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**MULTINOMIAL GROUP TESTING MODELS
WITH INCOMPLETE IDENTIFICATION**

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Multinomial Group Testing Models with Incomplete Identification

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Abstract

We study reliable multinomial probabilistic group testing models with incomplete identification. We assume that every of the pooled items has none or some of k attributes, one of them causing contamination. Any group possessing this latter attribute is discarded, while the others are collected and separated according to the attributes that were found in them. The objective is to choose an optimal group size for pooled screening so as to collect prespecified numbers of items of the various types with minimum testing expenditures. We derive exact results for the underlying distributions of the stopping times, enabling us to find optimal procedures by numerical methods.

Keywords: Group testing; multinomial trials; stopping time; optimal group size; optimal truncation.

1 Introduction

Basic group testing models deal with the classification of the items of some finite population in the two categories ‘good’ and ‘defective’. It is assumed that the items are group testable, i.e., for any subset of the population it is possible to carry out a simultaneous test (group test) with two possible outcomes: ‘success’, indicating that all items in the subset are good, and

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‘failure’, in which case at least one of the items in the subset is defective, without giving any clue which or how many are defective. Under the standard assumption that the items are defective independently of each other, each with the same probability, every group test constitutes a Bernoulli trial.

Since the pioneering work of Dorfman (1943) on pooled blood samples, numerous group testing procedures have been suggested and applied in various areas, not only to detect syphilis, HIV or other diseases or for DNA screening, but also in quality control for industrial production systems (e.g. Sobel and Groll (1959), Li (1962), Bar-Lev, Boneh and Perry (1990)) and communication networks. A key reference is the monograph by Du and Hwang (2000). Applications to HIV screening are given, among others, by Ham-mick and Gastwirth (1994), Litvak, Tu and Pagano (1994), Tu, Litvak and Pagano (1995), Wein and Zenios (1996), and Hung (2000) who used binomial grouping in hypotheses testing for the classification of quantitative covariables. Combinatorial questions in the context of DNA library screening were recently studied by Macula (1999a,1999b).

We propose a classification of group testing models according to the following five dichotomies. As these features can be combined freely, we obtain $2^5 = 32$ possible types of basic group testing models.

(a) *Probabilistic group testing (PGT) versus combinatorial group testing (CGT)*. In PGT a probability distribution on the number of defective items is assumed, while CGT deals with enumeration problems, using combinatorial techniques (see Du and Hwang (2000)).

(b) *Complete versus incomplete identification*. The objective can be a complete and correct division of the population into good and defective items via repeated group testing, or one can aim at finding some required number of good items (possibly subject to certain additional conditions). The latter models study optimal stopping times and optimization problems under constraints. Most of the references mentioned above discuss problems of complete identification. For the second type of models see Bar-Lev, Boneh and Perry (1990) and Bar-Lev, Stadje and Van der Duyn Schouten (2002a, 2002b).

(c) *Reliable versus unreliable testing*. In most studies it is assumed that the result of every group test is correct: a group is tested to be ‘good’ if and only if it does not contain any defective item. However, testing could also yield unreliable results: either false-positive, which means that a group is wrongly labeled contaminated, or false-negative in case a group is wrongly labeled good. The notions of false-positive and false-negative are commonly used in

medical experiments. In the group testing context, unreliable outcomes are discussed Litvak, Tu and Pagano (1994), Tu, Litvak and Pagano (1995) and Hung (2000).

(d) *Binomial versus multinomial.* In binomial models every group test is assumed to have one of two possible results, while in (strictly) multinomial models there are more than two possibilities. A multinomial CGT problem with complete identification and three outcomes has been studied by Christen (1983) in the context of the so-called candy factory model (see also Du and Hwang, 2000, pp. 118-123).

(e) *Time constraints versus arbitrary processing times.* Every group test is time consuming; the processing times of the conducted tests may or may not be taken into account. For example, there can be a time constraint by which all testing has to be terminated. Bernoulli PGT models with random i.i.d. processing times and incomplete identification have been studied in Bar-Lev, Stadjé and Van der Duyn Schouten (2002a).

The 32 types of possible group testing models generated by the above alternatives are summarized in Table 1.

Category	First Type	Second Type
Distributional	PGT	CGT
Identification	complete	incomplete
Reliability	reliable	false-positive, false-negative
Outcomes	Bernoulli	multinomial
Processing Times	with	without

Table 1: *Classification of group testing models.*

In this paper we study reliable multinomial PGT models with incomplete identification without processing times. We assume that each item possesses none or some of k possible attributes. One may think for example of blood samples in which the indicators of several different diseases and other factors can be present. Denote by $\mathbb{V} = \{v_1, \dots, v_k\}$ the set of these attributes and split it into two subsets, $\mathbb{V} = \{v_1, \dots, v_g\} \cup \{v_{g+1}, \dots, v_k\}$, $1 \leq g < k$, where $\mathbb{V}_g = \{v_1, \dots, v_g\}$ and $\mathbb{V}_d = \{v_{g+1}, \dots, v_k\}$ are considered to be the subsets of ‘good’ or ‘defective’ attributes, respectively. Now suppose that m such items are pooled together and group tested for the presence of elements of $\mathbb{V}$. If the test indicates that at least one element of $\mathbb{V}_d$ is present, then the group is defined to be contaminated and therefore discarded. Otherwise, if none of the elements of $\mathbb{V}$ or only those of $\mathbb{V}_g$ are found, the group is defined as clean (or good). These groups are accumulated and it is recorded which elements

of the $\mathbb{V}_g$, if any, were detected.

Since contaminated groups are not used further on, we may without restriction of generality fuse all elements of $\mathbb{V}_d$ into one so that $g = k - 1$ and $\mathbb{V}_d = \{v_k\}$, $\mathbb{V}_g = \{v_1, \dots, v_{k-1}\}$. For example, blood samples containing indicators for HIV, HTLV or Hepatitis A, B or C are obviously discarded, so that these defective attributes can be combined and considered as one factor. It should be noted that prior to screening blood donations for the presence of hepatitis, blood transfusions used to be the cause for more than 20% of all hepatitis cases.

A group in which v_k is not present is called clean; if no element of $\mathbb{V}$ is present, it is called purely clean. There are 2^{k-1} different types of clean groups which can be distinguished. Each group test constitutes a multinomial trial with $l = 2^{k-1} + 1$ possible outcomes, called purely clean, or clean of one of $2^{k-1} - 1$ distinguishable types, or contaminated.

The paper is organized as follows. In Section 2 we present in detail the general setting of the multinomial group testing models under consideration. We assume that a sufficiently large population is available for group testing, and there are demand requirements for the different clean item types. In Section 3 we show how to determine the probabilities of the various group types in terms of the model ingredients. In Section 4 appropriate stopping times are introduced depending on whether the demand requirements can be met or no more groups are left for further group tests. We derive the distributions of these stopping times in closed form. In Section 5 we introduce reasonable objective functions depending on the cost structure and the parameters involved. These functions have to be minimized subject to deterministic as well as probabilistic constraints. The decision variables are the group size m and the maximum number of possible group tests. The exact formulas for the objective functions and the constraints are very complicated, and only numerical optimization seems possible. In Section 6 we consider the trinomial case and study some numerical examples, including a sensitivity analysis of the objective functions and optimal solutions.

2 Model description

Items are testable in groups of any size m . (In practice, there may be a threshold $m \leq m_0$ for the group size.) Each item possesses some or none of the attributes $v_1, \dots, v_k$, where v_k is the defective attribute. The items are

stochastically independent. The number of items that can be purchased for testing is virtually infinite.

(ii) Regardless of the group size, any group test can result in one of $l = 2^{k-1} + 1$ types. The type indicates which of the attributes $v_1, \dots, v_k$ were found in the group. Clean groups are kept, aggregated and recorded according to their types; contaminated groups are discarded. A clean group is not further inspected for identifying the attributes of its individual items, but is put aside for possible future inspection.

(iii) The findings of any group test are 100% reliable. Thus no ‘false-negative’ or ‘false-positive’ errors occur.

(iv) Every item can have any combination of attributes independently of the other items. The outcomes of successive group tests are therefore independent. The population prevalence rates of all l types are assumed to be known in advance. (In medical studies these rates are indeed either known or can be accurately estimated.) Usually, the population prevalence rate of contaminated items is much smaller than those of the clean types taken together. In some applications (particularly in medicine) the occurrence of the k attributes $v_1, \dots, v_k$ in an item can be assumed to be independent. In this case we denote by p_i the probability that an item possesses attribute i and set $q_i = 1 - p_i$, $i = 1, \dots, k$.

(v) There are demand requirements for the various types of clean items. One possibility is to prespecify the numbers of required items for every clean type; a second option is to require say D clean items, among them at least d_1 purely clean ones. These or similar objectives determine the stopping time of the group testing process, which terminates when the requirement are met or some prespecified maximum number L of tests has been conducted.

(vi) The cost for buying and testing a group depend on its size m and is denoted by $c(m)$. For simplicity we assume that $c(m)$ has a fixed and a linear part, i.e., $c(m) = c_1 + c_2 m$ for some known cost parameters $c_1, c_2 \geq 0$. c_1 and c_2 are the cost per test and the cost per item, respectively. We also consider the possibility to buy clean items of type i at the price of b_i per item, $i = 1, \dots, l - 1$, from some secure source. We make such an alternative available in order to fulfill the demand requirements or to assess the cost of missing them. Finally, there may be a budget limit C for the entire testing process. As decision variables we take either m alone or m and L together.

(vii) In order to avoid some computational and analytical subtleties, we only consider group sizes m that divide all the demand quantities required for the

various clean items.

In this paper we do not consider several issues of practical importance for simultaneous group testing for various attributes; we mention interactions due to pooling, the effect of window periods (i.e., the time intervals between infections and the appearance of antibodies), constraints on processing times and expirations dates. Processing times can be incorporated in our model in the same way as in Bar-Lev, Stadje and Van der Duyn Schouten (2002a). The contaminating attributes can have different window periods so that at the time of group testing some or all of them cannot be detected. For those situations our model needs to be considerably refined. These and other challenging problems will be dealt with in further studies.

3 The probabilities of the group types

Consider the k attributes $v_1, \dots, v_k$ and fix the group size m . For a given group, let $(Z_{j1}, \dots, Z_{jk})$ be the random vector of '1's and '0's defined by

$$Z_{j\nu} = 1 \text{ if the } j\text{th item in the group possesses attribute } v_\nu,$$

and $Z_{j\nu} = 0$ if it does not. Let

$$\mathbf{Z} = (Z_{j\nu})_{j=1, \dots, m, \nu=1, \dots, k}$$

be the $(m \times k)$ -matrix of the $Z_{j\nu}$. For $1 \leq h \leq k$ and distinct indices $1 \leq s_1 < \dots < s_h \leq k$ we denote by $B_{s_1, \dots, s_h}$ the event that the attributes $v_{s_1}, \dots, v_{s_h}$ are present in at least one item of the given group while the other attributes are missing in all m items. Let B be the event that none of the attributes is present in the group. We can express the probabilities of these events in terms of the distribution of $\mathbf{Z}$. Indeed, we have

$$\begin{aligned} P(B_{s_1, \dots, s_h}) &= P\left(\sum_{j=1}^m Z_{js_\nu} \geq 1 \text{ for } \nu = 1, \dots, h, \sum_{j=1}^m Z_{js} = 0 \text{ for } s \notin \{s_1, \dots, s_h\}\right) \\ &= \sum P(\mathbf{Z} = \mathbf{a}) \end{aligned} \tag{3.1}$$

where the sum is over all matrices $\mathbf{a} = (a_{js})_{j=1, \dots, m, s=1, \dots, k}$ satisfying

$$\begin{aligned} a_{js} &\in \{0, 1\} \\ \sum a_{js_\nu} &\geq 1 \text{ for } \nu = 1, \dots, h \\ a_{js} &= 0, \quad s \notin \{s_1, \dots, s_h\}. \end{aligned}$$

Similarly,

$$P(B) = P(Z_{j\nu} = 0 \text{ for all } j, \nu). \quad (3.2)$$

The presence of attribute v_k contaminates a group so that we combine all types containing v_k into one; therefore we distinguish between the $l = 2^{k-1} + 1$ types

$$B_{s_1, \dots, s_h}, \quad 1 \leq h \leq k-1, \quad 1 \leq s_1 < \dots < s_h \leq k-1 \quad (3.3)$$

$$B \text{ and } \bigcup_{h=0}^{k-1} \bigcup_{1 \leq s_1 < \dots < s_h \leq k-1} B_{s_1, \dots, s_h, k}. \quad (3.4)$$

The types in (3.3) are the clean ones containing at least one of the attributes $v_1, \dots, v_{k-1}$; B is purely clean and the second type in 3.4 is the contaminated one. We number the types from 1 to l and call the types $B^{(1)}, \dots, B^{(l)}$, where $B^{(1)} = B$ and $B^{(l)}$ is the contaminated type.

Now let us consider the probabilities of the $B^{(i)}$. By the independence of the rows of $\mathbf{Z}$ (assumption (iv)) it follows that

$$P(B) = P(Z_{j\nu} = 0, \nu = 1, \dots, k)^m. \quad (3.5)$$

In particular, if the attributes are independent,

$$P(B) = \prod_{\nu=1}^k q_{\nu}^m. \quad (3.6)$$

The probabilities in (3.1) are difficult to compute in general. However, in the case of independent attributes it is easily seen that

$$P(B_{s_1, \dots, s_h}) = \prod_{\nu \notin \{s_1, \dots, s_h\}} q_{\nu}^m \prod_{i=1}^h (1 - q_{s_i}^m). \quad (3.7)$$

Finally,

$$P(B^{(l)}) = P\left(\sum_{j=1}^m Z_{jk} \geq 1\right) = 1 - q_k^m. \quad (3.8)$$

In the following we use the notation $\pi_i = P(B^{(i)})$ and $\pi = (\pi_i)_{i=1, \dots, l}$. If the dependence on the group size m becomes important, we write $\pi_i(m)$ and $\pi(m) = (\pi_i(m))_{i=1, \dots, l}$.

4 Stopping times and analysis

We denote by $M(n : r; \beta_1, \dots, \beta_r)$ the multinomial distribution with n trials, each having r possible outcomes with probabilities $\beta_1, \dots, \beta_r$, respectively.

Now assume that a sequence of independent samples of size m is group tested. Let $Y_{in} = 1$ if the n th group is tested to be of type i , and $Y_{in} = 0$ otherwise. Then obviously

$$\left(\sum_{n=1}^N Y_{1n}, \dots, \sum_{n=1}^N Y_{ln} \right) \sim M(N : l, \pi). \quad (4.1)$$

The random vector in (4.1) counts the number of groups of each of the l types in N group tests of size m .

Two kinds of stopping times for this group testing process are of special interest. We fix certain target values $D_1, \dots, D_{l-1}$ for the first procedure and D, D_1 for the second one. These values have to be multiples of m . Let $d_i = D_i/m$, $i = 1, \dots, l-1$, and $d = D/m$.

(a) Stop as soon as prespecified numbers $d_1, \dots, d_{l-1}$ of groups of types $B^{(1)}, \dots, B^{(l-1)}$ have been obtained or exceeded. This means stopping at

$$T_1 = T_1(m) = \inf \left\{ n \mid \sum_{j=1}^n Y_{ij} \geq d_i, \text{ for } i = 1, \dots, l-1 \right\}. \quad (4.2)$$

Figure 1 illustrates this stopping rule for $l = 3$. The lattice points on the polygonal line give the successive values of $(S_{n,1}, S_{n,2}) = (\sum_{j=1}^n Y_{1j}, \sum_{j=1}^n Y_{2j})$, $n = 1, 2, \dots$; the process is stopped as soon as a point (d_1, k_2) or (k_1, d_2) with $k_1 \geq d_1, k_2 \geq d_2$ is reached.

(b) Fix positive integers $d_1 < d$ and stop as soon as one of the following events has occurred: (i) d non-contaminated groups have been obtained, among them at most $d - d_1$ groups not of type 1; (ii) more than $d - d_1 =$ groups not of type 1 and at least d_1 of type 1 have been obtained. (Note that in this case the demands of clean types 2 to $l-1$ are aggregated.) Formally, stop at

$$T_2 = T_2(m) = \inf \left\{ n \mid \sum_{j=1}^n \sum_{i=2}^{l-1} Y_{ij} \leq d - d_1, \sum_{j=1}^n \sum_{i=1}^{l-1} Y_{ij} = d \right. \\ \left. \text{or } \sum_{j=1}^n \sum_{i=2}^{l-1} Y_{ij} > d - d_1, \sum_{j=1}^n Y_{1j} = d_1 \right\}. \quad (4.3)$$

Figure 1: the rule T_1 and its stopping region

Figure 2 shows the stopping region for $T_2(m)$ and a typical path of $(S_{n,1}, S_{n,2}) = (\sum_{j=1}^n Y_{1j}, \sum_{j=1}^n Y_{jn})$ for $l = 3$.

Figure 2: the rule T_2 and its stopping region

A natural generalization of (b) is as follows. Divide the clean types into the two subclasses $A_1 = \{1, \dots, r\}$ and $A_2 = \{r+1, \dots, l-1\}$. Fix positive integers $d_i, i \in \{1, \dots, r\}$, and d satisfying $\sum_{i=1}^r d_i < d$. Keep on testing until d clean groups have been obtained. If there are at least d_i groups of type i among them for every $i \in A_1$, stop. Otherwise, continue until these requirements are all met. This stopping time can be dealt with in the same way as T_2

(which is the special case $r = 1$).

In practice, there is often an upper bound L on the number of group tests that can be conducted. Therefore, we define the truncated stopping times

$$T_{i,L}(m) = \min(T_i(m), L), \quad i = 1, 2 \quad (4.4)$$

which determine the two group testing policies considered in this paper. We also need to introduce the random variables that count the number of clean items of the various types missing at the end of the testing procedure to meet the demand requirements. (Recall that by Assumption (vi) there is an option to purchase type i clean items at the price of b_i per item.) These numbers of missing items will be used in the objective functions in Section 5. For the stopping time $T_{1,L}$ they are given by the components of the random vector

$$R_1 = (R_{1k})_{k=1,\dots,l-1} = \left(m(d_1 - \sum_{j=1}^{T_{1,L}} Y_{1j})_+, \dots, m(d_{l-1} - \sum_{j=1}^{T_{1,L}} Y_{l-1,j})_+ \right). \quad (4.5)$$

For the stopping time $T_{2,L}$ the demand $D_1 = md_1$ of purely clean items will be fully satisfied if and only if $T_2 \leq L$; the other clean types are not distinguished and the total number of those items missing after the procedure is

$$R_2 = m(d - d_1 - \sum_{j=1}^{T_{2,L}} \sum_{i=2}^{l-1} Y_{ij})_+. \quad (4.6)$$

In the following theorem we give expressions for the probability distributions of T_1 and T_2 . Note that the two distributions have the same support $S_d = \{d, d+1, \dots\}$. We need the multinomial coefficients

$$\mu_j^{(N)}(k_1, \dots, k_j) = \binom{N}{k_1, \dots, k_j}.$$

Theorem 1 For every $n \in S_d$ we have

$$P(T_1 = N) = \sum_{i=1}^{l-1} \sum_{k_j \geq 0 \ (j \neq i)} \mu_l^{(N-1)}(d_1 + k_1, \dots, d_{i-1} + k_{i-1}, \\ d_i - 1, d_{i+1} + k_{i+1}, \dots, d_l + k_l) \pi_i^{d_i} \prod_{j \neq i} \pi_j^{d_j + k_j} \quad (4.7)$$

$$P(T_2 = N) = \sum_{k=1}^{d-d_1} \mu_3^{(N-1)}(d_1 + k - 1, d - d_1 - k, N - d) \pi_1^{d_1 + k - 1} \\ \times \left[\sum_{i=2}^{l-1} \pi_i \right]^{d-d_1-k} \pi_l^{N-d} \sum_{i=1}^{l-1} \pi_i \\ + \sum_{k=0}^{N-d} \mu_3^{(N-1)}(d_1 - 1, d - d_1 + k, N - d - k) \pi_1^{d_1} \\ \times \left[\sum_{i=2}^{l-1} \pi_i \right]^{d-d_1+k} \pi_l^{N-d-k}. \quad (4.8)$$

Proof. Let $(W_1, \dots, W_l)$ be distributed according to $M(N-1 : l, \pi)$ and let A_i be the event that in an $M(1 : l, \pi)$ trial independent of $(W_1, \dots, W_l)$ the outcome is i , $i \in \{1, \dots, l\}$. The event $\{T_1 = N\}$ occurs if and only if for the first $N-1$ tests there exists a type i such that for all types $j \neq i$ at least d_j groups of type j and exactly $d_i - 1$ groups of type i have been tested, and then in the N th test another group of type i appears. This yields

$$P(T_1 = N) = \sum_{i=1}^{l-1} P(W_i = d_i - 1, W_j \geq d_j \text{ for all } j \neq i) P(A_i) \\ = \sum_{i=1}^{l-1} \sum_{k_j \geq 0 \ (j \neq i)} P(W_i = d_i - 1, W_j = d_j + k_j, \text{ for all } j \neq i) \pi_i. \quad (4.9)$$

Inserting explicit expressions for the multinomial probabilities in (4.9) yields (4.7).

The event $\{T_2 = N\}$ occurs if and only if:

- (i) either the total number of non-contaminated groups among the first $N-1$ ones is $d-1$, types $2, \dots, l-1$ have altogether occurred less than $d-d_1$ times, and then in the N th test a group is tested to be non-contaminated;

(ii) or the total number of groups of types $2, \dots, l-1$ among the first $N-1$ ones is at least $d-d_1$, type 1 has occurred exactly d_1-1 times, and then in the N th test a group is tested to be purely clean.

This decomposition yields

$$\begin{aligned}
P(T_2 = N) &= \sum_{k=1}^{d-d_1} P(W_2 + \dots + W_{l-1} = d-d_1-k, W_1 = d_1+k-1) \\
&= \times [P(A_1) + \dots + P(A_{l-1})] \\
&\quad + \sum_{k=0}^{\infty} P(W_2 + \dots + W_{l-1} = d-d_1+k, W_1 = d_1-1) P(A_1).
\end{aligned} \tag{4.10}$$

Again inserting the multinomial probabilities leads to (4.8).

5 Objective functions

Now let us consider the cost of the group testing procedures when using one of the stopping times $T_{i,L}(m)$, $i = 1, 2$. We take into account the cost factors

$$C_{1,i}(m, L) = (c_1 + c_2 m) T_{i,L}(m), \quad i = 1, 2 \tag{5.1}$$

$$C_{2,1}(m, L) = \sum_{j=1}^{l-1} b_j m (d_j - \sum_{j=1}^{T_{1,L}(m)} Y_{1j})_+ \tag{5.2}$$

and

$$\begin{aligned}
C_{2,2}(m, L) &= b_1 m (d_1 - \sum_{j=1}^{T_{2,L}(m)} Y_{1j})_+ + b_1 R_2 \\
&= b_1 m (d_1 - \sum_{j=1}^{T_{2,L}(m)} Y_{1j})_+ + b_2 m (d - d_1 - \sum_{j=1}^{T_{2,L}(m)} \sum_{i=2}^{l-1} Y_{ij})_+.
\end{aligned} \tag{5.3}$$

$C_{1,i}(m, L)$, $i = 1, 2$, is composed of the purchase cost of $m T_{i,L}(m)$ items used for group testing and the cost for running the group tests. The constants c_1 and c_2 denote the cost per item and the cost per test, respectively. $C_{2,1}(m, L)$ is the total cost, when using stopping time $T_{1,L}(m)$, of purchasing the missing

clean items at the price of b_i per clean item of type i , $i = 1, \dots, l - 1$. Under stopping times $T_{2,L}$ the clean types $2, \dots, l - 1$ are not distinguished, so that we assume a common price $b_2 > b$ for buying one of them from a secure source. Then $C_{2,2}(m, L)$ gives the total cost of purchasing the missing clean items after using $T_{2,L}(m)$.

We consider two expected cost minimization problems for $T_{1,L}(m)$. In both problems, the decision variables are the group size m and the truncation threshold L . Only values of m satisfying

$$D_i/m \in \mathbb{N} \text{ for } i = 1, \dots, l - 1 \quad (5.4)$$

are admissible, and we may restrict m further by imposing an upper bound:

$$m \leq m_0, \quad (5.5)$$

To ensure that the demand will be met with high probability we introduce the constraint

$$P(T_i(m) > L) \leq \alpha, \quad i = 1, 2 \quad (5.6)$$

for some preassigned value $\alpha \in (0, 1)$, which in practice will of course be small.

If no clean items can be acquired after the testing, the budget constraint

$$P(C_{1,i}(m, L) \leq C) \geq 1 - \beta, \quad i = 1, 2 \quad (5.7)$$

is of interest. It assures that, with reliability of at least $100(1 - \beta)\%$, the total cost of the testing process does not exceed the preassigned budget limit C .

The constraint

$$P(C_{1,i}(m, L) + C_{2,i}(m, L) \leq C) \geq 1 - \beta, \quad i = 1, 2. \quad (5.8)$$

relates to the situation with extra purchase option; it requires that the total cost for buying items, running the testing process and acquiring the missing clean items does not exceed C .

The two optimization problems for the policies $T_{i,L}(m)$, $i = 1, 2$, can now be formulated as follows:

Problem 1. Under the constraints (5.4)-(5.7) find

$$\min_{m,L} \{E(C_{1,i}(m, L))\}. \quad (5.9)$$

Problem 2. Under the constraints (5.4)-(5.6) and (5.8) find

$$\min_{m,L} \{E(C_{1,i}(m, L) + C_{2,i}(m, L))\}. \quad (5.10)$$

These minimization problems cannot be solved analytically. The objective functions and the constraints can, however, be expressed in terms of complicated sums of multinomial probabilities, as specified in Theorem 1. In the final section we discuss some numerical examples for the trinomial case.

6 Some numerical analysis in the trinomial case

Now let $k = 2$, i.e. every item possesses none or at least one of two attributes v_1, v_2 . Then the three types of group testing results are: $B^{(1)}$, the purely clean type, $B^{(2)}$, the case when v_1 but not v_2 is present, and $B^{(3)}$, the case when v_2 is present.

As an example, consider the case of blood samples which have to be tested for the presence of a rare blood type (such as AB having Rh negative) and of HIV antibodies. Then $B^{(1)}$ stands for the rare blood type without HIV antibodies, while $B^{(2)}$ represents HIV infected serum.

We assume that the attributes are independently distributed in the population. Then in a group test of size m the probabilities of the three different outcomes are

$$\begin{aligned} \pi_1 &= P(B^{(1)}) = q_1^m q_2^m \\ \pi_2 &= P(B^{(2)}) = q_2^m (1 - q_1^m) \\ \pi_3 &= P(B^{(3)}) = 1 - q_2^m \end{aligned} \quad (6.1)$$

(cf. (3.6)-(3.8)). These probabilities can now be used in (4.7) and (4.8). The other ingredients in these formulas are trinomial coefficients $\binom{N-1}{k_1, k_2, k_3}$. The exact distributions of $T_{1,L}(m)$ and $T_{2,L}(m)$ form the basis of the following numerical calculations.

The columns in Tables 1 and 2 display the following quantities for different values of L , the maximum number of group tests:

(a) $\min_m E(C_{1,1}(m, L));$

- (b) the value $\hat{m} = \hat{m}(L)$ of the group size m minimizing $m \mapsto E(C_{1,1}(m, L))$;
- (c) the constraint probabilities $P(T_1(\hat{m}) > L)$ and $P(C_{1,1}(\hat{m}, L) \leq C)$.

In both cases we have chosen $D_1 = 60$ and $D_2 = 120$ as the target numbers of items. Thus the possible group sizes (divisors of D_1 and D_2) are $m = 1, 2, 3, 4, 5, 6, 10, 12, 15, 20, 30$. The parameters have been fixed as follows:

- (a) for Table 1: $q_1 = 0.97$, $q_2 = 0.97$, $c_1 = 10$, $c_2 = 1$, $C = 1300$;
- (b) for Table 2: $q_1 = 0.92$, $q_2 = 0.97$, $c_1 = 10$, $c_2 = 1$, $C = 900$.

In the situation of Table 1 we have $P(T_1(m) > L) = 1$ and $P(C_{1,1}(m, L) \leq C) = 0$ for all m if $L < 35$, i.e. no constraint, however weak, can be satisfied for $L < 35$. The optimal m is 30 for $35 \leq L \leq 40$ and 20 for $L > 40$. The best values of L and $\hat{m}$ depend on the bounds for the constraints that one wants to impose. For $\alpha = 0.01$ and $\beta = 0.95$ we find in Table 1 the optimal values to be $L = 49$, $\hat{m} = 20$. The global minimum of $E(C_{1,1}(m, L))$ is attained for $L = 41$ and $\hat{m} = 20$; if $\alpha = 0.04$ is a satisfactory bound in the first constraint, these values of L and $\hat{m}$ would be the right choice. It is interesting that $L \mapsto \min_m E(C_{1,1}(m, L))$ is neither unimodal nor monotone.

L	$\min_m E(C_{1,1}(m, L))$	$\hat{m}(L)$	$P(T_1(\hat{m}(L)) > L)$	$P(C_{1,1}(\hat{m}(L)) < C)$
35	763.498	30	0.035	0.941
36	766.119	30	0.030	0.941
37	768.375	30	0.025	0.941
38	770.312	30	0.021	0.941
39	771.973	30	0.017	0.941
40	773.395	30	0.015	0.941
41	724.166	20	0.039	1.000
42	726.412	20	0.033	1.000
43	728.366	20	0.027	1.000
44	730.062	20	0.023	0.973
45	731.528	20	0.019	0.973
46	732.794	20	0.016	0.973
47	733.882	20	0.013	0.973
48	734.816	20	0.011	0.973
49	735.615	20	0.009	0.973
50	736.298	20	0.008	0.973
51	736.879	20	0.006	0.973
52	737.372	20	0.005	0.973
53	737.791	20	0.004	0.973
54	738.145	20	0.004	0.973
55	738.443	20	0.003	0.973
56	738.695	20	0.002	0.973
57	738.907	20	0.002	0.973
58	739.084	20	0.002	0.973
59	739.233	20	0.001	0.973
60	739.357	20	0.001	0.973

Table 1: $\min_m E(C_{1,1})$ for different L in the trinomial case with $q_1 = 0.97$, $q_2 = 0.97$, $D_1 = 60$, $D_2 = 120$, $c_1 = 10$, $c_2 = 1$, $C = 1300$.

For Table 2 the results are similar. For $L < 36$ we have $P(T_1(m) > L) = 1$ and $P(C_{1,1}(m, L) \leq C) = 0$ for all m . The optimal group size is 12 (if $36 \leq L \leq 40$) or 10 (if $L > 40$). Again the optimal selection of L and m depends on the desired constraint probabilities. Note that $\min_m E(C_{1,1}(m, L))$ is an increasing function of L in this case.

L	$\min_m E(C_{1,1})$	$\hat{m}$	$P(T_1 > L)$	$P(C_{1,1} < C)$
36	555.205	12	0.045	1.000
37	557.887	12	0.036	1.000
38	560.076	12	0.028	1.000
39	561.854	12	0.022	1.000
40	563.294	12	0.018	1.000
41	586.128	10	0.039	1.000
42	588.608	10	0.030	1.000
43	590.648	10	0.023	1.000
44	592.310	10	0.018	1.000
45	593.653	10	0.013	1.000
46	594.729	10	0.010	0.987
47	595.585	10	0.008	0.987
48	596.261	10	0.006	0.987
49	596.790	10	0.004	0.987
50	597.202	10	0.003	0.987
51	597.521	10	0.002	0.987
52	597.766	10	0.002	0.987
53	597.954	10	0.001	0.987
54	598.096	10	0.001	0.987
55	598.203	10	0.001	0.987
56	598.284	10	0.000	0.987
57	598.345	10	0.000	0.987
58	598.390	10	0.000	0.987
59	598.423	10	0.000	0.987
60	598.448	10	0.000	0.987

Table 2: $\min_m E(C_{1,1})$ for different L in the trinomial case with $q_1 = 0.92$, $q_2 = 0.97$, $D_1 = 60$, $D_2 = 120$, $c_1 = 10$, $c_2 = 1$, $C = 900$.

Tables 3 and 4 provide examples for minimizing $E(C_{1,2}(m, L))$, i.e., using the stopping time $T_{2,L}(m)$. The values of the parameters are given in the captions. Any constraints can only be kept for $L > 38$ (Table 1) or for $L > 43$ (Table 2). The optimal group size as a function of L can jump downwards (from 8 to 6 in Table 3) or upwards (from 6 to 8 in Table 4). In Table 4 $L \mapsto \min_m E(C_{1,21}(m, L))$ is unimodal, in Table 3 it is not.

L	$\min_m E(C_{1,2})$	$\hat{m}$	$P(T_2 > L)$	$P(C_{1,2} < C)$
39	376.996	8	0.063	0.920
40	379.386	8	0.050	0.920
41	353.315	6	0.047	1.000
42	355.933	6	0.033	1.000
43	357.982	6	0.023	1.000
44	359.548	6	0.016	1.000
45	360.719	6	0.011	1.000
46	361.578	6	0.007	0.989
47	362.197	6	0.005	0.989
48	362.636	6	0.003	0.989
49	362.954	6	0.002	0.989
50	363.176	6	0.001	0.989
51	363.324	6	0.001	0.989
52	363.421	6	0.001	0.989
53	363.483	6	0.001	0.989
54	363.526	6	0.000	0.989
55	363.556	6	0.000	0.989

Table 3: $\min_m E(C_{1,2})$ for different L (trinomial case with $q_1 = 0.92$, $q_2 = 0.92$, $D_1 = 48$, $D = 120$, $c_1 = 5$, $c_2 = 1$, $C = 500$).

L	$\min_m E(C_{1,2})$	$\hat{m}$	$P(T_2 > L)$	$P(C_{1,2} < C)$
44	825.378	5	0.011	0.954
45	827.109	5	0.008	0.954
46	791.899	6	0.010	0.929
47	793.715	6	0.008	0.929
48	795.028	6	0.008	0.929
49	795.700	6	0.007	0.929
50	796.078	6	0.007	0.929
51	796.339	6	0.007	0.929
52	796.555	6	0.007	0.929
53	796.754	6	0.007	0.929
54	796.947	6	0.007	0.929
55	797.138	6	0.007	0.929
56	797.328	6	0.007	0.929
57	797.518	6	0.007	0.929
58	797.707	6	0.007	0.929
59	797.897	6	0.007	0.929
60	798.087	6	0.007	0.929

Table 4: $\min_m E(C_{1,2})$ for different L (trinomial case with $q_1 = 0.9$, $q_2 = 0.94$, $D_1 = 60$, $D = 120$, $c_1 = 20$, $c_2 = 1$, $C = 1000$).

Finally, Table 5 provides, again for $T_{2,L}(m)$, the values of the objective function and the probability constraints for a fixed L ($L = 40$) and *all* possible values of m . It is seen that $m \mapsto P(T_2(m) > L)$ is unimodal, but the behavior of $m \mapsto E(C_{1,2}(m, L))$ is irregular. Sufficiently small values of $P(T_2(m) > L)$ and $P(C_{1,1}(m, L) \geq C)$ are only attained for two values of the group size, namely for $m = 5, 6$; $m = 6$ gives the minimal value of the objective function. Similar phenomena occur in all other examples that we have computed.

L	m	$E(C_{1,2}(m, L))$	$P(T_2(m) > L)$	$P(C_{1,2}(m, L) \leq C)$	
40	1	840.000	1.000	1.000	
40	2	880.000	1.000	1.000	
40	3	919.452	0.999	1.000	
40	4	812.687	0.256	1.000	
40	5	807.868	0.046	1.000	
40	6	778.869	0.044	0.929	
40	10	890.927	0.212	0.603	
40	12	1013.391	0.361	0.404	
40	15	1212.974	0.588	0.188	
40	20	1512.558	0.834	0.054	
40	30	1980.103	0.971	0.006	
40	60	3198.631	0.999	0.000	

Table 5: $E(C_{1,2})$ for different m and $L = 40$ (trinomial case with $q_1 = 0.9$, $q_2 = 0.94$, $D_1 = 60$, $D = 120$, $c_1 = 20$, $c_2 = 1$, $C = 1000$).

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References

- [1] Bar-Lev, S.K., Boneh, A. and Perry, D. (1990) "Incomplete identification models for group-testable items", *Nav. Res. Logistics* 37, 647-659.
- [2] Bar-Lev, S.K., Stadje, W. and Van der Duyn Schouten (2002a) "Group testing models with incomplete identification and processing times". Submitted.
- [3] Bar-Lev, S.K., Stadje, W. and Van der Duyn Schouten (2002b) "Hypergeometric group testing with incomplete information". To appear in: *Prob. Engin. Inf. Sci.*
- [4] Christen, C. (1983) "Optimal detection of two complementary defectives", *SIAM J. Alg. Discr. Methods* 4, 101-110.
- [5] Du, Ding-Zhu and Hwang, F.K. (2000) *Combinatorial Group Testing and Its Applications* (2nd ed), Singapore: World Scientific.
- [6] Dorfman, R. (1943) "The detection of defective members of large populations", *Ann. Math. Statist.* 14, 436-440.
- [7] Hammick, P.A. and Gastwirth, J.L. (1994) "Group testing for sensitive characteristics: extensions to higher prevalence", *Int. Statist. Rev.* 62, 319-331.
- [8] Hung, M.C. (2000) "Use of binomial group testing in tests of hypotheses for classification or quantitative covariables", *Biometrics* 56, 204-212.

- [9] Li, C.H. (1962) "A sequential method for screening experimental variables", *J. Amer. Statist. Assoc.* 57, 455-477.
- [10] Litvak, E., Tu, X.M. and Pagano, M. (1994) "Screening for the presence of a disease by pooling sera samples", *J. Amer. Statist. Assoc.* 89, 424-434.
- [11] Macula, A.J. (1999a) "Probabilistic nonadaptive group testing in the presence of errors and DNA library screening", *Ann. Combin.* 3, 61-69.
- [12] Macula, A.J. (1999b) "Probabilistic nonadaptive and two-stage group testing with relatively small pools and DNA library screening", *J. Combin. Optim.* 2, 385-397.
- [13] Sobel, M. and Groll, P.A. (1959) "Group testing to = eliminate efficiently all defectives in a binomial sample", *Bell System Techn. J.* 28, 1179-1252.
- [14] Tu, X.M., Litvak, E. and Pagano, M. (1995) "On the informativeness and accuracy of pooled testing in estimating prevalence of a rare disease: application to HIV screening", *Biometrika* 82, 287-297
- [15] Wein, L.M. and Zenios, S.A. (1996) "Pooled testing for HIV screening: capturing the dilution effect", *Oper. Res.* 44, 543-569.