Hermite Polynomial Closure Approximations for Stochastic Epidemic Models

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Abstract

Moment closure approximations have been developed to provide simple approximations to non-linear stochastic models. They can give tremendous insight into the qualitative and quantitative behavior of stochastic models. They are also important because they can be used to mimic behavior observed in simulation studies, or in some cases, validate the dynamics of rigorous limit theorems. In most stochastic epidemic models, most researchers tend to focus on the mean and the variance of the model. This is because of rigorous limit theorems such as the strong law of large numbers and the central limit theorem. As a result, much of the literature tends to focus on the mean and variance and neglect the importance of higher moments, which may provide valuable information about the stochastic dynamics. Understanding the higher moments are crucial since many of the populations models have extinction, which tend to skew the distributions to absorbing states. In this paper, we address this problem by exploring the skewness of our Markovian (susceptible-infected-susceptible) SIS model via expanding our SIS model in terms of Hermite polynomials. We then use this finite Hermite expansion to develop first, second, and third order approximations for our stochastic population model. Using methods developed in the queueing theory literature, we also derive closed form expressions for the cumulative density function (cdf) and probability density function (pdf) of our approximate model. Finally, we show through simulations that our method is better at approximating of real behavior of the stochastic model, especially the asymmetry in the empirical distributions for high values of skewness.

1 Introduction

Markov processes are very important modeling tools in biology, epidemiology, and ecology. The development of Markovian stochastic models has made a profound impact on the way we understand complex dynamics in these fields of study. One particular way to explore the dynamics of these interactions in biological settings is to study the behavior of the
transition probabilities. However, the transition probabilities typically depend non-linearly on the current state of the process, which tends to make the dynamics non-trivial. Moreover, if the state space is quite large, in the case of a moderately sized population, then the it is almost intractable to really understand the behavior of the stochastic process through its transition probabilities. Thus, new techniques and ways of understanding the stochastic dynamics must be developed, especially ones that are low dimensional and require a small computation burden. One such development is the idea of (Bailey 1963) called linearization, where one can study small perturbations around the fixed point of deterministic dynamics. Furthermore, one can also investigate the quasi-equilibrium probabilities which give a picture of the distribution independent of time while conditioning on extinction not having occurred; this approach was developed by (Renshaw 1991). These approaches of studying the stochastic dynamics are very important, yet limited because they only apply around fixed points or to processes that have reached their equilibrium state. Moreover, these approaches do not work as well for time inhomogenous models, where much of the equilibrium and fixed point analysis is not helpful.

To fill the void of the transition probability literature, moment closure approximation methods were developed to give more insight into the dynamics of the stochastic models. Moment closure approximations can explain equilibrium and transient behavior of the stochastic models, and are not limited to just time homogenous models. One such closure approximation that has been used widely is the truncation procedure as seen in (Matis et al 1996, 1999). In this approximation, all cumulant moments less than or equal to k are approximated by setting all cumulants of order higher than k to 0. However, a paper by (Gillespie and Renshaw 2007) shows that this approximation may not be warranted and may produce inaccuracies in the moment estimates and error in the underlying probabilistic structure of the model. They propose using a refined saddlepoint approximation to correct these inaccuracies. Another approximation method initially developed by (Whittle 1957) is to make some distributional assumptions on the process and to use those distributions to compute the moments needed in the approximation. More recently, (Krishnarajaha et al 2005, 2007) have used mixture moment closure approximations to handle the inherent skewness, bi-modality, and possibility of extinction. However, they only study time homogenous models, and make arbitrary distributional assumptions on the model that we believe are not natural or intrinsic to the stochastic model itself. We take a very different approach that we believe is novel.

Inspired by techniques developed in the queueing theory literature for dynamic rate queues by (Massey and Pender 2011) we introduce a third order moment closure approximation for the time varying (susceptible-infected-susceptible) SIS model. Our method is very different from the traditional moment closure literature and novel because it does not assume an arbitrary distribution or mixtures of distributions to fit to the real stochastic model. Moreover, we use a continuous distribution to approximate the dynamics, which differs from most of the current literature for closure approximations. Our approximation is motivated by low dimensional projections of our stochastic epidemic process. We use a finite dimensional projection of the infinite dimensional stochastic process via a Hermite polynomial expansion. This allows us to expand our stochastic process onto a finite basis of Hermite polynomials, which we then use to approximate the true distribution. This is quite natural because if one were to expand the process in the infinite basis, it would converge
to the true distribution of our stochastic process. The Hermite expansion also allows us to capture the skewness, transient, and time varying dynamics of the model that other two and three dimensional models cannot capture. Moreover, we can give closed form expressions for the cdf and pdf of our approximate model, which are quadratic function of Gaussian random variables. This separates our model from others since we can clearly show how the skewness effects the stochastic dynamics and how it can provide valuable information about the underlying stochastic process.

This paper is organized as follows. Section 2 introduces the time varying SIS model that is used throughout the paper. We also give a motivation of why the mean and variance is not enough to characterize the real distribution or transient dynamics of our stochastic population model. Section 3 introduces Hermite polynomials and constructs a deterministic and Gaussian approximation for the dynamics of the SIS model. The construction of these lower dimensional approximations is to illuminate the general procedure that we will use throughout the rest of the paper. Section 4 introduces our new skewness approach and develops this new approximation for the SIS model. Moreover, we show that the cdf and pdf of our approximation can be computed in closed form. This leads us to show numerically that the skewness approximation is better at approximating the real dynamic behavior of our time varying model. Section 5 gives concluding remarks and possible extensions of our model. Finally the Appendix provides an introduction to Hermite polynomials and all the of proofs and derivations needed for our main results.

2 Probabilistic Analysis of SIS Model

In this section, we consider a stochastic SIS epidemic model with a fixed population size, $\tilde{N}$. The number of infected individuals at time $t$ is denoted as $N(t)$ and the number of susceptibles at time $t$ is denoted by $\tilde{N} - n(t)$. We assume that the rates of recovery and infection are given by the transition probabilities of a Markov chain. Mathematically, this means that the changes in the population of infected individuals in a small time interval are determined by the following probabilities

$$\mathbb{P}\{\Delta N(t + \Delta t) = 1\} = \alpha(t) \cdot N \cdot (\tilde{N} - N) \Delta t$$

$$\mathbb{P}\{\Delta N(t + \Delta t) = -1\} = \beta(t) \cdot N \Delta t$$

It is assumed that the time interval $\Delta t$ is sufficiently small to eliminate the possibility of multiple events occurring in the time interval can be ignored. Here we allow the parameter $\alpha$, known as the contact rate, to be time dependent. However, without loss of generality, we set $\beta = 1$, to normalize our simulation experiments.

As a result we also have the following representation of our population process in terms of Poisson random measures as

$$N(t) = N(0) + \Pi_1 \left( \int_0^t (\alpha(s) \cdot N(s) \cdot (\tilde{N} - N(s)))ds \right) - \Pi_2 \left( \int_0^t \beta \cdot N(s)ds \right)$$
Each $\Pi_i$ is an independent, unit rate Poisson process. This representation induces a probabilistic interpretation of the parameters of the model. From the random time change theorem for Poisson process, we have that $\alpha(t)$ represents the exponentially distributed infection times of mean $1/\alpha(t)$ and $\beta(t)$ represents the exponentially distributed recovery times of mean $1/\beta(t)$. The numerical example that we analyze in this paper, to demonstrate the effectiveness of our approximation methods evolves over the time interval $(0,50]$, has an contact rate function $\alpha(t) = .05 + .02 \sin(t)$, a recovery rate $\beta = 1.0$, total population size $\tilde{N} = 50$, and initial infected population size of $n_0 = 20$. We simulate using 10,000 independent sample paths.

To better understand our population model, we simulate our stochastic model in Figure 1. It is observed that the mean, variance, and skewness are all non-zero quantities. It is also observed that the skewness of the model is negative and has a slightly negative slope over the time interval we analyzed. This behavior of negative skewness is often typical in population models because there is a non-zero probability that the infection dies out or becomes extinct. This also suggests that using just one or two moments in a moment closure approximation may not be enough to get extract relevant information about the transient behavior of the original stochastic model. This problem naturally leads us to capture the skewness in our model and is the initial motivation of the paper.

![Figure 1: Simulated Mean and Variance (Left). Simulated Skewness (Right)](image)

### 3 First and Second Order Expansions

Our approach for our moment closure approximation is very novel and has not been explored in the population dynamics literature. In this section, we explain why our approach is useful and natural for stochastic processes. Moreover, we show how to expand our stochastic
process via Hermite polynomials and produce the low dimensional projections of our infinite dimensional stochastic process. The Hermite polynomials are essential to our analysis since they are an orthonormal basis for square integrable stochastic processes. Consequently, we have the following Hermite polynomial expansion of our population process:

\[ N(t) = N(t, X) \triangleq \sum_{j=0}^{\infty} \frac{n_j(t)}{\sqrt{j!}} \cdot h_j(X) \quad (3.1) \]

where \( h_j(X) \) are the Hermite polynomials as described in the Appendix and where there terms \( n_j(t) \) are defined as

\[ n_j(t) = \int_{-\infty}^{\infty} \frac{e^{-x^2/2}}{\sqrt{2 \cdot \pi}} \cdot \frac{h_j(x)}{j!} \cdot N(t, x) \, dx. \quad (3.2) \]

With this decomposition, we can show that

\[ E[N(t)] = n_0(t) \quad \text{and} \quad E[N^2(t)] = \sum_{j=0}^{\infty} n_j^2(t) \cdot j! \quad (3.3) \]

As a result of the properties of the Hermite polynomials, one can easily prove the following proposition.

**Proposition 3.1.** Let

\[ W_n(t) = \sum_{j=0}^{n} \frac{n_j(t)}{\sqrt{j!}} \cdot h_j(X) \quad \text{and} \quad W(t) = \sum_{j=0}^{\infty} \frac{n_j(t)}{\sqrt{j!}} \cdot h_j(X) \quad (3.4) \]

, then we have that

\[ \lim_{n \to \infty} E[|W(t) - W_n(t)|^2] = 0 \quad (3.5) \]

**Proof.**

\[
\begin{align*}
\lim_{n \to \infty} E[|W(t) - W_n(t)|^2] &= E[W^2(t)] + \lim_{n \to \infty} \left( E[W_n^2(t) - 2 \cdot W(t) \cdot W_n(t)] \right) \\
&= \sum_{j=0}^{\infty} n_j^2(t) \cdot j! + \lim_{n \to \infty} \left( \sum_{j=0}^{n} n_j^2(t) \cdot j! - 2 \cdot \sum_{j=0}^{n} n_j^2(t) \cdot j! \right) \\
&= \lim_{n \to \infty} \sum_{j \geq n+1} n_j^2(t) \cdot j! \\
&= 0
\end{align*}
\]

This proposition is the inspiration of our idea as one notices that as we add subsequent Hermite polynomials to approximate our random process, the squared error of the approximate process and the original process converges to zero as \( n \to \infty \). This implies that if
we approximate our infinite dimensional population process by a finite number of terms, we should expect to get a good approximation of the original stochastic process. To illustrate the effectiveness of this method, we will only consider the first three terms of the expansion. One can use more terms, but there are diminishing returns to using more additional polynomials. It is also important to note that since we have approximate convergence in $L^2$ i.e. ($W_n(t) \overset{L^2}{\approx} W(t)$ ), we should also expect to have the same type of approximate convergence in distribution as well i.e. ($W_n(t) \overset{d}{\approx} W(t)$) via the Chebyshev inequality. Additionally, we provide more information about the Hermite polynomials and their properties in the Appendix. The above proposition leads us to approximate our epidemic process with the following sequence of approximations

\[
N(t) \approx W_0 = n_0(t) \\
N(t) \approx W_1 = n_0(t) + n_1(t) \cdot h_1(X) = n_0(t) + n_1(t) \cdot X \\
N(t) \approx W_2 = n_0(t) + n_1(t) \cdot h_1(X) + n_2(t) \cdot h_2(X) = n_0(t) + n_1(t) \cdot X + n_2(t) \cdot (X^2 - 1)
\]

Now we consider the first term in the Hermite polynomial expansion.

### 3.1 Deterministic Mean Approximation

We define the deterministic mean approximation (DMA) by basing it on the mean behavior of the population process. To do this we assume that $N \equiv n$, a deterministic process \{n(t)|t \geq 0\}. From the Hermite polynomial expansion perspective, we are approximating the epidemic with the first term in the expansion, which is a deterministic function of time.

From the Kolmogorov forward equations we have the following differential equation for the mean dynamics

\[
\dot{E}[N(t)] = (\alpha \cdot \bar{N} - \beta) \cdot E[N(t)] - \alpha \cdot E[N^2(t)].
\]

Now $n = E[N]$ and having it solve the same differential equation for the mean as $N$, gives us

\[
\dot{n} = (\alpha \cdot \bar{N} - \beta) \cdot E[N(t)] - \alpha \cdot E[N^2(t)]
\]

\[
= (\alpha \cdot \bar{N} - \beta) \cdot n - \alpha \cdot n^2
\]

Unlike $E[N]$, $n$ solves and autonomous ordinary differential equation. Note that this dynamical system $n$ is also the mean field limit or limit derived from the functional strong law of large numbers scaling. As the Figure 2 suggests, this approximation is well suited for determining the mean behavior of the network when the number of people $\bar{N}$ is large. However, this deterministic approximation does not capture the deviations of the population process from the mean. It also says nothing about the distributional behavior of the model. This approximation also naturally assumes that all higher cumulant moments of the
distribution of our process are zero. This is a unrealistic assumption since we know that the distribution of our population process has a non-negative variance. Thus, this leads us to a second order approximation for the population process where we further expand our stochastic process by adding the second term in the Hermite polynomial expansion.

3.2 Gaussian Variance Approximation

Following the same steps from the DMA, we now write the Kolmogorov forward equations for both the first and second moments of our population model, thus we get

\[ \dot{E}[N(t)] = (\alpha \cdot \tilde{N} - \beta) \cdot E[N(t)] - \alpha \cdot E[N^2(t)] \]
\[ \dot{E}[N^2(t)] = (\alpha \cdot \tilde{N} + \beta) \cdot E[N(t)] + (2 \cdot \alpha \cdot \tilde{N} - \alpha - 2 \cdot \beta) \cdot E[N^2(t)] - 2 \cdot \alpha \cdot E[N^3(t)] \]

By adding the second term of the Hermite polynomial expansion, we therefore assume that \( N \) is approximately Gaussian i.e.

\[ N \equiv n(t) + \sqrt{v(t)} \cdot X, \quad (3.8) \]

where \( X \) is a Gaussian(0,1) random variable and \( \{n(t), v(t) \geq 0|t \geq 0\} \) are deterministic functions of time representing the \( n = E[N] \) and \( v = \text{Var}[N] \) respectively. We call this second order expansion the \textit{Gaussian-Variance Approximation} (GVA).

Unlike DMA, this second order approximation can explain some of the deviations of the stochastic model from its mean approximation or mean-field limit.

**Theorem 3.2.** If we assume that the epidemic process \( N \) has the distribution of Equation 3.8, then we have the following modified differential equations for the mean and variance of
our epidemic process as:

\[
\begin{align*}
\dot{n} &= (\alpha \cdot \tilde{N} - \beta) \cdot n - \alpha \cdot (n^2 + v) \\
\dot{v} &= (\alpha \cdot \tilde{N} + \beta) \cdot n + (2 \cdot \alpha \cdot \tilde{N} - \alpha - 2 \cdot \beta) \cdot (n^2 + v) - 2 \cdot \alpha \cdot n \cdot (n^2 + v)
\end{align*}
\]

Remark 3.3. Note that we have the convergence to the DMA equation when we let \( v \to 0 \). Thus, GVA can be interpreted as a generalized form of the DMA that serves to explain the stochastic fluctuations from from DMA.

Figure 3: Comparison of DMA, GVA and Simulated Means (Left). Comparison of GVA and Simulated Variances (Right)

Remark 3.4. The Gaussian distributional assumption is similar to the approach of (Isham 1991, 1993, 1995) and Whittle (1957). However, neither author analyzed the particular model that we are considering in this paper.

We now numerically integrate the differential equations derived from the GVA and compare them to the simulated mean and variance in Figure 3. On the left of Figure 3 we see that the GVA does well at improving the mean approximation. However, it does not do an excellent job of approximating the variance. However, it is important to note that by adding a second term, we do improve our approximations for the mean behavior. This means that by adding a more information about the true distribution, we can not only improve our information about the variance, but will also improve our estimates of the mean behavior. Thus, we show that the information contained in the higher moments of our population process can be useful for correcting the lower moments. Moreover, it suggests that errors made in
the approximation of the higher moments can propagate through to the lower moments and incorrectly affect the estimates of the lower moments. Since the variance is not well approximated by the GVA, it is important that we improve the estimates of the higher moments. We will do this in the next section by expanding our stochastic population process with yet another term from the Hermite polynomial expansion. This will lead us to exploring not only the mean and variance, but also the skewness of our population model.

4 Gaussian Skewness Approximation

Now we introduce our new method by adding a third term in the Hermite polynomial expansion. Similar to GVA, we now approximate our population process with the new process

$$N \equiv n + \sqrt{v} \cdot \left( \cos \theta \cdot X + \sin \theta \cdot \frac{X^2 - 1}{\sqrt{2}} \right) = n + \sqrt{v} \cdot Y_\theta$$

where $Y_\theta$ is defined as

$$Y_\theta \equiv \cos \theta \cdot X + \sin \theta \cdot \frac{X^2 - 1}{\sqrt{2}}$$

and $X$ is a Gaussian(0,1) random variable. Two properties of the $Y_\theta$ are

$$E[Y_\theta] = 0 \text{ and } \text{Var}[Y_\theta] = 1. \quad (4.11)$$

These allow us to preserve the same mean and variance as the DMA and GVA methods. We call this third order expansion the Gaussian-Skewness Approximation (GSA). The GSA is a natural extension of the DMA and GVA as it preserves DMA and GVA i.e. the mean and variance are identical. This follows from the orthogonality property of the Hermite polynomials and the fact that all polynomials of degree one and higher have expectation zero. By expanding our process in terms of higher order Hermite polynomials also allows us to interpret our approximation geometrically. Each approximation can be viewed as a projection of our infinite dimensional stochastic process onto finite dimensional subspaces. DMA, GVA, and GSA map the original population process into one, two, and three dimensional subspaces respectively.

Similar to DMA and GVA, we derive the Kolmogorov forward equations for the first, second, and third moments of our population process as

$$\begin{align*}
\dot{E}[N(t)] &= (\alpha \cdot \tilde{N} - \beta) \cdot E[N(t)] - \alpha \cdot E[N^2(t)] \\
\dot{E}[N^2(t)] &= (\alpha \cdot \tilde{N} + \beta) \cdot E[N(t)] + (2 \cdot \alpha \cdot \tilde{N} - \alpha - 2 \cdot \beta) \cdot E[N^2(t)] - 2 \cdot \alpha \cdot E[N^3(t)] \\
\dot{E}[N^3(t)] &= (\alpha \cdot \tilde{N} - \beta) \cdot E[N(t)] + (3 \cdot \alpha \cdot \tilde{N} - \alpha + 3 \cdot \beta) \cdot E[N^2(t)] \\
&+ (3 \cdot \alpha \cdot \tilde{N} - 3 \cdot \alpha - 3 \cdot \beta) \cdot E[N^3(t)] - 3 \cdot \alpha \cdot E[N^4(t)].
\end{align*}$$

Now by inserting our new approximate process $N$ into the forward equations we derive the following theorem.
Theorem 4.1. Under the assumptions of GSA, we have the following differential equations for the mean \((n)\), variance \((v)\), and third moment \((k)\)

\[
\begin{align*}
\dot{n} &= (\alpha \cdot \tilde{N} - \beta) \cdot n - \alpha \cdot (n^2 + v) \\
\dot{v} &= (\alpha \cdot \tilde{N} + \beta) \cdot n + (2 \cdot \alpha \cdot \tilde{N} - \alpha - 2 \cdot \beta) \cdot (n^2 + v) \\
&\quad - 2 \cdot \alpha \cdot (n^3 + 3 \cdot n \cdot v + 2 \cdot \sin^2 \theta \cdot n \cdot v + \sqrt{2} \cdot \sin \theta \cdot \sqrt{v^3} \cdot (2 + \cos^2 \theta)) \\
&\quad - 2 \cdot n^2 \cdot (\alpha \cdot \tilde{N} - \beta) + 2 \cdot \alpha \cdot n \cdot (n^2 + v) \\
\dot{k} &= (\alpha \cdot \tilde{N} - \beta) \cdot n + (3 \cdot \alpha \cdot \tilde{N} - \alpha + 3 \cdot \beta) \cdot (n^2 + v) \\
&\quad + (3 \cdot \alpha \cdot \tilde{N} - 3 \cdot \alpha - 3 \cdot \beta) \cdot (n^3 + 3 \cdot n \cdot v + 2 \cdot \sin^2 \theta \cdot n \cdot v + \sqrt{2} \cdot \sin \theta \cdot \sqrt{v^3} \cdot (2 + \cos^2 \theta)) \\
&\quad - 3 \cdot \alpha \cdot \left(n^4 + 2 \cdot n^2 \cdot v + v^2 + 4 \cdot \cos^2 \theta \cdot n^2 \cdot v + 8 \cdot \cos^2 \theta \cdot \sin^2 \theta \cdot v^2 + 8 \cdot \sqrt{2} \cdot \cos \theta \cdot \sin \theta \cdot n \cdot \sqrt{v^3}\right) \\
&\quad - 3 \cdot \alpha \cdot \left(2 \cdot (1 + 2 \cdot \sin^2 \theta + \sin^4 \theta) \cdot v^2 + 4 \cdot \sin^2 \theta \cdot n^2 \cdot v + 4 \cdot \sqrt{2} \cdot (1 + \sin^2 \theta) \cdot n \cdot \sqrt{v^3}\right) \\
&\quad - 3 \cdot \alpha \cdot \left(12 \cdot \sin^2 \theta \cdot \cos^2 \theta \cdot v^2 + 6 \cdot \sin^4 \theta \cdot v^2\right).
\end{align*}
\]

Proof. The proof is found in the Appendix.

Remark 4.2. Note that we do not calculate the skewness of the model directly as it is easier to work with the third moment and then calculate the skewness from the following equation

\[
\text{Skew}[N] = \frac{E[N^3] - 3 \cdot E[N] \cdot \text{Var}[N] - E[N]^3}{\sqrt{\text{Var}[N]^3}} \tag{4.12}
\]

Remark 4.3. Note that we have subsequent convergence to the GVA and DMA by sending \(\theta \to 0\) and \(v \to 0\) respectively. Thus, GSA is a generalized form of the GVA that serves to explain the deviations from GVA.

On the left of Figure 4, we compare the means of DMA, GVA, and GSA against the simulated values. We see that GSA does a better job of approximating the mean behavior of the real stochastic process. On the right of Figure 4, we compare the variances and we also see that GSA does the best job of approximating the variance of our stochastic process. However, it seems like the improvement of our new approximation in Figure 4 is very small. Thus, in Figure 5 we look at a more refined comparison of the log relative error of the difference of each approximation against the simulated values. It is apparent in both the mean and variance comparisons that GSA is doing the best job of approximating the real behavior of our stochastic model. It is important to note that GSA improves the estimate of the variance the most, however, it still does improve the estimate of the mean. This once again suggests that better approximations of the higher moments are needed to improve estimates of the lower moments.

In Figure 6, we compute the L1-norm of the error over time and GSA does a much better job of approximating the mean and variance of the stochastic process over time. These figures suggest that GSA is superior to DMA and GVA and does a good job of mimicking the real behavior of our stochastic population process.
4.1 Empirical Distribution of SIS Model

Unlike many other models, we can also compute in closed form the cdf and the pdf of our approximate processes. If we let $\gamma = \frac{a-n}{\sqrt{v}}$, then we have the following proposition.

Proposition 4.4. If $\Psi_\theta$ is the cdf for $Y_\theta$, then

$$\Psi_\theta(a) = (\Phi \circ z_+ - \Phi \circ z_-)(\theta, a)$$

Moreover, the cdf of our approximate population process is:

$$P\{N \leq a\} = \Psi_\theta\left(\frac{a-n}{\sqrt{v}}\right).$$

and its density is given by

$$\frac{d}{da} P\{N \leq a\} = \frac{(\phi \circ z_+ - \phi \circ z_-)(\theta, \frac{a-n}{\sqrt{v}})}{\sqrt{1 + 2 \cdot \frac{\sqrt{2}}{\gamma} \cdot \sin \theta + \sin^2 \theta}}$$

where we define $z_+(\theta, \gamma)$ and $z_-(\theta, \gamma)$ to be the two roots of the quadratic polynomial below

$$z^2 \cdot \sin \theta + z \cdot \cos \theta - \left(\gamma + \frac{\sin \theta}{\sqrt{2}}\right) = 0$$
Figure 5: Relative Error (Log Scale) of DMA, GVA, and GSA Means (Left). Relative Error (Log Scale) of GVA and GSA Variances (Right)

\[ z_+(\theta, \gamma) = \frac{\sqrt{2} \cdot \sin \theta + 2 \cdot \gamma}{\cos \theta + \sqrt{1 + 2\sqrt{2} \cdot \gamma \sin \theta + \sin^2 \theta}} = \gamma + \frac{1}{\sqrt{2}}(\gamma^2 - 1)\theta + O(\theta^2) \]

and

\[ z_-(\theta, \gamma) = \frac{\cos \theta + \sqrt{1 + 2\sqrt{2} \cdot \gamma \sin \theta + \sin^2 \theta}}{-\sqrt{2} \cdot \sin \theta} = -\frac{\sqrt{2}}{\theta} - \gamma + O(\theta) \]

as \( \theta \to 0 \).

**Proof.** The proof is a direct application of the quadratic formula.

On the left of Figure 7 we show the empirical distribution of the population process evaluated at the time of the lowest number of infectives and on the right we show the empirical distribution of the population process evaluated at the time of the highest number of infectives. We compare the empirical distributions of the population processes with their analytical approximations given by GVA and GSA. GSA seems to do a better job of approximating the real behavior, but it is very slight as these time points do not contain much skewness.

However, in Figure 8, we show the empirical distribution of the population process evaluated at the time of the peaked level of skewness. It is at these points where there is a large difference in the empirical distributions for GVA and GSA. GSA is much better at approximating the real empirical distribution in these areas and is able to capture the asymmetry in
the empirical distribution unlike GVA. Thus, it is clear that GSA is a powerful tool, when the real stochastic processes have non-zero levels of skewness as is the case in many population models with extinction. Moreover, when the level of skewness is small is converges back to GVA, which does well in areas of low skewness.

5 Additional Numerical Examples

In this section, we provide additional numerical examples to support the effectiveness of our new method of estimating the moments of the stochastic epidemic process.

5.1 Sinusoidal Time Varying Infection Rate in the Sub-Critical Regime

Our first additional numerical example considers the sub-critical regime with a time varying sinusoidal infection rate function. The parameters that correspond to this numerical example are given in Table 1. The figures illustrating the dynamics of Table 1 correspond to Figures 10 and 11. On the left of Figure 10, we see that the GVA and GSA are effective at approximating the mean dynamics of the epidemic process. On the right of Figure 10, we see that GSA is the best at estimating the time varying variance dynamics of the epidemic process. This gives us more support that GSA is a great tool for estimating the time varying moments of the population process. To distinguish the performance of GVA and GSA, Figure 11 gives the log relative error between the GVA and GSA approximations with simulated values. It is apparent on the left of 11 that GSA is doing a better job of estimating the mean behavior,
Distribution of \( N(t) \) at \( t = 11.78 \) : Lowest Number of Infectives (Left). Distribution of \( N(t) \) at \( t = 2.135 \) Highest Number of Infectives (Right)

However, this difference is a slight improvement. However, on the right of Figure 11 it is more apparent that GSA is doing a much better job of reproducing the time varying dynamics of the stochastic process. Lastly, we see in Figure 12 that we are doing a good job of estimating the skewness of the epidemic process as well. This is an important quantity as many epidemic models are heavily skewed because of the absorbing states of the model.

\[
\begin{array}{l|l}
\text{Parameter} & \text{Value (at time } t) \\
\hline
\alpha & 0.05 + 0.02 \sin(t) \\
\beta & 1.0 \\
T & 50 \\
n_0 & 20 \\
\end{array}
\]

### Table 1: Sub-Critical Sinusoidal Parameters

5.2 Constant Infection Rate in the Sub-Critical Regime

Our second additional numerical example considers the sub-critical regime with a constant infection rate function. The parameters that correspond to this numerical example are given in Table 2. The figures illustrating the dynamics of Table 2 correspond to Figures 13 and 14. On the left of Figure 13, we see that the GVA and GSA are effective at approximating the mean dynamics of the epidemic process. On the right of Figure 13, we see that GSA is the best at estimating the time varying variance dynamics of the epidemic process. This gives us more support that GSA is a great tool for estimating the time varying moments of the population process. To distinguish the performance of GVA and GSA, Figure 14 gives
the log relative error between the GVA and GSA approximations with simulated values. It is apparent on the left of Figure 13 that GSA is doing a better job of estimating the mean behavior, however, this difference is a slight improvement. However, on the right of Figure 14 it is more apparent that GSA is doing a much better job of reproducing the time varying dynamics of the stochastic process. Lastly, we see on the right of Figure 15 that we are doing a good job of estimating the skewness of the epidemic process as well since the log relative error of the skewness is negative. This is an important quantity as many epidemic models are heavily skewed because of the absorbing states of the model.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value (at time $t$)</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\alpha$</td>
<td>.05</td>
</tr>
<tr>
<td>$\beta$</td>
<td>1.0</td>
</tr>
<tr>
<td>$T$</td>
<td>50</td>
</tr>
<tr>
<td>$n_0$</td>
<td>20</td>
</tr>
</tbody>
</table>
5.3 Constant Infection Rate in the Meta-Stable Regime

Our third additional numerical example considers the meta-stable regime with a constant infection rate function. The parameters that correspond to this numerical example are given in Table 3. The figures illustrating the dynamics of Table 3 correspond to Figures 16 and 17. On the left of Figure 16, we see that the GVA and GSA are effective at approximating the mean dynamics of the epidemic process. On the right of Figure 16, we see that GSA is the best at estimating the time varying variance dynamics of the epidemic process. This gives us more support that GSA is a great tool for estimating the time varying moments of the population process. To distinguish the performance of GVA and GSA, Figure 17 gives the log relative error between the GVA and GSA approximations with simulated values. It is apparent on the left of 16 that GSA is doing a better job of estimating the mean behavior, however, this difference is a slight improvement. However, on the right of Figure 17 it is more apparent that GSA is doing a much better job of reproducing the time varying dynamics of the stochastic process. Lastly, we see in Figure 18 that we are doing a good job of estimating the skewness of the epidemic process as well. This is an important quantity as many epidemic models are heavily skewed because of the absorbing states of the model.
Figure 10: DMA, GVA, GSA, and Simulated Means (Left). GVA, GSA and Simulated Variances (Right).

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value (at time t)</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\alpha$</td>
<td>.25</td>
</tr>
<tr>
<td>$\beta$</td>
<td>1.0</td>
</tr>
<tr>
<td>$T$</td>
<td>50</td>
</tr>
<tr>
<td>$n_0$</td>
<td>20</td>
</tr>
</tbody>
</table>

Table 3: Sub-Critical Sinusoidal Parameters

5.4 Discontinuous Infection Rate Sub-Critical Regime

Our fourth additional numerical example considers the sub-critical regime with a discontinuous infection rate function. In fact the rate function oscillates between a high infection rate and a low infection rate. This type of infection rate function can mimic any measurable rate function since it is a comprised of step functions. The parameters that correspond to this numerical example are given in Table 4. The figures illustrating the dynamics of Table 4 correspond to Figures 19 and 20. On the left of Figure 19, we see that the GVA and GSA are effective at approximating the mean dynamics of the epidemic process. On the right of Figure 19, we see that GSA is the best at estimating the time varying variance dynamics of the epidemic process. This gives us more support that GSA is a great tool for estimating the time varying moments of the population process. To distinguish the performance of GVA and GSA, Figure 20 gives the log relative error between the GVA and GSA approximations with simulated values. It is apparent on the left of 19 that GSA is doing a better job of estimating the mean behavior, however, this difference is a slight improvement. However, on the right of Figure 20 it is more apparent that GSA is doing a much better job of reproducing...
the time varying dynamics of the stochastic process. Lastly, we see in Figure 21 that we are
doing a good job of estimating the skewness of the epidemic process as well.

Table 4: Discontinuous Infection Rate Function Parameters

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value (at time $t$)</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\alpha$</td>
<td>.07 if $2k \leq t/\pi &lt; 2k + 1$, otherwise .03</td>
</tr>
<tr>
<td>$\beta$</td>
<td>1.0</td>
</tr>
<tr>
<td>$T$</td>
<td>50</td>
</tr>
<tr>
<td>$n_0$</td>
<td>20</td>
</tr>
</tbody>
</table>

5.5 Discontinuous Infection Rate Meta-Stable Regime

Our last additional numerical example considers the meta-stable regime with a discontinuous
infection rate function. Like in the previous example, the rate function oscillates between
a high infection rate and a low infection rate. The parameters that correspond to this
numerical example are given in Table 5. The figures illustrating the dynamics of Table 5
 correspond to Figures 22 and 23. On the left of Figure 22, we see that the GVA and GSA
are effective at approximating the mean dynamics of the epidemic process. On the right of
Figure 22, we see that GSA is the best at estimating the time varying variance dynamics of
the epidemic process. This gives us more support that GSA is a great tool for estimating the
time varying moments of the population process. To distinguish the performance of GVA
and GSA, Figure 23 gives the log relative error between the GVA and GSA approximations.
with simulated values. It is apparent on the left of Figure 22 that GSA is doing a better job of estimating the mean behavior, however, this difference is a slight improvement. However, on the right of Figure 23 it is more apparent that GSA is doing a much better job of reproducing the time varying dynamics of the stochastic process. Lastly, we see in Figure 24 that we are doing a good job of estimating the skewness of the epidemic process as well.

Table 5: Discontinuous Infection Rate Parameters

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value (at time t)</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\alpha$</td>
<td>$0.35$ if $2k \leq t/\pi &lt; 2k + 1$, otherwise $0.15$</td>
</tr>
<tr>
<td>$\beta$</td>
<td>$1.0$</td>
</tr>
<tr>
<td>$T$</td>
<td>$50$</td>
</tr>
<tr>
<td>$n_0$</td>
<td>$20$</td>
</tr>
</tbody>
</table>

6 Conclusions and Future Work

In this paper we present a new moment closure approximation for the time varying SIS epidemic model. We show through simulations that our model is significantly better than than two moment approximations as we are able to capture the skewness of the distribution. Our approximation is novel and significant for three reasons. The first is that we use a continuous distribution for approximating the distributional behavior of the stochastic model, which is motivated by the limiting behavior of epidemic processes as the population size tends to $\infty$. The second is that we motivate the use of the Hermite polynomial expansion
for approximating the population process distribution. Lastly, we can give closed form approximations for the true empirical distribution of the stochastic model. We have shown through our simulation experiments that we are able to approximate the transient dynamics of our population process significantly better using the Gaussian skewness approximation. The best improvement is seen in the approximation of the variance. Although it is less noticeable, the mean dynamics are also improved by our method. Moreover, we have shown that in areas of peaked skewness, we are able to approximate the true empirical distribution of the stochastic process and capture its asymmetry. We are also able to capture accurate tail behavior in using this closed form approximation of the empirical distribution.

However, we also see in Figure 9 that the skewness it is not well approximated in longer time horizons. This can be explained by the absorbing states of the SIS model, which will skew the distribution towards the absorbing states as time grows. This hints at using an additional Hermite polynomial and subsequently an additional differential equation to correct this behavior. We plan to pursue this higher order kurtosis expansion in another paper. However, we should note that one may see diminishing returns for higher order approximations when trying to mimic the mean and variance behavior. Moreover, it is easy to extend this results to higher dimensional processes as it is no harder than integrating polynomials against a multivariate Gaussian distribution. We also plan to pursue this higher dimensional version in a subsequent paper.

Another idea for further work is a comparison of all existing moment closure methods for reproducing the mean, variance, and skewness behavior of the stochastic processes. This would highlight the similarities and differences in each method and hopefully give tremendous insight in understanding the best methods to use in particular situations or regions.
Figure 14: Log Relative Error of DMA, GVA, and GSA Means (Left). Log Relative Error of GVA and GSA Variances (Right).

Acknowledgements

The author would like to thank Dr. Simon Levin for encouragement to write this paper and his advice on the first draft of the paper.

7 Appendix

In this section, we provide a brief introduction to Hermite polynomials and some of their properties. We also provide the proofs of our main results and show the importance of the Hermite polynomials in our analysis.

7.1 Hermite Polynomials

The Hermite polynomials (probabilistic) are defined as:

\[ h_n(x) \equiv e^{x^2/2} \left( -\frac{d}{dx} \right)^n e^{-x^2/2} \]

We give the first five probabilistic Hermite polynomials for future reference.

\[ h_0(x) = 1, \ h_1(x) = x, \ h_2(x) = x^2 - 1 \]
\[ h_3(x) = x^3 - 3x, \ h_4(x) = x^4 - 6x^2 + 3 \]
Figure 15: GSA and Simulated Skewness (Left). Log Relative Error of GSA Skewness (Right).

Remark 7.1. It is important to note that all of the Hermite polynomials evaluated at X, except for the first one have expectation zero. This will simplify the analysis of future computations to come since many expectations with respect to some of these polynomials will vanish.

Theorem 7.2. If X is a standard Gaussian random variable, then

$$E[f(X) \cdot h_n(X)] = E[f^{(n)}(X)]$$

where f is any generalized function.

This follows easily from integration by parts since the Gaussian density is a smooth density. From this result follows the orthogonality property of Hermite polynomials,

Theorem 7.3. Hermite polynomials satisfy the following orthogonality properties,

$$E[h_i(X)] = \begin{cases} 1 & \text{if } i = 0, \\ 0 & \text{if } i \neq 0. \end{cases}$$

$$E[h_i(X) \cdot h_j(X)] = \begin{cases} j! & \text{if } i = j, \\ 0 & \text{if } i \neq j. \end{cases}$$

$$E[h_i(X) \cdot h_j(X) \cdot h_k(X)] = \begin{cases} \frac{i! \cdot j! \cdot k!}{(s-i)! \cdot (s-j)! \cdot (s-k)!} & \text{if } i + j + k = 2s ; i, j, k \leq s, \\ 0 & \text{if otherwise}. \end{cases}$$
Figure 16: DMA, GVA, GSA, and Simulated Means (Left). GVA, GSA and Simulated Variances (Right).

**Proof.** This follows easily from integration by parts since the Gaussian density is a smooth density.  

**Theorem 7.4.** \((\frac{1}{\sqrt{n!}} H_n)\) is an orthonormal basis of \(L^2(\mathbb{R}, \nu)\) where \(\nu\) is the Gaussian measure.

**Proof.** It suffices to show that the Hermite polynomials are orthogonal and that the set of Hermite polynomials \((H_n)_{n \geq 0}\) is complete in \(L^2(\mathbb{R}, \nu)\), i.e. the set of linear combinations of Hermite polynomials is dense in \(L^2(\mathbb{R}, \nu)\). The first part was proven in the previous theorem. The second part can be found in (Nualart 2001).

**Theorem 7.5.** Any \(L^2\) function can be written as an infinite sum of Hermite polynomials of \(X\), i.e.

\[
f(X) \stackrel{L^2}{=} \sum_{n=0}^{\infty} \frac{1}{n!} E[f^{(n)}(X)] \cdot h_n(X)
\]

\[
E[f(X) \cdot g(X)] = \sum_{n=0}^{\infty} \frac{1}{n!} \cdot E[f^{(n)}(X)] \cdot E[g^{(n)}(X)]
\]

and

\[
\text{Cov}[f(X), g(X)] = \sum_{n=1}^{\infty} \frac{1}{n!} \cdot E[f^{(n)}(X)] \cdot E[g^{(n)}(X)].
\]
Proof. These results follow easily from the previous three theorems.

Remark 7.6. Note that for any random variable $Y$, we have that

$$Y \overset{d}{=} F_Y^{-1} \circ \Phi(X).$$  \hfill (7.17)

Hence any distribution can be achieved with some appropriate function of $X$. Moreover, any such function can be approximated by polynomials uniformly. This gives us some hope that we can use the Hermite polynomials as a proxy for approximating the distribution of our stochastic population process.

### 7.2 Derivation of Moment Forward Equations

Now we show how to prove the main results of our paper. We prove the results for GSA, which imply the results for GVA and DMA, by sending $\theta \to 0$ and $v \to 0$. If we use the GSA as our population process where

$$\mathcal{N} = n + \sqrt{v} \cdot Y_\theta$$  \hfill (7.18)

where $Y_\theta$ is defined as

$$Y_\theta \equiv \cos \theta \cdot X + \sin \theta \cdot \frac{X^2 - 1}{\sqrt{2}}$$  \hfill (7.19)

The following lemma is essential for deriving the moments of our dynamical system approximation of our population process model.
Figure 18: GSA and Simulated Skewness (Left). Log Relative Error of GSA Skewness (Right).

**Lemma 7.7.** We have the following values for the derivatives of the population process

\[
\begin{align*}
E \left[ \frac{d}{dX} N \right] &= \sqrt{v} \cdot \cos \theta \\
E \left[ \frac{d^2}{dX^2} N \right] &= \sqrt{2} \cdot \sin \theta \cdot \sqrt{v} \\
E \left[ \frac{d}{dX} N^2 \right] &= 2n \cdot \cos \theta \cdot \sqrt{v} + 2\sqrt{2} \cos \theta \cdot \sin \theta \cdot v \\
E \left[ \frac{d^2}{dX^2} N^2 \right] &= (2 + 2 \cdot \sin^2 \theta) \cdot v + 2 \cdot \sqrt{2} \cdot \sin \theta \cdot n \cdot \sqrt{v} \\
E \left[ \frac{d^3}{dX^3} N^2 \right] &= 6\sqrt{2} \cdot \sin \theta \cdot \cos \theta \cdot v \\
E \left[ \frac{d^4}{dX^4} N^2 \right] &= 12 \sin^2 \theta \cdot v
\end{align*}
\]

**Proof.** These follow easily from simple differentiation.

We are now ready to give explicit expressions for the moments of our population process. These are given in the following theorem.

**Theorem 7.8.** We have the following expressions for the moments of our population process
under the assumption of GSA:

\[
\begin{align*}
E[N] &= n \\
E[N^2] &= n^2 + v \\
E[N^3] &= n^3 + 3 \cdot n \cdot v + 2 \cdot \sin^2 \theta \cdot n \cdot v + \sqrt{2} \cdot \sin \theta \cdot \sqrt{v^3} \cdot (2 + \cos^2 \theta) \\
E[N^4] &= n^4 + 2 \cdot n^2 \cdot v + v^2 + 4 \cdot \cos^2 \theta \cdot n^2 \cdot v + 8 \cdot \cos^2 \theta \cdot \sin^2 \theta \cdot v^2 + 8 \cdot \sqrt{2} \cdot \cos^\theta \cdot \sin \theta \cdot n \cdot \sqrt{v^3} \\
&\quad + 2 \cdot (1 + 2 \cdot \sin^2 \theta \cdot \sin^4 \theta) \cdot v^2 + 4 \cdot \sin^2 \theta \cdot n^2 \cdot v + 4 \cdot \sqrt{2} \cdot (1 + \sin^2 \theta) \cdot n \cdot \sqrt{v^3} \\
&\quad + 12 \cdot \sin^2 \theta \cdot \cos^2 \theta \cdot v^2 + 6 \cdot \sin^4 \theta \cdot v^2
\end{align*}
\]

Proof. The first moment is simple. However, the last three moments can be calculated using the Hermite calculus developed in (Massey and Pender 2013). We now show how to use the seamless Hermite calculus to calculate those moments. Now by exploiting Theorem 10, we
Figure 20: Log Relative Error of DMA, GVA, and GSA Means (Left). Log Relative Error of GVA and GSA Variances (Right).

have that

\[
E[\mathcal{N}^2] = E[\mathcal{N} \cdot \mathcal{N}]
\]

\[
= \sum_{j=0}^{2} E \left[ \frac{d^j}{dX^j} \mathcal{N} \right]^2
\]

\[
= E[\mathcal{N}]^2 + E \left[ \frac{d}{dX} \mathcal{N} \right]^2 + \frac{1}{2} \cdot E \left[ \frac{d^2}{dX^2} \mathcal{N} \right]^2
\]

\[
= n^2 + v \cdot \cos^2 \theta + v \cdot \sin^2 \theta
\]

\[
= n^2 + v.
\]

For the third moment, we have

\[
E[\mathcal{N}^3] = E[\mathcal{N}^2 \cdot \mathcal{N}]
\]

\[
= \sum_{j=0}^{2} E \left[ \frac{d^j}{dX^j} \mathcal{N} \right] \cdot E \left[ \frac{d^j}{dX^j} \mathcal{N} \right]
\]

\[
= E[\mathcal{N}^2] \cdot E[\mathcal{N}] + E \left[ \frac{d}{dX} \mathcal{N} \right] \cdot E \left[ \frac{d}{dX} \mathcal{N} \right] + \frac{1}{2} \cdot E \left[ \frac{d^2}{dX^2} \mathcal{N} \right] \cdot E \left[ \frac{d^2}{dX^2} \mathcal{N} \right] + \frac{1}{2} \cdot E \left[ \frac{d^2}{dX^2} \mathcal{N} \right] \cdot E \left[ \frac{d^2}{dX^2} \mathcal{N} \right] + \frac{1}{2} \cdot E \left[ \frac{d^2}{dX^2} \mathcal{N} \right] \cdot E \left[ \frac{d^2}{dX^2} \mathcal{N} \right]
\]

\[
= n^3 + 3 \cdot n \cdot v + 2 \cdot \sin^2 \theta \cdot n \cdot v + \sqrt{2} \cdot \sin \theta \cdot \sqrt{v^3} \cdot (2 + \cos^2 \theta)
\]

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and now for the fourth moment, we have

\[
\begin{align*}
E[N^4] &= E[N^2 \cdot N^2] \\
&= \sum_{j=0}^{4} E \left[ \frac{d^j}{dX^j} N^2 \right]^2 \\
&= E[N^2]^2 + E \left[ \frac{d}{dX} N^2 \right]^2 + \frac{1}{2} \cdot E \left[ \frac{d^2}{dX^2} N^2 \right]^2 \\
&\quad + \frac{1}{6} \cdot E \left[ \frac{d^3}{dX^3} N^2 \right] + \frac{1}{24} \cdot E \left[ \frac{d^4}{dX^4} N^2 \right]^2 \\
&= n^4 + 2 \cdot n^2 \cdot v + v^2 + 4 \cdot \cos^2 \theta \cdot n^2 \cdot v + 8 \cdot \cos^2 \theta \cdot \sin^2 \theta \cdot v^2 + 8 \cdot \sqrt{2} \cdot \cos^\theta \cdot \sin \theta \cdot n \cdot \sqrt{v^3} \\
&\quad + 2 \cdot (1 + 2 \cdot \sin^2 \theta \cdot \sin^4 \theta) \cdot v^2 + 4 \cdot \sin^2 \theta \cdot n^2 \cdot v + 4 \cdot \sqrt{2} \cdot (1 + \sin^2 \theta) \cdot n \cdot \sqrt{v^3} \\
&\quad + 12 \cdot \sin^2 \theta \cdot \cos^2 \theta \cdot v^2 + 6 \cdot \sin^4 \theta \cdot v^2
\end{align*}
\]

7.3 Algorithms and Sample Code

In this section we provide algorithms for the three different approximations that we analyze in the paper. We give algorithms for the DMA, GVA, GSA methods.
Figure 22: DMA, GVA, GSA, and Simulated Means (Left). GVA, GSA and Simulated Variances (Right).

7.3.1 Algorithm for DMA

In this section, we provide the sample code for the Deterministic Mean Approximation algorithm. This algorithm estimates the mean of the epidemic model and assumes the variance is zero.

```matlab
function[mean] = DMA(alpha, beta, T, dt)
    for i=1:T/(delta t)
        mean(i+1) = mean(i) + dt*( (alpha(i)*N - beta(i) )*mean(i) - alpha(i)*mean(i)^2);
    end
end
```

7.3.2 Algorithm for GVA

In this section, we provide the sample code for the Gaussian Variance Approximation algorithm. This algorithm estimates the mean and variance of the epidemic model.

```matlab
function[mean, var] = GVA((alpha, beta, T, dt)
    for i=1:T/(delta t)
        n1(i+1) = n1(i) + dt*( (alpha(i)*N - beta(i) )*n1(i) - alpha(i)*(m1(i)) );
        m1(i+1) = m1(i) + dt*( (alpha(i)*N + beta(i) )*n1(i) +...
                           (2*alpha(i)*N - alpha(i) - 2*beta(i))*m1(i) -...
                           2*alpha(i)*(n1(i)^3 + 3*n1(i)*(m1(i) - n1(i)^2)) );
        v1(i+1) = m1(i+1) - n1(i+1)^2;
    end
```
7.3.3 Algorithm for GSA

Lastly, we provide the sample code for the Gaussian Skewness Approximation algorithm. This algorithm estimates the mean, variance, and skewness of the epidemic model.

```matlab
function [mean, var, skew] = GSA(\alpha, \beta, T, dt)
for i = 1:T/(\delta t)
    theta(i+1) = findtheta(k(i),1);
    a = cos(theta(i+1))*sqrt(v(i));
    b = sin(theta(i+1))*sqrt(v(i)/2);
    m4 = m1(i)^4 + 24*a^2*b*m1(i) + 12*b^2*m1(i)^2 + 32*b^3*m1(i) + ...
        6*a^2*m1(i)^2 + 60*a^2*b^2 + 3*a^4 + 60*b^4;
    m1(i+1) = m1(i) + dt*( (alpha(i)*N - beta(i)) *m1(i) - alpha(i)*m2(i) );
    m2(i+1) = m2(i) + dt*( (alpha(i)*N + beta(i)) *m1(i) + ...
            (2*alpha(i)*N - alpha(i) - 2*beta(i))*m2(i) - ...
            2*alpha(i)*m3(i) );
    m3(i+1) = m3(i) + dt*((alpha(i)*N - beta(i))*n2(i) + ...
            (3*alpha(i)*N - alpha(i) + 3*beta(i))*m2(i) + ...
            (3*alpha(i)*N - 3*alpha(i) - 3*beta(i))*m3(i) - 3*alpha(i)*m4 );
end
```

Figure 23: Log Relative Error of DMA, GVA, and GSA Means (Left). Log Relative Error of GVA and GSA Variances (Right).
v(i+1) = m2(i+1) - m1(i+1)^2;
\[ k(i+1) = \frac{m3(i+1) - 3*v(i+1)*m1(i+1) - m1(i+1)^3}{v(i)^{1.5}}; \]
end
mean= m1;
var = v;
skew = k;
end

Figure 24: GSA and Simulated Skewness (Left). Log Relative Error of GSA Skewness (Right).

References


