{3.9}$$

This matrix L basically drives the evolution. Each step depends on a linear combo of the previous two values [1].

Proposition 8. (Spectral Radius Threshold: [5]). Let us define $\rho(L)$ as the spectral radius of the matrix L in simple terms, it's the largest absolute value of the eigenvalues. We will call that $\rho(L)$. Depending on its value, we get,

- If $\rho(L) > 1$, the infection spreads and fast.
- If $\rho(L) < 1$, the whole thing eventually dies out.

Proof. The system evolves like this,

$$V_n = L^n V_0 \tag{3.10}$$

Now, according to spectral theory, the norm of V_n behaves like $\rho(L^n)$ for large n. So, if $\rho(L) > 1$, that means the exponential growth game is over and if its $\rho(L) < 1$, the outbreak fades out.

Proposition 9. (Explicit Solution via Resultant: [3])

$$Z_n = \frac{(Z_1 - x_2 Z_0)x_1^n - (Z_1 - x_1 Z_0)x_2^n}{x_1 - x_2} \tag{3.11}$$

Theorem 10. (Cumulative Infection Sum). *Suppose the sequence* $\{Z_n\}$ *follows the standard Gaussian Fibonacci rule*,

$$Z_n = Z_{n-1} + Z_{n-2}$$

with starting values $Z_0, Z_1 \in \mathbb{C}$. Then the total infected population up to time n, defined as $S_n = \sum_{k=0}^{n} Z_k$, can be calculated super simply,

$$S_n = Z_{n+2} - Z_1 \tag{3.12}$$

Proof: From the recurrence relation,

$$Z_{k+2} = Z_{k+1} + Z_k$$
$$\Rightarrow Z_k = Z_{k+2} - Z_{k+1}$$

Now, let's sum both sides from $k = 0\ to\ n$,

$$S_n = \sum_{k=0}^{n} Z_k = \sum_{k=0}^{n} (Z_{k+2} - Z_{k+1}) \tag{3.13}$$

$$(Z_2 - Z_1) + (Z_3 - Z_2) + \cdots + (Z_{n+2} - Z_{n+1}) = -Z_1 + Z_{n+2}$$

So,

$$S_n = Z_{n+2} - Z_1$$

Epidemiological Insight

The intriguing aspect is that without calculating every Z, we can estimate the total number of infections up to time n. The total is determined by only two values, 1 at the start and $(n + 2)$ at the end [8].

Theorem 11. (Stability of Delayed Control). *We consider the generalized linear recurrence with a delayed control term, for* $m \geq 3$,

$$Z_n = \mathbb{c}_1 Z_{n-1} + \mathbb{c}_2 Z_{n-2} + d.Z_{n-m} \tag{3.14}$$

$\mathbb{c}_1, \mathbb{c}_2, d \in \mathbb{C}$ are complex parameters.

The term $d.Z_{n-m}$ models a delayed intervention, such as a vaccination campaign or treatment introduced after a fixed lag time m.The system is said to be asymptotically stable $(i.e., Z_n \to 0\ as\ n \to \infty)$ if and only if all roots r of the following characteristic equation satisfy $|x| < 1$ where the equation is

$$x^m - \mathbb{c}_1 x^{m-1} - \mathbb{c}_2 x^{m-2} - d = 0 \tag{3.15}$$

Proof: Assume a trial solution of the form $Z_n = x^n$*, and substitute into the recurrence,*

$$x^n = \mathbb{c}_1 x^{n-1} + \mathbb{c}_2 x^{n-2} + d.x^{n-m} = 0$$
$$x^m - \mathbb{c}_1 x^{m-1} - \mathbb{c}_2 x^{m-2} - d = 0$$

The general solution of the recurrence takes the form,

$$Z_n = \sum\nolimits_j A_j x_j^n$$

where each x_j is a root of the characteristic polynomial.

For the system to stabilize $(i.e., Z_n \to 0)$, every term $A_j x_j^n$ must vanish $as\ n \to \infty$, which holds if and only if,

$$|x_j| < 1\ for\ all\ j$$

- If $x = 0$, then substituting into the characteristic equation yields $-d = 0 \to$ contradiction unless $d = 0$.

Epidemiological Insight

This result reveals that delayed responses such as postponed vaccination or interventions applied too late can significantly impact the stability of an epidemic model [9], [10]

- If $|d|, |\mathbb{c}_1|, or\ |\mathbb{c}_2|$ are too large, or if m (the delay) is too long, the system may become unstable, leading to resurgent outbreaks.
- This framework offers a quantitative handle on when control strategies will work and when they might backfire.

Numerical Example

Let's take a specific set of parameters, $\mathbb{c}_1 = 0.4$, $\mathbb{c}_2 = 0.3$, $d = -0.2$, and $m = 4$, the characteristic equation becomes,

$$x^4 - 0.4x^3 - 0.3x^2 + 0.2 = 0$$

Solving this (numerically), we get roots

$$x \approx 0.78, 0.45, -0.62 \pm 0.28i$$

Each root satisfies $|x| < 1$, so the system is asymptotically stable.

Theorem 12. (Nonhomogeneous Recurrence with Migration Effects). *Let the sequence* $\{Z_n\}$ *be defined by the nonhomogeneous recurrence relation*

$$Z_n = \mathbb{c}_1 Z_{n-1} + \mathbb{c}_2 Z_{n-2} + K \tag{3.16}$$

where $K = k_{\mathcal{A}} + ik_{\mathcal{B}} \in \mathbb{C}$, denotes a constant migration factor. Then for $\mathbb{c}_1 + \mathbb{c}_2 \neq 1$,

$$Z_n = \mathcal{A}x_1^n + \mathcal{B}x_2^n + \frac{K}{1 - \mathbb{c}_1 - \mathbb{c}_2} \tag{3.17}$$

where x_1, x_2 are the characteristic roots of the quadratic equation $x^2 - \mathbb{c}_1 x - \mathbb{c}_2 = 0$, and the constants $\mathcal{A}, \mathcal{B}$ are uniquely determined by the initial conditions via the system:

$$\begin{cases} \mathcal{A} + \mathcal{B} = Z_0 - \dfrac{K}{1 - \mathbb{c}_1 - \mathbb{c}_2}, \\ \mathcal{A}x_1 + \mathcal{B}x_2 = Z_1 - \dfrac{K}{1 - \mathbb{c}_1 - \mathbb{c}_2} \end{cases} \tag{3.18}$$

Proof: Since the associated homogeneous recurrence is

$$Z_n^{(h)} = \mathbb{c}_1 Z_{n-1}^{(h)} + \mathbb{c}_2 Z_{n-2}^{(h)}$$

Thus,

$$Z_n^{(h)} = \mathcal{A}x_1^n + \mathcal{B}x_2^n$$

Assume $Z_n^{(p)} = \alpha$ (a constant). Then $\alpha = \mathbb{c}_1\alpha + \mathbb{c}_2\alpha + k$

$$\alpha = \frac{K}{1 - \mathbb{c}_1 - \mathbb{c}_2}$$

The general solution is

$$Z_n = Z_n^{(h)} + Z_n^{(p)} = \mathcal{A}x_1^n + \mathcal{B}x_2^n + \frac{K}{1 - \mathbb{c}_1 - \mathbb{c}_2}$$

Applying the initial condition Z_0, Z_1. We obtain $\mathcal{A}, \mathcal{B}$:

$$\begin{cases} \mathcal{A} + \mathcal{B} = Z_0 - \dfrac{K}{1 - \mathbb{c}_1 - \mathbb{c}_2}, \\ \mathcal{A}x_1 + \mathcal{B}x_2 = Z_1 - \dfrac{K}{1 - \mathbb{c}_1 - \mathbb{c}_2} \end{cases}$$

Theorem 13. (Decaying Oscillations in Seasonal Diseases). *Consider the nonhomogeneous recurrence relation for $D \in \mathbb{C}$,*

$$Z_n = \mathbb{c}_1 Z_{n-1} + \mathbb{c}_2 Z_{n-2} + (-1)^n D \tag{3.19}$$

where *D* represents periodic seasonal forcing. Let the companion matrix be

$$L = \begin{bmatrix} \mathbb{c}_1 & \mathbb{c}_2 \\ 1 & 0 \end{bmatrix}, \rho(L) = max\{|x_1|, |x_2|\} \tag{3.20}$$

Then

(i) If $1 + \mathbb{c}_1 - \mathbb{c}_2 \neq 0$ (non-resonant case), the general solution is

$$Z_n = \mathcal{A}x_1^n + \mathcal{B}x_2^n + (-1)^n \frac{D}{1 + \mathbb{c}_1 - \mathbb{c}_2} \tag{3.21}$$

(ii) If $1 + \mathbb{c}_1 - \mathbb{c}_2 = 0$ (resonant case), the particular solution grows linearly and

$$Z_n = \mathcal{A}x_1^n + \mathcal{B}x_2^n + (-1)^n \frac{D}{\mathbb{c}_1 - 2\mathbb{c}_2} \tag{3.22}$$

(iii) The long-term asymptotic behaviour is:

$$|Z_n| \sim \begin{cases} \left|\frac{D}{1+\mathbb{c}_1-\mathbb{c}_2}\right|, \rho(L)<1, non-resonant, \\ \left|\frac{D}{\mathbb{c}_1-2\mathbb{c}_2}\right| n, \rho(L)<1, resonant, \\ \mathbb{C}\rho(L)^n, \rho(L)>1, \end{cases} \tag{3.23}$$

where $\mathbb{C}$ depends on the initial conditions.

Proof: We first construct a particular solution. Assume $Z_n^{(p)} = (-1)^n P$ for some constant P. Then

$$\begin{gathered} (-1)^n P = \mathbb{c}_1(-1)^{n-1}P + \mathbb{c}_2(-1)^{n-2}P + (-1)^n D \\ \Longrightarrow P = -\mathbb{c}_1 P + \mathbb{c}_2 P + D \\ \Longrightarrow P(1+\mathbb{c}_1-\mathbb{c}_2) = D \end{gathered}$$

Hence, in the non-resonant case $1+\mathbb{c}_1-\mathbb{c}_2 \neq 0$, we obtain a particular solution

$$Z_n^{(p)} = (-1)^n \frac{D}{1+\mathbb{c}_1-\mathbb{c}_2}$$

In that resonant case, we upgrade to $Z_n^{(p)} = n(-1)^n P_1$. Substitution gives $P_1 = \frac{D}{\mathbb{c}_1-2\mathbb{c}_2}$, so the resonant particular solution becomes

$$Z_n^{(p)} = n(-1)^n \frac{D}{\mathbb{c}_1-2\mathbb{c}_2}$$

Turning to the homogeneous recurrence

$$Z_n^{(h)} = \mathbb{c}_1 Z_{n-1}^{(h)} + \mathbb{c}_2 Z_{n-2}^{(h)}$$

The general solution is

$$Z_n^{(h)} = \mathcal{A}x_1^n + \mathcal{B}x_2^n$$

Since $L = \begin{bmatrix} \mathbb{c}_1 & \mathbb{c}_2 \\ 1 & 0 \end{bmatrix}$ denotes the companion matrix, then the homogeneous part grows or decays according to the spectral radius $\rho(L) = max\{|x_1|, |x_2|\}$, so that $\left|Z_n^{(h)}\right| \sim \mathbb{C}\rho(L)^n$ for some constant $\mathbb{C}$.

Combining the homogeneous and particular parts, the full solution is

$$Z_n = Z_n^{(h)} + Z_n^{(p)} = \begin{cases} \mathcal{A}x_1^n + \mathcal{B}x_2^n + (-1)^n \frac{D}{1+\mathbb{c}_1-\mathbb{c}_2}, 1+\mathbb{c}_1-\mathbb{c}_2 \neq 0 \\ \mathcal{A}x_1^n + \mathcal{B}x_2^n + (-1)^n \frac{D}{\mathbb{c}_1-2\mathbb{c}_2}, 1+\mathbb{c}_1-\mathbb{c}_2 = 0\,, \end{cases}$$

Asymptotically, if $\rho(L) < 1$ and non-resonant, the homogeneous contribution vanishes and

$$Z_n \to (-1)^n \frac{D}{1+\mathbb{c}_1-\mathbb{c}_2}, |Z_n| \to \left|(-1)^n \frac{D}{1+\mathbb{c}_1-\mathbb{c}_2}\right|$$

If $\rho(L) < 1$ but resonance occurs, then the homogeneous part again decays, but the particular solution grows linearly,

$$|Z_n| \sim \left|\frac{D}{\mathbb{c}_1 - 2\mathbb{c}_2}\right| n$$

If $\rho(L) > 1$ the homogeneous component dominates regardless of resonance, and the growth is exponential,

$$|Z_n| \sim \mathbb{C}\rho(L)^n$$

Theorem 14. (Boundedness Criterion for Sub exponential Growth). *Let the infection sequence* $\{Z_n\}$ *evolve according to the second-order recurrence for* $n \geq 2$,

$$Z_n = \mathbb{c}_1 Z_{n-1} + \mathbb{c}_2 Z_{n-2}$$

with complex initial condition $Z_0, Z_1 \in \mathbb{C}$. If the coefficients satisfy the contraction condition

$$|\mathbb{c}_1| + |\mathbb{c}_2| < 1,$$

Then the infection trajectory remains bounded by a decaying exponential envelope:

$$|Z_n| \leq \kappa \mu^n,$$

where $\mu = \frac{|\mathbb{c}_1| + \sqrt{\mathbb{c}_1^2 + 4|\mathbb{c}_2|}}{2}$, $\kappa = max\left(|Z_0|, \frac{|Z_0|}{\mu}\right)$.

Proof: Characteristic equation $x^2 - \mathbb{c}_1 x - \mathbb{c}_2 = 0$ with roots $x_{1,2} = \frac{|\mathbb{c}_1| + \sqrt{\mathbb{c}_1^2 + 4|\mathbb{c}_2|}}{2}$. The asymptotic magnitude of Z_n is controlled by $max(|x_1|, |x_2|)$, by the inequality

$$max(|x_1|, |x_2|) \leq \frac{|\mathbb{c}_1| + \sqrt{\mathbb{c}_1^2 + 4|\mathbb{c}_2|}}{2} = \mu$$

we obtain an explicit upper bound.

To ensure the bound holds for all *n*, set $\kappa = max\left(|Z_0|, \frac{|Z_0|}{\mu}\right)$. Since $|\mathbb{c}_1| + |\mathbb{c}_2| < 1$, it follows that $\mu < 1$. Hence, $|Z_n| \leq \kappa \mu^n \xrightarrow[n\to\infty]{} 0$. Thus, the infection dynamics are subexponentially bounded and eventually vanish.

4. DISCUSSION AND LIMITATIONS

The Gaussian Fibonacci framework we have put together brings some real advantages for studying how epidemics interact. Because it's analytically tractable, the math stays manageable instead of spiralling into something unreadable, yet it still captures the big-picture exponential growth, scaled transmission, and those more tangled interactions involving complex coefficients. The theorems push the framework even further. They make it possible to quickly calculate cumulative infections, assess the stability of interventions that roll out with delays, and incorporate both migration and seasonal effects without breaking the model. Put simply, this approach gives us a flexible, practical toolkit for forecasting outbreaks and guiding smart public health planning.

5. CONCLUSIONS

This research sets up a Gaussian Fibonacci framework to model disease spread, built around three core recurrence relations: exponential growth, scaled transmission, and generalized dynamics with complex coefficients. The theorems developed here extend the framework's reach in meaningful ways. Closed-form solutions make cumulative infection counts directly computable, while stability results carefully outline how interventions work when latency is involved.

We have included migratory and seasonal forcing to account for both travel-driven influxes and oscillatory breakouts. Subexponentially bounds provide robust guarantees under weak transmission, and golden ratio approximations allow for fast large-scale projections. Together, these enhancements improve the model's analytical accessibility and flexibility, providing researchers with more powerful tools for controlling and forecasting epidemics shaped by complex interactions and external factors. The next steps will involve adding stochastic effects and testing the framework with real data.

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