

A DISCRETE TIME MODEL FOR A S-I-S INFECTIOUS DISEASE WITH A RANDOM NUMBER OF CONTACTS BETWEEN INDIVIDUALS

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Abstract—A chain-binomial deterministic model for the spread of an infectious disease of the S-I-S type is formulated that accounts explicitly for the distribution of the number of contacts made by each susceptible during one time interval. Under certain hypotheses, a threshold theorem for endemicity is derived, bounds for the endemic level are constructed, and the transient behavior of the epidemic process is investigated.

1. INTRODUCTION

In a recent paper, Ingenbleek and Lefèvre[1] have investigated a discrete time model for the interactive diffusion of an information in a social group. In the epidemiological context, this model can be used to describe the spread of an infectious disease of the S-I-S (susceptible-infectious-susceptible) type. More specifically, the chain-binomial process considered is the following Markov chain. A closed and homogeneously mixing population of N individuals is subdivided in two disjoint classes: the infectives, in number $I(t)$ at time t , and the susceptibles, in number $S(t) = N - I(t)$ at time t , $t = 0, 1, 2, \dots$. The propagation of the disease is governed by two independent processes. On the one hand, each of the $I(t)$ infectives has the probability g , $0 < g \leq 1$, to recover and return to the susceptible state at time $t + 1$ (recovery process). On the other hand, each of the $N - I(t)$ susceptibles becomes infectious at time $t + 1$ if he has at least one effective contact with an infective during $(t, t + 1]$; such a contact between two given individuals occurs with the probability p , $0 < p < 1$ (infection process). Consequently, given the state $I(t)$, $I(t + 1)$ is defined as the following sum of two independent binomial variables:

$$I(t + 1) \sim \text{Binomial}[I(t), 1 - g] + \text{Binomial}[N - I(t), 1 - (1 - p)^{I(t)}]. \quad (1)$$

The deterministic model associated with (1) is constructed in a phenomenological way by identifying the conditional expectation $E[I(t + 1) | I(t)]$ to $I(t + 1)$. Let us denote this quantity by $i(t + 1)$. We then obtain that $i(t + 1)$ obeys the following first-order difference equation:

$$i(t + 1) = (1 - g)i(t) + [N - i(t)][1 - (1 - p)^{i(t)}]. \quad (2)$$

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The reader is referred to Ingenbleek and Lefèvre[1] for a study and comparison of the stochastic and deterministic formulations.

A limitation of this model is that the infection process does not account for the distribution of the number of contacts made by each susceptible during one time interval. A similar criticism has been pointed out by Dietz and Schenzle[2] for the classical Reed–Frost epidemic model, which is a chain-binomial model of the S-I-R (susceptible-infectious-removed) type (see, e.g., Bailey[3]). The purpose of the present work is precisely to introduce this factor in the above model and to examine its implications for the propagation of the infectious disease. The problem will be discussed here only for the deterministic version of the model, but we hope to be able to treat the stochastic version in the near future.

The paper is structured as follows. We present in Sec. 2 the new modeling of the infection process. Under certain hypotheses, we derive in Sec. 3 a threshold theorem which states the conditions leading to an endemic situation; we then construct in Sec. 4 upper and lower bounds for the endemic level; and we finally investigate in Sec. 5 the transient behavior of the disease process.

2. MODELING OF THE INFECTION PROCESS

Let us consider the population of size N described in the introduction. Following Dietz and Schenzle[2], we suppose that during one time interval, each susceptible can make a random number R of contacts with other individuals of the population. The distribution of R is assumed independent of the number of infectives present; it can, however, depend on the population size N . We denote by $G(z) = \sum_{j=0}^{\infty} p_j z^j$, $0 \leq z \leq 1$, the probability generating function (PGF) of R , and for the sequel, we make the natural hypothesis $0 < E(R^2) < \infty$.

As announced, the present work is only concerned with the deterministic version of the model. Let us suppose that at time t , there are $i(t)$ infectives in the population. For simplicity, we omit the argument t in this section, and we denote by $y = y(t)$ the proportion of infectives at time t , that is, $y = i/N$. The probability for a given susceptible at t who meets another individual during $(t, t + 1]$ to have an infectious contact depends, of course, on the proportion y of infectives present at t . This probability is denoted by $\varphi(y)$, and we now specify its functional form. It is clear that most often, $\varphi(y) = \varphi y$, $0 < \varphi \leq 1$, which means that each infective can transmit the infectious agent independently and with the same probability φ . This is the hypothesis made implicitly by Dietz and Schenzle[2] (with $\varphi = 1$), and it corresponds to the standard case treated in the literature. This specification for $\varphi(y)$ will receive a particular attention in the next sections. In some situations, however, $\varphi(y)$ might have a more complicated nonlinear form, such as (i) $\varphi(y) = \varphi y^a$, $0 < \varphi \leq 1$, $a > 0$, or (ii) $\varphi(y) = \varphi by / (b - 1 + y)$, $0 < \varphi \leq 1$, $b > 1$. Similar types of interaction terms have been considered by Severo[4] and Capasso and Serio[5], respectively. In fact, a general hypothesis which seems reasonable in practice is that $\varphi(y)$ is a continuous increasing function of y , with $\varphi(0) = 0$ and $0 < \varphi(1) \leq 1$. This assumption is therefore retained for the sequel. In addition, for technical reasons, we will also suppose that the function $\varphi(y)$ is concave—this is verified, for example, if $\varphi(y)$ has the above expression (i) with $0 < a \leq 1$, or (ii). The case where $\varphi(y)$ is not concave leads to qualitatively different results and is not examined here.

Let us denote by C the random variable representing the total number of infectious contacts made by a given susceptible during one time interval. By adapting the argument of Dietz and Schenzle[2], we then deduce that the PGF of C during $(t, t + 1]$ is equal to

$$E(z^C | y) = G[1 - \varphi(y) + \varphi(y)z], \quad 0 \leq z \leq 1. \quad (3)$$

Finally, let us make the usual assumption that a given susceptible becomes infectious if he has at least one effective contact with an infective during one time interval. Thus a given susceptible at t will become infectious at $t + 1$ with the probability $P_1(y)$ given by

$$\begin{aligned}
 P_1(y) &= P[C \geq 1 | y] \\
 &= 1 - G[1 - \varphi(y)].
 \end{aligned}
 \tag{4}$$

It is interesting to show that this modeling of the infection process generalizes in some sense the one considered in the introduction.

Particular case. Let us suppose that $R \sim \text{Poisson}(\lambda N)$ and $\varphi(y) = \varphi y$. Putting $p = 1 - \exp(-\lambda\varphi)$, we obtain from (4) that

$$P_1(y) = 1 - (1 - p)^{Ny},
 \tag{5}$$

with $Ny = i$, which is precisely the interaction term introduced in (2). Therefore, the standard hypothesis of a constant probability p for an effective contact between any given pair of individuals can be viewed as corresponding to a particular case of the above modeling. This result has been pointed out and commented by Dietz and Schlenzle[2] (with $\varphi = 1$).

We close by mentioning that an extension of the model allowed by this approach consists in supposing that a susceptible becomes infectious if the number C of his infectious contacts is at least equal to $k + 1$, where k is a nonnegative integer. This situation has been studied by Lefèvre[6] in the case where $g = 1$ and $\varphi(y) = y$.

3. THRESHOLD THEOREM WHEN $\varphi(y)$ IS CONCAVE

Let us incorporate this new infection process in the deterministic epidemic model presented in the introduction. From (4), the recurrence relation (2) for $i(t)$ becomes

$$\begin{aligned}
 i(t + 1) &= (1 - g)i(t) + [N - i(t)]P_1[y(t)] \\
 &= (1 - g)i(t) + [N - i(t)]\{1 - G[1 - \varphi(y(t))]\}.
 \end{aligned}
 \tag{6}$$

Dividing (6) by N , we deduce that $y(t) = i(t)/N$ is solution of the first-order difference equation

$$y(t + 1) = f[y(t)],
 \tag{7}$$

where

$$f[y(t)] = (1 - g)y(t) + [1 - y(t)]\{1 - G[1 - \varphi(y(t))]\}.
 \tag{8}$$

We note that the function $f(y)$ is continuous and maps $[0, 1]$ into $[0, 1]$, with $f(0) = 0$ and $f(1) = 1 - g < 1$.

Since by hypothesis, $\varphi(y)$ is concave, it is directly verified that $f(y)$ is concave too. Consequently, we can now establish the following theorem which generalizes the theorem 2 proved by Lefèvre[6]. Let $m_1 = G'(1) = E(R)$.

Theorem 1. If $m_1\varphi'(0) \leq g$, the sequence $y(t)$ converges to 0 as $t \rightarrow \infty$ for any $0 \leq y(0) \leq 1$. If $m_1\varphi'(0) > g$, the function $f(y)$ has two fixed points, 0 and y^* , the last one being the positive root of the equation

$$y = (1/g)(1 - y)\{1 - G[1 - \varphi(y)]\}.
 \tag{9}$$

The state 0 is unstable, while the state y^* is globally stable in the sense that $y(t)$ converges to y^* as $t \rightarrow \infty$ for any $0 < y(0) \leq 1$.

Proof. As $f(y)$ is continuous and concave, with $f(0) = 0$ and $f(1) = 1 - g < 1$, the state 0 is necessarily a fixed point of $f(y)$, and there exists another fixed point $y^* > 0$ iff $f'(0) > 1$, that is, $m_1\varphi'(0) > g$. Clearly, y^* is the positive solution of (9) and is locally stable. By a theorem of Rosenkranz[7], a necessary and sufficient condition for the global stability of y^* is that if $f(y)$ has a maximum in $y_M \in (0, y^*)$, then $f[f(y)] > y$ for all $y \in (y_M, y^*)$. From (8), we find that $f'(y) > -1$ for all $y \in (0, 1)$, and it is easily seen that this inequality implies that the Rosenkranz condition is well satisfied.

Comments. The theorem states that if $m_1\varphi'(0) \leq g$, the disease dies out ultimately, while if $m_1\varphi'(0) > g$, the infection becomes endemic: This is the threshold phenomenon. The condition $m_1\varphi'(0) \geq g$ is rather intuitive. Indeed, it can be rewritten as $m_1\varphi(\epsilon) \leq g\epsilon$ as $\epsilon \rightarrow 0$ and consists thus in comparing the expected numbers of infectious contacts $[m_1\varphi(\epsilon)]$ and recoveries $[g\epsilon]$ during one time interval where the proportion of infectives is infinitely small [$y = \epsilon \rightarrow 0$]. An equivalent interpretation of the result is that the expected number of contacts m_1 has to be greater than a critical value $g/\varphi'(0)$ in order that the infection becomes endemic. We emphasize that this condition depends on the distribution of R only through its expectation m_1 . We note, however, that the temporal evolution of the disease and the endemic level y^* are function of the PGF of R . Finally, we remark that as m_1 is generally an increasing function of N , the theorem implies also that a sufficiently large population size is needed to maintain endemicity in the population. For example, in the particular case considered in Sec. 2 where $R \sim \text{Poisson}(\lambda N)$ and $\varphi(y) = \varphi y$, the critical population size is simply $g/\lambda\varphi$.

It is worth underlining that if $\varphi(y)$ is not concave, the threshold theorem 1 is no more valid. Indeed, in that case, the recurrence relation (7) can admit several positive fixed points, so that the asymptotic behavior of the disease process becomes more complex. This problem is actually under study.

4. ON THE ENDEMIC LEVEL WHEN $\varphi(y) = \varphi y$

Let us make the standard hypothesis $\varphi(y) = \varphi y$, and consider the situation where the infection becomes endemic, which occurs iff $m_1\varphi > g$. The endemic level y^* is then the positive root of Eq. (9), with $\varphi(y) = \varphi y$.

The explicit expression of y^* can only be obtained for some particular distributions for R . This is the case, for example, when the PGF of R is a fractional linear function (FLF). We recall that a FLF has the form

$$g(z; m_1, c) = 1 - m_1(1 - c) + m_1(1 - c)^2 z / (1 - cz), \quad 0 \leq z \leq 1, \quad (10)$$

with $m_1 = g'(1; m_1, c) > 0$ and $0 \leq c < 1$; it is a PGF iff $m_1(1 - c) \leq 1$. When the PGF $G(z)$ is a FLF of the type (10), some simple calculations give

$$P_1(y) = m_1(1 - c)\varphi y / (1 - c + c\varphi y),$$

and if $m_1\varphi > g$,

$$y^* = (m_1 - g/\varphi) / [m_1 + gc/(1 - c)]. \quad (11)$$

In particular, for $c = 0$, then $R \sim \text{Bernoulli}(m_1)$ and if $m_1\varphi > g$,

$$y^* = (m_1 - g/\varphi) / m_1.$$

For $m_1 = c/(1 - c)$, then $R \sim \text{Geometric}(1 - c)$ and if $m_1\varphi > g$,

$$y^* = (m_1 - g/\varphi)/m_1(1 + g).$$

These two cases will be reexamined in Sec. 5.

Generally, however, y^* cannot be determined explicitly. It is then useful to construct simple bounds for y^* in terms of some important parameters of the distribution of R . Another interest of these bounds comes from that quite often, it is difficult to know exactly the complete distribution of R . The two following theorems give such lower and upper bounds for y^* .

Theorem 2.

• Let $m_2 = G''(1) = E[R(R - 1)]$, and suppose that only m_1 and m_2 are known. Let

$$\begin{aligned} \alpha &= \text{the integer part of } (m_1 + m_2)/m_1, \\ A &= m_2/(\alpha + 1) - m_1(\alpha - 1)/(\alpha + 1), \\ B &= m_1 - m_2/\alpha, \\ C &= A + B = 2m_1/(\alpha + 1) - m_2/\alpha(\alpha + 1). \end{aligned} \tag{12}$$

Then the best lower bound for y^* is the state $y_{bl} = (1 - z_l)/\varphi$, where z_l is the root smaller than 1 of the equation $H_l(z) = 0$ with

$$H_l(z) = \varphi + [z - (1 - \varphi)][Az^{\alpha-1} + Bz^\alpha - (C + g)]/g, \quad 1 - \varphi \leq z \leq 1. \tag{13}$$

• Let $p_0 = G(0) = P(R = 0)$, and suppose that only m_1 and p_0 are known. Let

$$\begin{aligned} \beta &= \text{the integer part of } m_1/(1 - p_0), \\ \eta &= m_1 - \beta(1 - p_0). \end{aligned} \tag{14}$$

Then the best upper bound for y^* is the state $y_{bu} = (1 - z_u)/\varphi$, where z_u is the root smaller than 1 of the equation $H_u(z) = 0$ with

$$H_u(z) = \varphi + [z - (1 - \varphi)][\eta z^{\beta+1} + (1 - p_0 - \eta)z^\beta - (1 - p_0 + g)]/g, \quad 1 - \varphi \leq z \leq 1. \tag{15}$$

Proof. The construction of bounds for y^* involves bounding of the function $G(1 - \varphi y)$ in (9). We first derive the lower bound y_{bl} . Recently, Narayan[8] has obtained the best upper bound for a PGF $G(z) = \sum_{j=0}^{\infty} p_j z^j$, $0 \leq z \leq 1$, with $m_1 > 0$ and $m_2 < \infty$ fixed. This bound is a PGF $G_u(z)$, $0 \leq z \leq 1$, with $G'_u(1) = m_1$, $G''_u(1) = m_2$, and is given by

$$G(z) \leq G_u(z) = Az^{\alpha-1} + Bz^\alpha - C + 1, \quad 0 \leq z \leq 1, \tag{16}$$

where α, A, B, C are defined in (12). Inserting (16) in (8), we then find that

$$f[y(t)] \geq f_l[y(t)] = (1 - g)y(t) + [1 - y(t)]\{1 - G_u[1 - \varphi y(t)]\}.$$

Clearly, the function $f_l(y)$ has the same properties as $f(y)$, and the recurrence relation

$$y(t + 1) = f_l[y(t)]$$

has a positive fixed point y_{bl} iff $m_1\varphi > g$. We thus deduce that y_{bl} is the best lower bound for y^* when m_1 and m_2 are known. After some calculations, we obtain that $z_l = 1 - \varphi y_{bl}$ is the root smaller than 1 of the equation $H_l(z) = 0$ where $H_l(z)$ is given by (13). We note that the function $H_l(z)$ is convex, with $H_l(1 - \varphi) = \varphi$, $H_l(1) = 0$, and has a minimum in the interval $(1 - \varphi, 1)$. We now derive the upper bound y_{bu} . In his work, Narayan[8] has also obtained a lower bound for $G(z)$, $0 \leq z \leq 1$, in terms of the three first factorial moments. This bound is rather complicated and is not always a PGF. It is the reason why we have preferred another bound given by Heyde and Schuch[9] which is the best lower bound for a PGF $G(z) = \sum_{j=0}^{\infty} p_j z^j$, $0 \leq z \leq 1$, with $0 < m_1 < \infty$ and p_0 fixed. This bound is a PGF $G_l(z)$, $0 \leq z \leq 1$, with $G_l(1) = m_1$, $G_l(0) = p_0$, and is given by

$$G(z) \geq G_l(z) = \eta z^{\beta+1} + (1 - p_0 - \eta)z^{\beta} + p_0, \quad 0 \leq z \leq 1. \tag{17}$$

where β, η are defined in (14). Inserting (17) in (8), we find that

$$f[y(t)] \leq f_u[y(t)] = (1 - g)y(t) + [1 - y(t)]\{1 - G_l[1 - \varphi y(t)]\}.$$

By the same argument as for y_{bl} , we then deduce that y_{bu} defined above is the best upper bound for y^* when m_1 and p_0 are known. We note that the graph of $H_u(z)$ is similar to that of $H_l(z)$.

In theorem 3 below, we derive explicit lower and upper bounds for y^* . These bounds, however, are less tight than those obtained in the theorem 2.

Theorem 3 (in the notations of the theorem 2).

- Suppose that m_1 and m_2 are known. Then a lower bound for y^* is the state y_l given by the formula (11) where c takes the following value c_l :

$$c_l = [\alpha(\alpha - 1)m_1 + m_2]/\alpha(\alpha + 1)m_1. \tag{18}$$

- Suppose that m_1 and p_0 are known. Then an upper bound for y^* is the state y_u given by the formula (11) where c takes the following value c_u :

$$c_u = [\eta - m + \beta(\eta + m)]/(\eta + m)(\beta + 1). \tag{19}$$

Proof. To derive this result, we bound the function $G(1 - \varphi y)$ in (9) by using FLFs ww of the form (10). As shown by Lefèvre *et al.*[10], an upper bounding FLF for a PGF $G(z) = \sum_{j=0}^{\infty} p_j z^j$, $0 \leq z \leq 1$, with $m_1 > 0$ and $m_2 < \infty$ fixed is $g(z; m_1, c_l)$ with c_l given by (18), and a lower bounding FLF for $G(z)$, $0 \leq z \leq 1$, when $0 < m_1 < \infty$ and p_0 are fixed is $g(z; m_1, c_u)$ with c_u given by (19). Applying the same method as for the theorem 2 and then using the result (11), we finally get the theorem.

Table 1.

p_0	$g = 0.25$					$g = 0.75$				
	y_l	y_{bl}	y^*	y_{bu}	y_u	y_l	y_{bl}	y^*	y_{bu}	y_u
0.05	0.733	0.749	0.783	0.790	0.840	0.428	0.481	0.511	0.535	0.588
0.15	0.698	0.721	0.753	0.764	0.799	0.349	0.405	0.424	0.454	0.480
0.25	0.664	0.691	0.716	0.729	0.757	0.270	0.318	0.327	0.354	0.368
0.35	0.611	0.644	0.669	0.679	0.698	0.164	0.202	0.206	0.220	0.224
0.45	0.569	0.590	0.605	0.613	0.626	0.037	0.044	0.044	0.047	0.047
0.55	0.494	0.507	0.514	0.520	0.527	—	—	—	—	—
0.65	0.362	0.369	0.372	0.376	0.378	—	—	—	—	—
0.75	0.114	0.116	0.116	0.117	0.118	—	—	—	—	—

Table 2.

p_0	$g = 0.25$					$g = 0.75$				
	y_l	y_{bl}	y^*	y_{bu}	y_u	y_l	y_{bl}	y^*	y_{bu}	y_u
0.05	0.658	0.661	0.789	0.792	0.877	0.384	0.394	0.549	0.559	0.699
0.15	0.638	0.648	0.765	0.773	0.849	0.347	0.380	0.496	0.529	0.630
0.25	0.611	0.631	0.733	0.749	0.815	0.300	0.352	0.429	0.481	0.545
0.35	0.579	0.611	0.692	0.716	0.767	0.240	0.300	0.341	0.397	0.431
0.45	0.535	0.577	0.636	0.666	0.702	0.157	0.207	0.221	0.265	0.276
0.55	0.472	0.518	0.556	0.585	0.610	0.035	0.047	0.048	0.059	0.059
0.65	0.360	0.408	0.429	0.449	0.461	—	—	—	—	—
0.75	0.182	0.197	0.200	0.209	0.210	—	—	—	—	—

It is very simple to compute these bounds numerically. For illustration, some examples are presented below. The states $y_l, y_{bl}, y^*, y_{bu}, y_u$ are given for different values of p_0 and g in the case where $\varphi = 1$ and $R \sim \text{Poisson}(m_1)$ (Table 1) or $R \sim \text{Geometric}(1 - c)$ (Table 2).

5. THE TRANSIENT BEHAVIOR WHEN $\varphi(y)$ IS CONCAVE

The iterated values of $y(t)$ can be computed directly from (7) and (8). In theorem 4 below, we show that when $\varphi(y)$ is concave, the sequence $y(t)$ converges either monotonically (to 0 or y^*) or by oscillating around y^* . The important factors of the discussion are the existence or not of the fixed point y^* , the existence or not of an interior maximum for $f(y)$ in $y_M \in (0, 1)$, and the relative positions of y^* and y_M . The proof of the theorem is immediate and omitted. We just remark that $f(y)$ has a maximum in $y_M \in (0, 1)$ iff $f'(1) < 0$, that is, $G[1 - \varphi(1)] < g$.

Theorem 4. Three qualitatively different transient behaviors for $y(t)$ are possible.

- Case (I): $m_1\varphi'(0) \leq g$. Then $y(t)$ decreases to 0 for any $0 \leq y(0) \leq 1$.
- Case (II): $m_1\varphi'(0) > g$ and either $G[1 - \varphi(1)] \geq g$, or $G[1 - \varphi(1)] < g$ and $y_M \geq y^*$. Then $y(t)$ increases to y^* if $0 < y(0) \leq y^*$, and decreases to y^* if $y^* \leq y(0) \leq y_0$, where y_0 is either the value 1 if $G[1 - \varphi(1)] \geq g$, or $G[1 - \varphi(1)] < g$ and $y^* \leq 1 - g$, or the largest root of the equation $f(y) = y^*$, $y \in (0, 1)$, if $G[1 - \varphi(1)] < g$ and $y_M \geq y^* > 1 - g$. If $y_0 < y(0) \leq 1$, $y(1) < y^*$ and $y(t)$, $t \geq 2$, increases to y^* .
- Case (III): $m_1\varphi'(0) > g$, $G[1 - \varphi(1)] < g$ and $y_M < y^*$. Then $y(t)$ converges by oscillating around y^* as soon as it takes a value in the interval $(y_0^-, y_0^-]$, where y_0^- is the smallest root of the equation $f(y) = y^*$, $y \in (0, 1)$, and y_0^- is either the value 1 if $y_0^- \leq 1 - g$, or the largest root of the equation $f(y) = y_0^-$, $y \in (0, 1)$, if $y_0^- > 1 - g$. If $0 < y(0) < y_0^-$, $y(t)$ begins by increasing until it enters into the interval $(y_0^-, y_0^-]$. If $y(t) = y_0^-$ for some t , then $y(t + 1) = y^*$. If $y_0^+ < y(0) \leq 1$, $y(1) < y_0^-$ and $y(t)$, $t \geq 2$, evolves as indicated above.

We now illustrate this theorem for three particular distributions of R and under the assumption $\varphi(y) = \varphi y$. If $R \sim \text{Bernoulli}(m_1)$, the convergence is always monotone, and the cases (I) or (II) (with $y_0 = 1$) occur according as $m_1\varphi \leq g$ or $m_1\varphi > g$. If $R \sim \text{Geometric}(1 - c)$, the cases (I), (II), and (III) are possible; in function of the parameters $1 - c$ and g , they occur, for a given value of φ , as shown in Fig. 1, where the functions h_i , $i = 1, 2$, are defined by

$$h_1 = c\varphi/(1 - c),$$

$$h_2 = (1/2)\{-1 + c\varphi/(1 - c) - \{[-1 + c\varphi/(1 - c)]^2 - 4\}^{1/2}\}.$$

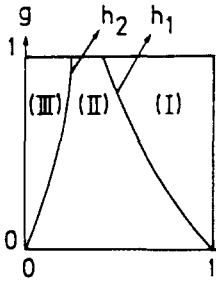


Fig. 1.

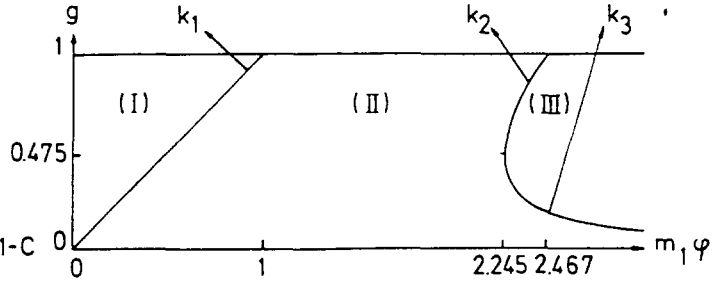


Fig. 2.

If $R \sim \text{Poisson}(m_1)$, the three cases are possible too; in function of the parameters m_1 and g , they occur as shown in Fig. 2, where the functions k_i , $i = 1, 2, 3$, are defined by

$$k_1 = m_1 \varphi,$$

$$k_2 = [1 + m_1 \varphi(1 - y_1)] \exp(-m_1 \varphi y_1),$$

$$k_3 = [1 + m_1 \varphi(1 - y_2)] \exp(-m_1 \varphi y_2),$$

y_1 and y_2 being the smallest and largest roots, when they exist, of the equation

$$(1 - y)[\exp(m_1 \varphi y) - m_1 \varphi y] = 1, \quad 0 < y < 1.$$

The calculations leading to these results are elementary but tedious, and are not given here.

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