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A MULTIVARIATE STOCHASTIC ORDERING BY THE MIXED DESCENDING FACTORIAL MOMENTS WITH APPLICATIONS[1]

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A stochastic order relation for discrete random vectors is introduced that relies on the mixed descending factorial moments. Connection with more usual orderings is pointed out through a hierarchical classification. The order relation is then used for comparing the state of a population which is subjected to certain damage processes by death, sampling or infection. In particular, for the multipopulation collective epidemic model, it allows us to establish in which sense the ultimate numbers of susceptibles do decrease with the infectivity level of the infectives. This paper extends to the multivariate case a recent work by the authors.

1. Introduction

In a previous paper (Lefèvre and Picard (1991)), we introduced an order relation for $\mathbb{N}$-valued random variables, unusual in the literature, that relies on the descending factorial moments; for this reason, we called it *the factorial ordering.* Our original motivation came from the epidemic context, namely to make precise in which probabilistic terms the total damage caused by the disease in a collective Reed-Frost epidemic model can indeed be viewed as an increasing function of the infection intensity exerted by the infectives. Further applications occur when comparing certain sampling procedures through the number of unsampled individuals. In particular, we used the ordering to obtain qualitative results for a reinforcement-depletion urn model and for a non-linear death process.

Our purpose here is to construct a multivariate version of this ordering based on the mixed descending factorial moments, and then to illustrate its relevance with some applications in the same fields. The ordering is derived in Section 2 through a hierarchical classification of various potential order

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relations for discrete random vectors. Connection with more classical orderings follows easily. In Section 3, we use it to compare the size of a population subjected to certain damage schemes. This allows us to generalize the qualitative analysis for the urn model and the death process mentioned above. Section 4 is concerned with the collective epidemic model, this time for an heterogeneous population. Thanks to the ordering, we are in a position to establish a monotonicity property of the ultimate numbers of susceptibles with respect to the infectivity level of the infectives. To this end, we adopt the approach developed recently in Picard and Lefèvre (1990) and which has recourse to a special family of polynomials with several variables defined in Lefèvre and Picard (1990). The method is direct, though rather technical, and has the merit to emphasize the interest and the flexibility of these polynomials.

2. Ordering Random Vectors by the Mixed Descending Factorial Moments

A number of stochastic order relations have been proposed to compare random vectors (see, e.g., Stoyan (1983)). We are going to derive a hierarchical classification of various potential multivariate stochastic orderings for discrete vectors. As a consequence, the ordering of interest by the mixed descending factorial moments will then emerge in a simple and natural way. For simplicity, but without loss of generality, we only consider bidimensional random vectors. We mention that the presentation below extends the one followed in Lefèvre and Picard (1991) for the univariate case; a letter I will be added to the numbering when referring to the associated formula in that paper.

2.1. *A Sequence of Remarkable Cones of Functions*

Let us consider the cone $\mathcal{F}_2$ of the functions $f(x_1, x_2)$ from $\mathbb{N}^2$ to $\mathbb{R}^+$. We start by constructing in $\mathcal{F}_2$ a sequence of remarkable cones $\mathcal{F}_2^{(1)}, \ldots, \mathcal{F}_2^{(6)}$. Put $1(A)$ as the indicator function of A, and for $i, j \in \mathbb{N}$, let $j_{[i]} = j(j-1)\ldots(j-i+1)$ and $j^{[i]} = j(j+1)\ldots(j+i-1)$, with $j_{[0]} = j^{[0]} = 1$.

DEFINITION 2.1 For $j = 1, \ldots, 5$ and $(i_1, i_2) \in \mathbb{N}^2$, let

$$e^{(j)}_{i_1,i_2}(x_1, x_2) = e^{(j)}_{i_1}(x_1) e^{(j)}_{i_2}(x_2), \tag{2.1}$$

with $e_i^{(j)}(x)$ given respectively by

$$\begin{aligned} &e_i^{(1)}(x) = 1(x \geq i), \\ (2.2) \qquad &e_0^{(2)}(x) = 1 \text{ and } e_i^{(2)}(x) = (x - i + 1)^+, i = 1, 2, \ldots \\ &e_i^{(3)}(x) = x_{[i]} \quad , \quad e_i^{(4)}(x) = x^i \quad , \quad e_i^{(5)}(x) = x^{[i]}. \end{aligned}$$

Then, $\mathcal{F}_2^{(j)}$, $j = 1, \ldots, 5$, is defined as the cone of the functions $f(x_1, x_2)$ in $\mathcal{F}_2$ that can be expressed as a linear combination (finite or not) with positive coefficients of the functions of the family $\{e_{i_1,i_2}^{(j)}(x_1, x_2), (i_1, i_2) \in \mathbb{N}^2\}$; in short, $\mathcal{F}_2^{(j)}$ is said to be generated by the $e_{i_1,i_2}^{(j)}(x_1, x_2)$. Similarly, $\mathcal{F}_2^{(6)}$ is the cone generated by the elements of the family $\{e_{a_1,a_2}^{(6)}(x_1, x_2)$, for any reals $a_1, a_2 > 1\}$, where

$$e_{a_1,a_2}^{(6)}(x_1, x_2) = e_{a_1}^{(6)}(x_1) e_{a_2}^{(6)}(x_2),$$

with

$$(2.3) \qquad e_a^{(6)}(x) = a^x.$$

The first three cones can be characterized equivalently as follows. We denote by $\Delta^{i_1,i_2}(\nabla^{i_1,i_2})f(j_1, j_2)$, (i_1, i_2) and $(j_1, j_2) \in \mathbb{N}^2$, the forward (backward) difference of $f(x_1, x_2)$ of orders i_1 in x_1 and i_2 in x_2 evaluated at $(x_1, x_2) = (j_1, j_2)$. For $i, j \in \mathbb{N}$, we put $i \wedge j = \min(i, j)$.

PROPERTY 2.2 *$\mathcal{F}_2^{(j)}$, $j = 1, 2, 3$, is the cone of the functions $f(x_1, x_2)$ in $\mathcal{F}_2$ such that, for $(i_1, i_2) \in \mathbb{N}^2$, $\nabla^{1\wedge i_1, 1\wedge i_2} f(i_1, i_2) \geq 0$ when $j = 1$, $\nabla^{2\wedge i_1, 2\wedge i_2} f(i_1, i_2) \geq 0$ when $j = 2$, and $\Delta^{i_1,i_2} f(0, 0) \geq 0$ when $j = 3$.*

PROOF Fix $j = 1, 2$ or 3. We first observe that any function $f(x_1, x_2)$ in $\mathcal{F}_2$ can be expanded in terms of the $e_{i_1,i_2}^{(j)}(x_1, x_2)$ as

$$(2.4) \qquad f(x_1, x_2) = \sum_{i_1=0}^{\infty} \sum_{i_2=0}^{\infty} \alpha_{i_1,i_2}^{(j)} e_{i_1,i_2}^{(j)}(x_1, x_2)$$

for some appropriate coefficients $\alpha_{i_1,i_2}^{(j)}$. Indeed, by (2.1) and (2.2), the summation in (2.4) is, for any given $(x_1, x_2) \in \mathbb{N}^2$, a finite sum, so that the $\alpha_{i_1,i_2}^{(j)}$ may be determined recursively. Now, we proved in (I, 2.2) and (I, 2.5) that

$$(2.5) \qquad \nabla^{1\wedge i} e_k^{(1)}(i) = \nabla^{2\wedge i} e_k^{(2)}(i) = \Delta^i e_k^{(3)}(0)/i! = 1(k = i) \quad , \quad i, k \in \mathbb{N}.$$

Combining (2.5) with (2.1), (2.2) and (2.4), we obtain successively that

$$\begin{aligned} &\nabla^{1\wedge i_1, 1\wedge i_2} f(i_1, i_2) = \alpha_{i_1,i_2}^{(1)}, \\ (2.6) \qquad &\nabla^{2\wedge i_1, 2\wedge i_2} f(i_1, i_2) = \alpha_{i_1,i_2}^{(2)}, \\ &\Delta^{i_1,i_2} f(0, 0)/i_1! i_2! = \alpha_{i_1,i_2}^{(3)}, \quad (i_1, i_2) \in \mathbb{N}^2. \end{aligned}$$

By definition, $f(x_1,x_2)$ is in $\mathcal{F}_2^{(j)}$ iff the $\alpha_{i_1,i_2}^{(j)}$ are in $\mathbb{R}^+$. From (2.6), the above characterizations of $\mathcal{F}_2^{(j)}$, $j = 1,2,3$, are then straightforward. □

REMARK 2.3 From Property 2.2, we easily deduce that $\mathcal{F}_2^{(j)}$, $j = 1,2,3$, contains any function $f(x_1,x_2)$ in $\mathcal{F}_2$ that can be factorized as

$$f(x_1,x_2) = f_1(x_1)f_2(x_2), \tag{2.7}$$

where $f_1(x)$ and $f_2(x)$ are functions from $\mathbb{N}$ to $\mathbb{R}^+$ which are increasing for $j = 1$, increasing and convex for $j = 2$, and such that $\Delta^i f_1(0)$ and $\Delta^i f_2(0) \geq 0$, $i \in \mathbb{N}$, for $j = 3$.

We now show that the six cones decrease in the inclusion sense.

PROPERTY 2.4 $\mathcal{F}_2^{(j)} \supset \mathcal{F}_2^{(j+1)}$, $j = 1,\ldots,5$.

PROOF Using Property 2.2, we observe that $\mathcal{F}_2^{(1)} \supset \mathcal{F}_2^{(2)}$ obviously, and $\mathcal{F}_2^{(2)} \supset \mathcal{F}_2^{(3)} \supset \mathcal{F}_2^{(4)}$ because by (2.1) and (2.2),

$$\nabla^{2\wedge i_1,2\wedge i_2} e_{k_1,k_2}^{(3)}(i_1,i_2) = \nabla^{2\wedge i_1} i_{1,[k_1]} \nabla^{2\wedge i_2} i_{2,[k_2]} \geq 0,$$

$$\nabla^{i_1,i_2} e_{k_1,k_2}^{(4)}(0,0) = \Delta^{i_1} 0^{k_1} \Delta^{i_2} 0^{k_2} \geq 0,$$

for (i_1,i_2) and $(k_1,k_2) \in \mathbb{N}^2$, respectively. Moreover, $\mathcal{F}_2^{(4)} \supset \mathcal{F}_2^{(5)} \supset \mathcal{F}_2^{(6)}$ since $x^{[i]}$, $i \in \mathbb{N}$, can be generated by the x^j, $j \in \mathbb{N}$, and a^x, $a > 1$, by the $x^{[j]}$, $j \in \mathbb{N}$ (see (I, 2.7)). □

2.2. *The Induced Stochastic Order Relations*

Let us denote by $\mathcal{D}_2$ the space of the $\mathbb{N}^2$-valued random vectors. To each of the cones of Definition 2.1, we can associate an order relation on $\mathcal{D}_2$ as follows. Let $\mathbf{X} = (X_1,X_2)$ and $\hat{\mathbf{X}} = (\hat{X}_1,\hat{X}_2)$ be r.v.s in $\mathcal{D}_2$.

DEFINITION 2.5 $\mathbf{X}$ is smaller than $\hat{\mathbf{X}}$ in the $\leq_j$ sense (written $\mathbf{X} \leq_j \hat{\mathbf{X}}$), $j = 1,\ldots,6$, when

$$E[f(X_1,X_2)] \leq E[f(\hat{X}_1,\hat{X}_2)] \text{ for any function in } \mathcal{F}^{(j)}, \tag{2.8}$$

that is, equivalently,

$$\begin{aligned} E[e_{i_1,i_2}^{(j)}(X_1,X_2)] &\leq E[e_{i_1,i_2}^{(j)}(\hat{X}_1,\hat{X}_2)] \text{ for } (i_1,i_2) \in \mathbb{N}^2, \\ & \text{ when } j = 1,\ldots,5, \\ E[e_{a_1,a_2}^{(6)}(X_1,X_2)] &\leq E[e_{a_1,a_2}^{(6)}(\hat{X}_1,\hat{X}_2)] \text{ for } a_1,a_2 > 1, \\ & \text{ when } j = 6. \end{aligned} \tag{2.9}$$

REMARK 2.6 From (2.8), (2.9) and Remark 2.3, we obtain directly the following characterization of the first three orderings. For $j = 1,2,3$, $\mathbf{X} \leq_j \hat{\mathbf{X}}$ iff

$$E[f_1(X_1)f_2(X_2)] \leq E[f_1(\hat{X}_1)f_2(\hat{X}_2)] \tag{2.10}$$

for any functions f_1 and f_2 from $\mathbb{N}$ to $\mathbb{R}^+$ that are increasing when $j = 1$, increasing and convex when $j = 2$, and such that $\Delta^i f_1(0)$ and $\Delta^i f_2(0) \geq 0$, $i \in \mathbb{N}$, when $j = 3$.

The orderings $\leq_1$ and $\leq_2$ correspond to those introduced by Bergmann (1978), for discrete or not random vectors. At our knowledge, the four others have not been investigated so far in the literature. In fact, from (2.1), (2.2) and (2.9), we see that $\leq_3$ compares the mixed descending factorial moments of $\mathbf{X}$ and $\hat{\mathbf{X}}$, $\leq_4$ their moments about zero, $\leq_5$ their ascending factorial moments and $\leq_6$ the expected value of increasing exponentials of their components.

By Property 2.4, the six orderings in Definition 2.5 decrease in the strength sense.

PROPERTY 2.7 $\mathbf{X} \leq_j \hat{\mathbf{X}}$ *implies* $\mathbf{X} \leq_{j+1} \hat{\mathbf{X}}$, $j = 1, \ldots, 5$.

These order relations generalize those defined in (I, Section 2) for $\mathbb{N}$-valued random variables. Furthermore, the following connection is immediate from (2.9).

PROPERTY 2.8 *For* $j = 1, \ldots, 6$,

$$\mathbf{X} \leq_j \hat{\mathbf{X}} \textit{ implies } X_1 \leq_j \hat{X}_1 \textit{ and } X_2 \leq_j \hat{X}_2. \tag{2.11}$$

When X_1, X_2, *as well as* $\hat{X}_1, \hat{X}_2$, *are independent, then the converse of (2.11) is true.*

2.3. *The So-Called Factorial Ordering*

For the sequel, we will mainly use the order relation $\leq_3$. As it compares random vectors through their mixed descending factorial moments, we keep the name given in I of *factorial ordering*, with the notation $\leq_F$. In addition, we will limit our attention to the subspace $\mathcal{D}_{n_1,n_2}$ in $\mathcal{D}_2$ of the random vectors $\mathbf{X} = (X_1, X_2)$ with X_1 and X_2 valued in the sets $\{0, 1, \ldots, n_1\}$ and $\{0, 1, \ldots, n_2\}$, respectively. Thus, for $\mathbf{X}, \hat{\mathbf{X}} \in \mathcal{D}_{n_1,n_2}$, $\mathbf{X} \leq_F \hat{\mathbf{X}}$ when

$$E[X_{1,[i_1]}X_{2,[i_2]}] \leq E[\hat{X}_{1,[i_1]}\hat{X}_{2,[i_2]}] \quad , \quad 0 \leq i_1 \leq n_1, 0 \leq i_2 \leq n_2. \tag{2.12}$$

We note that within $\mathcal{D}_{n_1,n_2}$, all the orderings of Definition 2.5 satisfy the axioms of partial order relation. Moreover, $\leq_6$ is now closely tied with the probability generating function ordering ($\leq_g$ in Stoyan (1983)). For $\mathbf{X}, \hat{\mathbf{X}} \in \mathcal{D}_2$, $\mathbf{X} \leq_g \hat{\mathbf{X}}$ when

$$E\left(z_1^{X_1} z_2^{X_2}\right) \geq E\left(z_1^{\hat{X}_1} z_2^{\hat{X}_2}\right) \quad , \quad 0 \leq z_1, z_2 \leq 1. \tag{2.13}$$

From (2.3) and (2.9), we thus deduce that for $\mathbf{X}, \hat{\mathbf{X}} \in \mathcal{D}_{n_1,n_2}$,

$$\mathbf{X} \leq_6 \hat{\mathbf{X}} \text{ iff } \mathbf{n} - \mathbf{X} \geq_g \mathbf{n} - \hat{\mathbf{X}}, \tag{2.14}$$

where $\mathbf{n} - \mathbf{X}$ denotes the vector $(n_1 - X_1, n_2 - X_2)$. As a consequence, when comparing $\leq_F$ with more usual orderings, we have the following implications: for $\mathbf{X}, \hat{\mathbf{X}} \in \mathcal{D}_{n_1,n_2}$,

$$\mathbf{X} \leq_2 \hat{\mathbf{X}} \Rightarrow \mathbf{X} \leq_F \hat{\mathbf{X}} \Rightarrow \mathbf{n} - \mathbf{X} \geq_g \mathbf{n} - \hat{\mathbf{X}}. \tag{2.15}$$

3. Comparison of the Outcome of Certain Damage Procedures

We are going to show that the factorial ordering is a well-adapted notion when comparing certain damage procedures through the number of unhurt individuals. As main applications, we will use it for two particular situations, namely a non-linear death process and a reinforcement-depletion urn model. The results extend in several ways those obtained in (I, Section 3) - and earlier ones.

3.1. *A Single Population Subjected to a Death Risk*

Consider a population of initial size n which shares a death risk. We denote by $T_i, i = 1, \ldots, n$, the lifetime of individual i. The T_i are assumed to be exchangeable; this hypothesis, however, could be removed without difficulty. We are interested in the number X_t of individuals surviving at time $t, t \in \mathbb{R}^+$ (or $\mathbb{N}$).

Let t_1, t_2 be any two instants with $t_1 < t_2$. Fix then k_1 and k_2 in $[1, n]$. We can write that

$$\binom{X_{t_1}}{k_1} = \sum 1(T_{\alpha_1} > t_1, \ldots, T_{\alpha_{k_1}} > t_1), \tag{3.1}$$

where the sum is over the $\binom{n}{k_1}$ groups of k_1 distinct individuals $\alpha_1, \ldots, \alpha_{k_1}$. An analogous formula is valid for $\binom{X_{t_2}}{k_2}$. From (3.1), we then obtain that

$$\binom{X_{t_1}}{k_1}\binom{X_{t_2}}{k_2} = \tag{3.2}$$

$$\sum 1(T_{\alpha_1} > t_1, \ldots, T_{\alpha_{k_1}} > t_1; T_{\beta_1} > t_2, \ldots, T_{\beta_{k_2}} > t_2),$$

where the sum is over the $\binom{n}{k_1}\binom{n}{k_2}$ groups of k_1 distinct individuals $\alpha_1, \dots, \alpha_{k_1}$ and k_2 distinct individuals $\beta_1, \dots, \beta_{k_2}$. Certain of the α_i and β_j individuals may be identical, of course; in fact, there can exist $k = 0, \dots, \min(k_1, k_2)$ individuals in common. For a given value of k, since $t_1 < t_2$, the sum contains $\binom{n}{k_1-k,k_2}$ indicator functions of the type $1(T_1 > t_1, \dots, T_{k_1-k} > t_1$ - provided $k_1 - k \geq 1$; $T_{k_1+1} > t_2, \dots, T_{k_1+k_2} > t_2)$. Therefore, taking the expectation in (3.2) yields for the mixed descending factorial moments

$$E\left[X_{t_1,[k_1]}X_{t_2,[k_2]}\right] = \sum_{k=0}^{\min(k_1,k_2)} k_{1,[k]}n_{[k_1+k_2-k]}P(T_1 > t_1, \dots, T_{k_1-k} > t_1; \\ T_{k_1+1} > t_2, \dots, T_{k_1+k_2} > t_2). \tag{3.3}$$

We note that when k_2 (e.g.)$= 0$, (3.3) is easily adapted and becomes

$$E\left[X_{t_1,[k_1]}\right] = n_{[k_1]}P(T_1 > t_1, \dots, T_{k_1} > t_1). \tag{3.4}$$

Consider now a similar model characterized by the lifetimes $\hat{T}_i, i = 1, \dots, n$. Let $\hat{X}_t, t \in \mathbb{R}^+$, be the state of the population at time t. Using the factorial ordering (2.12), we deduce from (3.3) and (3.4) the following comparison.

PROPOSITION 3.1 *Let $t_1 \neq t_2$. If for any $\tau_1, \dots, \tau_i$, $i \in [1, n]$, taken in $\{t_1, t_2\}$,*

$$P(T_1 > \tau_1, \dots, T_i > \tau_i) \leq P(\hat{T}_1 > \tau_1, \dots, \hat{T}_i > \tau_i), \tag{3.5}$$

then

$$(X_{t_1}, X_{t_2}) \leq_F (\hat{X}_{t_1}, \hat{X}_{t_2}). \tag{3.6}$$

3.1.1. A non-linear death process

A special case of the model arises when $X_t, t \in \mathbb{R}^+$, is governed by a non-linear Markovian death process. Here, given $X_t = x$, $x = 1, \dots, n$, each of the x individuals still alive at t can die, during $(t, t + dt)$, independently of the others and with the probability $\xi(x)dt$, where $\xi(x)$ is some positive function of the current state x.

Now, the (unconditional) lifetimes T_i are clearly exchangeable and interdependent. Ball and Donnelly (1987) investigated the nature of that dependence; see also Lefèvre and Michaletzky (1990) and an amendment by Donnelly (1991). They proved that if

$$(3.7)\qquad \xi(x), x = 1, \ldots, n, \text{ forms an increasing (decreasing) sequence,}$$

then for any $\tau_1, \ldots, \tau_i, i \in [1, n]$,

$$(3.8)\qquad P(T_1 > \tau_1, \ldots, T_i > \tau_i) \leq (\geq) P(T_1 > \tau_1) \ldots P(T_i > \tau_i).$$

We can use this result to compare the model with an approximated one where the individuals would behave independently. Specifically, consider a population of n individuals whose lifetimes $\hat{T}_i, i = 1, \ldots, n$, are i.i.d., with the same marginal distribution as the original T_i. Thus, for any $\tau_1, \ldots, \tau_i$, $i \in [1, n]$,

$$(3.9)\qquad P(\hat{T}_1 > \tau_1, \ldots, \hat{T}_i > \tau_i) = P(T_1 > \tau_1) \ldots P(T_i > \tau_1).$$

Let $\hat{X}_t, t \in \mathbb{R}^+$, be the new population state at time t. From (3.7), (3.8), (3.9) and Proposition 3.1, we then deduce that

$$(3.10)\quad \text{the condition (3.7) implies } (X_{t_1}, X_{t_2}) \leq_F (\geq_F)(\hat{X}_{t_1}, \hat{X}_{t_2}), \quad t_1 \neq t_2.$$

3.1.2. A reinforcement-depletion urn model

We turn now to an urn model, developed by Shenton (1981), with successive reinforcement-depletions of random size. The urn contains initially n white balls and m black balls. At stage $t, t = 1, 2, \ldots$, the black balls are reinforced by the addition of a random number R_t of extra black balls. All the balls are then uniformly mixed, and depletion occurs as a sample of balls, of the same size R_t, is drawn without replacement from the urn. Attention centers on the number X_t of white balls that remain in the urn just after stage t.

This model can be viewed as a particular case of the model above by simply assimilating the sampling of a white ball from the urn to its death. Thus, $T_i, i = 1, \ldots, n$, represents here the time period white ball i will spend in the urn. These T_i are exchangeable. Moreover, let $\tau_1 \leq \tau_2 \leq \ldots \leq \tau_i$, $i \in [1, n]$, be the termination time of various stages. By conditioning on the event $A = [R_t = r_t, t = 1, \ldots, \tau_i]$, we obtain

$$(3.11)\qquad P(T_1 > \tau_1, \ldots, T_i > \tau_i | A) =$$
$$\prod_{j=1}^{i} \prod_{u_j = \tau_{j-1}+1}^{\tau_j} \binom{n + m + r_{u_j} - (i - j + 1)}{r_{u_j}} \Big/ \binom{n + m + r_{u_j}}{r_{u_j}},$$

where we put $\tau_0 = 0$ and $\prod_{u_j} = 1$ when $\tau_{j-1} = \tau_j$. From (3.11), we then deduce that

$$(3.12) \quad P(T_1 > \tau_1, \ldots, T_i > \tau_i) = \left\{ \prod_{j=1}^{i} \left[(n+m)_{[i-j+1]} \right]^{\tau_j - \tau_{j-1}} \right\} \times E \left\{ 1 / \prod_{j=1}^{i} \prod_{u_j = \tau_{j-1}+1}^{\tau_j} (n + m + R_{u_j})_{[i-j+1]} \right\}.$$

Recently, Donnelly and Whitt (1989;Section 4) examined for the model some effects of more variable reinforcement-depletion sizes. Their results can be strengthened, as shown below for their Corollary 4.1; for brevity, that corollary is not recalled. We begin by introducing a further stochastic ordering for random vectors which was proposed before by Bergmann (1978). In the notations of Section 2, $\mathbf{X}$ is smaller that $\hat{\mathbf{X}}$ in the $\leq_{2d}$ sense when the inequality (2.10) holds for any functions f_1 and f_2 from $\mathbb{N}$ to $\mathbb{R}^+$ that are decreasing and convex. It is easily seen that an analogous inequality is then valid for the cone of the functions $f(x_1, x_2)$ in $\mathcal{F}_2$ that are generated by the elements of the family $\{(i_1 - x_1)^+(i_2 - x_2)^+, (i_1, i_2) \in \mathbb{N}^2\}$. Now, consider another urn model with random sizes $\hat{R}_t, t = 1, 2, \ldots$, and let $\hat{T}_i, i = 1, \ldots, n$, be the lifetime of white ball i. We observe that (3.12) is the expectation of the product of τ_i functions with arguments $R_t, t = 1, \ldots, \tau_i$, respectively, each of these functions being decreasing and convex. Therefore, applying $\leq_{2d}$, we deduce from (3.12) and Proposition 3.1 that

$$(3.13) \qquad (R_t, t = 1, \ldots, t_2) \leq_{2d} (\hat{R}_t, t = 1, \ldots, t_2) \text{ implies } (X_{t_1}, X_{t_2}) \leq_F (\hat{X}_{t_1}, \hat{X}_{t_2}), t_1 < t_2.$$

3.2. *A Multipopulation Subjected to a Sampling*

Consider a bipopulation of n_1 individuals of type 1 and n_2 individuals of type 2, subjected jointly to a sampling procedure. Let $B_{1,i}(B_{2,j})$ be the event that individual i in population 1 (j in population 2) is not drawn. The $B_{1,i}$, $i = 1, \ldots, n_1$, are supposed to be exchangeable, as well as the $B_{2,j}$, $j = 1, \ldots, n_2$; this hypothesis, however, is not essential. We are concerned with the vector (X_1, X_2) of the numbers of unsampled individuals from populations 1 and 2, respectively.

Fix k_1 in $[1, n_1]$ and k_2 in $[1, n_2]$. Arguing as for (3.2), we obtain that

$$(3.14) \quad \binom{X_1}{k_1} \binom{X_2}{k_2} = \sum 1 \left(B_{1,\alpha_1} \cap \ldots \cap B_{1,\alpha_{k_1}} \cap B_{2,\beta_1} \cap \ldots \cap B_{2,\beta_{k_2}} \right),$$

where the sum is over the $\binom{n_1}{k_1}\binom{n_2}{k_2}$ groups of k_1 distinct individuals $\alpha_1,\ldots,\alpha_{k_1}$ in population 1 and k_2 distinct individuals $\beta_1,\ldots,\beta_{k_2}$ in population 2. Let $q(k_1,k_2)$ denote the probability that any given group of individuals of that kind is not drawn from the population; thus

$$q(k_1,k_2) = P(B_{1,1}\cap\ldots\cap B_{1,k_1}\cap B_{2,1}\cap\ldots\cap B_{2,k_2}). \tag{3.15}$$

From (3.14) and (3.15), we then deduce that

$$E\left[X_{1,[k_1]}X_{2,[k_2]}\right] = n_{1,[k_1]}n_{2,[k_2]}q(k_1,k_2). \tag{3.16}$$

We note that when k_2 (e.g.)= 0, (3.16) is still true provided we put $q(k_1,0) = P(B_{1,1}\cap\ldots\cap B_{1,k_1})$, with $q(0,0) = 1$.

Suppose now that another sampling is based on the parameters $\hat{q}(k_1,k_2)$, $0\le k_1\le n_1$, $0\le k_2\le n_2$, and let $(\hat{X}_1,\hat{X}_2)$ be the resulting size of the unsampled populations. The characterization of $\underset{F}{\le}$ below follows then directly from (3.16).

PROPOSITION 3.2

(3.17) $(X_1,X_2)\le_F(\hat{X}_1,\hat{X}_2)$*iff*

$$q(k_1,k_2)\le\hat{q}(k_1,k_2)\ ,\ 0\le k_1\le n_1, 0\le k_2\le n_2.$$

3.2.1. A sampling with random size

Let us examine the special sampling that consists in taking, with or without replacement, random numbers of individuals R_1 and R_2, possibly dependent, from populations 1 and 2, respectively. Such a situation can arise, for instance, when modelling the infection process in epidemic models (see 4.3(i) below).

For a sampling with replacement, we obtain, for $0\le k_1\le n_1$, $0\le k_2\le n_2$,

$$q(k_1,k_2) = E\left\{[(n_1-k_1)/n_1]^{R_1}[(n_2-k_2)/n_2]^{R_2}\right\}. \tag{3.18}$$

Consider a similar sampling with random sizes $\hat{R}_1$ and $\hat{R}_2$. Using the definition (2.13) of the $\le_g$ ordering, we then deduce from (3.17) and (3.18) that

$$(R_1,R_2)\ge_g(\hat{R}_1,\hat{R}_2) \text{ implies } (X_1,X_2)\le_F(\hat{X}_1,\hat{X}_2). \tag{3.19}$$

When the sampling is done without replacement, we have, for $0\le k_1\le n_1$, $0\le k_2\le n_2$,

$$q(k_1,k_2) = E\left[(n_1-R_1)_{[k_1]}(n_2-R_2)_{[k_2]}\right]/n_{1,[k_1]}n_{2,[k_2]}, \tag{3.20}$$

so that from (3.17) and (3.20),

$$(X_1, X_2) \leq_F (\hat{X}_1, \hat{X}_2) \text{ iff } (n_1 - R_1, n_2 - R_2) \leq_F (n_1 - \hat{R}_1, n_2 - \hat{R}_2). \tag{3.21}$$

3.2.2. An extended urn model

We generalize the reinforcement-depletion urn model described in 3.1.2 by putting in the urn balls of three different colours, white, red and black, in initial numbers n_1, n_2 and m, respectively. As before, at stage $t, t = 1, 2, \ldots$, the black colour is reinforced with a random number R_t of balls, and just after, R_t balls are drawn without replacement from the urn. Interest centers on the vector (X_{1,t_1}, X_{2,t_2}) where $X_{1,t_1} (X_{2,t_2})$ represents the number of white (red) balls that remain in the urn immediately after stage $t_1 (t_2)$.

From (3.15) and (3.16), we have, for $k_1 \in [1, n_1]$, $k_2 \in [1, n_2]$,

$$E\left[X_{1,t_1,[k_1]} X_{2,t_2,[k_2]}\right] = n_{1,[k_1]} n_{2,[k_2]} q(k_1, k_2; t_1, t_2), \tag{3.22}$$

where $q(k_1, k_2; t_1, t_2)$ denotes the probability that any given group of k_1 white balls and k_2 red balls is still in the urn just after stages t_1 and t_2, respectively. Choose $t_1 \leq t_2$, for example. By first conditioning on $[R_t, t = 1, \ldots, t_2]$, we then obtain

$$\begin{aligned} q(k_1, k_2; t_1, t_2) & \\ &= E\left\{ \prod_{j=1}^{2} \prod_{u_j = t_{j-1}+1}^{t_j} \frac{\binom{n_1 + n_2 + m + R_{u_j} - k_j - k_{j+1}}{R_{u_j}}}{\binom{n_1 + n_2 + m + R_{u_j}}{R_{u_j}}} \right\} \\ &= \left\{ \prod_{j=1}^{2} \left[(n_1 + n_2 + m)_{[k_j + k_{j+1}]} \right]^{t_j - t_{j-1}} \right\} \\ &\quad \times E\left\{ 1 \Big/ \prod_{j=1}^{2} \prod_{u_j = t_{j-1}+1}^{t_j} (n_1 + n_2 + m + R_{u_j})_{[k_j + k_{j+1}]} \right\}, \end{aligned} \tag{3.23}$$

where we put $t_0 = 0$, $k_3 = 0$ and $\prod_{u_2} = 1$ if $t_1 = t_2$. We note that the formulae (3.22) and (3.23) are easily adapted when k_2 (e.g.)$= 0$.

Consider now another urn model with random sizes $\hat{R}_t, t = 1, 2, \ldots$, and let $\hat{X}_{1,t_1} (\hat{X}_{2,t_2})$ be the resulting number of white (red) balls just after stage $t_1 (t_2)$. Using, as for (3.13), the $\leq_{2d}$ ordering, we deduce from (3.17), (3.22) and (3.23) that

$$\begin{aligned} &(R_t, t = 1, \ldots, t_2) \leq_{2d} (\hat{R}_t, t = 1, \ldots, t_2) \text{ implies} \\ &\qquad (X_{1,t_1}, X_{2,t_2}) \leq_F (\hat{X}_{1,t_1}, \hat{X}_{2,t_2}), t_1 \leq t_2. \end{aligned} \tag{3.24}$$

4. Comparison of the Final Outcome of Collective Epidemics

In (I, Section 4), we showed the effect of increased infection intensity on the total damage caused by a collective epidemic process. We are going to generalize our analysis by examining this time the case of an heterogeneous population. For clarity, that population is supposed to contain only two different groups of individuals. The approach relies on results derived in Lefèvre and Picard (1990) and Picard and Lefèvre (1990); these results will be referred with a supplementary letter II or III, respectively. We begin by establishing a comparison property that involves a family of polynomials with several variables introduced in II. We then apply it to the epidemic model formulae obtained in III.

4.1. *A Property of the Family of Polynomials*

Let us recall the definition (II, 4.1) of these polynomials, given here for two variables. For $j = 1, 2$, let $U^{(j)} = \{u^{(j)}_{i_1,i_2}, (i_1, i_2) \in \mathbb{N}^2\}$ be a fixed family of real numbers. To $U^{(1)}, U^{(2)}$ is attached a unique family of polynomials $G_{k_1,k_2}(x_1, x_2|U^{(1)}, U^{(2)})$ of degrees k_1 in x_1, k_2 in x_2, $(k_1, k_2) \in \mathbb{N}^2$, defined recursively by

$$G_{0,0}(x_1, x_2|U^{(1)}, U^{(2)}) = 1,$$

and when $k_1 + k_2 \geq 1$,

$$G_{k_1,k_2}(x_1, x_2|U^{(1)}, U^{(2)}) = \frac{x_1^{k_1}}{k_1!}\frac{x_2^{k_2}}{k_2!} - \tag{4.1}$$

$$\sum_{D(k_1,k_2)} \left[\frac{(u^{(1)}_{i_1,i_2})^{k_1-i_1}}{(k_1-i_1)!} \frac{(u^{(2)}_{i_1,i_2})^{k_2-i_2}}{(k_2-i_2)!} \right] G_{i_1,i_2}(x_1, x_2|U^{(1)}, U^{(2)}),$$

where $D(k_1, k_2)$ denotes the set of indexes $\{(i_1, i_2)$, with $0 \leq i_1 \leq k_1$, $0 \leq i_2 \leq k_2$ and $i_1 + i_2 < k_1 + k_2\}$. Observe that $G_{k_1,k_2}(\ )$, $k_1 + k_2 \geq 1$, depends only on the $u^{(1)}_{i_1,i_2}$ and $u^{(2)}_{i_1,i_2}$ with $(i_1, i_2) \in D_{k_1,k_2}$.

For our purpose, we need to establish a monotonicity property of certain expansions constructed from these polynomials with respect to the parameters in $U^{(1)}$ and $U^{(2)}$. Let $f(x_1, x_2)$ be a function with derivatives $f^{(i_1,i_2)}(x_1, x_2)$, $(i_1, i_2) \in \mathbb{N}^2$, and let $\hat{A}, A, \hat{U}^{(1)}, \hat{U}^{(2)}, U^{(1)}, U^{(2)}$ be six families of real numbers $\hat{a}_{i_1,i_2}, a_{i_1,i_2}, \hat{u}^{(1)}_{i_1,i_2}, \hat{u}^{(2)}_{i_1,i_2}, u^{(1)}_{i_1,i_2}, u^{(2)}_{i_1,i_2}$, respectively, $(i_1, i_2) \in \mathbb{N}^2$. Given these elements, fix $(k_1, k_2) \in \mathbb{N}^2$ and consider the polynomial

$$
\begin{aligned}
(4.2)\qquad & h_{k_1,k_2}(x_1,x_2|\hat{A},\hat{U}^{(1)},\hat{U}^{(2)},f,A,U^{(1)},U^{(2)})\\
&= \sum_{i_1=0}^{k_1}\sum_{i_2=0}^{k_2} \hat{a}_{i_1,i_2} f^{(i_1,i_2)}(\hat{u}^{(1)}_{i_1,i_2},\hat{u}^{(2)}_{i_1,i_2}) G_{i_1,i_2}(x_1,x_2|\hat{U}^{(1)},\hat{U}^{(2)})\\
&- \sum_{i_1=0}^{k_1}\sum_{i_2=0}^{k_2} a_{i_1,i_2} f^{(i_1,i_2)}(u^{(1)}_{i_1,i_2},u^{(2)}_{i_1,i_2}) G_{i_1,i_2}(x_1,x_2|U^{(1)},U^{(2)}).
\end{aligned}
$$

Note that $h_{k_1,k_2}(\ )$, $(k_1,k_2)\in \mathbb{N}^2$, depends only on the $\hat{a}_{i_1,i_2}, \hat{u}^{(1)}_{i_1,i_2}$, $\hat{u}^{(2)}_{i_1,i_2}$, $a_{i_1,i_2}, u^{(1)}_{i_1,i_2}$, $u^{(2)}_{i_1,i_2}$ with $0\le i_1\le k_1$, $0\le i_2\le k_2$. We remark that the two sums in (4.2) correspond to finite Abel expansions of the function $f(x_1,x_2)$ of the type given in (II, 4.5).

PROPERTY 4.1 *Let* $(k_1,k_2)\in\mathbb{N}^2$. *If for* $j=1,2$ *and* $0\le i_1\le k_1$, $0\le i_2\le k_2$, *the following conditions hold*

(4.3)

$u^{(j)}_{i_1,i_2}$ *and* $\hat{u}^{(j)}_{i_1,i_2}$ *are decreasing sequences in* i_1*(*i_2 *fixed) and* i_2*(*i_1 *fixed),*
$\hat{u}^{(j)}_{i_1,i_2}\ge u^{(j)}_{i_1,i_2}$,
$\hat{a}_{i_1,i_2}\ge \max\{0, a_{\ell_1,\ell_2}$, *for* $i_1\le \ell_1\le k_1, i_2\le \ell_2\le k_2\}$,
$f^{(i_1,i_2)}(u^{(1)}_{i_1,i_2},u^{(2)}_{i_1,i_2})\ge 0$, *and*
$f^{(k_1+1,k_2)}(x_1,x_2)$ *and* $f^{(k_1,k_2+1)}(x_1,x_2)\ge 0$ *for* $x_1\ge u^{(1)}_{k_1,k_2}, x_2\ge u^{(2)}_{k_1,k_2}$,

then

$$
(4.4)\qquad h_{k_1,k_2}(x_1,x_2|\hat{A},\hat{U}^{(1)},\hat{U}^{(2)},f,A,U^{(1)},U^{(2)})\ge 0 \quad \text{for } x_1\ge \hat{u}^{(1)}_{0,0}, x_2\ge \hat{u}^{(2)}_{0,0}.
$$

PROOF This can be shown by extending to the multivariate case the argument by induction followed for Property (I, 4.2). The proof is then direct, though rather technical, and uses properties of the polynomials given in (II, Section 4); it is omitted. □

4.2. *Varying Infectivity in Collective Epidemics*

The multipopulation collective epidemic model introduced in (III, Section 4) describes the spread of an infectious disease in a closed population subdivided in several (here two) groups (men and women, for example). Each group j, $j=1,2$, is partitioned in three classes of individuals, the susceptibles, the infectives and the removed cases. Initially, these are in numbers n_j, m_j and 0, respectively, and infection is then propagated as follows. Any infective remains infected during a random period of time. All the infectious periods are independent and, for j given, identically distributed, the common distribution being that of a variable D_j, say. These D_j are in general $\mathbb{R}$-valued, but can be discrete and possibly constant. While infected, the individual behaves independently of the others and can contact susceptibles of the two groups. Specifically, he will fail to transmit the infectious agents within any given set of k_1 susceptibles in group 1 and k_2 susceptibles in group 2, k_1 in $[1, n_1]$ and k_2 in $[1, n_2]$, with a random probability that depends on his infectious period. We make for these random variables, k_1, k_2 fixed, the same hypotheses as for the infectious periods, the common distribution for j given being that of a variable $Q_j(k_1, k_2)$, say. After that, the infective becomes a removed case and plays no further role in the infection process.

Let T denote the end of the epidemic, when there are no more infectious present in the population. We are interested by the vector $(S_{1,T}, S_{2,T})$ that represents the ultimate numbers of susceptibles surviving the disease in groups 1 and 2, respectively. Using the polynomials (4.1), we obtained, inter alia, in (III, 4.15) the formula (4.5) below for the mixed descending factorial moments of that vector. For $j = 1, 2$ and $k_1 \in [1, n_1]$, $k_2 \in [1, n_2]$, let

$$q_j(k_1, k_2) = E[Q_j(k_1, k_2)] \tag{4.5}$$

be the expected value of the different probabilities of non-infection; when k_2 (e.g)= 0, put $q_j(k_1, 0) = q_j(k_1, -)$, with $q_j(0, 0) = 1$. Then, for $0 \le k_1 \le n_1$, $0 \le k_2 \le n_2$,

$$\begin{aligned} E\left[S_{1,T,[k_1]} S_{2,T,[k_2]}\right] = \sum_{i_1=k_1}^{n_1} \sum_{i_2=k_2}^{n_2} & \Big\{ n_{1,[i_1]} n_{2,[i_2]} [q_1(i_1, i_2)]^{n_1+m_1-i_1} \\ & \times [q_2(i_1, i_2)]^{n_2+m_2-i_2} \Big\} G_{i_1-k_1, i_2-k_2}\left[1, 1 | \mathcal{E}^{k_1,k_2} U^{(1)}, \mathcal{E}^{k_1,k_2} U^{(2)}\right], \end{aligned} \tag{4.6}$$

where for $j = 1, 2$, $\mathcal{E}^{k_1,k_2} U^{(j)}$ is the family $\{u^{(j)}_{k_1+i_1, k_2+i_2}, (i_1, i_2) \in \mathbb{N}^2\}$, with

$$u^{(j)}_{i_1,i_2} = q_j(i_1, i_2) \quad , \quad 0 \le i_1 \le n_1, 0 \le i_2 \le n_2, \tag{4.7}$$

the $u^{(j)}_{i_1,i_2}$ for other indexes being superfluous and omitted.

Intuitively, one expects that lower infectivity levels translated by smaller $q_j(k_1, k_2)$ should generate larger ultimate numbers of susceptibles. Hereafter, we prove that this is indeed true provided comparison on $(S_{1,T}, S_{2,T})$ is made through the factorial ordering. Thus, consider a similar bipopulation collective epidemic characterized now by the variables $\hat{D}_j$ and $\hat{Q}_j(k_1, k_2)$, $j = 1, 2$ and $0 \le k_1 \le n_1$, $0 \le k_2 \le n_2$. Let $\hat{q}_j(k_1, k_2)$ be the associated expectations (4.5), and denote by $(\hat{S}_{1,T}, \hat{S}_{2,T})$ the resulting final numbers of susceptibles.

PROPOSITION 4.2 *If for $j = 1,2$ and $0 \le i_1 \le n_1$, $0 \le i_2 \le n_2$,*

$$q_j(i_1,i_2) \le \hat{q}_j(i_1,i_2), \tag{4.8}$$

then

$$(S_{1,T},S_{2,T}) \le_F (\hat{S}_{1,T},\hat{S}_{2,T}). \tag{4.9}$$

PROOF We have to show that for $0 \le k_1 \le n_1$, $0 \le k_2 \le n_2$,

$$E\left[\hat{S}_{1,T,[k_1]}\hat{S}_{2,T,[k_2]}\right] - E\left[S_{1,T,[k_1]}S_{2,T,[k_2]}\right] \ge 0. \tag{4.10}$$

Define $\mathcal{E}^{k_1,k_2}A = \{a_{k_1+i_1,k_2+i_2},(i_1,i_2) \in \mathbb{N}^2\}$, with

$$a_{i_1,i_2} = \left(u^{(1)}_{i_1,i_2}\right)^{m_1}\left(u^{(2)}_{i_1,i_2}\right)^{m_2}, \quad 0 \le i_1 \le n_1, 0 \le i_2 \le n_2, \tag{4.11}$$

the other a_{i_1,i_2} being superfluous for the discussion. Putting

$$f(x_1,x_2) = x_1^{n_1-k_1}x_2^{n_2-k_2}, \tag{4.12}$$

(4.6) can be expressed as

$$\begin{aligned} E\left[S_{1,T,[k_1]}S_{2,T,[k_2]}\right] = n_{1,[k_1]}n_{2,[k_2]} &\sum_{i_1=0}^{n_1-k_1}\sum_{i_2=0}^{n_2-k_2} \\ &a_{k_1+i_1,k_2+i_2}f^{(i_1,i_2)}\left(u^{(1)}_{k_1+i_1,k_2+i_2},u^{(2)}_{k_1+i_1,k_2+i_2}\right) \\ &\times G_{i_1,i_2}\left[1,1|\mathcal{E}^{k_1,k_2}U^{(1)},\mathcal{E}^{k_1,k_2}U^{(2)}\right]. \end{aligned} \tag{4.13}$$

Write then the formula (4.13) associated with the alternative model. Using the definition (4.2), we see that the difference in (4.10) just corresponds to

$$\begin{aligned} n_{1,[k_1]}n_{2,[k_2]}h_{n_1-k_1,n_2-k_2}&\left[1,1|\mathcal{E}^{k_1,k_2}\hat{A},\mathcal{E}^{k_1,k_2}\hat{U}^{(1)},\mathcal{E}^{k_1,k_2}\hat{U}^{(2)},\right. \\ &\left. f,\mathcal{E}^{k_1,k_2}A,\mathcal{E}^{k_1,k_2}U^{(1)},\mathcal{E}^{k_1,k_2}U^{(2)}\right]. \end{aligned} \tag{4.14}$$

Now, let us examine $h_{n_1-k_1,n_2-k_2}(\ )$ in (4.14). It is easily verified that thanks to the hypothesis (4.8), the conditions (4.3) in Property 4.1 are well satisfied. Since $1 \ge \hat{u}^{(1)}_{k_1,k_2}$ and $\hat{u}^{(2)}_{k_1,k_2}$, we deduce (4.10) from (4.4) and (4.14). □

The factorial ordering between final epidemic outcomes has been obtained under rather weak conditions on the model parameters $q_j(k_1,k_2)$. We will show in a forthcoming paper how it can be strengthened under stronger conditions on these parameters.

4.3. *Some Specific Applications*

For illustration, let us discuss some applications of this comparison result for two particular cases of the model.

(i) Suppose that the infectious periods are of length 1 ($D_1 = D_2 = 1$), and each infective can contact, independently of the others, a random number of individuals per time unit. All these numbers of contacts are independent, and for infectives of group $j, j = 1,2$, identically distributed, the common distribution for contacts within groups 1 and 2 being that of the vector $(R_{j,1}, R_{j,2})$, say. The contacts then occur with or without replacement amongst the $N_1 = n_1 + m_1$ and $N_2 = n_2 + m_2$ individuals of these groups.

Clearly, the model here can be viewed as the iterative version of a sampling scheme such as described in 3.2.1. For the case with replacement, we have, for $j = 1,2$ and $0 \leq k_1 \leq n_1$, $0 \leq k_2 \leq n_2$,

$$q_j(k_1,k_2) = E\left\{[(N_1 - k_1)/N_1]^{R_{j,1}}[(N_2 - k_2)/N_2]^{R_{j,2}}\right\}. \tag{4.15}$$

From (4.15) and Proposition 4.2, we then deduce that (in obvious notations)

$$(R_{j,1}, R_{j,2}) \geq_g (\hat{R}_{j,1}, \hat{R}_{j,2}), j = 1,2, \text{ implies (4.9)}\ . \tag{4.16}$$

In a similar way, for the sampling without replacement,

$$q_j(k_1,k_2) = E\left[(N_1 - R_{j,1})_{[k_1]}(N_2 - R_{j,2})_{[k_2]}\right]/N_{1,[k_1]}N_{2,[k_2]}, \tag{4.17}$$

and we deduce that

$$(N_1 - R_{j,1}, N_2 - R_{j,2}) \leq_F (N_1 - \hat{R}_{j,1}, N_2 - \hat{R}_{j,2}), \quad j = 1,2, \text{ implies (4.9)}\ . \tag{4.18}$$

(ii) Consider the situation above where the infectious periods are r.v.s which are independent and, for infectives of group $j, j = 1,2$, distributed as D_j. Suppose now that while infected, each infective can contact, independently of the others, any susceptible present at the points of a Poisson process. All these processes are independent, and for infectives of group $j, j = 1,2$, the associated contact rates within groups 1 and 2 are equal to $\beta_{j,1}$ and $\beta_{j,2}$, respectively. Here thus, for $j = 1,2$ and $0 \leq k_1 \leq n_1$, $0 \leq k_2 \leq n_2$,

$$Q_j(k_1,k_2) = \exp\left[-(k_1\beta_{j,1} + k_2\beta_{j,2})D_j\right]. \tag{4.19}$$

The so-called general epidemic model corresponds to the case where the D_j are exponentially distributed. When $D_1 = D_2 = 1$, then $Q_j(k_1,k_2) = (q_{j,1})^{k_1}(q_{j,2})^{k_2}$ with $q_{j,1} = \exp(-\beta_{j,1})$, $q_{j,2} = \exp(-\beta_{j,2})$, and the model reduces to the Reed-Frost process (see, e.g., Bailey (1975)).

We start by assessing the effect of varying the infectious periods. For this, we are going to use a weak stochastic ordering based on the Laplace-Stieltjes transform ($\leq_L$ in Stoyan (1983)): for random variables $X_1, \hat{X}_1$ valued in $\mathbb{R}^+$, $X_1 \leq_L \hat{X}_1$ when

$$E[\exp(-\theta X_1)] \geq E[\exp(-\theta \hat{X}_1)] \ , \ \theta \in \mathbb{R}^+. \tag{4.20}$$

From (4.19), (4.20) and Proposition 4.2, we thus deduce that

$$D_j \geq_L \hat{D}_j, j = 1,2, \text{ implies } (4.9) \ . \tag{4.21}$$

This result can be exploited to construct bounds for the ultimate numbers of suceptibles when only partial information on the D_j is available. For example, suppose that D_j, $j = 1,2$, are known to belong to the $\mathcal{L}(\bar{\mathcal{L}})$ class introduced by Klefsjö (1983); in other words, we have

$$D_j \geq_L (\leq_L) Exp(\mu_j), \tag{4.22}$$

where $\mu_j = E(D_j)$ and $Exp(\mu_j)$ denotes an exponential variable with the same mean μ_j. From (4.21) and (4.22), we then obtain that the general epidemic with exponential infectious periods with the same means provides an upper (lower) $\leq_F$ bound for the statistic $(S_{1,T}, S_{2,T})$.

Another comparison of interest is between the original epidemic model with random infectious periods and an approximated Reed-Frost process in which, by definition, infectious periods are all equal to 1. Take first the expectation in (4.19). Using the fact that the set of a single random variable is associated (Esary, Proschan and Walkup (1967)), we can write that for $j = 1,2$ and $0 \leq k_1 \leq n_1$, $0 \leq k_2 \leq n_2$,

$$q_j(k_1, k_2) \geq \{E[\exp(-k_1\beta_{j,1}D_j)]\} \{E[\exp(-k_2\beta_{j,2}D_j)]\} . \tag{4.23}$$

Then, applying twice Jensen's inequality in (4.23), we obtain that

$$q_j(k_1, k_2) \geq (\hat{q}_{j,1})^{k_1}(\hat{q}_{j,2})^{k_2} \geq (q^*_{j,1})^{k_1}(q^*_{j,2})^{k_2}, \tag{4.24}$$

where for $i = 1,2$,

$$\left\{ \begin{array}{l} \hat{q}_{j,i} = E[\exp(-\beta_{j,i}D_j)], \\ q^*_{j,i} = \exp[-\beta_{j,i}E(D_j)]. \end{array} \right. \tag{4.25}$$

Therefore, from (4.24), (4.25) and Proposition 4.2, we deduce that the Reed-Frost model with the $\hat{q}_{j,i}$ as probabilities of non-infection yields to a lower $\leq_F$ bound for $(S_{1,T}, S_{2,T})$. Moreover, replacing the infectious periods by their mean leads to a further Reed-Frost model that predicts an even $\leq_F$ smaller number of susceptibles. We mention that for the latter comparison, the factorial ordering could be strengthened.

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