

Static versus Dynamic Group-Screening Models

Dieter Claeys, Joris Walraevens, Bart Steyaert, Herwig Bruneel
SMACS Research Group, Department TELIN
Ghent University
Ghent, Belgium
Email: Dieter.Claeys@telin.ugent.be

Abstract—Group screening can lead to a tremendous reduction in number of tests and costs, and therefore has attracted considerable attention in literature. For several decades, a model from Robert Dorfman was the de facto standard to determine the optimal group size. However, more recently, it has been pointed out that the model from Dorfman is rather static, i.e., a predetermined large number of items has to be screened, whereas in reality the context is rather dynamic: items arrive at random moments in time, in groups of different and random size.

In this paper, we investigate to what extent the optimal group size in the static model from Dorfman remains efficient in a dynamic context. This is of vital importance for practitioners, as the model from Dorfman was the de facto standard for several decades and thus has to be validated. On top of that, even though dynamic models exist nowadays, these are much harder to implement and require a time-consuming processing time, due to the numerical work that is involved, such as repeatedly calculating zeroes of functions and solving sets of equations.

Keywords-group screening; optimal group size; static model; dynamic model; model validation

I. INTRODUCTION

Classification of items as good or bad can often be achieved more economically by screening the items in groups rather than individually. The underlying reason is that when a test on a group returns good, it can be concluded (after one test only) that all items within the group are good. Dorfman [1] was the first to introduce the paradigm of group screening and he found an immediate application in the detection of syphilitic men drafted into military service during WWII. He suggested to apply this procedure also to manufacturing processes where the defective goods have to be eliminated from the collection of all produced goods. Later on, many researchers applied this paradigm to screen blood for the presence of HIV [2][3][4][5][6][7], Influenza [8] and West Nile Virus [9] (group screening is in this context generally referred to as blood pooling). The range of application even stretches further. Macula [10] and Manoli et al. [11] applied group screening to DNA screening and Dean and Lewis [12] (chapter 3), Xie et al. [13] and Zhu et al. [14] utilized it for drug discovery. Finally, group screening has also found its entrance in the field of computer science, for instance in the study of web services [15][16], image compression

[17], multiple access protocols [18], optical networks [19], encryption [20], etc.

When group screening is feasible, the *selection of the group size is crucial*: the larger a group size, the more items can be screened by only one test, but the more likely it becomes that one or more items of the group are bad, inferring that retesting becomes necessary. This can, for instance, be achieved by retesting all items of the group individually, which is often referred to as *group-individual screening policy* (see, e.g., [2]). However, in many occasions, a *group-subgroup screening policy* is adopted, whereby the group is divided into subgroups which are each subjected to a new group test. Traditionally, a bad group is divided in two subgroups of equal size whereby the items of a bad subgroup are retested individually [21].

For several decades, a mathematical model from Robert Dorfman [1] was the de facto standard to determine the optimal group size. This model is essentially **static**: it postulates that a population consisting of a predetermined large number of items has to be screened whereby all items are present from the beginning. However, Abolnikov and Dukhovny [2] correctly pointed out that the practical context is usually **dynamic**: items are not all present from the start, and arrive at random moments in time, possibly in groups of different and random size. For instance, trucks from various regions of a country arrive at the blood screening laboratory at random moments of the day, with a variable number of blood samples to be screened. Abolnikov and Dukhovny [2] dealt with the dynamic nature by relying on queueing theory. Since then, Bar-Lev et al. [22] and Claeys et al. [21] further developed and analyzed queueing models to better include the dynamic nature of item arrivals.

An important disadvantage of dynamic models and analyses, is that they are *much harder to implement* and the *processing time is slow* due to the numerical work that is involved, such as repeatedly calculating zeroes of functions and solving sets of equations. A natural question crucial to practitioners is thus the following: **under which circumstances does the static model yield accurate results in a dynamic context?** This is the question we wish to

answer in this paper. More specifically, we examine to what extent the optimal group size in the static model from Dorfman [1] remains optimal or efficient in the dynamic (queueing) model from Claeys et al. [21]. We compare with [21] and not with the dynamic model from Bar-Lev et al. [22] as they study an incomplete-identification scenario, which means that when a group test returns bad, the whole group is discarded. In Claeys et al. [21] and Dorfman [1] on the other hand, the bad items need to be separated from the good, i.e., complete identification is necessary, incurring that retesting is essential. We also prefer to not adopt the model from Abolnikov and Dukhovny [2], as only the system content at service completion times is established in their paper.

The remainder of this paper is structured as follows: in Section II, we describe the static and the dynamic model in detail. Thereafter, we evaluate in Sections III and IV to what extent results obtained by the static model are valid in a dynamic context. Finally, conclusions are drawn in Section V.

II. DESCRIPTION OF THE MODELS

In this section, the static model of Dorfman [1] and the dynamic model of Claeys et al. [21] are reviewed in detail.

A. Static Model

In the static model, the bad items in a (huge) population have to be identified. Dorfman [1] has deduced a formula for the mean number of tests ($E[T]$) required to screen a population consisting of N items when the group-individual policy is adopted with group size c . Let \bar{p} characterise the probability that a random item is good. Then $(1 - \bar{p}^c)$ is the probability that a group of c items is bad (at least one item is bad), in which case c additional individual tests are necessary after this group test to actually identify the bad item(s). Hence, the mean number of tests to screen a group of c customers equals $1 + (1 - \bar{p}^c)c$. As the population is divided in N/c subgroups, the average number of tests to screen the entire population reads

$$E[T] = \frac{N}{c} + N(1 - \bar{p}^c) . \quad (1)$$

Along the same lines, it is possible to deduce an expression for the average number of required tests in case of other screening policies. For instance, for the group-subgroup policy whereby a bad group is divided in two subgroups of equal size which are retested individually when the (sub)group test returns bad, it can be found that

$$E[T] = \frac{N}{c} \left[1 + \left(1 - \bar{p}^{\lceil c/2 \rceil}\right) \bar{p}^{\lfloor c/2 \rfloor} (2 + \lceil c/2 \rceil) + \left(1 - \bar{p}^{\lfloor c/2 \rfloor}\right) \bar{p}^{\lceil c/2 \rceil} (2 + \lfloor c/2 \rfloor) + \left(1 - \bar{p}^{\lceil c/2 \rceil}\right) \left(1 - \bar{p}^{\lfloor c/2 \rfloor}\right) (2 + c) \right] . \quad (2)$$

The first term between brackets expresses that at least one test is required per group, the second represents the situation whereby only the first subgroup is bad, the third term corresponds with only the second subgroup being bad, whereas in the final term both subgroups are bad.

B. Dynamic Model

In [2], it was stated that the dynamic nature of the item arrivals can be captured by a queueing model. We here briefly recapitulate the queueing model that is presented in [21]. It is a discrete-time queueing model whereby the numbers of item arrivals during consecutive time slots are modelled by a sequence of independent and identically distributed random variables, with common mass function

$$a(n) \triangleq \Pr [n \text{ arrivals in a random slot}] ,$$

and probability generating function (PGF) $A(z)$, i.e.,

$$A(z) \triangleq \sum_{n=0}^{\infty} a(n)z^n .$$

The mean value, often referred to as mean arrival rate, is denoted by λ and is by definition equal to $A'(1)$ (we use primes to indicate derivatives).

The items join the queue in awaitance of being screened by the testing facility (“the server”). The items are screened (“served”) in groups, which is in queueing theory called batch service (e.g., [23][24][25][26]) or bulk service ([27][28][29][30]). It is assumed that a single test takes exactly one slot and that tests are initiated and completed at slot boundaries. In order to avoid confusion, we adopt the term group screening for the complete process, i.e., for the first test on the entire (original) group and the other tests (if any) on subgroups or individual items of the group. The “service time” of a group of items corresponds with the number of tests required to screen the group and can thus take several slots. As the number of tests required to screen a group depends on the number of items in that group, the service time of a group is dependent on the number of items within the group (a larger group has a larger probability of being bad). The service time of a group consisting of j items is represented by S_j and its corresponding PGF by $S_j(z)$. The following expression for $S_j(z)$ is established in [21] for the group-individual screening policy

$$S_1(z) = z ,$$

$$S_j(z) = \bar{p}^j z + (1 - \bar{p}^j) z^{j+1} , \quad j \geq 2 .$$

This can be comprehended as follows: a group consisting of one item requires only one test. In the other case, a group of size j is good with probability \bar{p}^j and thus requires one (group) test. When the group is bad (with probability

$(1 - \bar{p}^j)$), j additional individual tests are necessary, leading to a service time of $j + 1$ slots.

For the group-subgroup screening policy presented in Section II-A it was found in [21] that

$$S_1(z) = z ,$$

$$S_2(z) = \bar{p}^2 z + (1 - \bar{p}^2) z^3 ,$$

$$S_3(z) = \bar{p}^3 z + \bar{p}^2 p z^3 + (1 - \bar{p}^2) z^5 ,$$

$$S_j(z) = \bar{p}^j z + \bar{p}^{\lceil j/2 \rceil} (1 - \bar{p}^{\lceil j/2 \rceil}) z^{\lceil j/2 \rceil + 3} \\ + \bar{p}^{\lfloor j/2 \rfloor} (1 - \bar{p}^{\lfloor j/2 \rfloor}) z^{\lfloor j/2 \rfloor + 3} \\ + (1 - \bar{p}^{\lfloor j/2 \rfloor}) (1 - \bar{p}^{\lceil j/2 \rceil}) z^{j+3} , \quad j \geq 4$$

The cases $j < 4$ are considered separately to avoid that a bad group or subgroup consisting of one item gets retested. In the expression for $j \geq 4$, the first term corresponds with a good group, the second with only the first subgroup being bad, the third with only the second subgroup being bad and the final term with both subgroups being bad.

At this point, it is important to realize that the dynamic nature of the item arrivals entails **two additional differences** as compared to the static model. First, it is necessary to select a **minimum group size** next to the maximum c from the static model (in the sequel we denote this minimum by l), as it might occur that less items are present than the maximum group size when the testing facility is available. When less than l items are present, screening is postponed, whereas otherwise screening is initiated even if less than c items are present.

Second, whereas in the static model only the number of required tests to screen the entire population matters, **various performance measures** can be of importance in case of a dynamic model. In this paper, we restrict ourselves to the, in our opinion, most important, performance measures for dynamic models. The first is the *testing probability* f , defined as the fraction of slots during which the testing facility is busy. It is equal to the probability that the testing facility is testing (a group, a subgroup or an individual item) during a random time slot. This performance measure is especially of importance from an operational point of view: the smaller the testing probability, the cheaper the testing strategy. The second is the *mean delay* of items (\bar{D}), i.e., the average time that an item remains in the test center (the ‘‘system’’). More specifically, the delay of an item is the time, starting at the end of the time slot wherein the item arrives, until the item has been screened. As screening starts and ends at slot boundaries, the delay of an item is expressed as an integral number of time slots. As opposed to the testing probability, the mean delay is especially

of importance from the point of view of the items to be screened. For instance, when items represent blood samples, it is necessary to inform the patients as soon as possible whether or not they are infected by some disease and the mean delay is a measure for this. The following formulas have been deduced in [21] for these performance measures:

$$f = 1 - \sum_{n=0}^{l-1} d_n , \quad (3)$$

$$\bar{D} = \left[\frac{2cE[S_c] \lambda \sum_{n=0}^{l-1} d_n + c(c-1) \sum_{n=0}^{l-1} d_n + 2c \sum_{n=0}^{l-1} d_n n}{2\lambda(c - E[S_c] \lambda)} + \sum_{n=l}^{c-1} d_n g_n - c(c-1) + S_c''(1) \lambda^2 + E[S_c] A''(1) \right] \quad (4)$$

with

$$g_n \triangleq E[S_n] c [c - 1 + 2n] - E[S_c] n [n - 1 + 2c] \\ + 2\lambda(c - n) E[S_n] E[S_c] + \lambda [c S_n''(1) - n S_c''(1)] ,$$

and $E[S_n] = S_n'(1)$ by definition. The boundary probabilities d_n ($n = 0, \dots, c-1$) are the solutions of the following set of c linear equations:

$$\sum_{n=0}^{l-1} d_n z_i^n + \sum_{n=l}^{c-1} d_n \frac{z_i^n - S_n(A(z_i))}{1 - A(z_i)} = 0 , \quad 1 \leq i \leq c-1 ,$$

$$-c + E[S_c] \lambda = -c \sum_{n=0}^{l-1} d_n + \sum_{n=l}^{c-1} d_n [n E[S_c] - c E[S_n]] .$$

The z_i 's ($1 \leq i \leq c-1$) are the $c-1$ zeroes of $z^c - S_c(A(z))$ inside the closed complex unit disk $\{z \in \mathbb{C} : |z| \leq 1\}$ that are different from 1.

Before we compare results of the static and the dynamic model, it is important to stress that in order to determine optimal group sizes l and c , it is necessary to calculate (3) or (4) (whichever is the intended criterium) for various values of l and c and then select those values that minimize f or \bar{D} . On top of that, (3) and (4) rely on the d_n 's, which in turn are dependent on l and c . Therefore, **those boundary probabilities have to be calculated for every l and c , by each time calculating zeroes z_i and solving a set of equations**. Hence, this procedure is complicated for practitioners due to the numerical work involved and requires much processing time.

Remark 1: It should be noted that formulas (3) and (4) are valid under the assumption that the system is in steady state. The system can reach steady state if and only if

$$\lambda < \frac{c}{E[S_c]} .$$

This inequality guarantees that items that enter the test center will eventually (i.e., after a finite time) be screened. It expresses that the average number of items that enter the test center in a random slot must be smaller than the average number of items that can leave the test center at the end of a slot if many items are present. This is a natural assumption in practice.

In the remainder of this paper, we compare the optimal group size in the static model (in the sequel referred to as optimal static group size) with the minimum and maximum group sizes that produce the smallest testing probability f (Section III) and those that generate the smallest average delay \bar{D} (Section IV) in the dynamic model.

III. TESTING PROBABILITY

In this section, we compare the optimal static group size with the group sizes that minimize the testing probability (f) in the dynamic model. Note first that formulas (1)-(2) and (3)-(4) for the static and dynamic model do not consist of the same parameters. Before we can fairly compare the optimal group sizes, we have to study the influence of these parameters. We therefore represent in Tables I and II the optimal static group size versus the population size N for respectively the group-individual and the group-subgroup screening procedure as presented in Section II-A. To find the optima, we have calculated $E[T]$ for a wide range of values of c and selected the value that produces smallest $E[T]$ as optimum (see [21] for more information). We observe that the population size has no impact on the optimal static group size.

Next, we turn to the dynamic model and evaluate the influence of $A(z)$ on the group sizes that minimize f . The optimal maximum group size is illustrated in Tables III and IV for several values of λ and \bar{p} and for two distributions for the number of item arrivals during a random slot: the Poisson distribution, i.e., with PGF

$$A(z) = e^{\lambda(z-1)} ,$$

and the geometric distribution:

$$A(z) = \frac{1}{1 + \lambda - \lambda z} .$$

We perceive from Tables III and IV that the mean arrival rate λ and even the whole distribution $A(z)$ have no impact on the optimal maximum group size. Note that the **optimal minimum group size** is not mentioned as it is **equal to the**

Table I
GROUP SIZE THAT MINIMIZES $E[T]$ IN CASE OF GROUP-INDIVIDUAL SCREENING (STATIC MODEL)

	$\bar{p} = 0.95$	$\bar{p} = 0.975$	$\bar{p} = 0.99$
$N = 1000$	5	7	11
$N = 2000$	5	7	11
$N = 5000$	5	7	11
$N = 10000$	5	7	11

Table II
GROUP SIZE THAT MINIMIZES $E[T]$ IN CASE OF GROUP-SUBGROUP SCREENING (STATIC MODEL)

	$\bar{p} = 0.95$	$\bar{p} = 0.975$	$\bar{p} = 0.99$
$N = 1000$	8	10	14
$N = 2000$	8	10	14
$N = 5000$	8	10	14
$N = 10000$	8	10	14

optimal maximum group size when the testing probability has to be minimized.

These findings are of crucial importance: in order to compare the static and dynamic models, it is not necessary to “map” the parameter N of the (static) population size on the (dynamic) mean arrival rate λ and the PGF of the arrival process $A(z)$: **the exact values of N and λ and the exact expression for $A(z)$ do not have an influence** on the optimal group sizes. In addition, when comparing Tables I-II with Tables III-IV, it is clear that **the static and the dynamic model produce equal optimal group sizes.**

We now prove these findings. Let us start by inspecting the dynamic model. As already mentioned, the optimal minimum group size always equals the optimal maximum group size. The reasoning behind this is that when less items are present than the maximum group size, it is, from the point of view of minimizing the testing probability, better to wait until enough items are present, in order to fully exploit the benefit of group screening (less tests required). As a result, if the testing facility is screening (with probability f), it always screens a group consisting of c items. As a consequence, the average screening time equals $E[S_c]$ slots, so that in a random slot wherein the testing facility is screening, the ongoing screening is finished at the end of that slot with probability $1/E[S_c]$. Hence, the average number of items leaving the system in a slot because screening is completed equals $fc/E[S_c]$. We now rely on this result to translate the well-known “rate-in-rate-out” principle (see e.g., [31]) in terms of the system parameters. The “rate-in-rate-out” principle expresses that in a queueing system in steady state, the mean number of items entering the system per slot equals the mean number of items leaving the system per slot.

Table III

GROUP SIZE THAT MINIMIZES f IN CASE OF GROUP-INDIVIDUAL SCREENING (DYNAMIC MODEL); * MEANS THAT THE TEST CENTER IS NOT ABLE TO COPE WITH ALL SAMPLES, BECAUSE $\lambda \geq c/E[S_c]$ FOR EVERY VALUE OF c

	$\bar{p} = 0.95$ Poisson	$\bar{p} = 0.95$ geometric	$\bar{p} = 0.99$ Poisson	$\bar{p} = 0.99$ geometric
$\lambda = 1$	5	5	11	11
$\lambda = 2$	5	5	11	11
$\lambda = 3$	*	*	11	11
$\lambda = 4$	*	*	11	11
$\lambda = 5$	*	*	11	11

Table IV

GROUP SIZE THAT MINIMIZES f IN CASE OF GROUP-SUBGROUP SCREENING (DYNAMIC MODEL); * MEANS THAT THE TEST CENTER IS NOT ABLE TO COPE WITH ALL SAMPLES, BECAUSE $\lambda \geq c/E[S_c]$ FOR EVERY VALUE OF c

	$\bar{p} = 0.95$ Poisson	$\bar{p} = 0.95$ geometric	$\bar{p} = 0.99$ Poisson	$\bar{p} = 0.99$ geometric
$\lambda = 1$	8	8	14	14
$\lambda = 2$	8	8	14	14
$\lambda = 3$	*	*	14	14
$\lambda = 4$	*	*	14	14
$\lambda = 5$	*	*	14	14

Putting these elements together yields

$$\lambda = f \frac{c}{E[S_c]} \quad (5)$$

Next, define

$$g(c) \triangleq \frac{E[S_c]}{c} \quad (6)$$

As a result, (5) can be transformed into

$$f = \lambda g(c) \quad .$$

At this point, it is crucial to realize that $g(c)$ is independent of λ and $A(z)$, simply because $E[S_c]$ only depends on c and \bar{p} . As a result, the group size c that produces the smallest value f , minimizes $g(c)$ and is independent of λ and $A(z)$. In the static scenario on the other hand, the mean number of tests required to screen a population of size N is equal to

$$E[T] = \frac{N}{c} E[S_c] \quad ,$$

because the population is divided in N/c groups with average testing time $E[S_c]$. Owing to (6), we obtain

$$E[T] = Ng(c) \quad .$$

Analogously as for the dynamic model, we can state that the optimal group size minimizes $g(c)$ and that N has no impact. We can thus conclude that the optimal group size is the same in both models as it minimizes in essence the same function. Finally, it is worth noting that the proof is independent of the screening policy, which thus infers that the conclusions are valid for all screening policies.

In order to illustrate that the optimal group size minimizes $g(c)$ ($\triangleq E[S_c]/c$), $E[S_c]$ and $g(c)$ are shown in Table V, for various values of c and in case of the group-subgroup screening policy. We indeed notice that for $\bar{p} = 0.95, 0.975, 0.99$, $g(c)$ is minimized when $c = 8, 10, 14$ respectively (compare with Tables II and IV).

Table V

$E[S_c]$ AND $g(c)$ FOR VARIOUS VALUES OF c IN CASE OF GROUP-SUBGROUP SCREENING

	$E[S_c]$ $\bar{p} = 0.95$	$g(c)$ $\bar{p} = 0.95$	$E[S_c]$ $\bar{p} = 0.99$	$g(c)$ $\bar{p} = 0.99$
$c = 1$	1	1	1	1
$c = 2$	1.1950	0.5975	1.0398	0.5199
$c = 3$	1.4803	0.4934	1.0992	0.3664
$c = 4$	1.7610	0.4402	1.1584	0.2896
$c = 5$	2.0753	0.4151	1.2269	0.2454
$c = 6$	2.3856	0.3976	1.2952	0.2159
$c = 7$	2.7732	0.3962	1.3826	0.1975
$c = 8$	3.1571	0.3946	1.4697	0.1837
$c = 9$	3.6126	0.4014	1.5756	0.1751
$c = 10$	4.0647	0.4065	1.6813	0.1681
$c = 11$	4.5829	0.4166	1.8055	0.1641
$c = 12$	5.0982	0.4248	1.9295	0.1608
$c = 13$	5.6744	0.4365	2.0716	0.1594
$c = 14$	6.2479	0.4463	2.2136	0.1581
$c = 15$	6.8777	0.4585	2.3735	0.1582

IV. MEAN DELAY

In the previous section, we have shown that the minimum and maximum group sizes that minimize f in the dynamic model are both equal to the optimal static group size. In this section, we investigate whether this also holds when \bar{D} is minimized instead of f in the dynamic model. First, note that the **optimal minimum group size now equals 1**. Indeed, if very few items are present when the testing facility is available, these items would probably suffer a considerable delay if the testing facility would postpone screening until more items are present. In addition, the probability of a group of very few items to be infected is very small, so that most likely the screening of such a group only lasts one slot, in which case the testing facility will be available again at the beginning of the next slot for possible newly arrived items. As a result, we fix the minimum group size to 1.

Next, we illustrate the maximum group size that minimizes \bar{D} for various values of λ and \bar{p} , both for the group-individual (Table VI) and the group-subgroup screening policy (Table VII). We observe that the **optimal maximum group size increases as a function of λ** and that **for large enough λ it equals the static optimum**. The latter is a consequence of the fact that when the system is heavily loaded, nearly always many items are present, meaning that the system becomes almost equivalent with a static system. In the previous section, we have proved that the optimal

static group size minimizes $g(c)$, the average number of tests per item. It is thus natural to ask why for small and medium values of λ it is better to select a smaller maximum group size than the group size that minimizes the average number of tests per item. In order to understand this, we consider the example with the group-subgroup policy and with $\bar{p} = 0.975$ (Table VII). Assume that 10 items are present, the testing facility is available and $\lambda = 1$. It seems evident to execute 1 group test on the 10 items, as this would lead to the smallest average number of tests per item (Table IV). However, Table VII indicates that a maximum group size equal to 6 is the best option. Let us observe what happens if the maximum group size equals 6 instead of 10, by relying on Table V. When the 10 items are screened together, this takes on average 2.6364 slots. When, on the other hand, only the first 6 items are screened together, these 6 items are screened in, on average, 1.72 slots. Thereafter, the remaining 4 items can be screened, in other words, these items have already been delayed on average 1.72 slots before their screening is initiated. As $\lambda = 1$, on average 5.72 items are present when the screening of the first 6 items is completed. Assume that 6 items are present at that time. These items are screened together and it takes on average 1.72 slots. Hence, the first 6 items benefit and suffer on average a delay of 1.72 instead of 2.6364 slots, whereas the screening of the other 4 items is completed after on average 3.34 instead of 2.6364 slots. As a consequence, the average screening time of these 10 items is $(6 * 1.72 + 4 * 3.34)/10 = 2.368$, which is better than 2.6364 slots. This example thus illustrates why the maximum group size that minimizes \bar{D} can be smaller than the optimal static group size for smaller values of λ .

Table VI
GROUP SIZE THAT MINIMIZES \bar{D} IN CASE OF GROUP-INDIVIDUAL SCREENING; * MEANS THAT THE TEST CENTER IS NOT ABLE TO COPE WITH ALL SAMPLES, BECAUSE $\lambda \geq c/E[S_c]$ FOR EVERY VALUE OF c

	$\bar{p} = 0.95$	$\bar{p} = 0.975$	$\bar{p} = 0.99$
$\lambda = 1$	3	4	6
$\lambda = 2$	4	5	6
$\lambda = 2.25$	5	5	6
$\lambda = 2.5$	*	5	6
$\lambda = 3$	*	6	7
$\lambda = 3.25$	*	7	7
$\lambda = 3.5$	*	*	7
$\lambda = 4$	*	*	8
$\lambda = 5.11$	*	*	11

Hence, for low and medium λ , the static model overestimates the optimal group size if the mean delay of items has to be optimized. A question that arises in this context is: when the static optimal group size (say c_s) is selected instead of the group size that actually minimizes \bar{D} (we call this c_d),

Table VII
GROUP SIZE THAT MINIMIZES \bar{D} IN CASE OF GROUP-SUBGROUP SCREENING; * MEANS THAT THE TEST CENTER IS NOT ABLE TO COPE WITH ALL SAMPLES, BECAUSE $\lambda \geq c/E[S_c]$ FOR EVERY VALUE OF c

	$\bar{p} = 0.95$	$\bar{p} = 0.975$	$\bar{p} = 0.99$
$\lambda = 1$	4	6	8
$\lambda = 2$	6	6	8
$\lambda = 2.5$	8	8	8
$\lambda = 3$	*	8	10
$\lambda = 3.75$	*	10	10
$\lambda = 4$	*	*	10
$\lambda = 6$	*	*	14

what is the relative error

$$100(\bar{D}_s - \bar{D}_d)/\bar{D}_s ,$$

(in %), with \bar{D}_s the mean delay when $c = c_s$ and \bar{D}_d the mean delay when $c = c_d$. We have therefore depicted this relative error versus λ in Figures 1 and 2, for the group-individual and the group-subgroup screening policy respectively. We observe that the **relative error is extremely small for small values of λ** , that it **first increases as a function of λ** , and then **decreases again when λ becomes large**. When for instance $c = 14$ is selected instead of $c = 8$ for small values of λ , it does not matter much because it seldom occurs that more than 8 items are present when the testing facility is available. If λ increases, this occurs more, which then leads to a larger relative error. Finally, when λ becomes large, c_d tends to c_s , which leads to a decaying relative error.

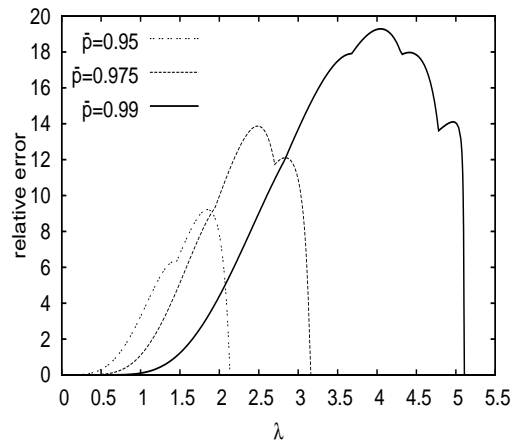


Figure 1. Relative error (in %) versus λ ; Group-individual screening policy

Remark 2: Even in those cases whereby it is necessary to adopt the dynamic model because the relative error is significant, this paper provides precious information. Indeed, we have pointed out that the optimal minimum group size equals one and that the optimal maximum group size is upper bounded by the optimal static group size. As a result, \bar{D} has to be calculated only for values of c not larger than

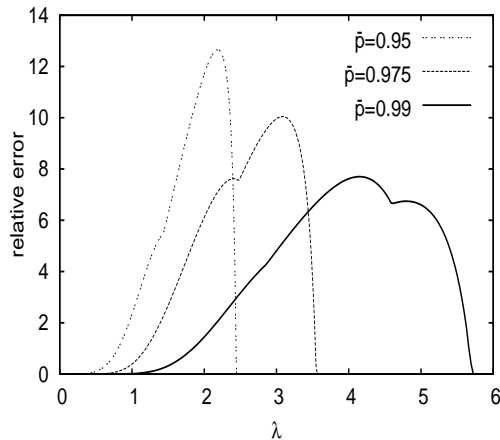


Figure 2. Relative error (in %) versus λ : Group-subgroup screening policy

the optimal static group size, instead of an extensive range of combinations of both l and c , which thus reduces the calculation time considerably.

V. CONCLUSION AND FUTURE WORK

In this paper, we have investigated to what extent the optimal static group size of Dorfman remains efficient in a dynamic context. We have explained that instead of one group size, a minimum and a maximum group size have to be determined in case of dynamic item arrivals. In addition, various performance measures exist, whereas only the number of tests required to screen the population matters in the static model. We have considered the testing probability and the mean delay of items. The former is especially of importance from an operational point of view, whereas the latter is crucial for the items to be tested.

We have shown that when the testing probability has to be minimized, both the optimal minimum and the maximum group size equal the optimal static group size. When, on the other hand, the average delay has to be minimized, the optimal minimum group size equals one, whereas the optimal maximum group size increases as a function of the mean arrival rate (λ) and eventually becomes equal to the optimal static group size for large mean arrival rates. We have demonstrated that selecting the optimal static group size instead of the optimal maximum group size, leads to a small relative error in the mean delay for sufficiently small or large mean arrival rates and to a larger relative error for medium mean arrival rates.

We can thus conclude that this paper clearly indicates under which circumstances the static model from Dorfman produces satisfying results in a dynamic context. This is of vital importance for practitioners, as the model from Dorfman was the de facto standard for several decades and thus has to be validated. On top of that, even though dynamic models exist nowadays, these are much harder to implement

and require a time-consuming processing time, due to the numerical work that is involved, such as repeatedly calculating zeroes of functions and solving sets of equations.

Finally, we would like to stress that even when it is necessary to rely on a dynamic model, this paper provides valuable insights which aid in reducing the calculation time considerably.

Although this paper provides precious insights, there are several directions for future research. First, the conclusions in this paper are based on numerical examples and intuitive reasoning. Therefore, we will continue our research in order to prove our findings on a rigorous manner. Next, we will investigate whether the conclusions from this paper also hold when the number of item arrivals during consecutive time slots is not independent and identically distributed, but exhibits some kind of correlation. Finally, we will also study other performance measures, such as the probability that the delay of an item exceeds some large threshold, the mean number of items waiting in the queue to be screened, etc.

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