

A stochastic death pairing process

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Abstract. In this article a stochastic death process in which particles of two types combine and are removed from the system at a rate proportional to the product of their numbers is considered. A simpler approximate process is also detailed and is shown numerically to compare very well with the exact process. The process has application in the modeling of bacteria harboring plasmids.

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1 Introduction

A plasmid is an independent self-replicating DNA molecule that carries only a few genes. In the modeling of the population size of bacteria harboring plasmids, one can consider a population which consists of two types of individuals that combine at a rate proportional to the product of their numbers.

If there are initially N type I individuals and $N + k$ type II individuals, where $k \geq 0$, then letting $x(t)$ be the number of type I individuals in the population at time t ; since the individuals combine in pairs, the number of type II individuals at time t will be $x(t) + k$, for $k \geq 0$.

A deterministic model that describes $x(t)$ is given as

$$(1.1) \quad \frac{d}{dt}x(t) = -\mu x(t)(x(t) + k)$$

with $x(0) = N$, and $\mu > 0$. This ordinary differential equation is readily solved to give

$$(1.2) \quad x(t) = \frac{Nk}{(N + k)e^{k\mu t} - N}.$$

This model for bacteria harboring plasmids has been considered by Esty, et al. [2].

Some plasmids have the ability to physically transfer from a plasmid-bearing donor cell to a plasmid-free recipient cell. The deterministic model given by equations (1.1)

and (1.2) describe the situation where recipient cells having received plasmids and the donor cells no longer play an active role in the process.

This article considers a birth-death process which is a stochastic formulation of this deterministic model and details an approximate process that may be simpler to handle in some applications.

2 A death process with paired removals

A stochastic version of the model described by equation (1.1) can be given by considering $X(t)$ a random variable which represents the number of type I individuals in the population at time t ; the number of type II individuals at time t will be $X(t) + k$, for $k \geq 0$. The transition for this process during the interval $(t, t + \delta t)$ can be described as shown in the following table

transition	rate
$j \rightarrow j - 1$	$\mu j(j + k)\delta t$,

where $\mu > 0$ is the combination rate for the two subpopulations. This stochastic process is an example of a *quadratic* death process.

If the process is assumed to initially start with N type I individuals, then the probabilities

$$p_j(t) = P[X(t) = j | X(0) = N]$$

of the Markov chain $\{X(t); t \geq 0\}$ in continuous time will satisfy the forward Kolmogorov equations

$$(2.1) \quad p'_j(t) = -\mu j(j + k)p_j(t) + \mu(j + 1)(j + 1 + k)p_{j+1}(t),$$

for $j = 1, \dots, N$ and for $j = 0$

$$p'_N(t) = -\mu N(N + k)p_N(t).$$

This system of equations can be solved recursively, though the resulting algebraic expressions are difficult to handle. One can also approach the solution more succinctly, using the probability generating function (p.g.f.) technique. Specifically, letting

$$\phi(z, t) = \sum_{j=0}^N p_j(t) z^j,$$

then the system of differential equations (2.1) can be expressed by the partial differential equation

$$(2.2) \quad \frac{\partial \phi(z, t)}{\partial z} = \mu(1 - z) \left((k + 1) \frac{\partial \phi(z, t)}{\partial z} + z \frac{\partial^2 \phi(z, t)}{\partial z^2} \right).$$

The solution of the partial differential equation, using the method of separation of variables, is straightforward, though tedious and is

$$(2.3) \quad \phi(z, t) = \sum_{j=0}^N d_j e^{-\mu j(k+j)t} {}_2F_1(-j, k + j, k + 1, z)$$

where

$$d_j = \frac{(-1)^j (2j+k)(k+j-1)! N!(N+k)!}{j! k! (N-j)! (N+k+j)!},$$

and ${}_2F_1(-j, k+j, k+1, z)$ is the hypergeometric function defined by the series

$${}_2F_1(a, b, c, z) = \sum_{\ell=0}^{\infty} \frac{(a)_\ell (b)_k}{(c)_\ell} \frac{z^\ell}{\ell!}$$

with

$$(a)_\ell = a(a+1)(a+2)\dots(a+\ell-1)$$

and $(a)_0 = 1$. Morgan [9], in a slightly different context, also obtained this solution.

Expanding the p.g.f. $\phi(z, t)$ in equation (2.3), one can obtain the transient probabilities as

$$(2.4) \quad p_j(t) = \frac{N!(N+k)!}{j!(j+k)!} \sum_{i=j}^N (-1)^{i-j} \left(\frac{(j+i+k-1)!(2i+k)}{(N-i)!(i-j)!(N+i+k)!} \right) e^{-\mu i(i+k)t}$$

for $j = 0, 1, \dots, N$.

A representative graph of a few of these probabilities with $\mu = 0.25$, $k = 5$ and $N = 10$ is shown in Figure 1.

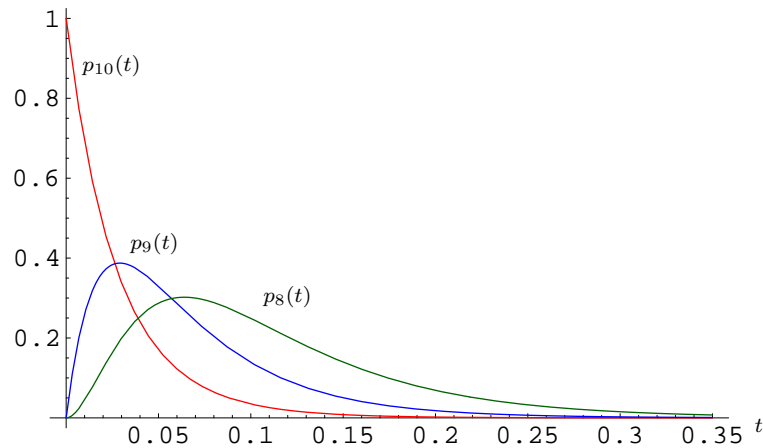


Figure 1: Representative graph of the probabilities $p_j(t)$ for $j = 10, 9, 8$ with $\mu = 0.25$, $k = 5$ and $N = 10$

The expected value of the process $X(t)$ is obtained from $\phi(z, t)$ as

$$(2.5) \quad \begin{aligned} E(X(t)) &= \frac{\partial}{\partial z} \phi(1, t) \\ &= N!(N+k)! \sum_{i=1}^N \left(\frac{(2i+k)(i-1)!(i+k)!}{(N-i)!(i+k)!(N+i+k)!} \right) e^{-\mu i(i+k)t}. \end{aligned}$$

M.J. Faddy & W.W. Esty [3] considered a diffusion approximation of the process $X(t)$ and showed numerically that this approximation behaved reasonably well. In the next section, another, perhaps simpler, approximation is proposed.

3 An approximation

An approximation of the process $\{X(t); t \geq 0\}$ can be obtained by replacing the transition rate $\mu j(j+k)\delta t$ of moving from state j to $j-1$ with the transition rate $\mu j(x(t)+k)\delta t$, where $x(t)$ is the deterministic value from equation (1.2).

This approximation method has seen many forms of application. J. Gani [4], [5] used it in his studies of bacteriophage; K. Tognetti and G. Winley [11] and P.R. Parthasarathy and B.K. Kumar [10] applied it in their studies of the logistic process; while recently, J. Gani and R.J. Swift [6], [7] have applied the same technique for the simple stochastic and carrier-borne epidemics. Some further examples of the technique were detailed in B.J.T. Morgan and J.P. Hinde [8].

In the context of the death pairing process of the previous section, the transition rates for the approximate process $\tilde{X}(t)$ are given by

$$\begin{array}{c|c} \text{transition} & \text{rate} \\ \hline j \rightarrow j-1 & \mu j \left(\frac{Nk}{(N+k)e^{k\mu t} - N} + k \right) \delta t, \end{array}$$

thus, writing

$$x(t) + k = \frac{Nk}{(N+k)e^{k\mu t} - N} + k = \frac{(N+k)k}{N+k - Ne^{-k\mu t}},$$

the probabilities

$$\tilde{p}_j(t) = P[\tilde{X}(t) = j | \tilde{X}(0) = N]$$

of the Markov chain $\{\tilde{X}(t); t \geq 0\}$ will satisfy the forward Kolmogorov equations

$$(3.1) \quad \tilde{p}'_j(t) = -\mu j \left(\frac{(N+k)k}{N+k - Ne^{-k\mu t}} \right) \tilde{p}_j(t) + \mu(j+1) \left(\frac{(N+k)k}{N+k - Ne^{-k\mu t}} \right) \tilde{p}_{j+1}(t),$$

for $j = 1, \dots, N$, and when $j = 0$

$$\tilde{p}'_N(t) = -\mu N \left(\frac{(N+k)k}{N+k - Ne^{-k\mu t}} \right) \tilde{p}_N(t).$$

The approximate number $\tilde{X}(t)$ of type I individuals in the population is thus a nonhomogeneous death process with a death rate $\mu y(t)$ where

$$y(t) = \frac{(N+k)k}{N+k - Ne^{-k\mu t}}$$

for $k \geq 0$. For further details on birth-death processes with time-dependent parameters, one may consult the text by Allen [1].

The p.g.f.

$$\psi(u, t) = \sum_{j=0}^N \tilde{P}_j(t) u^j$$

of this approximate process $\tilde{X}(t)$ is thus

$$(3.2) \quad \psi(u, t) = \left(ue^{-\mu Y(t)} + 1 - e^{-\mu Y(t)} \right)^N$$

where

$$(3.3) \quad \begin{aligned} Y(t) &= \int_0^t y(u) du = \int_0^t \frac{(N+k)k}{N+k - Ne^{-k\mu t}} du \\ &= \frac{1}{\mu} \ln \left[1 + \frac{N}{k} (1 - e^{-k\mu t}) \right] + kt. \end{aligned}$$

This gives the transient probabilities as $\tilde{X}(t)$ for $j = 0, 1, \dots, N$ as the following binomial probabilities

$$(3.4) \quad \begin{aligned} \tilde{p}_j(t) &= \binom{N}{j} e^{-j\mu Y(t)} \left(1 - e^{-\mu Y(t)} \right)^{N-j} \\ &= \binom{N}{j} \left(\frac{e^{-k\mu t}}{\left[1 + \frac{N}{k} (1 - e^{-k\mu t}) \right]} \right)^j \left(1 - \frac{e^{-k\mu t}}{\left[1 + \frac{N}{k} (1 - e^{-k\mu t}) \right]} \right)^{N-j} \\ &= \binom{N}{j} \left(\frac{k^j (N+k)^{N-j} e^{-kj\mu t} (1 - e^{-k\mu t})^{N-j}}{(k + N(1 - e^{-k\mu t}))^N} \right). \end{aligned}$$

The expected value of the approximate number $\tilde{X}(t)$ of type I individuals is

$$(3.5) \quad \begin{aligned} E[\tilde{X}(t)] &= \frac{\partial}{\partial u} \psi(1, t) = Ne^{-\mu Y(t)} \\ &= N \left(\frac{e^{-k\mu t}}{\left[1 + \frac{N}{k} (1 - e^{-k\mu t}) \right]} \right) \\ &= \frac{Nk}{(N+k)e^{k\mu t} - N}, \end{aligned}$$

which corresponds precisely to the deterministic model $x(t)$ given by equation (1.2).

A comparison of these approximate probabilities $\tilde{p}_j(t)$ with their exact values $p_j(t)$ can be seen in Figures 1 and 2, where representative plots are given for $\mu = 0.25$, $k = 5$ and $N = 10$. The agreement is very good. The behaviour for other values of parameters is similar.

Figure 3 shows a representative plot of the expectations $E(X(t))$ and $E(\tilde{X}(t))$ for $\mu = 0.25$, $k = 5$ and $N = 10$ and shows remarkably good agreement.

The approximation is good over a range of values. A graph of the difference

$$(3.6) \quad \begin{aligned} E(X(t)) - E(\tilde{X}(t)) &= N!(N+k)! \sum_{i=1}^N \left(\frac{(2i+k)(i-1)!(i+k)!}{(N-i)!(i+k)!(N+i+k)!} \right) e^{-\mu i(i+k)t} \\ &\quad - \frac{Nk}{(N+k)e^{k\mu t} - N} \end{aligned}$$

for $N = 10$ and $k = 5$ at different values of time t and for varying values of μ is shown in Figure 4. From this graph, one sees that the difference between the expected values

is small for values of $\mu > 0.25$; for this range of μ , there is less than a 3% error in approximation, where the percent error is calculated as

$$100\% \times \frac{E(X(t)) - E(\tilde{X}(t))}{E(X(t))}.$$

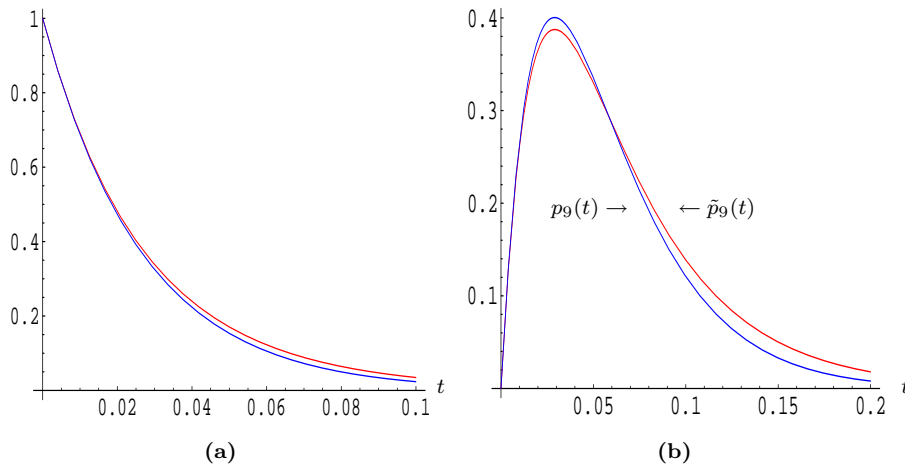


Figure 2: **(a)** $p_{10}(t)$ and $\tilde{p}_{10}(t)$ for $\mu = 0.25$, $k = 5$ and $N = 10$. **(b)** $p_9(t)$ and $\tilde{p}_9(t)$ for $\mu = 0.25$, $k = 5$ and $N = 10$.

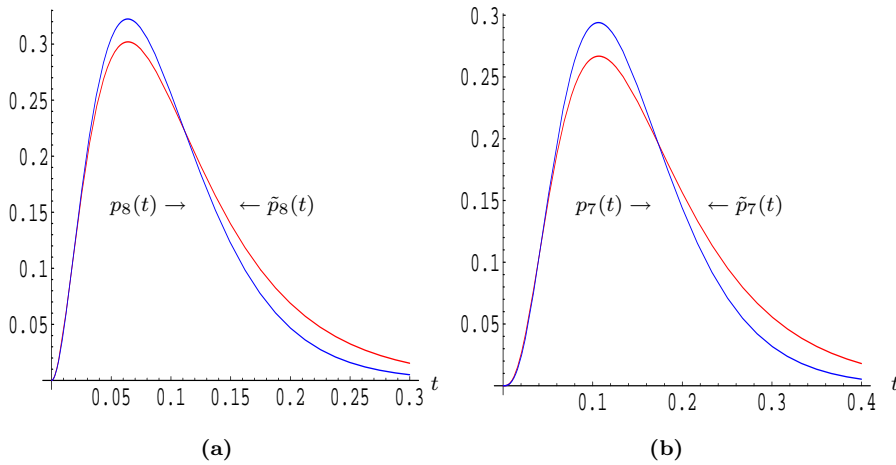


Figure 3: **(a)** $p_8(t)$ and $\tilde{p}_8(t)$ for $\mu = 0.25$, $k = 5$ and $N = 10$. **(b)** $p_7(t)$ and $\tilde{p}_7(t)$ for $\mu = 0.25$, $k = 5$ and $N = 10$.

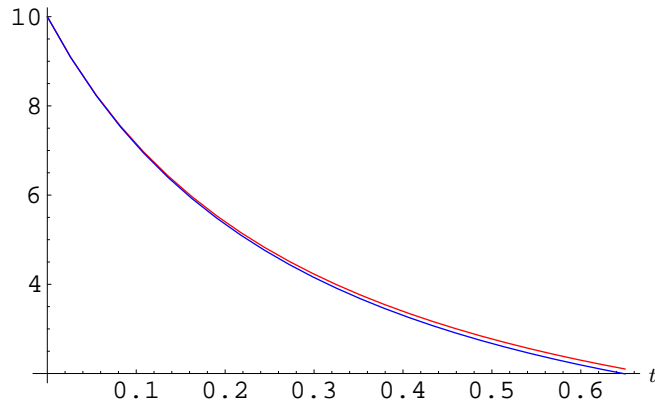


Figure 4: $E(X(t))$ and $E(\tilde{X}(t))$ for $\mu = 0.25$, $k = 5$ and $N = 10$.

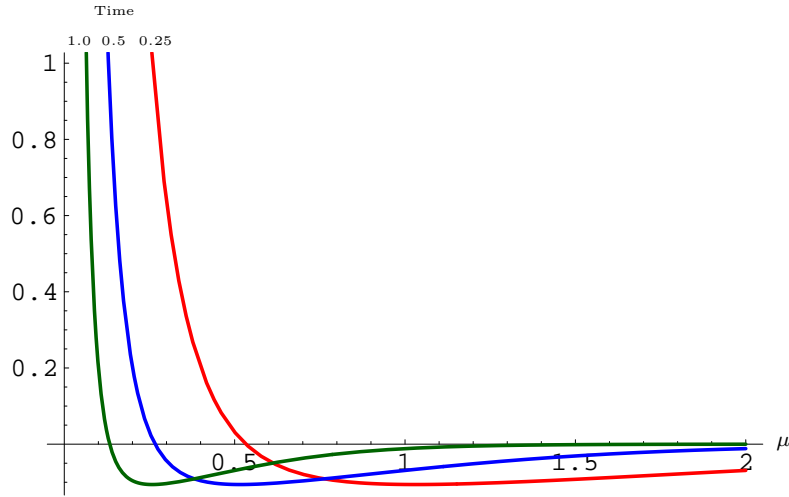


Figure 5: The difference $E(X(t)) - E(\tilde{X}(t))$ for varying μ , with $k = 5$ and $N = 10$ at different instances of time $t = 0.25, 0.5, 1.0$.

The approximation for the complicated expression (2.5) for the expected value of the process $X(t)$ appears to be quiet good and robust. Indeed, it is interesting to note that from equation (3.3) for $Y(t)$,

$$Y(t) = \frac{1}{\mu} \ln \left[1 + \frac{N}{k} (1 - e^{-k\mu t}) \right] + kt \approx \frac{N}{k\mu} (1 - e^{-k\mu t}) + kt.$$

using the approximation $\ln(1+x) \approx x$. Thus one may use the simpler expression $\frac{N}{\mu} (1 - e^{-\mu t}) + kt$ for $Y(t)$ for small values of k .

4 Concluding remarks

In this brief article, a natural approximation method has been employed on a death pairing process that is useful in modeling the population size of plasmids. This approximation provides simpler expressions for the transient probabilities and the expected population size and it is hoped that it will be of use to practitioners.

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References

- [1] L.J.S. Allen, *An Introduction to Stochastic Processes with Applications to Biology*, Pearson Education, 2003.
- [2] W.W. Esty, R.V. Miller, and D.C. Sands, *A model for fluctuations in the fraction of bacterial population harboring plasmids*. Theoret. Popn. Biol. **30**, (1986), 111-124.
- [3] M.J.Faddy and W.E. Esty, *A stochastic death process with elimination by pairing*, J. Appl. Prob. **24**, (1987), 241-245.
- [4] J. Gani, *Stochastic phage attachment to bacteria*, Biometrics, **21**, (1965), 134-139.
- [5] J. Gani, *Models for antibody attachment to virus and bacteriophage*, Proc. 5th Berkeley Symp. Math. Statist. Prob., **4**, (1967), 537-547.
- [6] J. Gani and R.J. Swift, *Approximating carrier-borne epidemics*, Australian & New Zealand Journal of Statistics, (to appear).
- [7] J. Gani and R.J. Swift, *An epidemic model approximating the spread of the common cold*, Australian Math. Soc. Gazette, (to appear).
- [8] B.J.T. Morgan and J.P. Hinde, *On an approximation made when analysing stochastic processes*, J. Appl. Prob. **13**, No. 4, (1976), 672-683.
- [9] B.J.T. Morgan, *On the solution of differential equations arising in some attachment models of virology*, J. Appl. Prob. **8**, (1971), 215-221.
- [10] P.R. Parthasarathy and B.K. Kumar, *A birth and death process with logistic mean population*, Commun. Statist, Theory, **20**, No. 2, (1991), 621-629.
- [11] K.P. Tognetti and G. Winley, *Stochastic growth models with logistic mean population*, J. Theor. Biol **82**, (1980), 167-169.

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