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A Simple Interpretation Of Two Stochastic Processes Subject To An Independent Death Process*

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Abstract

In this explanatory note, we interpret two known results for a death process and a birth process subject to an independent death process. The first example is the carrier-borne epidemic, while the second is the polymerisation chain reaction. The interpretations allow a more intuitive understanding of the resulting formulae for the probability generating functions of the processes.

1 Introduction

In some biological phenomena, the size of a population $X(t)$ at time $t \geq 0$ is influenced by an independent process $Y(t)$ and is often modeled as a continuous time bivariate Markov chain $\{(X(t), Y(t)) : t \geq 0\}$.

One classic example is the carrier-borne epidemic process detailed by Weiss (1965). In this process the number of susceptibles $X(t)$ are modeled as a death process subject to the number of infectious carriers $Y(t)$, which themselves follow an independent death process.

The bivariate Markov chain $\{(X(t), Y(t)) : t \geq 0\}$ for the process $X(t)$ subject to the independent process $Y(t)$ is often characterized by the probability generating function (p.g.f.) for the transient probabilities. The p.g.f. which usually arises as a solution of a partial differential equation is often difficult to interpret conceptually. In this brief article, we present a conceptual framework for the p.g.f. of two such processes.

2 The Carrier-Borne Epidemic

In the carrier-borne epidemic process, as outlined in Weiss (1965) and Daley & Gani (1999), infection spreads through contact between an infectious carrier and a susceptible. The carriers are subject to a pure death process while an infected susceptible is directly removed from the population.

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If there are initially n susceptibles and b infectious carriers at time $t = 0$, and we let the nonnegative integer-valued processes $X(t)$ and $Y(t)$ represent the numbers of susceptibles and carriers of the disease, then

$$\{(X(t), Y(t)) : t \geq 0\}$$

can be modeled as a continuous time bivariate Markov chain.

The transitions and rates for this chain in the interval $(t, t + \delta t)$ are described as

transition	rate
$(x, y) \to (x-1, y)$	$\beta x y \delta t$
$(x, y) \to (x, y-1)$	$\mu y \delta t$,

where β is the infection parameter and μ is the death parameter of the carriers.

The carrier process $\{Y(t) : t \geq 0\}$ is a pure death process with the well known p.g.f.

$$\psi_Y(v, t) = \mathrm{E}(v^{Y(t)}) = \left(ve^{-\mu t} + 1 - e^{-\mu t}\right)^b, \quad \text{for } 0 \leq v \leq 1,$$

so that

$$P(Y(t) = k \mid Y(0) = b) = \binom{b}{k} e^{-\mu k t}(1 - e^{-\mu t})^{b-k}, \;\; k = 0, \ldots, b.$$

The susceptible process $X(t)$ is subject to the influence of the process $Y(t)$, which is itself independent of $X(t)$.

If we let

$$P_{ij}(t) = Pr(X(t) = i, Y(t) = j | X(0) = n, Y(0) = b),$$

for $i = 0, \ldots, n,\;\; j = 0, \ldots, b$, then it can be shown that the p.g.f.

$$\phi(z, v, t) = E\left(z^{X(t)} v^{Y(t)}\right) = \sum_{i=0}^{n} \sum_{j=0}^{b} P_{ij}(t) z^i v^j$$

of the process satisfies the partial differential equation (p.d.e.)

$$\frac{\partial \phi}{\partial t} = \beta(1 - z)v \frac{\partial^2 \phi}{\partial z \partial v} - \mu(v - 1)\frac{\partial \phi}{\partial v}. \tag{1}$$

The solution of this p.d.e. is obtained using the separation of variables method and can be found in either Bailey (1975) or Daley & Gani (1999); the resulting p.g.f. is

$$\phi(z, v, t) = \sum_{i=0}^{n} (z - 1)^i \binom{n}{i} \left[\frac{\mu}{\mu + \beta i} + \left(v - \frac{\mu}{\mu + \beta i}\right) e^{-(\mu + \beta i)t}\right]^b. \tag{2}$$

Let us attempt to interpret the structure of this p.g.f.. Given that the number of susceptibles $X(t) = i$ is fixed, a single carrier will have the partial p.g.f.

$$ve^{-(\mu+\beta i)t} + \int_0^t \mu e^{-(\mu+\beta i)u}\, du = ve^{-(\mu+\beta i)t} + \frac{\mu}{\mu + \beta i}\left(1 - e^{-(\mu+\beta i)t}\right),$$

so that the b independent carriers will have the partial p.g.f.

$$\left[\frac{\mu}{\mu+\beta i}+\left(v-\frac{\mu}{\mu+\beta i}\right)e^{-(\mu+\beta i)t}\right]^b.$$

For $v=1$, this leads to the probability

$$P\{0\leq Y(t)\leq b|X(t)=i\}=\left[\left(\frac{\beta i}{\mu+\beta i}\right)e^{-(\mu+\beta i)t}+\frac{\mu}{\mu+\beta i}\right]^b=p_i^i(t),\ \text{(say)},$$

for the carriers when there are $X(t)=i$ susceptibles.

Now the susceptibles follow a binomial death distribution with probability $q_i(t)$ of death, and $p_i(t)=1-q_i(t)$, so that the p.g.f. is

$$\begin{aligned}[zp_i(t)+1-p_i(t)]^n &= [(z-1)p_i(t)+1]^n \\ &= \sum_{k=0}^{n}(z-1)^k\binom{n}{k}p_i^k(t).\end{aligned}$$

Thus if one writes for the ith term of a series $\sum_k a_k$, the indicator

$$I_i\left(\sum_k a_k\right)=a_i$$

then

$$\begin{aligned}\phi(z,1,t) &= \sum_{i=0}^{n} I_i\left[(z-1)p_i(t)+1\right]^n \\ &= \sum_{i=0}^{n}(z-1)^i\binom{n}{i}p_i^i(t) \\ &= \sum_{i=0}^{n}(z-1)^i\binom{n}{i}\left[\left(\frac{\beta i}{\mu+\beta i}\right)e^{-(\mu+\beta i)t}+\frac{\mu}{\mu+\beta i}\right]^b,\end{aligned}$$

which would ensue if the p.g.f. $E(z^{X(t)}v^{Y(t)})$ is

$$\phi(z,v,t)=\sum_{i=0}^{n}(z-1)^i\binom{n}{i}\left[\frac{\mu}{\mu+\beta i}+\left(v-\frac{\mu}{\mu+\beta i}\right)e^{-(\mu+\beta i)t}\right]^b.$$

3 The PCR Process

Recently, Gani & Swift (2007) considered the polymerisation chain reaction (PCR) process of enzyme molecules (DNA polymerase) that have the property of causing the replication of DNA strands, while themselves degrading after a certain period. They modeled this process as a DNA strand birth process subject to a death process for the enzymes.

Their model considers $X(t)$ DNA strands and $Y(t)$ enzyme molecules at time $t\geq 0$, with $X(0)=n$ and $Y(0)=b$ with the transitions and rates in $(t,t+\delta t)$ given by

transition	rate
$(x,y) \to (x+1,y)$	$\beta xy\delta t$
$(x,y) \to (x,y-1)$	$\mu y\delta t,$

The forward Kolmogorov equations for the probabilities

$$p_{i,j}(t) = P\{X(t)=i, Y(t)=j|X(0)=n, Y(0)=b\}$$

are

$$\frac{d}{dt}p_{i,j}(t) = -(\beta i+\mu)jp_{i,j}(t) + \mu(j+1)p_{i,j+1}(t) + \beta j(i-1)p_{i-1,j}(t),$$

for $n \le i < \infty, 0 \le j \le b$. The p.g.f.

$$\psi(u,v,t) = \sum_{i=n}^{\infty}\sum_{j=0}^{b} p_{i,j}(t)u^i v^j, \quad 0 \le u,v \le 1,$$

satisfies the p.d.e.

$$\frac{\partial\psi}{\partial t} = \mu(1-v)\frac{\partial\psi}{\partial v} + \beta uv(u-1)\frac{\partial^2\psi}{\partial u\partial v}.$$

The solution, obtained by separation of variables, is

$$\begin{aligned}\psi(u,v,t) &= \left(\frac{u}{1-u}\right)^n \sum_{i=0}^{\infty}(-1)^i\binom{n+i-1}{i}\left(\frac{u}{1-u}\right)^i \\ &\quad\times\left[\left(v-\frac{\mu}{\mu+\beta(i+n)}\right)e^{-(\beta(i+n)+\mu)t} + \frac{\mu}{\mu+\beta(i+n)}\right]^b \\ &= \left(\frac{u}{1-u}\right)^n \sum_{i=0}^{\infty}\binom{n+i-1}{i}\left(\frac{u}{u-1}\right)^i \\ &\quad\times\left[\left(v-\frac{\mu}{\mu+\beta(i+n)}\right)e^{-(\beta(i+n)+\mu)t} + \frac{\mu}{\mu+\beta(i+n)}\right]^b.\end{aligned}$$

The p.g.f. for the number of DNA strands $X(t)$ is found as

$$\begin{aligned}\psi(u,1,t) &= \sum_{i=0}^{\infty}(-1)^i\binom{n+i-1}{i}\left(\frac{u}{1-u}\right)^{n+i} \\ &\quad\times\left[\left(\frac{\beta(i+n)}{\mu+\beta(i+n)}\right)e^{-(\beta(j+n)+\mu)t} + \frac{\mu}{\mu+\beta(i+n)}\right]^b.\end{aligned}$$

To interpret the structure of this p.g.f., we follow a similar reasoning to that in Section 2. Given that $X(t)=i+n$ is fixed, a single enzyme will have the partial p.g.f.

$$ve^{-(\beta(i+n)+\mu)t} + \int_0^t \mu e^{-(\beta(i+n)+\mu)u}\,du = \left[\left(v-\frac{\mu}{\beta(i+n)+\mu}\right)e^{-(\beta(i+n)+\mu)t} + \frac{\mu}{\beta(i+n)+\mu}\right]$$

so that for the b independent enzymes, the partial p.g.f. will be

$$\left[\left(v-\frac{\mu}{\beta(i+n)+\mu}\right)e^{-(\beta(i+n)+\mu)t} + \frac{\mu}{\beta(i+n)+\mu}\right]^b.$$

For $v = 1$, this leads to the probability

$$\begin{aligned}P\{X(t)|X(t) = i+n\} &= \left[\left(\frac{\beta(i+n)}{\mu+\beta(i+n)}\right)e^{-(\beta(i+n)+\mu)t} + \frac{\mu}{\beta(i+n)+\mu}\right]^b \\ &= p_{n+i}^{n+i}(t), \text{ (say)}.\end{aligned}$$

Now the DNA strands follow a birth process with probability $p_{i+n}(t)$ of birth when $X(t) = i+n$ so that the p.g.f. is

$$\begin{aligned}\left(\frac{p_{i+n}(t)u}{1-u+p_{i+n}(t)u}\right)^n &= \left(\frac{p_{i+n}(t)\left(\frac{u}{1-u}\right)}{1+p_{i+n}(t)\left(\frac{u}{1-u}\right)}\right)^n \\ &= p_{i+n}^n(t)\left(\frac{u}{1-u}\right)^n \sum_{i=0}^{\infty}(-1)^i\binom{n+i-1}{i}\left(\frac{u}{1-u}\right)^i p_{i+n}^i(t).\end{aligned}$$

Writing once again

$$I_i\left(\sum_k a_k\right) = a_i$$

then

$$\begin{aligned}\psi(u,1,t) &= \sum_{i=0}^{\infty} I_i\left(\frac{p_{i+n}(t)\left(\frac{u}{1-u}\right)}{1+p_{i+n}(t)\left(\frac{u}{1-u}\right)}\right)^n \\ &= \left(\frac{u}{1-u}\right)^n \sum_{i=0}^{\infty}(-1)^i\binom{n+i-1}{i}\left(\frac{u}{1-u}\right)^i p_{i+n}^{i+n}(t) \\ &= \sum_{i=0}^{\infty}(-1)^i\binom{n+i-1}{i}\left(\frac{u}{1-u}\right)^{n+i} \\ &\quad \times\left[\left(\frac{\beta(i+n)}{\mu+\beta(i+n)}\right)e^{-(\beta(j+n)+\mu)t} + \frac{\mu}{\mu+\beta(i+n)}\right]^b\end{aligned}$$

as required. The ensuing p.g.f. for the bivariate process $\{(X(t), Y(t)) : t \geq 0\}$ would then be

$$\begin{aligned}\phi(z,v,t) &= \left(\frac{u}{1-u}\right)^n \sum_{i=0}^{\infty}\binom{n+i-1}{i}\left(\frac{u}{u-1}\right)^i \\ &\quad \times\left[\left(v - \frac{\mu}{\mu+\beta(i+n)}\right)e^{-(\beta(i+n)+\mu)t} + \frac{\mu}{\mu+\beta(i+n)}\right]^b.\end{aligned}$$

4 Concluding Remarks

We have attempted to provide a more intuitive approach to the rather complex formulae for the p.g.f.s of a death process and a birth process, each subject to an independent death process. Much yet remains to be done to make such formulae more accessible to workers in applied probability.

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