Response of a deterministic epidemiological system to a stochastically varying environment

J. E. Truscott* and C. A. Gilligan

Epidemiology and Modelling Group, Department of Plant Sciences, University of Cambridge, Downing Street, Cambridge CB2 3EA, United Kingdom

Edited by Simon A. Levin, Princeton University, Princeton, NJ, and approved May 20, 2003 (received for review October 16, 2002)

Fluctuations in the natural environment introduce variability into the biological systems that exist within them. In this paper, we develop a model for the influence of random fluctuations in the environment on a simple epidemiological system. The model describes the infection of a dynamic host population by an environmentally sensitive pathogen and is based on the infection of sugar beet plants by the endoparasitic slime-mold vector Polymyxa betae. The infection process is switched on only when the temperature is above a critical value. We discuss some of the problems inherent in modeling such a system and analyze the resulting model by using asymptotic techniques to generate closed-form solutions for the mean and variance of the net amount of new inoculum produced within a season. In this way, the variance of temperature profile can be linked with that of the inoculum produced in a season and hence the risk of disease. We also examine the connection between the model developed in this paper and discrete Markov-chain models for weather.

1. Introduction

Most analytical work on stochasticity in epidemics has focused on demographic variability (1, 2). However, in many instances, environmental variation can be a critical influence on the development of an epidemic. A wide range of economically and environmentally important fungi and invertebrates have a strong sensitivity to environmental factors. Many species of fungi, including the damping-off fungi (Rhizoctonia solani), mildews (Blumeria graminis), and rusts (Puccinia spp.), have threshold temperatures and humidity levels for germination to occur. Some pathogenic nematodes that cause severe disease in staple crops exhibit a critical sensitivity to soil moisture content, becoming inactive at low levels (3). A variety of insect pests and parasites are strongly influenced by environmental switching, most notably by diapause, a suspension of development often triggered by changes in temperature, light levels, or humidity (4).

In this paper, we analyze the resulting SDE in Section 3 by using asymptotic techniques to get closed-form solutions for the mean and variance of the solutions in terms of the properties of the driving environmental variable. In Section 4, we show how these results can be linked with a specific Markov-chain weather-generation model. In Section 5, we compare the results of the analysis with numerical simulations of the system and examine how the analysis can lead to testable hypotheses about the behavior of the system.

2. The Model

2.1. The Deterministic System. The biological system addressed is a susceptible-infectious epidemic driven by primary infection from a reservoir of inoculum (X) in which the force of infection is switched on and off above and below a critical temperature. The model presented below is motivated by work done on a sugar beet–P. betae model described and analyzed in refs. 7–10. The model comprises the following system of ordinary differential equations:

\[ \frac{dn}{dt} = f(n, t), \]  

\[ \frac{ds}{dt} = f(n, t) - ms - \Lambda_m X s, \]  

\[ \frac{di}{dt} = Q \Lambda_m X s, \]

with initial conditions, \( n(0) = s(0) = n_0, i(0) = 0 \). The variables \( n, s, \) and \( i \) represent the total population, the susceptible population at risk from the disease, and the inoculum generated.
Calculation. Clearly, Eq. 52 is not satisfied. Therefore, we can replace the function, $f(X, n)$, which represents the fraction of the total root length in a particular state, with a monomolecular function, $f(n, t) = r(1 - n)$, which is both representative and convenient for calculation. Clearly, Eq. 1 can be solved independently of the other equations, and hence we can replace the function, $f$, in Eq. 2 with $n_d(t)$, the derivative of the total population. We assume that newly generated inoculum is released as fully active for the next season. In the context of rhizomania, the variables $n, s, t$ and $i$ represent the fraction of the total root length in a particular state. The model contains only four parameters: $m, r$, the rate at which susceptibles become resistant to infection; $X$, the initial inoculum loading; $\lambda_m$, the force of infection, and $Q$, the amplification factor for new inoculum. Temperature dependence enters through the parameter, $\lambda_m$, as follows:

$$\Lambda_m(T) = \begin{cases} \lambda_m, & \text{if } T \geq T_e, \\ 0, & \text{otherwise.} \end{cases} \quad [4]$$

That is, for temperature less than the critical value, $T_e$, infection is effectively turned off, whereas for temperature above this value, the force of infection is constant.

2.2. The Fluctuating Environment. In the present context, we focus on temperature as the critical aspect of the environment. However, more generally, a range of possible factors could introduce stochastic effects into the system, such as rain, sunlight, and animal movement. These are discussed in more detail in Sections 4 and 6. During the growing season, the mean temperature rises considerably and passes through the critical temperature of the parasite. The obvious deterministic approach to this changing environment is to consider the parasite to be “switched off” until the mean temperature reaches $T_e$ and “switched on” afterwards. However, if we consider temperature to be a stochastically varying quantity, as experienced by the parasite, then the system will be switched on and off randomly while the variation in temperature spans $T_e$. Given that temperature can be taken to vary about the mean between definable extremes, the rising temperature profile can be divided into three temporal phases (Fig. 1) with respect to the parasite.

- Phase 1, in which temperature is always below $T_e$ and the infection process is always active ($t_1$ to $t_2$ in Fig. 1).
- Phase 2, in which temperature varies across the critical temperature and the infection process switches between quiescent and active ($t_1$ to $t_2$ in Fig. 1).
- Phase 3, in which the temperature is constantly above $T_e$ and the infection process is always active ($t_2$ to $t_3$ in Fig. 1).

Clearly the dynamics of Phase 1 are straightforward, assuming deterministic initial conditions. Phase 3 is once again deterministic but must describe the evolution of the mean and variance of the variables as they stand at the end of Phase 2. Phase 2, however, requires a new approach to integrate the stochasticity into the dynamics.

2.3. Stochastic Differential Equation (SDE) Model. An SDE is used to model the continuous-time stochastic process. The SDE comprises the deterministic mean behavior to which a noise term is added in the form of an infinitesimal Wiener process. The deterministic solution of Eqs. 1-3 is easily calculated in terms of the function, $f(n, t)$. It is now necessary to formulate the infection switching in terms of the Wiener process. Problems arise from the fact that the switching process is binary; i.e., it is either “on” or “off.” In trying to formulate a continuous-time representation of switching based on a Wiener process, one must take a limit as $dt \to 0$. As this limit is approached, the high-frequency elements in the Wiener process spectrum dominate, causing the variance and hence stochastic terms in the equation to vanish. Viewed from a physical or biological standpoint, the nature of the problem is clear. In the context of the sugar-beet rhizomania system, switching at high frequencies would require soil to heat up and the behavior of the parasite to change almost instantaneously. A more accurate description of the process would require either that the sharp step from “off” to “on” at $T_e$ be made into a smooth function or that the physical system be given some inertia in changing state. Of these two, the second can be approximated by assuming that there exists an effective correlation period over which the state of the system will not change. The system samples only the random variable between these periods. In Section 4, this approach is compared directly to discrete first-order Markov-chain models for generating stochastic data, as used in weather modeling (13, 14). The strong correspondence between the SDE formulation and such models allows us to directly include such environmental influences into SDE descriptions.

To derive a continuous-time stochastic differential equation representation of the system described above, we first calculate the mean and variance of the process. Consider the system described by Eqs. 1-3 at time, $t$, in state $(n, s, i)$. Let $p_+(t)$ be the probability that the temperature is above $T_e$ at time $t$, and let $\Delta T$, the effective correlation time, define the discrete time interval at which the system checks the temperature. We can interpret $\Delta T$ as a property of either the deterministic system or the driving stochastic variable. Within the deterministic system, it can represent the time for the force of infection to respond to a change in temperature. In the case of the vector for rhizomania, this could be the characteristic time of the vector for rhizomania, this could be the characteristic time scale for soil heating. From the viewpoint of temperature, it can represent a correlation time over which temperature remains unchanged. This possibility is discussed in detail in Section 4 with regard to discrete Markov-chain models.

The effective correlation time is assumed to be small compared to the time scale of evolution of the deterministic system. Considering just the changes over $\Delta T$ of the stochastically varying elements, $s$ and $i$,

$$\frac{ds}{dt} = \left( n(t) - \lambda m X s - ms \right) \Delta T,$$

with probability, $1 - p_-(t)$, and

$$\frac{ds}{dt} = \left( n(t) - \lambda m X s + ms \right) \Delta T,$$

with probability, $p_+(t)$. This gives a mean of
\[
\left( n_i(t) - p_+(t)\lambda_sX_s - ms \right)\Delta T,
\]
and a variance of
\[
\left( (p_+ - p_+^2)\lambda_s^2X_s^2 \right)\Delta T^2.
\]
We want these variances to be matched by the SDE,
\[
\left( ds \right) = \left( A_i \right) dt + \left( B_i \right) dW(t),
\]
where \(dW(t)\) represents the infinitesimal Wiener deviate at time, \(t\). Only one infinitesimal Wiener process is required, because there is only a single stochastic process operating. Considering again the period, \(\Delta T\), and assuming a slow evolution for the deterministic processes, we arrive at a mean of
\[
\left( A_i \right) \Delta T,
\]
and
\[
\text{Var}(ds) = B_i^2\Delta T, \quad \text{Var}(di) = B_i^2\Delta T,
\]
using the identity, \(dW(t)^2 = dt\) (15). By comparison with Eqs. 5 and 6, we have
\[
A_i = n_i(t) - p_+\lambda_sX_s - ms, \quad A_i = p_+\lambda_sX_s,
\]
\[
B_i = \pm \lambda_sX_s\sqrt{(p_+ - p_+^2)\Delta T}, \quad B_i = \pm Q\lambda_sX_s\sqrt{(p_+ - p_+^2)\Delta T}.
\]
Therefore, the SDE describing the dynamics of Phase 2 is
\[
dn = n_i(t)dt,
\]
\[
ds = (n_i - p_+\lambda_sX_s - ms)dt - \lambda_sX_s\Phi(t)dW(t),
\]
\[
di = p_+\lambda_sX_sdt + \lambda_sX_s\Phi(t)dW(t),
\]
where \(\Phi(t) = \sqrt{(p_+ - p_+^2)\Delta T}\). We have taken advantage of the degree of freedom in the signs of \(B_s\) and \(B_i\) to allow for material removed from \(s\) to be added to \(i\).

3. Analysis

By using Eqs. 1–3 for Phases 1 and 3 and Eqs. 7–9 for Phase 2, it is possible to describe the evolution of a single realization of the system through all three phases in the form of a stochastic integral (15). This solution is, in general, too complex to yield any practically useful information about the statistics of the system, such as mean and variance. To simplify the solution, we consider an asymptotic limit in which the stochasticity is small, thereby allowing a solution through asymptotic techniques. Non-dimensionalizing with respect to time and grouping parameters gives
\[
dn = n_i\,dt, \quad \text{[10]}
\]
\[
ds = (n_i - p_+s - s)dt - \phi(\tau)sdW(\tau), \quad \text{[11]}
\]
\[
di = p_+sdt + se\phi(\tau)dW(\tau), \quad \text{[12]}
\]
for the SDE and
\[
\frac{dn}{d\tau} = f'(n, \tau), \quad \text{[13]}
\]
\[
\frac{ds}{d\tau} = f'(n, \tau) - s - \lambda's, \quad \text{[14]}
\]
\[
\frac{di}{d\tau} = \lambda's, \quad \text{[15]}
\]
for the deterministic system, where
\[
t = \frac{\tau}{m}, \quad e = \frac{\lambda_sX_s}{m}, \quad \rho = \frac{r}{m},
\]
and using the identity, \(dW(\alpha\tau) = \sqrt{\alpha}dW(\tau)\). The parameter, \(\lambda' = 0\) in phase 1 and \(\lambda' = e\) in Phase 3.

Because the stochastic effects of Phase 2 enter through the force of the infection process and the parameter, \(\lambda_m\), the small-noise limit is analyzed by taking the limit in which the parameter, \(e \to 0\). We look for solutions of Eqs. 10–12 as a series in \(e\), i.e.,
\[
s(\tau) = s_o(\tau) + es_b(\tau) + e^2s_i(\tau), \ldots
\]
Substituting these series into the SDE gives for the first two terms
\[
s_o(\tau) = s_e^{-\tau} + e^{-\tau}\int_0^\tau e^{-\tau'}n_o(\tau')d\tau', \quad \text{[16]}
\]
\[
s_b(\tau) = e^{-\tau}\int_0^\tau e^{-\tau'}p_+(\tau')s_b(\tau')d\tau' - \int_0^\tau e^{-\tau}\phi(\tau)s_b(\tau)dW(\tau'), \quad \text{[17]}
\]
where \(n_o, s_i\) represent values at the start of Phase 2, and \(\tau\) is measured from the start of Phase 2. We are interested only in the first term of \(i\), which is \(i_o\)
\[
i_o(\tau) = \int_0^\tau p_+(\tau)s_o(\tau)d\tau' + \int_0^\tau \phi(\tau)s_b(\tau)dW(\tau'). \quad \text{[18]}
\]
It is easy to calculate the mean and variance of these quantities by using the identity,
\[
\left\langle \int_m^t G(t')dW(t') \right\rangle \int_m^t H(t')dW(t') = \left\langle \int_m^t G(t')H(t')dt' \right\rangle,
\]
(15), giving
\[
\text{Var}(s(\tau)) = e^{2\tau}e^{-2\tau}\int_0^\tau e^{2\tau'}\phi^2(\tau')s_o^2(\tau')d\tau', \quad \text{[19]}
\]
\[
\text{Var}(i(\tau)) = e^{2\tau}\int_0^\tau \phi^2(\tau')s_b^2(\tau')d\tau', \quad \text{[20]}
\]
\[
\text{Cov}(s(\tau), i(\tau)) = e^{2\tau}e^{-2\tau}\int_0^\tau e^{2\tau'}\phi^2(\tau')s_o^2(\tau')d\tau'. \quad \text{[21]}
\]
The \(O(e^2)\) for these terms reflects the fact that the infection process and hence its products are \(O(e)\). As yet, we have made no assumptions about the form of \(p_+(\tau)\) and hence \(\phi(\tau)\). The simplest assumption is that \(p_+(\tau)\) is constant through Phase 2, in which case \(\phi\) can be removed from the integrals in Eqs. 19–21. The simplest approximation to the time-dependent behavior illustrated in Fig. 1 is a linear rate of change for \(p_+\), which captures the smooth transition in \(p_+\) from 0 at the start of Phase 2 to Phase 1 at the end.
\[
p_+(\tau) = \tau/\Delta T_2 \quad \text{[22]}
\]
\[
\phi(\tau) = \frac{\tau}{\sqrt{\Delta T_2}} \left( 1 - \frac{\tau}{\Delta T_2} \right)^{\Delta T}, \tag{23}
\]

where \(\Delta T_2\) is the duration of Phase 2.

We can make a further simplification to the above expressions for variance when Phase 2 is short in comparison to the rate of change of \(s_0\). We can approximate
\[
s_0(\tau) = s_0(0) + \frac{ds_0}{d\tau}(0) \tau,
\]

where \(\tau\) is measured from the start of Phase 2. The derivative of \(s_0\) at the start of the phase can be expressed in terms of \(n_i\) and \(s_0\) through Eq. 14. With this approximation, the integrals in Eqs. 19-21 become analytically tractable. For example, the expression for the variance of \(i\) (Eq. 20) becomes
\[
\Var(i(\tau)) = \sigma^2 \int_0^\tau \left( 1 - \frac{\tau}{\Delta T_2} \right) \Delta T \left( s_0(0) + \frac{ds_0}{d\tau}(0) \right)^2 \, d\tau,
\]

which is simply the integral of a polynomial in \(\tau\).

The evolution of the mean and variance of \(s\) and \(i\) in the deterministic third phase is addressed in the Supporting Appendix, which is published as supporting information on the PNAS web site, www.pnas.org. Essentially, the development of these quantities in Phase 3 can be expressed as functions of the mean, variance, and covariance of \(s\) and \(i\) at the end of Phase 2.

### 4. Comparison of Results with Discrete First-Order Markov-Chain Models

Discrete first-order Markov-chain models are widely used in model weather-generating systems as a simple and accurate method of illustrating the connection between first-order Markov-chain models and that derived in Section 3. Using the relationships between SDE and Markov-chain models derived in this section, we can correctly parameterize an SDE to simulate the stochastic influence of a discrete Markov-chain environmental variable. The rainfall model assumes the weather to be in one of two states on any day: raining or dry. Hence the day is the fundamental unit of time, \(t_0\), over which the state of the system remains unchanged. The state on any day depends only on that of the previous day through the conditional probabilities,
\[
p_1 = p(\text{wet today} \mid \text{wet the previous day}),
\]
\[
p_0 = p(\text{wet today} \mid \text{dry the previous day}).
\]

It can be shown that over a period of \(n\) days the mean and variance of the cumulative length of time of rainy days, \(r\), are given by
\[
\bar{r} = n \pi t_0, \tag{25}
\]
\[
\Var(r) = \pi(1 - \pi)n \frac{1 + p_1 - p_0}{1 - p_1 + p_0} t_0^2, \tag{26}
\]
as \(n\) gets large, where \(\pi\) is the absolute probability of rain on any day,
\[
\pi = \frac{p_0}{1 + p_0 - p_1}.
\]

These expressions can be directly compared to those for the mean and variance of \(i\) in Section 3. The quantity, \(i\), represents the accumulation of inoculum generated by the stochastically switching infection process and is entirely analogous to the accumulation of rainy days in the Markov-chain weather model. If we consider the dynamics of the underlying model to be static through Phase 2, we can express the mean and variance of \(i\) as
\[
\langle i(t) \rangle = \lambda_i X_0 \sigma t, \tag{27}
\]
\[
\Var(i(t)) = \lambda_i X_0^2 \sigma^2 (1 - p_i) \Delta T t, \tag{28}
\]
in dimensional form. The parameter grouping \(\lambda_i X_0\) is a rate appearing in both expressions, converting time into the units of \(i\). Hence we can make a direct comparison between the time spent in an infectious state in Phase 2 and the time spent raining in the Markov-chain model, and we can associate the parameters of the two models:

**SDE model \leftrightarrow Markov-chain model**

\[
p_+ \leftrightarrow \pi, \tag{29}
\]
\[
\Delta T \leftrightarrow \frac{1 + p_1 - p_0}{1 - p_1 + p_0} t_0 = \Delta t_c. \tag{30}
\]

Both \(p_+\) and \(\pi\) are absolute probabilities, whereas the quantities in Eq. 30 are both functions of correlation parameters.

We can use this basis, therefore, to construct SDE models for systems governed by discrete Markov-chain stochastic processes over relatively long periods of time. Simulations show that the relative error in the variance as predicted by the SDE model decreases with increasing time. This decrease would of course be accompanied by a corresponding increase in error from the asymptotic approximation.

### 5. Numerical Results

The theory developed in Section 3 was tested against numerical simulations by using a fourth-order Runge–Kutta algorithm to integrate Eqs. 1-3 over the three phases of the system’s evolution. During the stochastic phase, the temperature of the system for any correlation period was chosen randomly according to the probability, \(p_+\). For all the following simulations, the temperature phases were defined as

| Phase 1 | \(0 \leq \tau < 1\) |
| Phase 2 | \(1 \leq \tau < 1.5\) |
| Phase 3 | \(1.5 \leq \tau \leq 3\) |

The parameters used were those presented in Table 1 unless stated otherwise. A monomolecular growth function was used for simulations for algebraic tractability.

Table 2 below compares values for variance of inoculum production at the end of Phase 3 between the numerical solution and the theoretical predictions from Section 3 for different correlation periods, \(\Delta T\). Predictions for the mean were found to be very accurate for all values of the period. For variance, the accuracy increases as the correlation period gets smaller. These results also illustrate the problem discussed in Section 2.3: as the correlation period is decreased toward zero, the variance in the system also vanishes.

![Graph showing variance over time](image)

Table 2 shows realizations of the stochastic process produced by the simulator. The thicker lines represent the mean and two standard deviations on either side as calculated from theory (Eq. 20). The region between these lines represents approximately a 98% confidence interval for the realizations, assuming a normal distribution. This assumption can be seen to be approximate from the fact that the lower curve goes negative at the start of the second phase.

<table>
<thead>
<tr>
<th>Name</th>
<th>Symbol</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Growth rate, (\text{d}^{-1})</td>
<td>(r)</td>
<td>0.1</td>
</tr>
<tr>
<td>Force of infection, (\text{d}^{-1})</td>
<td>(\Delta X)</td>
<td>0.007</td>
</tr>
<tr>
<td>Susceptible interval, (\text{d})</td>
<td>(1/m)</td>
<td>14</td>
</tr>
<tr>
<td>Correlation period, (\text{d})</td>
<td>(\Delta T)</td>
<td>1</td>
</tr>
</tbody>
</table>

Table 1: Dimensional parameter values
Nevertheless, they function well as bounds on the behavior of the realizations. Fig. 3 shows more clearly the variance of generated inoculum over the three phases of evolution. In particular, it shows the ongoing change in variance in the third deterministic phase.

Simulation and theory are in close agreement through the entire range of $p_i$. The shape of the curve reflects the dependence of the variance of inoculum on $\phi^2$ (Eq. 20), where $\phi = \sqrt{2T_p (1 - p^*_i)}$, giving a characteristic parabolic shape. A linear rate of change in variance of inoculum on $\phi^2$ shows that the improvement in the accuracy of the SDE described in Section 3 is outweighed by the accumulating errors from the asymptotic approximation and the assumption of linearity in $p_i$.

Dependence of variance in infected root against the length of Phase 2, showing that the improvement in the accuracy of the SDE described in Section 3 is outweighed by the accumulating errors from the asymptotic approximation and the assumption of linearity in $p_i$.

Table 2. Table of comparisons between simulation and theory for a range of values for $\Delta T$

<table>
<thead>
<tr>
<th>Correlation period, $\Delta T$, days</th>
<th>Inoculum variance</th>
<th>Simulation</th>
<th>Theory</th>
<th>%</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.0</td>
<td>$2.20 \times 10^{-5}$</td>
<td>$2.30 \times 10^{-5}$</td>
<td>4.3</td>
<td></td>
</tr>
<tr>
<td>0.5</td>
<td>$1.12 \times 10^{-5}$</td>
<td>$1.15 \times 10^{-5}$</td>
<td>2.7</td>
<td></td>
</tr>
<tr>
<td>0.2</td>
<td>$4.51 \times 10^{-6}$</td>
<td>$4.59 \times 10^{-6}$</td>
<td>1.7</td>
<td></td>
</tr>
</tbody>
</table>

Fig. 3. Variance in infected root over all three phases as predicted from theory.

For these particular parameter values, the deterministic value never exceeds $i_c$. For high values of $r$, the slow generation of new roots limits the quantity of inoculum generated. For low values, the majority of roots have already entered the resistant class before $T_c$ is reached and the disease process can develop strongly. Hence $P(i > i_c)$ has a local maximum as a function of $r$. For these particular parameter values, the deterministic value for $i$ never exceeds $i_c$. The stochastic model, however, indicates that there is a quite high probability ($P > 0.4$) of breaching the threshold for certain values of $r$.

6. Conclusion

The development of a model for this system falls into two distinct parts: first, the development of a conceptual model for the real system, and second, the development of a mathematical description of the conceptual model.

Fokker–Planck equations and stochastic differential equations are two different ways of representing the same underlying continuous-time stochastic process (15, 16). Stochastic differential equations describe the evolution of the random variables representing the state of the system, whereas Fokker–Planck equations describe the evolution of the probability distribution for the state of the system. From an analytic standpoint, they have a well-behaved deterministic limit as the effect of stochasticity is reduced. For systems such as the present one, in which the deterministic solutions are available, there is the possibility of generating asymptotic series around the small noise limit. In the analogous limit for Fokker–Planck equations, no such convenient form is obtained.

Results from Section 3 show that it is possible to construct an SDE for the stochastic-switching model developed in Section 2.3. Moreover, a closed-form solution to this system of equations can be found in the asymptotic limit and hence an analytical approximation for the stochastic process. This approach has broad
applicability to a range of epidemics and growth processes subject to environmentally controlled stochastic switching. In the present example, analytic tractability rests on the simplicity of the underlying epidemic model. For more complex systems, numerical techniques would be required.

Numerical results in Section 5 show that the solutions for the statistics of the inoculum, \( i \), calculated in Section 3 and the Supporting Appendix describe those of the simulation very well. Predictions for the mean value of the inoculum are very accurate, whereas that for the variance are typically \(<5\%\) out for the parameter values used. This accuracy is maintained across the whole range of \( p_i \). There is an implicit assumption in the construction of the SDE that the Wiener process can be used to describe what is the essentially binomial process of switching. One problem can be seen in Eq. \( \text{12} \), where \( dW(t) \) can be negative and large enough to allow \( di \) to be negative. Clearly, in the real system, \( di \geq 0 \). Hence, although the statistics predicted by the theory are reliable, individual realizations may be unrepresentative. As the stochastic period lengths, the accuracy of the estimate of variance declines (Fig. 4), because of the accumulation of errors from the approximation.

In Section 4, we explicitly compare the behavior of the SDE model to that of a discrete first-order Markov-chain model. The concept of Markov chains underlies many stochastic processes, and discrete first-order chains are widely used to model weather phenomena. Strong parallels can be drawn between such models and the SDE systems in terms of their statistics, in particular, the correlation period and the conditional probabilities of the Markov chain. That is,

\[ \Delta T = \frac{1 + p_1 - p_0}{1 - p_1 + p_0} t_0, \]

where \( t_0 \) is the length of the discrete time unit. Using this relationship and the approach outlined in this paper, we can include the stochastic influence of such Markov-chain environmental phenomena on evolving deterministic systems subject to stochastic switching.

For the specific model treated in this paper, we have considered stochastic forcing through fluctuating temperature in detail. This forcing is mediated through an extreme sensitivity to temperature in the parasite. A similar sensitivity to temperature would be found in plants vulnerable to frost damage and infection. In this case, the cutoff temperature is 0°C. Periods of rainfall or high humidity can also be triggers for infection and, as has been illustrated in Section 4, rainfall patterns are accurately simulated by Markov-chain models and hence SDEs. Other candidates include insolation and the movement of animal vectors.

By explicitly including stochastic effects into a deterministic model, we address properties of the system that are not recoverable from a purely deterministic description. The probability of exceeding a threshold shown in Fig. 5A and B is an example of such a property. Most biological experiments yield results of a statistical result of this nature based on many replicates, which can be tested against the probability distributions predicted by the model. Hence we can examine directly the nature and strength of the interaction between environmental phenomena and the biological systems they control.

The work presented here illustrates some of the difficulties inherent in representing the influence of stochastic processes on time-continuous systems. Simply taking the limit as \( dt \rightarrow 0 \) to get a continuous representation can fail to capture the variability of the system. It can “disappear” in the limit. This is the result of the fact that the variance of the Wiener process is proportional to time. Table 2 illustrates this point well. As the correlation period, \( \Delta T \), is made smaller, and variance shrinks proportionally. From a practical point of view, the problem lies with the infinitesimal properties of the Wiener distribution combined with the step-function nature of the switch. It could be said that the Wiener process is capable of finite changes in infinitesimally small periods of time. Because of inertia, no natural process behaves in this way. Hence for a switching process, it is necessary to include inertia artificially. In the present case, we included the effective correlation time to represent thermal inertia. An alternative approach is to replace the switching function with a smooth alternative. This would better represent the response of the system to an environmental influence. What form these functions should take and what effect their form will have on the transmission of variance into the system are the subjects of further work.

We gratefully acknowledge funding from the Biotechnology and Biological Sciences Research Council (J.E.T.) and the Royal Society and Leverhulme Trust (C.A.G.).

Supporting Appendix

Deterministic Solutions

In the three-phase scenario outlined in Section 2.2 and Fig. 1 of the paper, stochasticity within the system is generated only during phase 2. In this paper, we are interested in the evolution of the mean and variance of the elements of the system through all phases of development. We need to be able to track the mean and variance of the variables through the deterministic system operating in phases 1 and 3. We can calculate the mean and variance of \( s \) and \( i \) directly from these solutions \((n \) is assumed to be entirely deterministic and to have zero variance).

\[
\overline{s}(\tau) = \overline{s}_0 e^{-\alpha \tau} + \rho \left( \frac{1-n_0}{\rho - \alpha} \right) \left[ e^{-\alpha \tau} - e^{-\rho \tau} \right],
\]

\[
\overline{t}(\tau) = \overline{t}_0 + \frac{\epsilon}{\alpha} \overline{s}_0 (1 - e^{-\alpha \tau}) + \epsilon \rho \left( \frac{1-n_0}{\rho - \alpha} \right) \left[ \frac{(1 - e^{-\alpha \tau})}{\alpha} - \frac{(1 - e^{-\rho \tau})}{\beta} \right],
\]

\[
\text{Var}(i(\tau)) = \text{Var}(i_0) + \left( \frac{\epsilon}{\alpha} (1 - e^{-\alpha \tau}) \right)^2 \text{Var}(s_0) + \frac{2\epsilon}{\alpha} (1 - e^{-\alpha \tau}) \text{Cov}(i_0, s_0),
\]

\[
\text{Var}(s(\tau)) = \text{Var}(s_0) e^{-2\alpha \tau}.
\]

The presence of the covariance of \( s \) and \( i \) in the expression for evolution of \( \text{Var}(i) \) arises from the flow of material from the \( s \) to the \( i \) compartment. Because material gained by \( i \) is lost by \( s \), the covariance \( \text{Cov}(s_0, i_0) < 0 \).