A Note on Gani's Models on Phage Attachment to Bacteria

by

Prem S. Puri\*

Purdue University, Lafayette and University of California, Berkeley

Department of Statistics

Division of Mathematical Sciences

Mimeograph Series No. 121

September 1967

This investigation was supported in part by U. S. Public Health Service Grant GM-10525-04.

By PREM S. PURI\*

Purdue University, Lafayette

and

University of California, Berkeley

### Abstract

In this note, the solution for the distribution of the relevant random variables has been obtained for Gani's "general stochastic model" [1] for the attachment of phages to bacteria, for the special case with r = 1, where r the upper limit to the number of phage particles that can become attached to a bacterium. This distribution is then compared with the corresponding distribution already obtained by Gani [1] under his "simplified stochastic model". found that in general the simplified model appears to be a good approximation to the general model only when the total of phages is much larger than the total number of bacteria. The distribution of the time it takes before either all the bacteria (when  $n_{00} < v_{00}$ ) or all the phages (when  $n_{00} > v_{00}$ ) are exhausted, is also considered under the general model with r = 1.

<sup>\*</sup>This investigation was supported in part by U. S. Public Health Service Grant GM-10525-04.

### 1. Introduction

In a recent paper, Gani [1] has considered a stochastic analogue of a deterministic model for the attachment of phages to bacteria in suspension considered earlier by Yassky [3]. Among others, the underlying assumptions of these models are that the duration of observation is short enough not to cause any multiplications or deaths of both bacteria and phage particles and (ii) that there exists an upper limit r the number of phage particles that can become attached to a In [1] Gani first considers a general stochastic bacterium. model, henceforth called 'model A', where it is assumed that the probability of attachment during (t,t+t) of a phage to bacterium already carrying i phages is  $\lambda_i n_i(t) v_0(t) \tau + o(\tau)$ , where  $n_0(t)$ ,  $n_1(t)$ , ...,  $n_r(t)$  are the numbers of bacteria at time t with 0, 1, 2, ..., r phages respectively, with  $n_{00} = \Sigma_{i=0}^{r} n_{i}(t) = n_{0}(0)$  and the random variable  $v_{0}(t)$ the number of unattached phages at time t with  $v_0(0) = v_{00}$ . Here  $\lambda_i$ 's( $\lambda_i = 0$  for  $i \geq r$ ) are some nonnegative constants. In particular it is assumed that  $\lambda_i = i\alpha + \beta$ ; i =0, 1, 2,  $\cdots$ , r - 1 where  $\beta$  is nonnegative and  $\alpha$  is such that  $\lambda_i$  are nonnegative. Having found the differential equation associated with this model rather untractable to solution, Gani considers a simplified stochastic model, henceforth called as 'model B', where  $v_0(t)$  instead is a assumed to be nonrandom having the form originally given

by Yassky as

$$v_0(t) = \frac{v_{00}(m\alpha + \beta)}{m\alpha + \beta \exp\{n_{00}(m\alpha + \beta)t\}}, \qquad (1)$$

where  $m = v_{00}/n_{00}$ .  $v_0(t)$  as given in (1) may be regarded as the mean number of unattached phages at time t. It is assumed as before that the probability of attachment during  $(t,t+\tau)$  of a phage to bacterium already carrying i phages is  $\lambda_i n_i(t) v_0(t) \tau + o(\tau)$ , where  $v_0(t)$  is given by (1). The relevant distribution of the vector  $(n_0(t), \cdots, n_r(t))$  under model B turns out to be of the multinomial form. Reader is referred for details to Gani ([1], [2]).

The purpose of this note is two-fold. First is to find the exact distribution of the random variables involved under model A for the special case with r=1, where it was found possible to solve the equations directly using the laplace transform approach. The case of single infection (r=1) may be of interest by itself in its applications to this as well as other fields. In the present case however when  $v_{00} << v_{00}$ , the case with  $v_{0$ 

## 2. Gani's Stochastic Model A.

We shall restrict ourselves to the case with r=1, so that it is sufficient to consider the distribution of  $n_1(t)$ ,

since  $n_0(t) \equiv n_{00} - n_1(t)$  and  $v_0(t) \equiv v_{00} - n_1(t)$ . Let  $P_k(t) = Pr(n_1(t) = k)$ ;  $k = 0, 1, \dots, M$ , where  $M = \min(v_{00}, n_{00})$ . Following Gani, we have

$$\begin{cases} \frac{dP_0}{dt} = -\lambda_0 n_{00} v_{00} P_0 \\ \frac{dP_k}{dt} = -\lambda_0 (v_{00} - k) (n_{00} - k) P_k \\ + \lambda_0 (v_{00} - k + 1) (n_{00} - k + 1) P_{k-1}; k = 1, 2, \dots, M. \end{cases}$$

Let  $Q_{k}(\theta) = \int_{0}^{\infty} e^{-\Theta t} P_{k}(t) dt; k = 0, 1, \dots, M; Re(\theta) > 0. \quad (3)$ 

Next, the transforms of equations (2) are taken, using the boundary conditions  $P_k(0) = 1$  if k = 0 and zero if k > 0, leading to the recurrence relation between Q's as

$$\begin{cases} Q_0 = \frac{1}{\Theta + \lambda_0 n_{00} \nu_{00}}, \\ Q_k = \frac{\lambda_0 (\nu_{00} - k + 1) (n_{00} - k + 1)}{\Theta + \lambda_0 (\nu_{00} - k) (n_{00} - k)} Q_{k-1}; k = 1, 2, \dots, M, \end{cases}$$
(4)

and thence to their values

$$\begin{cases} Q_{0} = \frac{1}{\Theta + \lambda_{0} n_{00} v_{00}} \\ Q_{k} = \lambda_{0}^{k} \left[ \frac{v_{00}! \quad n_{00}!}{(v_{00}-k)! (n_{00}-k)!} \right] \cdot \prod_{i=0}^{k} \left[ \Theta + \lambda_{0} (v_{00}-i) (n_{00}-i) \right]^{-1} \end{cases}$$
(5)

Rewriting the product in  $Q_k$  of (5) in terms of partial fractions we have for  $k=0,1,\cdots,M$ ,

$$Q_{k} = \frac{v_{00}! \; n_{00}!}{(v_{00}-k)! (n_{00}-k)!} \sum_{i=0}^{k} \frac{C_{ik}}{\Theta + \lambda_{0}(n_{00}-i)(v_{00}-i)}$$
(6)

where  $C_{00} = 1$  and

$$C_{ik} = \frac{k}{\sum_{j=0}^{j=0}} [(i-j)(n_{00} + \nu_{00} - j-i)]^{-1}$$
(7)

Finally, taking the inverse of  $Q_k$  with respect to time t we immediately obtain the desired distribution of  $n_1(t)$  given for  $k=0,1,2,\cdots,M$  by

$$P_{k}(t) = \frac{v_{00}! n_{00}!}{(v_{00}-k)!(n_{00}-k)!} \sum_{i=0}^{k} C_{ik} \exp[-\lambda_{0}(n_{00}-i)(v_{00}-i)t].$$
(8)

Unfortunately the expressions for  $E(n_1)$  and higher moments of  $n_1(t)$  are rather involved and hence we shall not touch them here. It is clear however that since  $n_1(t)$  is a non-decreasing function of t,  $n_1(t)$   $\dagger$  M, a.s. as  $t \to \infty$ .

Again if T denotes the time it takes before either all the bacteria or all the phage particles are exhausted, depending upon whether  $n_{00} < v_{00}$  or  $n_{00} > v_{00}$ , we have

$$F(t) = Pr(T \le t) = P_{M}(t)$$

$$= \frac{v_{00}! n_{00}!}{(|n_{00} - v_{00}|)!} \sum_{i=0}^{M} C_{iM} \exp[-\lambda_{0}(n_{00} - i)(v_{00} - i)t], \quad (9)$$

with

$$F(\infty) = \frac{v_{00}! \; n_{00}!}{(|n_{00}-v_{00}|)!} \; C_{MM} = 1; \; F(0) = \sum_{i=0}^{M} \; C_{iM} = 0 \; . \tag{10}$$

From (9), one can easily find the moments of T, for instance

$$E(T) = \frac{v_{00}! \ n_{00}!}{(|n_{00}-v_{00}|)!} \sum_{i=0}^{M-1} \frac{-C_{iM}}{\lambda_0(n_{00}-i)(v_{00}-i)}. \tag{11}$$

# 3. Some limiting results and comparison between the two models

For the case with r=1, we must take  $\beta=-\alpha=\lambda_0$ , so that under model B,  $\nu_0(t)$  of (1) assumed to be nonrandom is given by

$$v_0(t) = \frac{v_{00}(n_{00} - v_{00}) \exp[-\lambda_0(n_{00} - v_{00})t]}{n_{00} - v_{00} \exp[-\lambda_0(n_{00} - v_{00})t]}.$$
 (12)

Under model B,  $n_1(t)$  turns out to be a binomial random variable. More specifically, if  $p_k(t)$  denotes  $Pr[n_1(t) = k]$  under model B, then from [1] we have for  $k = 0, 1, \dots, n_{00}$ 

$$p_k(t) = {n_{00} \choose k} a^k (1-a)^{n_{00}-k},$$
 (13)

where

$$a = \frac{v_{00}(1 - \exp[-\lambda_0(n_{00} - v_{00})t])}{n_{00} - v_{00} \exp[-\lambda_0(n_{00} - v_{00})t]} . \tag{14}$$

It may be remarked here that because of the introduction of a deterministic element in model B (namely, treating  $\nu_0(t)$  as nonrandom unlike in model A), one may be tempted to conclude that variance of  $n_1(t)$  should be smaller under model B than under model A. This however is not necessarily true as will be

exhibited below specially for the case where  $v_{00} < n_{00}$ , the case which arises fairly commonly in practice. One simple explanation for this is as follows: when  $v_{00} < n_{00}$ , whereas one starts with  $v_{00}$  phage particles at time zero and the number  $v_{0}(t)$  decreases with t deterministically under model B, there is always a positive probability of  $n_{1}(t)$  taking a value greater than the available total number  $v_{00}$  of phage particles; in fact

$$Pr(h_{1}(t) > v_{00}) = 1 - \sum_{k=0}^{v_{00}} p_{k}(t)$$

$$= n_{00} {n_{00}-1 \choose v_{00}} \cdot \int_{0}^{a} x^{v_{00}} (1-x)^{n_{00}-v_{00}-1} dx . \qquad (15)$$

It is this scatter of the distribution of  $n_1(t)$  beyond point  $v_{00}$  that is partly responsible for a greater variability in  $n_1(t)$  under model B than that under model A.

In the following we shall study the behavior of the distribution of  $n_1(t)$  under models A and B for three different limiting cases: (i) when  $t\to\infty$  (ii) when  $n_{00}\to\infty$  and  $\lambda_0\to0$  such that  $n_{00}\lambda_0\to\delta$  and (iii) when  $\nu_{00}\to\infty$  and  $\lambda_0\to0$  such that  $\nu_{00}\lambda_0\to\mu$ .

$$\lim_{t \to \infty} p_k(t) = {n_{00} \choose k} \left(1 - \frac{v_{00}}{n_{00}}\right)^{n_{00} - k} \left(\frac{v_{00}}{n_{00}}\right)^k . \tag{16}$$

Clearly in this case then, for large t, the variance of  $n_1(t)$  under model A is neglible; whereas under model B it is quite significant, unless  $v_{00} \approx n_{00}$ .

<u>Case (ii)</u>. If we let  $n_{00} \to \infty$  and  $\lambda_0 \to 0$  in such a manner that  $n_{00}\lambda_0 \to \delta$ , then we find under model A, for  $k=0,\,1,\,\cdots,\,\nu_{00};$  that

$$\lim P_{k}(t) = {\binom{v_{00}}{k}} e^{-\delta(v_{00}-k)t} (1 - e^{-\delta t})^{k} . \qquad (17)$$

Thus the random variable  $n_1(t)$  tends to be binomially distributed in the limit, with

$$E(n_1(t)) = v_{00}(1 - e^{-\delta t}); Var(n_1(t)) = v_{00} e^{-\delta t}(1 - e^{-\delta t})$$
 (18)

The situation is somewhat different under the simplified model B when we let  $n_{00} \to \infty$  and  $\lambda_0 \to 0$  in a similar manner. Here the limiting distribution is Poisson with parameter  $\nu_{00}(1-e^{-\delta t})$  so that for  $k=0,1,2,\cdots$ ,

$$\lim p_{k}(t) = \frac{1}{k!} \left[ v_{00}(1 - e^{-\delta t}) \right]^{k} e^{-v_{00}(1 - e^{-\delta t})}, \quad (19)$$

and in the limit

$$E(n_1(t)) = v_{00}(1 - e^{-\delta t}) = Var(n_1(t))$$
 (20)

On comparing (18) and (20), we find that whereas the  $E(n_1(t))$  is same for both models,  $Var(n_1(t))$  is again found to be smaller under model A than that under model B.

<u>Case (iii)</u>. If instead we let  $v_{00} \to \infty$  such that  $\lambda_0 v_{00} \to \mu$ , one finds as expected that the limiting distributions of  $n_1(t)$  under the two models coincide; the common limiting distribution is binomial with the

$$Pr(n_1(t) = k) = {n_{00} \choose k} e^{-\mu(n_{00}-k)t} (1 - e^{-\mu t})^k; \qquad (21)$$

for  $k = 0, 1, \dots, \nu_{00}$ .

In conclusion, we may remark that in general the simplified model B appears to be a good approximation to the stochastic model A, as far as the distribution of  $n_1(t)$  is concerned, only when  $\nu_{00}$  is much larger than  $n_{00}$ . However this is restricted only to the case with r=1; for the case with r>1, the present results are only suggestive.

### REFERENCES

- [1] Gani, J. (1965). Stochastic phage attachment to bacteria.

  Biometrics, 21, No. 1, 134-39.
- [2] Gani, J. (1965). Stochastic models for bacteriophage.

  J. Appl. Prob. 2, 225-268.
- [3] Yassky, D. (1962). A model for the kinetics of phage attachment to bacteria in suspension.

  Biometrics, 18, 185-91.