Poisson approximation to density dependent stochastic processes. 
A numerical implementation and test.

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Abstract

We implement the recently introduced Poisson approximation on a 
density dependent jump process corresponding to a simple, but not ex-
tactly solvable, epidemiological model. Statistics produced with $10^6$ inde-
pendent realizations of the Feller process are compared with equivalent 
statistics produced with Poisson, proper Gaussian and diffusion realiza-
tions. While in the Poisson approximation the statistical deviation can 
be reduced to a satisfactory level by reducing the time step of the sim-
ulation, and the Gauss approximation will only be rejected in the most 
demanding situations, the statistical deviation of the diffusion approxi-
mation can easily be perceived in a city with mean population of $\sim 10^4$ 
individuals. This deviation cannot be reduced decreasing the time step 
of the simulation.

1 Introduction

In several fields of Natural Sciences it is meaningful to count populations 
by the number of members of a given species, representing the state of 
the population with a single non-negative integer or a set of non negative 
integers when age-structured populations or a patchy environment (or 
other subpopulations) need to be considered. The evolution of such 
populations is then determined by the occurrence of several “events”, each 
one changing the quantities of the populations in a fixed and prescribed 
form.

It is also standard to consider that the probability of occurrence of 
the next event corresponds to independent Poisson processes with state-
dependent transition rates. Epidemic models\textsuperscript{1,2,3,4,5}, chemical reactions
laser photonics and ecological problems, can be meaningfully studied within this framework.

The observable evolution of the populations corresponds to realizations of Feller-type density dependent Markov processes. The computer implementation of such processes is simple but can put important demands on computer times (eventually impossible to satisfy). The description at this level will be event by event, and some times millions of events are produced between two subsequent observations of the natural system.

The question posed in many cases does not justify such degree of precision in the description, specially considering that the fine scale of the evolution will strongly depend on the realization. In such cases it is worth searching for alternative algorithms that describe the problem within a prescribed tolerance for the meaningful variables.

In addition, some systems follow a “generalized mass action law” which in essence states that interactions of individuals are expected to depend on the density of the populations they interact with, rather than on the total number. Hence, for large systems, scaling by a factor \( A \) all the populations will approximately multiply the rate of each kind of event by the same factor. For this class of systems there are some approximations available, known as the deterministic limit, and the fluctuations around the deterministic limit as well as the heuristic diffusion approximation.

We have recently introduced a new approximation (first at an intuitive level and later in a more rigorous form) able to produce results within a prescribed tolerance for small and large populations. Furthermore, the approximation can also be seen as a numerical algorithm for the problem under study.

The purpose of the present work is to test this novel approximation in a simple but non-trivial model of an endemic disease. We will present a simple implementation of the approximation testing its efficiency, the statistical deviations and the dependence of these deviations with control parameters. We will also discuss in light of the numerical results the proper implementation of the diffusion approximation.

In what follows we review the main results concerning the Poisson approximation (Section 2), the test problem and the numerical results (Section 3) and present our conclusions in Section 4.

2 Background

This section will be a review of the main features of the theoretical framework, advanced in a previous manuscript.

We will consider an event space \( E \) of finite dimension. Each event is described by a random variable \( \zeta \), taking nonnegative integer values.
Hence, the array \((\zeta_1, \zeta_2, \ldots, \zeta_E)\) may take the nonnegative integer values \((n_1, n_2, \ldots, n_E) \in \mathcal{E}\), describing the occurrence of \(n_j\) events of class \(j\), \(j = 1, \ldots, E\). The connection with “physical reality” is attained by the stochastic variable \(X = X_0 + \sum_{j=1}^{E} \delta_j \zeta_j\), which is a weighted sum of the stochastic variables \(\zeta_j\), with initial condition \(X_0\). \(\delta_j\) quantifies the effect of event-class \(j\) on the phase variable. The system is fully described when the probability \(P(\zeta_1 = n_1, \ldots, \zeta_E = n_E, t/X_0)\) is known. When no confusion arises we will lighten up the notation omitting obvious arguments.

We will need to distinguish between admissible states, border states and non-admissible states. Non-admissible states are given by the problem. They correspond to e.g., negative populations, and are assumed to have zero probability.

We define the border states as follows: Let \(B_j(X_0)\) be the set of events such that: \(X = X_0 + \sum_{i=1}^{E} \delta_i n_i\) is an admissible state while the state \(Y = X + \delta_j\) is not. In such cases, we shall say that \(\{n_i\} i = 1 \ldots E\) belongs to the \(j\)-th component of the border, \(B_j(X_0)\), of the admissible region (note that the different components of the border are not necessarily disjoint). In other words, a border state of class \(j\) is an admissible state where an increase by one unit in \(n_j\) would produce a non-admissible state.

The probabilities governing the process satisfy Kolmogorov’s forward equation:

\[
\frac{d}{dt} P(n_1 \ldots n_E, t/X_0) = \sum_{j=1}^{E} \left( W_j(X - \delta_j) P(n_1 \ldots n_j - 1 \ldots n_E, t/X_0) \right) - \left( \sum_{j=1}^{E} W_j(X) \right) P(n_1 \ldots n_E, t/X_0) \tag{1}
\]

where \(X = X_0 + \sum_{j=1}^{E} \delta_j n_j\) and \(P(n_1 \ldots n_E, 0/X_0) = \prod_{j=1}^{E} \delta_{n_j} (\delta_{ij}\) is the Kronecker delta). We notice that \(P(n_1 \ldots n_E, t/X_0) = 0\) whenever at least one \(n_j\) is negative.

The present Poisson approximation amounts to replacing the exact probabilities \(P(n_1, n_2, \ldots, n_E, t/X_0)\) for the admissible states which do not belong to the border by an approximated expression based on independent Poisson processes:

\[
P(n_1, n_2, \ldots, n_E, t/X_0) = \prod_{j=1}^{E} e^{-\lambda_j(t)} \frac{\left( \lambda_j(t) \right)^{n_j}}{n_j!} \tag{2}
\]
If \((n_1, n_2, \cdots, n_E) \in B_j(X_0)\) then the corresponding factor \(\tilde{P}^j\) in \(\tilde{P}\) reads:

\[
\tilde{P}^j(n_j, t/X_0) = 1 - e^{-\lambda_j(t)} \sum_{k=0}^{n_j-1} \frac{(\lambda_j(t))^k}{k!}
\tag{3}
\]

Here, the time-dependent Poisson parameters \(\lambda_j\) satisfy the following equation, with initial condition \(\lambda_j(0) = 0:\)

\[
N_j(t, X_0) \frac{d\lambda_j}{dt} = \sum_{\{n\} \notin B_j} W_j(X) \tilde{P}(n_1 \ldots n_E, t; X_0)
\equiv f_j(\lambda) N_j(t, X_0) \tag{4}
\]

where \(X = X_0 + \sum_j \delta_j n_j\) as above, \(N_j(t, X_0) = \sum_{\{n\} \notin B_j} \tilde{P}(n_1 \ldots n_E, t; X_0)\) denotes the sum of approximated probabilities excluding the border states, and the functions \(f_j(\{\lambda\})\) are defined by the right hand side of the equation.

The final basic assumption for this class of problems is the mass-action law, namely that the system under study is restricted to (or at least unlikely to escape) a region of phase space \(\|X\|_1 \sim \Theta \leq \Omega\) which we call the size of the system. The mass-action law is stated as the following assumption:

\[
W_j(X) = \Omega w_j(X/\Omega), \tag{5}
\]

namely that the transition probabilities scale with the size of the system.

The quality of the present approximation is established by the following theorems, where the exact and approximated generating functions are compared:

**Theorem 1 (Truncated Poisson approximation)** Let \(V_j\) be the minimum distance to the \(j\)-border states, i.e., the minimum of all \(n\) such that \(X_0 + \sum_{k \neq j} n_k \delta_k + n \delta_j \in B_j\). Assume also that the generalized mass-action law holds and that \(|W_j(X) - W_j(Y)| \leq C_j |X - Y|\) with \(C_j\) (\(j = 1 \ldots E\)) finite. Then, for \(\epsilon > 0\) sufficiently small and \(\epsilon < \nu_i \leq 0\), \(\Psi_X(\exp(\sum_j \nu_j/\Omega))\) converges uniformly to \(H_\nu(\nu)\) in the limit \(\Omega \to \infty\), provided that \(\forall j, \lambda_j/V_j < 1\).

The precise approximation statement reads:

\[
|\Delta(\exp(\nu/\Omega), t, X_0) - O(t \sqrt{\lambda_j/\sqrt{\Omega}})| \leq \sum_{j=1 \ldots E} \left( \sqrt{\lambda_j} C_j |\delta_j| \right) O(t^2 \epsilon/\sqrt{\Omega})
\tag{6}
\]

where \(\Delta = \phi - \psi\) is the difference between the exact and approximated generating functions and \(\tilde{\lambda}_j\) is as defined in the statement of the next Theorem.
Theorem 2 (Large-size limit) Under the conditions of the previous theorem and if, additionally, \( \lim_{\Omega \to \infty} \lambda_j/V_j = b_j < 1 \) then \( \Psi_X(\exp(\nu/\Omega)) \) converges uniformly to \( \exp(\sum_j \nu_j \hat{\lambda}_j) \), where \( \hat{\lambda}_j = \lim_{\Omega \to \infty} \lambda_j/\Omega \) satisfies the differential equation

\[
\frac{d\hat{\lambda}_j}{dt} = \lim_{\Omega \to \infty} \frac{f_j}{\Omega}.
\]

The precise approximation statement in this case reads:

\[
\exp(\sum_j \lambda_j(e^{\nu_j/\Omega} - 1)) = \exp(\sum_j \hat{\lambda}_j \nu_j) + O(\nu^2/\Omega) \tag{7}
\]

Corollary (Deterministic limit): In the conditions of the above theorems, the fluctuation of the variables \( x_i \) are zero; i.e., the variables have a deterministic behavior in the limit \( \Omega \to \infty \).

Theorem 3 (Poisson limit) Under the assumption of the mass-action law and if \( |W_j(X) - W_j(Y)| \leq C_j|X - Y| \) with \( C_j (j = 1 \ldots E) \) finite, then \( \Phi(z,t;X_0;\Omega) - \Psi(z,t;X_0;\Omega) \) converges uniformly to zero as a function of \( z \) in \([0,1]\) in the limit \( \Omega \to \infty \), \( t \to 0 \), while \( \lambda_j \) is kept bounded.

Sketch of Proof: The proof proceeds along the lines followed for Theorem 1 with a slightly modified estimate. Then, the two contributions to the error \( \Delta \) become of order \( O(t\sqrt{\lambda}) \) and \( O(t^2\sqrt{\lambda}) \) respectively. The latter is negligible in front of the first one for \( t \to 0 \). Both contributions go to zero in the conditions of the theorem when \( t \to 0 \) as \( 1/\Omega \).

The convergence in Theorem 1 can be improved to

\[
|\Delta(\exp(\nu/\Omega),t,X_0) - O(\varepsilon^2 t \sqrt{\hat{\lambda}/\Omega^{3/2}})| \leq \sum_{j=1 \ldots E} \left( \sqrt{\hat{\lambda}_j C_j|\delta_j|} \right) O(t^2 \varepsilon/\sqrt{\Omega}) \tag{8}
\]

Moreover, the exact mean values of \( n_j \) relate to the approximate ones as follows:

\[
|n_j| - |n_j|_{\tilde{P}} = \sum_{j=1 \ldots E} \left( \sqrt{\hat{\lambda}_j C_j|\delta_j|} \right) O(t^2 \varepsilon \sqrt{\Omega}), \tag{9}
\]

where \( |n_j|_{\tilde{P}} \) is the mean value of \( n_j \) using the Poisson weights \( \tilde{P} \).

Theorem 4 (Fluctuations around the deterministic limit) The fluctuations \( (n_j - <n_j>/\sqrt{\Omega})/\sqrt{\Omega} \) of \( n_j \) around its mean value \( <n_j> \), in the scale \( \sqrt{\Omega} \), converge towards a Brownian process under the conditions of Theorems (1,2) in the limit \( \Omega \to \infty \) for any fixed \( t < t^* \) and the proper does the motion in phase space for the variable \( (X - <X>)/\sqrt{\Omega} \).
From Theorems 1, 2 and the Corollary, we notice that the size-scaled populations \( x = X/\Omega \) obey the following deterministic equation in the limit \( \Omega \to \infty \):

\[
\frac{dx}{dt} = \sum_j \delta_j w_j(x)
\]

(10)

where, letting \( x_0 = \lim_{\Omega \to \infty} X_0/\Omega \), we have:

\[
x = x_0 + \sum_j \delta_j \hat{\lambda}_j
\]

(11)

a result that corresponds with the main theorem in Kurtz\(^{16}\): the law of large numbers.

In a similar way, the increments of \( x \) in a time interval \( dt \) on the scale of Theorem 4 are:

\[
dx = \left( \sum_j \delta_j w_j(x) + \zeta(t)/\sqrt{\Omega} \right) dt
\]

(12)

where \( \zeta \) is a normally distributed variable with zero mean and covariance matrix \([\zeta(t) \zeta^{\prime}(t')]\). This covariance can be estimated as: \([\zeta(t) \zeta^{\prime}(t')] \sim \delta(t - t') \sum_j \delta_j \hat{\lambda}_j w_j(x)\).

Expression (12) corresponds to a Langevin process or Brownian motion in phase space with a noise amplitude which is state dependent. This process is also known as the diffusion approximation\(^{15}\) and, as far as we know, it has always been introduced heuristically rather than as a limit case like in the present work\(^{15}\). The linearization of (12) assuming small departures of the solution of the stochastic process with respect to the deterministic solution leads to the Central Limit Theorem stated by Kurtz\(^{17}\). However, such linearization will drastically shorten the time range where the approximation can be used, a fact that is not apparent when \( \Omega \) can be taken as large as needed but matters when \( \Omega \) and the time are large but finite.

We will discuss some features of the Langevin approximation in the Results Section, showing the outcome of different “interpretations” of the Langevin approach.

3 Example

As a test model we will use one of the simplest, yet widely used, models for measles epidemics. The evolution of the susceptible, \( S \), and infected, \( I \), populations rests on just three different events:

- Event-type 1: *Birth*: Susceptible are born at a constant rate \( a = \Theta\bar{a} \).
• Event-type 2: Contagion: The susceptible population decreases by one while the infected population increases by one at a rate $\beta SI = \beta SI/\Theta$.

• Event-type 3: Recovery: Infected individuals are removed at a rate $bI = bI$.

The time between events is exponentially distributed with frequency $\tau^{-1} = a + \beta SI + bI$.

A deterministic version of the model was used by Soper\textsuperscript{21} in a study of periodicity of measles outbreaks, the stochastic counterpart was introduced by Bartlett\textsuperscript{1,2}. Several other authors have considered the model\textsuperscript{20,22,23,24} and it has been reviewed by Renshaw\textsuperscript{14} and Nåsell\textsuperscript{4}.

We will consider the Poisson approximation to $P(n_1, n_2, n_3, t; S_0 I_0)$ which represents the probability that starting from the state $(S_0, I_0)$ with certainty at $t = 0$, $(n_1, n_2, n_3)$ events of type birth, infection and recovery, respectively, have occurred up to time $t$. Let $n_{12} = n_1 - n_2$ and $n_{23} = n_2 - n_3$. Then, the total number of susceptible individuals at a given time will be $S = S_0 + n_{12}$ while the number of infected individuals will be $I = I_0 + n_{23}$. The evolution of $P(n_1, n_2, n_3, t; S_0 I_0)$ is described by the forward Kolmogorov’s equation:

$$
\frac{dP}{dt}(n_1, n_2, n_3) = aP(n_1 - 1, n_2, n_3)
+ \beta(S_0 + n_{12} + 1)(I_0 + n_{23} - 1)P(n_1 + 1, n_2 - 1, n_3)
+ b(I_0 + n_2 + 1 - n_3)P(n_1, n_2, n_3 - 1)
- (a + \beta(S_0 + n_{12})(I_0 + n_{23}) + b(I_0 + n_{23}))P(n_1, n_2, n_3)
$$

(13)

where the dependence on $t; S_0, I_0$ has been omitted, lightening the notation.

The equations for the parameters of the Poisson approximation (4) can be written as:

$$
d\lambda_1/dt = a
$$

$$
d\lambda_2/dt = \beta((S_0 + \lambda_1 - \lambda_2)(I_0 + \lambda_2 - \lambda_3) - (\lambda_2)
$$

$$
d\lambda_3/dt = b(I_0 + \lambda_2 - \lambda_3)
$$

(14)

In these equations the full Poisson distributions have been considered since the contributions of the tails represent a negligible error in the present example ($O(\exp(\lambda_j - V_j))$ where $V_j$ is the minimum distance from $(S_0, I_0)$ to $B_j$, as evaluated in the Appendix of our previous article\textsuperscript{19}. In this example $V$ is about one thousand while $\lambda_j$ remains around a couple of hundreds.

Simulations were performed for the full Feller process, its Poisson approximation without considering the borders and for two versions of
the diffusion (Gauss) approximation. The equations for the parameters (14) were integrated including up to $O(dt^2)$ terms, i.e., the same order of error than the error introduced in the mean value (9).

The two different interpretations of the Gauss process are as follows. We can consider that the deviations from the mean value of $(S_0/\Theta, I_0/\Theta)$ are approximated by $(\lambda_i/\sqrt{\Theta})\psi$ with $\psi$ a $N(0,1)$ random variable according to Theorem (4). This is the standard interpretation of the diffusion approximation. We shall call this interpretation “Gauss-B”.

Alternatively we can consider that the values of $(S,I)$ are given by $(S,I) = [(S_0 + \lambda_1 - \lambda_2 + \sqrt{\lambda_1}\psi_1 + \sqrt{\lambda_2}\psi_2, I_0 + \lambda_2 - \lambda_3 + \sqrt{\lambda_2}\psi_2 + \sqrt{\lambda_3}\psi_3]$ where $[X]$ stands for “integer nearest to $X$”. We shall call this approximation “Gauss-G”.

The essential difference between these two Gauss approximations is that in Gauss-G the variables at intermediate times are constrained to take integer values, while in Gauss-B they are real-valued. Both approximations satisfy the same limits (as stated in Theorem 4). We will reason about this fact in the following lines, leaving the detailed proofs for a future manuscript.

Recasted in the present context, it is clear that the goal of the Gauss-G approximation is to produce the integer pairs $(S,I)$ distributed according to the processes $\psi_k$ above in order to approximate the Feller process $X$. Since $x = X/\Omega$ we can recast Eq. (12) in terms of the unscaled variables:

$$dX = \left( \sum_j \delta_j W_j(X) + \sqrt{\Omega} \zeta(t) \right) dt$$

It is then natural that the outcomes of the Gauss or whichever other approximation of the left hand side are to be integers since nothing else exists in the original Feller process $X$. Since $x = X/\Omega$ we can recast Eq. (12) in terms of the unscaled variables:

It is then natural that the outcomes of the Gauss or whichever other approximation of the left hand side are to be integers since nothing else exists in the original Feller process $X$. In this context, the standard interpretation of the Langevin approach, Gauss-B, introduces then an extra error in that the phase space for intermediate values does not consist of integer triples but of real ones. This error is of the order $O(1/W_j)$ where $W_j$ is the size of the system at any integration step $dt$ (in this problem $W_j$ is of the order of $\Theta$).

This additional error in Gauss-B does not depend on the choice of time interval and cannot be diminished reducing the integration step. On the contrary, while in the Gauss-G approximation the errors can in principle be reduced decreasing the time step, the error introduced in Gauss-B by using real numbers may dominate the process for small enough time-steps. Yet, both interpretations of the Langevin approach have identical $\Omega \to \infty$ (with $W_j \to \infty$ together with $\Omega$ as assumed in the Mass-action Law) limit, but converge with different deviations.
3.1 Results

In order to compare the results obtained by the four simulations discussed above, we had to devise some simplified test. We fixed the parameter values as $\bar{a} = 1$, $\bar{\beta} = 10$, $b = 10$, $\Theta = 10000$ and run the four simulations for a time extent $T = 2$ which is close to the period of the damped oscillations in the deterministic model. The initial conditions for the simulations were in all the cases reported $(I_0, S_0) = (1000, 100031)$ which is close to the deterministic equilibrium value (endemic solution) $(I, S) = (1000, 10000)$.

The simulations produce results on a subset of $\mathbb{Z}^4$ which is too large for direct comparison using statistical tests, since it would require about $10^{10}$ simulation runs. On the other hand, the fact that the Poisson approach approximates the real process is already established by theorems so we aimed for a simpler test which only gives necessary conditions for having a satisfactory approximation.

To begin with, there is no need to compare $\lambda_1$ since it is computed in equivalent forms in all simulations. Note that the equation for $\lambda_1$ can be integrated exactly in closed form. Hence, we compared datasets of $\lambda_2$, $\lambda_3$ and $\lambda_2 - \lambda_3$ produced with $10^6$ runs for all four simulations using the Kolmogorov-Smirnov (KS) test to compare distributions. The choice of the third test is motivated since $\lambda_2$ and $\lambda_3$ present a large correlation. They are both of the order of 20000 while their difference is of the order of a few hundred.

Given a confidence level $\alpha \in (0, 1]$ and consequently a tolerance level $d(\alpha)$, the KS test helps to decide whether it makes sense to accept or reject the hypothesis that two given data sets come from the same process. The test computes a difference value $\bar{d}$ and thereafter a confidence level $\bar{\alpha} = P(x \geq \bar{d})$ ($x$ satisfying the null hypothesis) which has to be compared with $\alpha$. If $\bar{\alpha} \geq \alpha$ (hence $\bar{d} < d$) one cannot reject the hypothesis that both data sets come from the same process, and conversely.

There is a compromise in the choice of $\alpha$. It has to be a low number, otherwise in the hunt for detecting “false data sets” we would reject too many true data sets which happen to be somewhat different among themselves. On the other hand it cannot be too low, otherwise we would hardly distinguish true from false at all. It has to be kept in mind that such choices are always “at our own risk”. To fix ideas consider the confidence levels 0.1, 0.05 and 0.01, meaning that we risk to reject a “Feller” data set in 10%, 5% and 1% of the runs respectively.

A successful test indicates that the sets of values of $\lambda_2$, $\lambda_3$ and $\lambda_2 - \lambda_3$ coming from two runs are compatible with the null hypothesis, but this does not guarantee that the pairs $(\lambda_2, \lambda_3)$ are compatible, since our test does not consider the distribution of pairs but rather marginal distributions of the variables. Even if the figures are “the same”, we still
do not know if they came out with the proper distribution in terms of pairs. On the other hand, a failed test establishes that the pairs \((\lambda_2, \lambda_3)\) in two runs cannot come from the same process.

In Table I we show the \(\bar{\alpha}\) values computed with the KS test comparing some Feller and Poisson runs. “P0” denotes Poisson runs with a time-step of 0.02 (with approximately 600 events within each time step) while “P1x” \(x = 1, 2, 3\) denote three Poisson runs with time-step 0.001 (involving approximately 30 events within each time step). The Feller runs are denoted by “Tx” \(x = 1, 2, 3\).

<table>
<thead>
<tr>
<th>Dataset pair</th>
<th>(\lambda_2)</th>
<th>(\lambda_3)</th>
<th>(\lambda_2 - \lambda_3)</th>
</tr>
</thead>
<tbody>
<tr>
<td>P0 T1</td>
<td>0.054448</td>
<td>0.705083</td>
<td>0.000196</td>
</tr>
<tr>
<td>P0 T2</td>
<td>0.181261</td>
<td>0.507998</td>
<td>0.087076</td>
</tr>
<tr>
<td>P0 T3</td>
<td>0.720376</td>
<td>0.916048</td>
<td>0.002592</td>
</tr>
<tr>
<td>P11 T1</td>
<td>0.766497</td>
<td>0.366515</td>
<td>0.845375</td>
</tr>
<tr>
<td>P11 T2</td>
<td>0.260222</td>
<td>0.101213</td>
<td>0.302322</td>
</tr>
<tr>
<td>P11 T3</td>
<td>0.959234</td>
<td>0.802967</td>
<td>0.632484</td>
</tr>
<tr>
<td>P12 T1</td>
<td>0.138791</td>
<td>0.020574</td>
<td>0.112523</td>
</tr>
<tr>
<td>P12 T2</td>
<td>0.381672</td>
<td>0.169256</td>
<td>0.910722</td>
</tr>
<tr>
<td>P12 T3</td>
<td>0.027510</td>
<td>0.110272</td>
<td>0.858000</td>
</tr>
<tr>
<td>P13 T1</td>
<td>0.349022</td>
<td>0.082855</td>
<td>0.182363</td>
</tr>
<tr>
<td>P13 T2</td>
<td>0.338261</td>
<td>0.221951</td>
<td>0.752806</td>
</tr>
<tr>
<td>P13 T3</td>
<td>0.779957</td>
<td>0.211652</td>
<td>0.929525</td>
</tr>
</tbody>
</table>

Table I Comparison of Poisson and Feller runs (see text).

We realize that as expected the P0 data set compares worse than the P1x against the Feller runs, as two comparisons of \(\lambda_2 - \lambda_3\) are far under the \(\alpha = 0.01\) confidence level. The P1x and Feller runs cannot be distinguished at the \(\alpha = 0.01\) confidence level and hardly so at the \(\alpha = 0.1\) level, since only 2 out of 27 comparisons fail the test.

In Table II we show the \(\bar{\alpha}\) values computed with the KS test comparing with the Gaussian runs G and B. Actually, there is no need for further tests of the Gauss-B approximation in the present case since a plot of the cumulative distribution of \(I(2)\) shows the contrast between the Gauss-B and any of Feller, Poisson and Gauss-G approaches (see Figure 1). Notice further that decreasing the time step from \(dt = 0.02\) to \(dt = 0.001\) deteriorates the situation rather than improving it since the \(\Omega \to \infty\) and \(dt \to 0\) limits cannot be exchanged within the Gaussian approximation. This effect is not present in the Poisson approximation and is also less evident (but yet present) in the Gauss-G approximation.
Table II Comparison of G and B runs with P and Feller runs (see text).

<table>
<thead>
<tr>
<th>Dataset pair</th>
<th>$\lambda_2$</th>
<th>$\lambda_3$</th>
<th>$\lambda_2 - \lambda_3$</th>
</tr>
</thead>
<tbody>
<tr>
<td>P11 G</td>
<td>0.252950</td>
<td>0.218046</td>
<td>0.034904</td>
</tr>
<tr>
<td>P12 G</td>
<td>0.001751</td>
<td>0.000470</td>
<td>0.001281</td>
</tr>
<tr>
<td>P13 G</td>
<td>0.008090</td>
<td>0.003931</td>
<td>0.004159</td>
</tr>
<tr>
<td>T1 G</td>
<td>0.106936</td>
<td>0.272261</td>
<td>0.165325</td>
</tr>
<tr>
<td>T2 G</td>
<td>0.090212</td>
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<tr>
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Figure 1: Cumulative statistics of $I(2)$ produced with four different methods. At the resolution level of the figure there are no differences between the Feller, Poisson and Gauss-G processes. The Gauss-B1 set corresponds to a time step $dt = 0.02$ while the Gauss-B2 set corresponds to $dt = 0.001$.

It is clear from Table II that the B run cannot be mistaken with the Feller or P1x runs since the comparisons fail the test for any confidence.
level. The G run is somewhat better: 2 out of 9 comparisons with the Feller process fail the test at the $\alpha = 0.01$ confidence level while 7 out of 9 fail at the $\alpha = 0.1$ level. However, the G results are far worse than the P1x comparisons. It is noteworthy that G compares somewhat worse with P1x than with the Feller runs: 5 out of 9 comparisons fail the test at the $\alpha = 0.01$ level.

The strength of the Poisson approximation can be further illustrated by comparing the computational times for the different runs. Time differences are just illustrative, since they are machine and optimization dependent. No optimization was attempted in either run. On a fast (> 2.5 GHz) Pentium computer with large internal memory, the Feller runs required about 23200 seconds, the P1x about 7400 seconds while the Gauss runs needed about 1800 seconds.

![Figure 2](image)

Figure 2: Average orbit ($10^5$ runs) for the Feller, Poisson and Gauss-G processes. The orbit resulting from abusing of Eq. (14) by integrating it over large ($O(1)$) times is also displayed.

In Figure 2 we can see a further illustration of the quality of the Poisson approximation. The figure shows the average over $10^5$ runs of the
evolution produced with the Feller process, the Poisson and the Gauss-G approximations. Also displayed is \((S, I)(t)\) as it would result from integrating (14) over characteristic times for the deterministic evolution and the corresponding deterministic approximation. Notice that the Poisson approximation degrades gracefully with time.

4 Concluding remarks

We have illustrated the use of our recently introduced Poisson approximation to a Feller process in a simple epidemiological model.

Considering the situation of a relatively small city of about \(\Theta = 10000\) individuals, we have found no significant deviations between the Feller process and the Poisson approximation in \(10^6\) runs and a slight systematic deviation when further approximation is introduced producing the Gauss-G simulations.

As a numerical method, even considering that no effort has been made to optimize the code, the Poisson approximation runs a factor of 4 faster than the Feller process with the possibility of improving the performance using longer time-steps if lesser statistical significance can be tolerated.

This study also illustrates the critical role that the discrete phase space has. When intermediate values of the populations are allowed to be real, as in the standard diffusion approximation, large errors are introduced which cannot be controlled adjusting the time step of the process. Nevertheless, even the Gauss-G approximation is expected to fail close to extinction situations \(^{18}\).

Acknowledgments

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