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A BATCH ARRIVAL QUEUE PROVIDING A CLASS OF TRUNCATED GEOMETRIC DISTRIBUTION FOR MODELING DISTRIBUTION OF ANIMAL POPULATIONS

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Abstract. We consider a batch arrival queueing system $M^{(i)}/M/1/m/$ of varying cluster arrival sizes I . The arrival process thus constitutes an independent compound Poisson stream of rate λ_r where

$$r = \sum_{i=1}^{\infty} i\alpha_i, \quad pr(I = i) = \alpha_i \quad (i \geq 1)$$

and $pr(I \geq i) = \beta_i$ with $\beta_k = 0$ for $k \leq 0$.

Acceptance into system is further limited by available space m thus implying a truncation of an otherwise infinite domain.

With the aid of certain combinatoric analysis of partitions and compositions the steady state distributions under various forms of arrival size pattern have been explicitly obtained in terms of system specifications. It is demonstrated that the results can perfectly provide one more class of truncated geometric distribution for a less idealistic modeling of the complex natural process of aggregation, congregation and abundance for such animals as soil microarthropods. A numerical illustration is provided using some copious data from the biological literature.

1. INTRODUCTION

Queueing system of the form $M^{(i)}/M/1/m/$ where units arrive in compound but truncated streams of various sizes (I), acceptances are limited by available space m as units in excess of those to fill up space are allowed to overflow and units depart singly are common in practice. Incidentally this may model the natural spatial and temporal distribution of microorganisms in certain instances. Soil microarthropods may arrive into an appropriate sampling unit of a discrete habitat in batches of various sizes.

The arrival sizes may be limited by the sampling unit and plan, and such other inherent differences in the ecology of the various species as represented by their average ambit and reaction to biotic and abiotic factors in the environment. In other words differences in spatial distribution may be attributed to the physiognomy and other soil characteristics of the forest as well as other conditions as temperature and moisture content in the different seasons. The species also die or disappear from the sampling unit at specific rates depending on the share for the species or niche from a complex resource apportioning mechanism in a community. The result is that one specie may aggregate while another may not and the species that strongly aggregate under a microenvironmental condition may only weakly aggregate under a different latitudinal pattern. The various conditions can be captured by the choice of birth or arrival rates λ , the mean arrival size r , death or departure rates μ and the available space m for the birth and death queueing model. We assume that $p_r \{I = i\} = \alpha_i, p_r \{I \geq i\} = \beta_i$ such that the mean bulk arrival size

$$r = \sum_{i=1}^{\infty} i\alpha_i$$

We also define a somewhat truncated mean

$$r_k = \sum_{i=1}^k \beta_i = \sum_{i=1}^{k-1} i\alpha_i + k\beta_k = r - \sum_{i=k}^{\infty} (i - k) \alpha_i$$

Readily available in the literature are such relevant results as the Pollaczec-khinchin $P - K$ formula (*Kleinrock, 1975*) for specific time- point steady -state distribution of

queue size for $M^{(x)}/M/c$, $M^{(x)}/M/c/c$ /loss system as well as such other generalisations as $M^{(x)}/G/1$ with bulk arrival (*Medhi,1991*). Our contribution is to utilise a simple combinatoric interpretation for solving for bulk systems of varying or fixed cluster or batch sizes. This may also clearly bring out the relevance of the model to biological and other population systems. It is important to note that the $P - K$ mean value formula actually shows that the mean queue length for an $M/G/1$ grows linearly with the squared coefficient variation of the service time distribution, and that the coefficient of variation for any distribution is a measure of its aggregation. Also this can generally be increased by sending a unit through a parallel arrangement of queues. Our own results suggest a weighted combination of truncated geometric distributions may be an appropriate alternative model for spatial distribution of such animal populations as soil arthropods that have been poorly fit by a pure geometric distribution (*Maguran,1988*).

2. THE SYSTEM EQUATIONS

We denote as follows:

q_j = The steady- state probability of j ($0 \leq j \leq m$) units in the queue at a random time point.

Q_j = The corresponding cumulative probability of j or less units in the queue.

$G_{(j)}$ = A function of system parameters λ , μ and β which is proportional to the steady-state distribution of units in the system (as identified shortly).

The steady - state difference equations for our $M^{(i)}/M/1/m/$ system are given by

$$\begin{aligned}\lambda q_0 &= \mu q_1 \\ q_j (\lambda + \mu) &= \mu q_{j+1} + \lambda \sum_{k=0}^{j-1} q_k \alpha_{j-k}, \quad 0 < j < m \\ q_m \mu &= \lambda \sum_{k=0}^{m-1} q_k \beta_{m-k}\end{aligned}$$

The system thus satisfies the equation

$$q_j = \rho \sum_{k=0}^{j-1} q_k \beta_{j-k}, \quad j = 1, 2, \dots, m \quad (0)$$

where $\rho = \lambda/\mu$, or

$$q_j = q_0 G(j), \quad j = 0, 1, \dots, m \quad (1)$$

where

$$G(j) = \rho \sum_{k=1}^j G(j-k) \beta_k \quad j = 1, 2, \dots, m \quad (2)$$

with $G(0) = 1$, $\beta_k = 0$ ($k \leq 0$) so that

$$q_j = \frac{G(j)}{\sum_{j=0}^m G(j)} \quad j = 0, 1, \dots, m \quad (3)$$

and

$$q_0^{-1} = \sum_{j=0}^m G(j)$$

We note that the first few terms for $G(j)$ are

$$\begin{aligned} G(0) &= 1 \\ G(1) &= \rho\beta_1 \\ G(2) &= \rho\beta_2 + (\rho\beta_1)^2 \\ G(3) &= \rho\beta_3 + 2\rho^2\beta_1\beta_2 + (\rho\beta_1)^3 \\ G(4) &= \rho\beta_4 + \rho^2(2\beta_1\beta_3 + \beta_2^2) + 3\rho^3\beta_1^2\beta_2 + (\rho\beta_1)^4 \\ G(5) &= \rho\beta_5 + 2\rho^2(\beta_1\beta_4 + \beta_2\beta_3) + 3\rho^3(\beta_1^2\beta_3 + \beta_1\beta_2^2) \\ &\quad + 4\rho^4\beta_1^3\beta_2 + (\rho\beta_1)^5 \\ G(6) &= \rho\beta_6 + \rho^2(2\beta_1\beta_5 + 2\beta_2\beta_4 + \beta_3^2) \\ &\quad + \rho^3(6\beta_1\beta_2\beta_3 + \beta_2^3 + 3\beta_1^2\beta_4) + \rho^4(6\beta_1^2\beta_2^2 + 4\beta_1^3\beta_3) \\ &\quad + 5\rho^5\beta_1^4\beta_2 + (\rho\beta_1)^6 \end{aligned} \quad (4)$$

In general $G(j)$ can be generated by the number of compositions for the composed number j (for the different partitions) with the convention of using exponents for repeated parts. Of course, the number of compositions of the composed number j into k parts is given by $\binom{j-1}{k-1}$ so that, for example, the number 5 has 6 compositions into 3 parts namely: 113, 131, 311, 122, 212, and 221 as simply identified by $3(\beta_1^2\beta_3 + \beta_1\beta_2^2)$ in the expression for $G(5)$. In short $G(j)$ is given by

$$G(j) = \sum_{k=1}^j \rho^k \sum_{\Lambda(j,k)} \prod_{i=1}^k \beta_i^{n_i}, \quad j = 1, 2, \dots \quad (5)$$

where the inner summation is over the $\binom{j-1}{k-1}$ compositions in $\Lambda(j, k)$ = (compositions such that $\sum_{i=1}^k n_i = j$), $n_i = 0, 1, 2, \dots$ and $G(0) = 1$.

3. SPECIAL CASES OF FIXED ARRIVAL SIZE (l)

It is instructive to note that the general case of varying arrival is only some convex combination of the special cases of fixed l sized system when arrivals are in batches of fixed bulk size l ($l = 1, 2, \dots$) when $\beta_i = 1$ for $i = 1, 2, \dots, l$ and $\beta_i = 0$ for $i > l$.

We denote as follows:

$q_{jl} = (q_j, \text{ for particular fixed } l \text{ sized system})$

$Q_{jl} = (Q_j, \text{ for particular fixed } l \text{ sized system})$

$G_l(j) = (G(j), \text{ for particular fixed } l \text{ sized system}), j = 0, 1, \dots, m$

$G(l, k, j,) = \text{number of compositions of } j \text{ into exactly } k \text{ } (k < j) \text{ parts no part of which exceeds } l,$

$[x] = \text{integral part of } x$

The function $G_l(j)$ is given by inspection of equations (4) as

$$G_l(j) = \sum_{k=1}^j G(l, k, j) \rho^k, \quad j = 1, 2, \dots, m; l = 1, 2, \dots \quad (6)$$

with $G(0) = 1$. The function $G(l, k, j,)$ can be identified as the number of options in the classical problem of dividing a line of k elements to give j sections of interval but with the maximum number of elements contained in a section being l . The functions $G(l, k, j)$ are given by the coefficient of x^j in the expansion of $(x + x^2 + \dots + x^l)^k$. Further more the functions $G(l, k, j)$ are given by the recurrence

$G(l, 0, 0) = 1, \quad G(l, k, j) = 0, \quad j \geq k + 1$ and

$$G(l + 1, k, j) = \sum_{r=0}^{j-k} \binom{k}{r} G(l, r, j - k) \quad (7)$$

so that $G(l, k, j,)$ is explicitly given (see Barton and David, 1959) by

$$G(l, k, j) = \sum_{i=0}^a \binom{k}{i} (-1)^i \binom{j - li - 1}{k - 1} \quad (8)$$

with $a = \min(k, [(j - k)/l])$ and $j - k + 1 \geq l \geq [(j + k - 1)/k]$. We note in passing that

(i) Recurrence relation (7) follows from the identity

$$(x + x^2 + \dots + x^{l+1})^k = x^k \sum_{r=0}^k \binom{k}{r} (x + x^2 + \dots + x^l)^r$$

(ii) Equation (8) follows from a recursive application of relation (7)

(iii) Equation (8) is easy to evaluate for small j and k , and it is also widely tabulated in the literature (*Smart, 1976*) for various l , j and k . For $l = 3$, for example, the relevant points are

$$G(3, 1, 5) = G(3, 2, 5) = 0, G(3, 3, 5) = 6, G(3, 4, 5) = 4 \text{ and } G(3, 5, 5) = 1.$$

(iv) For the some what extreme cases of $l = 1$ and $l = m$ in particular a quick inspection of the pattern in equations (4) or (5) gives

$$G(1, j, j) = 1, \quad G(1, k, j) = 0 \quad (9)$$

for $k \neq j$ and $G(m, k, j) = \binom{j-1}{k-1}$ giving straight away (following equations(3))

$$G_1(j) = \rho^j \text{ so that } q_{j1} = \frac{(1-\rho)\rho^j}{1-\rho^{m+1}} = q_{01}\rho^j, \quad j \geq 1 \text{ and}$$

$$G_m(j) = \rho(1+\rho)^{j-1} \quad (10)$$

so that $q_{jm} = \rho(1+\rho)^{j-1-m} = q_{om}\rho(1+\rho)^{j-1}$, $j \geq 1$ where $q_{01} = (1-\rho)/(1-\rho^{m+1})$ and $q_{om} = 1/(1+\rho)^m$

(v) A direct application of equations (7) and (9) (or alternatively (8)) gives, for the next case of $l = 2$, the function

$$G(2, k, j) = \binom{k}{j-k} \text{ and subsequently by equation(3) and (6)}$$

$$G_2(j) = \sum_{k=\lceil(j+1)/2\rceil}^j \binom{k}{j-k} \rho^k \text{ so that}$$

$$q_{j2} = q_{02} \sum_{k=\lceil(j+1)/2\rceil}^j \binom{k}{j-k} \rho^k, \quad j \geq 1 \quad (11)$$

where

$$q_{02}^{-1} = \sum_{k=0}^m \left(2^k - \sum_{j=m-k+1}^m \binom{k}{j} \right) \rho^k$$

A typical value for q_{02} , when $m = 5$, is $q_{02} = (1 + 2\rho + 4\rho^2 + 7\rho^3 + 5\rho^4 + \rho^5)^{-1}$ with $q_{12} = \rho q_{02}$ and other points given by the identity

$$q_{j2} = \rho(q_{j-2,2} + q_{j-1,2}), \quad j \geq 2 \quad (12)$$

(vi) A handy way of obtaining $G_l(j)$ and consequently q_{jl} for small m or l close to m is to use some set of recursive relationships. A particularly useful set is

$$\begin{aligned} G_{l+1}(j) &= G_l(j), & j \geq l \\ G_{l+1}(l+1) &= G_l(l+1) + \rho \\ G_{l+2}(l+2) &= G_l(l+2) + 2\rho^2 \end{aligned} \quad (13)$$

(vii) In any case the nested equation (0) gives, for the queue size distribution, in the general l case, the nested result

$$q_{jl} = \rho \sum_{s=1}^{j'} q_{j-s,l}, \quad j \geq 1$$

or

$$G_l(j) = \rho \sum_{s=1}^{j'} G_l(j-s), \quad j \geq 1$$

where $j' = \min(j, l)$, or equivalently,

$$q_{jl} = \begin{cases} \rho^j(1+\rho)Q_{jl}, & 1 \leq j \leq l \\ \rho(1+\rho)(Q_{jl} - Q_{j-l-1}), & j > l \end{cases} \quad (14)$$

Equation (14) connects the probability distribution q_{jl} and the cumulative probability distribution Q_{jl} so that a graph of q_{jl} against Q_{jl} , for $j = 1$ to l , is a straight line of gradient $\rho/(1+\rho)$. It thus provides a basis for a graphical estimation or any other estimation of ρ .

Furthermore, we claim that equation (14) indicates that the steady state queue size distributions q_{jl} for general l consists of a linear piece l for $1 \leq j \leq l$ and “out of step” jumps at $j = 0, l+1, l+2, \dots, m-1, m$. This is essentially a truncated geometric distribution. For $l = m$ there is only one jump at $j = 0$, there is one additional jump at $j = m$ for $l = m - 1$ and two additional jumps at $j = m$ and $j = m - 1$ for $l = m - 2$.

4. DERIVATIONS OF QUEUEING MEASURES FOR (l) CLOSE TO (m)

Three measures of interest for ecological applications for each fixed batch size l are the empty state probability q_{0l} , the k^{th} moment $E[X_l^k]$ for the number X_l of units in the queue and the information entropy $H(X_l)$. The measures are completely determined by the combinatoric functions $G_l(j)$ as follows:

$$q_{0l} = \left(\sum_{j=1}^m G_l(j) \right)^{-1}, \quad E[X_l^k] = q_{0l} \sum_{j=0}^m j^k G_l(j)$$

$$H(X_l) = -\ln q_{0l} - q_{0l} \sum_{j=0}^m G_l(j) \ln G_l(j) \quad (15)$$

To examine the effect of the closeness of l to m we establish connections between the different measures for $l = m - 2$, $l = m - 1$, $l = m$. Incidentally the results for general l are derivable from those of $l = m$ with a little algebra. From equation (10)

$$G_m(j) = \begin{cases} 1, & j = 0 \\ \rho(1 + \rho)^{j-1}, & 1 \leq j \leq m \end{cases}$$

Putting $l = m - 1$ or $l = m - 2$ in equation (13), we have

$$G_{m-1}(j) = \begin{cases} G_m(j), & 0 \leq j \leq m - 1 \\ G_m(m) - \rho, & j = m \end{cases}$$

while

$$G_{m-2}(j) = \begin{cases} G_m(j), & 0 \leq j < m - 2 \\ G_m(m - 1) - \rho, & j = m - 1 \\ G_m(m) - 2\rho^2, & j = m \end{cases} \quad (16)$$

It follows by equations (3) and (16) that

$$q_{om-1}^{-1} = q_{om}^{-1} - \rho, \quad q_{om-2}^{-1} = q_{om}^{-1} - \rho - 2\rho^2$$

so that by equation (10), we obtain the empty state probabilities as;

$$\begin{aligned} q_{om} &= (1 + \rho)^{-m} \\ q_{om-1} &= ((1 + \rho)^m - \rho)^{-1} \\ q_{om-2} &= ((1 + \rho)^m - \rho(1 + 2\rho))^{-1} \end{aligned} \quad (17)$$

The result is that we have as members of a class of truncated piecewise geometric distributions: For $l = m$,

$$q_{jm} = \begin{cases} (1 + \rho)^{-m}, & j = 0 \\ q_{0m}\rho(1 + \rho)^{j-1}, & 1 \leq j \leq m \end{cases} \quad (18)$$

Also for $l = m - 1$,

$$\begin{aligned} q_{om}(1 - \rho q_{om})^{-1} &= \frac{1}{(1 + \rho)^{m - \rho}} \quad j = 0 \\ q_{jm-1} &= q_{om-1}G_m(j) = q_{jm}(1 - \rho q_{om}) = \frac{\rho(1 + \rho)^{j-1}}{(1 + \rho)^{m - \rho}} \quad 1 \leq j \leq m - 1 \\ q_{om-1}(G_m(m) - \rho) &= \frac{q_{mm} - \rho q_{om}}{1 - \rho q_{om}} = \frac{\rho(1 + \rho)^{m-1-1}}{(1 + \rho)^{m - \rho}} \quad j = m \end{aligned} \quad (19)$$

and for $l = m - 2$

$$q_{jm-2} = \begin{cases} q_{om}(1 - \rho q_{om}(1 + 2\rho))^{-1}, & j=0 \\ q_{om-2}G_m(j) = q_{jm}(1 - \rho q_{om}(1 + 2\rho))^{-1}, & 1 \leq j \leq m - 2 \\ q_{om-2}(G_m(m - 1) - \rho) = (q_{m-1m} - \rho q_{om})(1 - \rho q_{om}(1 + 2\rho))^{-1}, & j=m-1 \\ q_{om-2}(G_m(m) - 2\rho^2) = (q_{mm} - 2\rho^2 q_{om})(1 - \rho q_{om}(1 + 2\rho))^{-1}, & j=m \end{cases} \quad (20)$$

Equations (18), (19) and (20) give three options for distributions that can be used to fit data once the value of m is settled. Apparently the closer l is to m the lower the value of q_{ol} for the same ρ . The less batchy an animal is the higher the chance of finding a quadrat of sampling without the animal, all other things (λ, μ) balancing out.

The k^{th} moment for the steady state number in the queue at random time point is given for $l = m$ by

$$\begin{aligned} E[X_m^k] &= q_{om}\rho \sum_{j=1}^m (1+\rho)^{j-1} j^k \\ &= q_{om}\rho \left(1 + \sum_{j=1}^{m-1} (1+\rho)^j \sum_{r=0}^k \binom{k}{r} j^r \right) \\ &= -q_{om} + (1+\rho) \sum_{r=0}^k \binom{k}{r} (E[X_m^r] - m^r \rho (1+\rho)^{m-1}) \end{aligned} \quad (21)$$

so that

$$E[X_m^o] = 1, \quad E[X_m] = m - \frac{1}{\rho} + \frac{1}{\rho(1+\rho)^m}$$

and

$$E[X_m^k] = (m+1)^k - \frac{(1+\rho)}{\rho} \sum_{r=0}^{k-1} E[X_m^r] \binom{k}{r} + \frac{1}{\rho(1+\rho)^m}, \quad k \geq 1 \quad (22)$$

Similarly, $E[X_{m-1}^k]$ is obtainable from

$E[X_{m-1}^k] = \sum_{j=1}^m j^k q_{jm-1}$, which by relations (19) gives

$$E[X_{m-1}^k] = \frac{1}{1-\rho q_{om}} (E[X_m^k] - \rho q_{om} m^k) \quad (23)$$

which combined with (22) gives

$$E[X_{m-1}^k] = (m+1)^k - \frac{1+\rho}{\rho} \sum_{r=0}^{k-1} E[X_{m-1}^r] \binom{k}{r} + \frac{1/\rho + m^k - (m+1)^k}{(1+\rho)^m - \rho} \quad (24)$$

with $E[X_{m-1}] = m + 1/\rho - (1-\rho)/\rho((1+\rho)^m - \rho)$

In the same way relations (19) give, for $l = m - 2$,

$$\begin{aligned} E[X_{m-2}^k] &= \frac{1}{1-\rho q_{om}(1+2\rho)} (E[X_m^k] - \rho q_{om}(m-1)^k - 2\rho^2 q_{om} m^k) \\ &= (m+1)^k - \frac{1+\rho}{\rho} \sum_{r=0}^{k-1} E[X_{m-2}^r] \binom{k}{r} + \frac{\frac{1}{\rho} + ((m-1)^k - m^k) + \rho(m^k - (m+1)^k)}{(1+\rho)^m - \rho(1+2\rho)} \end{aligned} \quad (25)$$

with

$$E[X_{m-2}] = m - \frac{1}{\rho} + \frac{1 - \rho - \rho^2}{\rho((1 + \rho)^m - \rho(1 + 2\rho))}$$

Equations (22), (23), (24), and (25) explicitly give all moments (including means and variances) for the number X_i in the queue at random time points for $l = m - 2$, $m - 1$, and m . To establish relations between information entropy as batch size l gets closer to maximum available space m , we note from (14) that

$$H(X_l) + \ln q_{ol} + q_{ol} \sum_{j=0}^m G_l(j) \ln G_l(j) = 0 \quad \text{for all } l \quad (26)$$

Equating relation (26) for $l = m$ and $l = m - 1$ and applying the relations (16), we obtain the connection

$$\frac{H(X_m) + \ln q_{om} + q_{mm} \ln G_m(m)}{q_{om}} = \frac{H(X_{m-1}) + \ln q_{om-1} + q_{mm-1} \ln G_{m-1}(m)}{q_{om-1}} \quad (27)$$

Similarly by equating relation (26) for $l = m$ and $l = m - 2$ and applying relations (16), we obtain the connection

$$\begin{aligned} & \frac{H(X_m) + \ln q_{om} + q_{m-1m} \ln G_{m-2}(m-1) + q_{mm} \ln G_m(m)}{q_{om}} \\ &= \frac{H(X_{m-2}) + \ln q_{om-2} + q_{m-1,m-2} \ln G_{m-2}(m-1) + q_{mm-2} \ln G_{m-2}(m)}{q_{om-2}} \end{aligned} \quad (28)$$

Equations (27) and (28) provide a basis for studying the effect of natural processes that may manifest as increasing the batch size l toward m on such natural phenomena as aggregation.

5. DERIVATION OF MOMENTS FOR LOW (l)

In anticipation of the requirements for a numerical illustration in Section 6 we give the k^{th} moments for the queue size X_1 and X_2 corresponding to systems for $l = 1$ and $l = 2$. The k^{th} moment $E[X_1^k]$ for X_1 is given simply from equations (9) and (15) by

$$E[X_1^k] = \frac{1 - \rho}{1 - \rho^{m+1}} \sum_{j=1}^m j^k \rho^j$$

With a little algebra, this gives

$$E[X_1^k] = \frac{\rho}{1-\rho} \sum_{j=0}^{k-1} \binom{k}{j} E[X_1^j] - \frac{\rho^{m+1}}{1-\rho^{m+1}} (m+1)^k, \quad k \geq 1 \quad (29)$$

so that, for example, the mean $E[X_1]$ and variance $\text{var}[X_1]$ are given by (as well known)

$$E[X_1] = \frac{\rho}{1-\rho} - \frac{(m+1)\rho^{m+1}}{1-\rho^{m+1}} \quad (30)$$

$$\text{Var}[X_1^k] = \frac{\rho}{1-\rho} + \left(\frac{\rho}{1-\rho}\right)^2 - \frac{(m+1)^2 \rho^{m+1}}{(1-\rho^{m+1})^2} \quad (31)$$

The k^{th} moment $E[X_2^k]$ for queue size X_2 is similarly given by

$$\begin{aligned} E[X_2^k] &= q_0 \rho \left(1 + \sum_{j=2}^m j^k (G_2(j-1) + G_2(j-2))\right) \\ &= \frac{\rho}{1-2\rho} \left(\sum_{r=0}^{k-1} E[X_2^r] (1 + 2^{k-r}) \binom{k}{r} - A_k(m) - B_k(m)\right) \end{aligned} \quad (32)$$

where $A_k(m) = q_{m2} \left((m+2)^k + (m+1)^k\right)$, $B_k(m) = (m+1)^k q_{m-1,2}$ and with q_{m2} and $q_{m-1,2}$ given by equation (11).

In particular the first two moments for X_2 give

$$\begin{aligned} E[X_2] &= \frac{\rho}{1-2\rho} (3 - A_1(m) - B_1(m)) \text{ and} \\ \text{Var}[X_2] &= \frac{\rho}{1-2\rho} (5 - A_2(m) - B_2(m)) + \left(\frac{\rho}{1-2\rho}\right)^2 (9 - (A_1(m) + B_1(m))^2) \end{aligned} \quad (33)$$

6. NUMERICAL ILLUSTRATION

In Table 1 we reproduce for a revisit the frequency data on two cohabiting rare animals namely Centipede *Lithobius Crassipes* (L. koch) and the large wood louse *Philoscia muscorum* (scopoli) as collected from thirty-seven contiguous hexagonal quadrats (each of area $.08\text{m}^2$) of beech litter at Wythamwoods, near Oxford and reported by *Lloyd(1967)*. We demonstrate the potential in fitting steady state queue size denoted $X(l,m)$ to both sets of data. It is required that we estimate fixed arrival size l , ambit (or sample unit) m and ρ . Our distribution is amenable to various methods of estimation. We have adopted here the technique of constraining on the observed x_{ol}

| | L.Koch | L.Koch Fitted | Scopoli | Scopoli Fitted |
|-------------------|----------|-----------------------|----------|-----------------------|
| Count per quadrat | observed | X(1,3) $\rho = .5621$ | observed | X(2,5) $\rho = .3372$ |
| 0 | 18 | 18.000 | 15 | 15.0000 |
| 1 | 10 | 10.1172 | 5 | 5.0581 |
| 2 | 7 | 5.6866 | 9 | 6.7638 |
| 3 | 2 | 3.1962 | 4 | 3.9864 |
| 4 | 0 | 0.0000 | 2 | 3.6250 |
| 5 | 0 | 0.0000 | 2 | 2.5667 |
| X_2 with df | | .00290 2 | | 1.2061 3 |

Table 1: Goodness of fit of the proposed distributions X(1, 3) for L. Koch and X(2, 5) for Scopoli.

of empty quadrats and using the Newton's iterative scheme. Thus for the centipede (L.koch) we fix $l = 1$ and $m = 3$ and use the iterative equation

$$\rho_{n+1} = \rho_n - \frac{(1 - \rho_n)/(1 - \rho_n^{m+1}) - x_{oi}/\sum x_{i1})(1 - \rho_n^{m+1})^2}{(m + 1)(1 - \rho_n)\rho_n^m - (1 - \rho_n)^{m+1}}$$

with the starting value $\rho_0 = x_{m1}/x_{01}$ where x_{j1} is the observed frequency of species of size j . For the wood louse(scopoli) data we fix $l = 2$ and $m = 5$ and use the iterative equation

$$\rho_{n+1} = \rho_n + (c^{-1}(\rho_n) - x_{02}/\sum x_{i2})/c^{-2}(\rho_n)c'(\rho_n)$$

where $c(\rho) = 1 + 2\rho + 4\rho^2 + 7\rho^3 + 5\rho^4 + \rho^5$ and with the starting value $\rho_0 = x_{12}/x_{02}$. The choice of l and m is informed by the dynamics of the data and graphical application of equation (14). Both algorithms converge very smoothly and fastly (as early as step 2 in some cases). It would certainly appear that our proposed distribution perfectly fits L Koch data based on arrival in singles while it fits Scopoli data on arrival in pairs. We note that the larger the fitted value of l the higher the tendency for the species to crowd around itself. Our values of $l = 1$ for L. Koch and $l = 2$ for Scopoli also appear to be in the same line with Lloyd's (1967) observation that L. Koch is more locally random and less crowded than the Scopoli. The centipede is essentially a more lonely animal than the woodlouse. Further more our results (formula and fitting) give measures $\mu = .840$, $\sigma_2 = .960$ compared with sample values $\bar{x} = .811$, $s^2 = .856$ for the centipede as well as $\mu = 1.564$, $\sigma^2 = 2.692$ compared with sample

values $\bar{x} = 1.432$ and $s^2 = 2.245$ for the woodlouse. To the extent that we are dealing with small sizes these results recommend our model for favourable consideration for fitting purposes.

7. CONCLUSIONS

In this paper we have (a) provided a solution to the system equations for the $M^{(i)}/M/1/m$ system in situations of varying or fixed batch sizes in terms of our $G_l(j)$ functions (b) demonstrated the extent to which spatial distribution for animals can be fitted by the model subject to some system parameters and (c) suggested that in the likelihood that l can be chosen very close to m it may be reasonable to consider using a weighted combination of a class of truncated geometric distribution. This is an important step in the unending quest for models that provide less idealistic explanations for the complex natural processes of aggregation, congregation and abundance on soil microathropods.

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