Abstract

When screening for rare diseases in large populations, conducting individual tests can be expensive and time-consuming. In group testing, individuals are pooled and tested together. If a group is tested negative, then all individuals in that group are declared negative. Otherwise, it is concluded that at least one individual in that group is positive. Group testing can be used to classify the individuals with respect to their disease status, to estimate the prevalence in the target population, or to conduct a hypothesis test on the unknown prevalence. In this work, we consider both the case when the population is not stratified and when it is stratified, the latter leading to multiple test problems. We define single- and two-stage randomized $p$-values for a model pertaining to the proportion of positive individuals in binomial distribution and in group testing. Randomized $p$-values are less conservative compared to non-randomized $p$-values under the null hypothesis, but they are stochastically not smaller under the alternative. We show that the proposed $p$-values are valid in the binomial model. Testing individuals in pools for a fixed number of tests improves the power of the tests based on the $p$-values. The power of the tests based on randomized $p$-values as a function of the sample size is also investigated. Simulations and real data analysis are used to compare and analyze the different considered $p$-values.

1 Introduction

We are concerned with the problem of screening large populations for the presence or absence of a particular trait of interest, for example, an infection in humans or animals. In such a situation, conducting individual tests is expensive and time-consuming. In group testing, the individuals are put into groups and a single test is used for each group. If the test for a group is negative, then all the individuals in that group are declared to be tested negative, and testing stops for that group. If the test is positive, then at least one individual in that group is assumed having been tested positive. Individuals from these latter groups can then be tested one by one until all the positive individuals are identified. Group testing as just described was introduced by Dorfman (1943), first as an economical way of screening soldiers for the presence of syphilis. In general, group testing is used to screen large populations and is especially beneficial when the trait of interest is rare; cf. Mutesa et al. (2021).

Compared to individual testing, group testing in most cases utilizes a lower number of tests, leading to savings in testing costs and time. Also, Swallow (1985) showed that for a low prevalence rate $\theta$ (which is the proportion of infected individuals in the considered population) of the trait of interest (e. g., $\theta < 0.1$) and a fixed total number of tests, grouping individuals for each test instead of doing individual tests provides more precise estimates of $\theta$. In the same setting, Tebbs and Swallow (2003) showed that the power of the likelihood ratio test increases when one tests items in groups instead of testing them individually. Another benefit of group testing is that it provides individual anonymity within positively tested groups, cf. Uhl et al. (2001).

Group testing is widely applied in infectious disease testing such as for the West Nile virus in Khan et al. (2017), for HIV/AIDS detection as in Kim and Hudgens (2009) and most recently by Mutesa et al. (2021) in SARS-COV-2 screening. It is also applied in drug discovery studies as reported by Kainkaryam and Woolf (2009) and Hughes-Oliver (2006). Pasquali et al. (2014) used group testing for studies involving food contamination detection. Diagnosis of faulty network sensors using group
testing was illustrated by Lo et al. (2013). In the industry, it is used to identify leaking devices in a set of devices and also to identify defective bulbs by connecting the bulbs in series and applying a voltage across the whole batch, cf. Sobel and Groll (1959), among many other applications.

In the group testing literature, one distinguishes between classification and estimation problems. The classification problem consists in the identification of individuals having the trait of interest, where the aim is to use as few tests as possible. Individuals from positive groups are retested until they are all classified as either positive or negative. In the estimation problem, the goal of group testing is to estimate the unknown prevalence rate. Here, it is only necessary to test at the group level. Testing ends at the group level since retesting of positive groups offers very little benefit in terms of a cost function like the mean squared error or the cost per unit information, cf. Chen and Swallow (1990). The same authors indicate that retesting is not always possible, and that retesting (even if possible) can complicate and prolong the process of data collection.

Recently, group testing has also included conducting hypothesis tests and constructing confidence intervals for the prevalence rate. For example, Tebbs and Bilder (2004) considered exact and approximate intervals when equal group sizes are used. Pairwise comparisons for the prevalence rates were investigated by McCann and Tebbs (2007). The goal of the study was to identify significant differences between strata in the case of a stratified sampling scheme, and to also rank the strata in terms of their prevalence rates. In the context of point hypothesis testing, Ornaghi et al. (1999) used a two sample \( t \)-test to compare individual transmission probabilities between the two genders of an insect. Hung and Swallow (2000) investigated group testing where the prevalence rate \( \theta \) is assumed to depend on a single qualitative or quantitative covariate; a chi-square test and regression techniques were used, respectively. Tebbs and Swallow (2003) investigated the usage of the likelihood ratio test (LRT) for testing whether the prevalence rates for different strata are equal against an ordered alternative. Tebbs and Bilder (2006) considered the LRT, the angular-transformed statistic and Bartholomew’s statistic when testing for or against a simple order among the prevalence rates. Large sample likelihood-based tests (Wald, score and likelihood ratio), for multiple-vector transfer designs with \( r \geq 2 \) strata for equal and unequal group sizes were considered by Tebbs and McCann (2007).

The objective of this paper is to investigate the usage of randomized \( p \)-values in this context. Alike randomization of tests, which aims at an exact equality between size and level, randomization of \( p \)-values aims at exact uniformity of the \( p \)-value under the null. We consider both the case when there is no stratification and the case when the population has been stratified, the latter leading to a multiple test problem. It has been demonstrated in prior work (cf. among others, Dickhaus et al. (2012); Dickhaus (2013); Hoang and Dickhaus (2022b,a)) that randomization techniques for \( p \)-values can improve the performance of multiple tests considerably.

For stratified group testing, the population is first divided into different strata and pooling is conducted within each stratum separately, independently of the other strata. The motivation for stratification is to divide the population based on some factor that may influence the prevalence rate. Stratification also arises in multiple-vector transfer experiments where a group of insects is exposed to and left to feed on an infected plant. These infected insects are then moved to uninfected test plants (organized in strata) which are observed for developing symptoms of infections, cf. Swallow (1985), Tebbs and Swallow (2003), Tebbs and Bilder (2004), and McCann and Tebbs (2007).

The rest of this paper is organized as follows. General preliminaries are provided in Section 2. In Section 3 we describe the proposed randomization procedures for a general discrete model and a composite null hypothesis. In Section 4 we define the one- and two-stage randomized \( p \)-values, and we calculate their cumulative distribution functions (CDFs) for the general binomial model. We also compare the power of the test based on the randomized \( p \)-values for different sample sizes in that section. An application in group testing when there is no stratification is considered in Section 5. Multiple testing in group screening when the population is divided into strata is considered in Section 6. Finally, we discuss our results in Section 7.

## 2 General Preliminaries

Throughout the remainder, we assume that the tests conducted on the group level are perfect and therefore a group is tested positive (negative) if and only if it is truly positive (negative). We assume that the sampling scheme is such that the total number of positively tested groups in each stratum is binomially distributed. The binomial distribution with parameters \( n \in \mathbb{N} \) (number of trials) and \( \theta \in [0, 1] \) (success probability) will be denoted by \( \text{Bin}(n, \theta) \). In the case of \( n = 1 \), we have the Bernoulli
distribution with success parameter $\theta$, Bernoulli($\theta$) for short. To avoid pathologies, we will restrict attention to $\theta \in (0,1)$ at some occasions. We denote the (random) data by $X = (X_1, \ldots, X_n)^\top$, where each $X_i$ is a real-valued, observable random variable, $1 \leq i \leq n$, and all $X_i$ are stochastically independent and identically distributed (i.i.d.). We assume that the marginal $p$-value $p(X)$ derived from the test statistic $T = T(X)$ is valid, that is, it holds $P_\theta(p(X) \leq \alpha) \leq \alpha$ under any parameter value $\theta$ in the null hypothesis and for all $\alpha \in [0,1]$. If in this condition a parameter value $\theta_{LFC}$ maximizes the left-hand side for all $\alpha$, we call $\theta_{LFC}$ the least favorable parameter configuration (LFC). Valid $p$-values are under the null stochastically not smaller than the uniform distribution on the unit interval $[0,1]$, which we denote by UNI$[0,1]$. Especially in the case of discrete models, valid $p$-values are typically strictly stochastically larger than UNI$[0,1]$, as investigated by, among many others, Finner and Strassburger (2007), Habiger and Pena (2011), Dickhaus et al. (2012), and Habiger (2015). In the case of a composite null hypothesis, a deviation of $p$-values from uniformity occurs when marginal test statistics do not have a unique distribution under the null hypothesis. This implies that they cannot be calibrated precisely with respect to their type I error probabilities. Dickhaus et al. (2012); Dickhaus (2013) proposed randomized $p$-values for discrete and continuous models, respectively, as a solution. The approach by Dickhaus (2013) has recently been extended by Hoang and Dickhaus (2022b). In this paper we utilize both approaches in one- and two-stage randomization procedures: In the one-stage randomization, we apply the approach proposed by Hoang and Dickhaus (2022b), but with a minor modification; see Section 4. In the two-stage randomization procedure, we first take care of the discreteness of the $p$-values by applying the randomization proposed by Dickhaus et al. (2012). Under LFCs this leads to exactly uniformly distributed randomized $p$-values. However, these $p$-values are still conservative under non-LFCs. Therefore, we apply the approach by Hoang and Dickhaus (2022b) on these $p$-values in the second stage. For these randomized $p$-values to be valid, we require their non-randomized versions to be so-called uniformly valid, cf. Whitt (1980); Whitt (1982), Lynch et al. (1987), and Zhao et al. (2019), among others. Throughout the remainder, we will be concerned with one-sided test problems of the form $H : \theta \leq \theta^*$ versus $K : \theta > \theta^*$, where $\theta^*$ is a pre-specified constant. It is known that uniform validity holds for $p$-values of one-sided tests for such test problems, if the distributions of the test statistic have monotone likelihood ratios, cf. Zhao et al. (2019). For example, one-sided tests in the binomial model that we are investigating have this property, due to the structure of a one-dimensional exponential family for the likelihood functions. We provide further details on this in Lemma 1.

3 Randomization Procedures

3.1 Introduction

As mentioned before, we will consider both single- and two-stage randomization procedures. For single-stage randomization, a modification of the randomized $p$-value given by Hoang and Dickhaus (2022a) is utilized. For the two-stage randomization, the first stage is carried out using the approach proposed in Appendix II of Dickhaus et al. (2012). This transforms the discrete $p$-value based on $T$ into a continuous $p$-value. In the second stage, the approach given by Hoang and Dickhaus (2022a) is applied to deal with the conservativeness of the $p$-value resulting from the first stage. This conservativeness is due to the composite nature of the hypothesis $H$. We first give a description of the single-stage procedure and then one for two-stage randomization.

3.2 Single-stage randomization

Suppose we wish to randomize only once. In that case, we can make use of the single-stage randomized $p$-value defined by Hoang and Dickhaus (2022a) with a slight modification. The LFC-based $p$-value for our hypothesis is defined as

$$P_{LFC}(X) = 1 - F_{\theta^*}(T(X)), \quad (1)$$

where $F_{\theta^*}$ is the CDF of the test statistic $T$ under the LFC $\theta^*$. We use $p$-LFC and $P_{LFC}(X)$ interchangeably to denote the $p$-value defined in (1). The CDF of $p$-LFC is given by

$$P_\theta(P_{LFC}(X) \leq t) = 1 - F_\theta(F_{\theta^*}^{-1}(1 - t)). \quad (2)$$

Hoang and Dickhaus (2022a) defined a randomized $p$-value as follows: Let $U$ be a UNI$[0,1]$-distributed random variable that is stochastically independent of $X$. For a given constant $c \in (0,1]$, the randomized
The \( p \)-value \( P_{\text{rand}}(X, U, c) \) based on \( P^{LFC}(X) \) is then defined as
\[
P_{\text{rand}}(X, U, c) = U1\{P^{LFC}(X) \geq c\} + \frac{P^{LFC}(X)}{c^*}1\{P^{LFC}(X) < c\},
\]
and \( P_{\text{rand}}(X, U, 0) = U \). We propose to let \( c^* = \mathbb{P}_\theta\{P^{LFC}(X) < c\} \) (instead of \( c^* = c \) as in Hoang and Dickhaus (2022a)), which is our proposed modification for discretely distributed \( p \)-value.

If \( P^{LFC}(X) \) is \( \text{UNI}[0,1] \)-distributed under the LFC parameter, then both versions are equivalent. Notice that \( c^* \) is the largest support point of \( P^{LFC}(X) \) under an LFC parameter \( \theta^* \) such that \( c^* \leq c \).

The interpretation of \( P_{\text{rand}}(X, U, c) \) is such that, when \( P^{LFC}(X) < c \) then \( P^{LFC}(X) \) is transformed by dividing it by \( c^* \), otherwise it is replaced by the random variable \( U \). This division by \( c^* \) is needed to ensure (conditional) validity of \( P_{\text{rand}}(X, U, c) \), and it has its conceptual origins in the general approach to selective inference; see the discussion around Definition 3.1 in Hoang and Dickhaus (2022b). The CDF of \( P_{\text{rand}}(X, U, c) \) is given by
\[
\mathbb{P}_\theta\{P_{\text{rand}}(X, U, c) \leq t\} = t\mathbb{P}_\theta\{P^{LFC}(X) > c\} + \mathbb{P}_\theta\{P^{LFC}(X) \leq tc^*\},
\]
\[
= \mathbb{P}_\theta\{P_{\text{rand}}(X, U, c^*) \leq t\}.
\]

The second equality in (4) holds due to \( c^* \leq c \), so that \( \mathbb{P}_\theta\{P^{LFC}(X) > c\} = \mathbb{P}_\theta\{P^{LFC}(X) > c^*\} \) (assuming the support points of \( p \)-LFC do not depend on \( \theta \), since there is no other support point between \( c \) and \( c^* \). Single-stage randomization deals with the discreteness of the model and the composite nature of the hypothesis all at once. However, it fails to remove the conservativity of \( P^{LFC}(X) \) arising from the discreteness of the model completely. This will be seen more clearly in the plots in Section 4. This is the motivation for the two-stage randomization procedure which we describe next.

### 3.3 Two-stage randomization

We now turn our attention to the two-stage randomization procedure and describe it in detail. For the first stage, we make use of the following randomized \( p \)-value for discrete models from Dickhaus et al. (2012): Assume that the real-valued test statistic \( T \) tends to larger values under the alternative. Assume \( U \) to be a \( \text{UNI}[0,1] \)-distributed random variable which is stochastically independent of \( X \).

Then, the randomized \( p \)-value pertaining to \( T \) that we are considering in the sequel is given by
\[
P_{T}^{\text{rand}} = \sum_{y: T(y) > T(X)} f_{\theta^*}(y) + U \sum_{y: T(y) = T(X)} f_{\theta}(y),
\]
where \( f_{\theta^*} \) denotes the probability mass function (pmf) of \( X \) under \( \theta^* \). The CDF of \( P_{T}^{\text{rand}} \) is given by
\[
\mathbb{P}_\theta\{P_{T}^{\text{rand}} \leq t\} = 1 - F_{\theta}(g(t)) + g(t)f_{\theta}(y(t)),
\]
where \( g(t) = \{F_{\theta^*}(y(t)) - (1 - t)\}^{-1} \), \( y(t) = F_{\theta^*}^{-1}(1 - t) \), and where \( F_{\theta^*} \) and \( F_{\theta^*}^{-1} \) are the CDF and the quantile function of \( T \) under the LFC parameter \( \theta^* \), respectively. We note that thresholding \( P_{T}^{\text{rand}} \) at \( \alpha \) for making a test decision is under certain conditions equivalent to utilizing the well-known (potentially randomized) uniformly most powerful (UMP) level \( \alpha \) test based on \( T \) (which is in such cases a deterministic transformation of the likelihood ratio of the statistical model under consideration). In the case of a one-sided test under a binomial model, the aforementioned equivalence holds true. Therefore, we sometimes refer to \( P_{T}^{\text{rand}} \) as the UMP \( p \)-value in our context.

In discrete models, non-randomized \( p \)-values are usually conservative, i.e. under the null hypothesis they are valid and \( \mathbb{P}(p(X) \leq \alpha) < \alpha \) for some \( \alpha \in (0,1) \). Tests conducted using these \( p \)-values will fail to exhaust the significance level. This non-uniformity is not a problem for single tests, but can lower the multiple power of multiple tests as noted by Dickhaus et al. (2012). Our proposed solution to this is to use the \( p \)-value \( P_{T}^{\text{rand}} \) in a first stage of randomization, in order to transform the discrete test statistic into a continuously distributed \( p \)-value.

The proposed second stage of randomization using the randomization technique from Hoang and Dickhaus (2022a) can now be applied to deal with the conservativeness of \( P_{T}^{\text{rand}} \) that results from the composite nature of our null hypothesis. To this end, let \( \tilde{U} \) be another \( \text{UNI}[0,1] \)-distributed random variable which is stochastically independent of the data \( X \) and stochastically independent of \( U \).

Assume
also that a constant \(c \in (0, 1]\) is given. The randomized \(p\)-value \(Pr^\text{rand}_2(X, U, \tilde{U}, c)\) in the second stage is defined as
\[
Pr^\text{rand}_2(X, U, \tilde{U}, c) = U \mathbb{1}\{Pr^\text{rand}_1(X, U) \geq c\} + Pr^\text{rand}(X, U)(c)^{-1}\mathbb{1}\{Pr^\text{rand}(X, U) < c\}.
\] (7)

Furthermore, we define \(Pr^\text{rand}_2(X, U, \tilde{U}, 0) = \tilde{U}\). The CDF of \(Pr^\text{rand}_2\) is given by
\[
\mathbb{P}_\theta\{Pr^\text{rand}_2(X, U, \tilde{U}, c) \leq t\} = t\mathbb{P}_\theta\{Pr^\text{rand}_1(X, U) > c\} + \mathbb{P}_\theta\{Pr^\text{rand}_1(X, U) \leq tc\}.
\] (8)

Under parameter values in the null hypothesis, randomized \(p\)-values are typically in distribution closer to UNI\([0, 1]\) than non-randomized \(p\)-values (cf. Dickhaus (2013)). For easier reference, Table 1 below gives an overview of all the \(p\)-values described in this section, together with their corresponding CDFs.

| \(p\)-LFC | \(Pr^\text{LFC}(X) = 1 - F_{\theta^*}(T(X))\) |
| --- | --- |
| CDF | \(\mathbb{P}_\theta\{Pr^\text{LFC}(X) \leq t\} = 1 - F_{\theta^*}(1 - t)\) |

| RAND1 | \(Pr^\text{rand}_1(X, U, c) = \tilde{U} \mathbb{1}\{Pr^\text{LFC}(X) \geq c\} + Pr^\text{LFC}(X)(c)^{-1}\mathbb{1}\{Pr^\text{LFC}(X) < c\}\) |
| --- | --- |
| CDF (Eq 4) | \(\mathbb{P}_\theta\{Pr^\text{rand}_1(X, U, c) \leq t\} = t\mathbb{P}_\theta\{Pr^\text{LFC}(X) > c\} + \mathbb{P}_\theta\{Pr^\text{LFC}(X) \leq tc\}\) |

| PT-RAND | \(Pr^\text{rand}(X, U) = \sum_{y:T(y) > T(X)} f_{\theta^*}(y) + \tilde{U} \sum_{y:T(y) = T(X)} f_{\theta^*}(y)\) |
| --- | --- |
| CDF | \(\mathbb{P}_\theta\{Pr^\text{rand}(X, U) \leq t\} = 1 - F_{\theta^*}(y(t)) + g(t)f_{\theta^*}(y(t)),\) 
| & \(g(t) = \{F_{\theta^*}(y(t)) - (1 - t)\}^{-1}\{f_{\theta^*}(y(t))\}\) |
| & \(y(t) = F_{\theta^*}(1 - t)\) |

| RAND2 | \(Pr^\text{rand}_2(X, U, \tilde{U}, c) = \tilde{U} \mathbb{1}\{Pr^\text{rand}_1(X, U) \geq c\} + Pr^\text{rand}(X, U)(c)^{-1}\mathbb{1}\{Pr^\text{rand}(X, U) < c\}\) |
| --- | --- |
| CDF (Eq 8) | \(\mathbb{P}_\theta\{Pr^\text{rand}_2(X, U, \tilde{U}, c) \leq t\} = t\mathbb{P}_\theta\{Pr^\text{rand}_1(X, U) > c\} + \mathbb{P}_\theta\{Pr^\text{rand}_1(X, U) \leq tc\}\) |

With the randomized \(p\)-values so defined we are now in a position to apply them to the general binomial model and later in group testing.

## 4 Randomization in the General Binomial Model

### 4.1 General properties

In this section, we demonstrate how the proposed randomized \(p\)-value can be used when the data are constituted by Bernoulli indicators. Suppose we are interested in testing the hypothesis \(H : \theta \leq \theta^*\) versus \(K : \theta > \theta^*\), where \(\theta\) is the unknown binomial success parameter and \(\theta^*\) is a pre-specified constant. Let \(X = (X_1, \ldots, X_n)^T\) be \(n\) i.i.d. Bernoulli random variables with mean \(\theta \in (0, 1)\). The test statistic \(T(X) = \sum_{i=1}^n X_i\) follows the \(Bin(n, \theta)\) distribution, and it tends to larger values under the alternative. Throughout this section, we let \(F_{\theta}\) denote the \(n\)-fold product of Bernoulli(\(\theta\)) and we let \(F_{\theta^*}\) denote the CDF of \(Bin(n, \theta^*)\), with corresponding quantile function \(F_{\theta^*}^{-1}\).

With these specifications, the LFC-based \(p\)-value under the binomial model is given by (1), and the corresponding CDF for \(p\)-LFC is given by (2). The single-stage randomized \(p\)-value is given by (3)
using the LFC-based $p$-value described in the first sentence of this paragraph. Equation (4) gives the CDF for the single-stage randomized $p$-value under the binomial model.

Turning our attention to the two-stage randomization procedure, the randomized $p$-value in the first stage for the binomial model is given by (5) with the corresponding CDF given by (6). Similarly, the randomized $p$-value in the second stage for the binomial model is given by (7) with the corresponding CDF given by (8).

Figure 1 displays the CDFs of the LFC-based $p$-value (denoted by LFC), the UMP $p$-value $P_{\text{rand}}$ (denoted by UMP), the single-stage randomized $p$-value (denoted by RAND1), and the two-stage randomized $p$-value (denoted by RAND2) under the null ($\theta = 0.20$) and the alternative hypothesis ($\theta = 0.37$), where $n = 50$, $\theta^* = 0.25$, and $c = 0.5$.

Figure 1 indicates that under the alternative hypothesis the test based on $P_{\text{rand1}}$ is the least powerful one, followed by that based on $P_{\text{rand2}}$. On the other hand, $P_{\text{rand2}}$ is the least conservative of the considered $p$-values under the null hypothesis, meaning that its CDF is closest to the main diagonal.
in the unit square. The latter property is very useful in situations where closeness of the p-value distribution to UNI[0, 1] under the null is required. For example, this is the case when estimating proportion of true null hypotheses by means of an estimator which is based on the empirical CDF of all p-values in a multiple testing context; see Dickhaus (2013) and Hoang and Dickhaus (2022a) for more details.

The p-value \( P^{\text{rand1}} \) is partially discrete as can be seen by the slanting steps in its CDF under both the null and alternative hypothesis. We also note that \( P^{\text{rand2}}(X, U, \tilde{U}, 1) = P^{T}_{T}(X, U) \), which is always stochastically smaller than \( \tau \)-LFC. The distribution of \( P^{\text{rand2}} \) moves closer to UNI[0, 1] distribution if \( c \to 0 \). However, for \( c \) less but close to 1, the test based on \( P^{\text{rand2}} \) can still be more powerful than that based on \( \tau \)-LFC for many significance levels \( \alpha \in (0, 1) \).

**Lemma 1** (Validity of the proposed p-values). Under the binomial model, the LFC-based p-value \( P^{\text{LFC}}(X) \), single-stage randomized p-value \( P^{\text{rand1}}(X, U, c) \), UMP p-value \( P^{\text{rand}}(X, U) \), and the two-stage randomized p-value \( P^{\text{rand2}}(X, U, \tilde{U}, c) \) are all valid p-values, for all \( c \in [0, 1] \).

We provide the proof for Lemma 1 in Web Appendix A of the Supporting information for this article.

### 4.2 Sample size versus power

We now investigate the relationship between the powers of the tests based on the four considered p-values (UMP, LFC, \( P^{\text{rand1}} \), and \( P^{\text{rand2}} \)) and an increasing sample size. In comparing the power of the tests based on the p-values with different sample sizes, we are particularly interested in assessing whether there is an increase in power with an increase in sample size, as one would (usually) expect.

When testing for a binomial parameter in the composite null hypothesis, Finner and Strassburger (2001) showed that the power function at a sample size \( n \) can be higher than at some \( n + i, i \geq 1 \) for the non-randomized p-value (LFC-based p-value), which seems paradoxical. This paradox also occurs in permutation tests, in Fisher's exact test, and when comparing ratios or differences between two binomial success parameters. This drop in power when the sample size increases slightly can occur since power depends on the actual alpha rather than the nominal alpha. An increased sample size leads to a decreased actual alpha. The drop in power is also caused by the discrete nature of the test statistic involved in the definition of the LFC-based p-value.

In Figure 2, we compare the powers of the tests based on the LFC-based p-value, the UMP p-value and the randomized p-values \( P^{\text{rand1}} \) and \( P^{\text{rand2}} \) for different sample sizes, \( \theta^* = 0.25, \theta = 0.5, c = 0.5 \), and \( \alpha = 0.05 \). Indeed, Figure 2 demonstrates that the power of the test based on \( \tau \)-LFC is not monotonically increasing in the sample size. The power function of the test based on \( P^{\text{rand1}} \) shows a similar behaviour to the one based on \( \tau \)-LFC. Instead, the power function is monotonically increasing in \( n \) when utilizing \( P^{\text{rand2}} \) or \( P^{T}_{T} \). Of course, the test based on the UMP p-value \( P^{\text{rand}} \) is the most powerful of all the tests based on the four p-values. The p-value \( P^{\text{rand1}} \) is based on \( \tau \)-LFC, while \( P^{\text{rand2}} \) is based on the stochastically smaller \( P^{T}_{T} \). Therefore, it is expected that the test based on \( P^{\text{rand2}} \) is also more powerful and less conservative than that based on \( P^{\text{rand1}} \). This behavior is verified in Figures 1 and 2.

### 4.3 Power and level of conservativeness for different values of \( c \)

We now investigate the CDFs for the two randomized p-values \( P^{\text{rand1}} \) and \( P^{\text{rand2}} \) when different values of \( c \) are used. In Figure 3, we display graphically the CDFs for \( P^{\text{rand2}} \) under the null and alternative hypothesis. The power function of the test based on \( P^{\text{rand1}} \) when \( c^* \) (which is a support point for \( \tau \)-LFC) is used is displayed in Figure 4.

Under the null hypothesis in Figure 3, as \( c \) increases, the CDF departs from the diagonal line (\( c = 0 \)) which is the least conservative, to the CDF of the UMP p-value (\( c = 1 \)) which is the most conservative. Under the alternative hypothesis, the pointwise largest CDF occurs when \( c = 1 \), and the pointwise smallest CDF occurs when \( c = 0 \).

In Figure 4, the power function of the test based on \( P^{\text{rand1}}(X, U, c^*) \) is displayed. We indicate the graph of this function by RAND1(S) in Figure 4. In addition, we display in Figure 4 two further curves, indicated by RAND1(AS) and RAND1(BS). These are the graphs of the power functions of the test based on the single-stage randomized p-values when \( c^* + \varepsilon \) or \( c^* - \varepsilon \) are used, respectively, where \( \varepsilon \) is small.
For any support point $c^*$, RAND1(AS) and RAND1(S) are equal as explained after (4). The $p$-values RAND1(S) and RAND1(BS) have different CDFs regardless of the size of $c$ since the support point in RAND1(BS) is always smaller than the support point $c^*$ in RAND1(S). Unlike $P_{rand2}$, the single-stage randomized $p$-value $P_{rand1}$ is not stochastically ordered in $c$.

5 Application in Group Testing

5.1 Introduction

This section illustrates how the four $p$-values $p$-LFC, $P_{rand1}$, UMP, and $P_{rand2}$ can be used in (unstratified) group testing. Assume that we have a population of size $N$ that can be divided into $g$ groups, each of size $s$. The individuals in each group are either positive (denoted by 1) or negative (denoted by 0) with respect to the target event, and this outcome is random. Furthermore, let $Q_\ell = 1$ if the $\ell$-th group is positive and $Q_\ell = 0$ otherwise, for $\ell = 1, \ldots, g$. In this, we call a group positive if it contains at least one positive individual, and negative otherwise. We assume that the trait under consideration and the sampling scheme are such that $Q_1, \ldots, Q_g$ are i.i.d. Bernoulli random variables, each with mean $\pi$, where $\pi = 1 - (1 - \theta)^s$. Letting $R = \sum_{\ell=1}^{g} Q_\ell$ denote the total number of positive groups, we have that $R \sim Bin(g, \pi)$. A realization of $R$ will be denoted by $r$.

The maximum likelihood estimator (MLE) for $\theta$ is $\hat{\theta} = 1 - (1 - \hat{\pi})^{1/s}$, where $\hat{\pi} = r/g$ is the proportion of positive groups out of the $g$ groups. The pair of composite hypotheses $H : \pi \leq \pi^*$ versus $K : \pi > \pi^*$ considered in Section 4 is similar to the case for individual testing, that is, when $s = 1$. This pair of hypotheses is equivalent to $H_s : \pi \leq \pi^*$ versus $K_s : \pi > \pi^*$ for group testing where $\pi^* = 1 - (1 - \theta^*)^s$ and $\pi = 1 - (1 - \theta)^s$. We consider a test statistic $T = T(Q)$, where $Q = (Q_1, \ldots, Q_g)^T$. The computations for the CDFs of the four $p$-values for the hypothesis $H_s : \pi \leq \pi^*$ versus $K_s : \pi > \pi^*$ follow the same process as in Section 4, but with $\theta^*, \theta$, and $n$ replaced by $\pi^*$, $\pi$, and $g$, respectively.

We compare the power of the tests based on the four $p$-values for different group sizes $s$ under two scenarios, namely (i) for a fixed number of tests (Section 5.2), and (ii) for a fixed number of individuals (Section 5.3).

Figure 2: Graphic display of power versus sample size for LFC, UMP, single-, and two-stage randomized $p$-values (RAND1) and (RAND2), respectively, for significance level $\alpha = 0.05$, $\theta^* = 0.25$, and $c = 0.5.$
Figure 3: An illustration of the CDF for two-stage randomized p-value (RAND2) in the null ($\theta = 0.20$) and alternative ($\theta = 0.35$) hypotheses under different values of $c$ for $n = 50$ and $\theta^* = 0.25$. 
Figure 4: Graphic illustration of the CDF for single-stage randomized \( p \)-value in support-RAND1(S), below support-RAND1(BS), and above support-RAND1(AS) for \( n = 50, \theta^* = 0.25, \theta = 0.35, \) and \( c = 0.5 \).

### 5.2 Fixed number of tests

We consider here the power of the tests based on the four \( p \)-values for different group sizes \( s \) when the number of tests \( g \) is fixed, but the total number of individuals varies. This is common, for example, in multiple-vector transfer designs where the number of tests is limited by the available number of test plants, green house spaces, or isolation cages for the test plants. However, any number of insects can be used since the cost of obtaining an insect is small, see Swallow (1985), Tebbs and Swallow (2003), and McCann and Tebbs (2007) for more details.

It is expected that testing items in groups when the number of tests is fixed will improve the power of the tests based on the four \( p \)-values compared to performing (the same number of) individual tests. It is also expected that the power of the tests based on the four \( p \)-values will further increase with an increase in group size as long as the proportion of positive individuals in a group is low. We verify these claims in Figure 5 and in web Figure 1 of the supporting information for this article.

Increasing the group size \( s \) increases the power first (as demonstrated in Figure 5), then eventually the power drops towards zero for large group sizes \( s \) and a large prevalence rate as illustrated in web Figure 1. The aforementioned drop in power occurs since \( \pi^* \) increases in \( s \), and for \( s \) too large \( K_s : \pi > \pi^* \) becomes too difficult to detect. The power functions of tests based on \( p \)-LFC and \( Prand1 \) in Figure 5 just like in Figure 2 do not increase monotonically with an increase in the group size \( s \). Generally for a high prevalence rate \( \theta \), the power functions increase faster and drop earlier compared to a low prevalence rate. For a large \( \theta^* \) the power functions drop earlier compared to a low \( \theta^* \). Of course, the power of the test based on the UMP \( p \)-value is the highest (among the four tests). The test based on \( Prand1 \) has the lowest power throughout while the tests based on \( p \)-LFC and \( Prand2 \) are competing. The optimal group size based on web Figure 1 is in the vicinity of \( s = 10 \).

### 5.3 Fixed number of individuals

We can also have a situation where the total number of individuals is fixed but the number of groups varies. We give a graphic display in web Figure 2 of the supporting information for this article of how the power of the tests based on all the four \( p \)-values decreases with an increase in group size.

We set \( \theta^* = 0.1, \theta = 0.2, c = 0.5, \alpha = 0.05, \) and \( s \times g = 300 \). The power of the tests based on \( Prand2 \)
Figure 5: A graphic display of power versus different group sizes $s$ for LFC, UMP, single- (RAND1) and two-stage (RAND2) randomized $p$-values for fixed number of tests. We use $\theta^* = 0.01$, $\theta = 0.02$, $c = 0.5$, and $g = 50$.

and UMP $p$-value drops to $\alpha$ and stays that way throughout never dropping to zero. The CDF of $P_{\text{rand}^2}$ lies between the CDF of $P_{T^\text{rand}}$ and the CDF of UNI[0, 1], cf. Hoang and Dickhaus (2022a), which implies that when the CDF of $P_{T^\text{rand}}$ at $\alpha$ goes to $\alpha$ then the CDF of $P_{T^\text{rand}}$ at $\alpha$ will also converge to $\alpha$.

The tests based on all the four $p$-values have a higher power when doing individual testing ($s = 1$) compared to the case of group testing ($s > 1$). This is because individual testing provides the maximum amount of information when the number of individuals is fixed and hence a higher power than when using group testing (Tebbs and Swallow (2003)). The power gained by the tests in the case of individual testing is not much and may not justify the additional testing costs. For example, when $\theta = 0.008$, under individual testing, the power of tests based on $p$-LFC is 69.3% and the maximum number of tests, in this case 300, is required. At the same prevalence when using group testing with $s = 10$, the power of tests based on $p$-LFC is 68.5% and only 30 tests are used. In this example, the slight gain in power by the tests based on $p$-LFC under individual testing requires ten times more tests compared to when the same $p$-value is used in group testing. Therefore, in applications where the testing budget is limited, group testing will still remain very useful despite the slight loss in power.

5.4 A summary of the two cases

In both cases considered above, for large group sizes ($s \geq 20$) as seen in web Figures 1 and 2 of the supporting information for this article, the power of the tests based on $p$-LFC and $P_{T^\text{rand}}$ drops to zero, the one for $P_{T^\text{rand}}$ rises again to 0.05 and stays that way throughout, the one for $p$-LFC stays at zero throughout. The power of the tests based on $p$-LFC drops to zero when the critical value equals the sample size (number of groups in this case) and hence the CDF at the critical value equals one. When this happens, the term after the “$+$” sign in (4) equals zero and hence the CDF of $P_{T^\text{rand}}$ at $\alpha$ rises to $\alpha$.

In general, the power of tests based on the four $p$-values increases with an increase in group size when only the number of tests is fixed and decreases with an increase in group size when only the number of individuals is fixed. These two findings are analogous to the findings of Tebbs and Swallow (2003) who used LRT and Tebbs and Bilder (2006) who used LRT, angular-transformed, and Bartholomew’s statistics in testing for simply ordered proportions in group testing. Generally in group testing, the
group sizes are kept small since large group sizes increase the risk of all the groups in a stratum testing positive and hence increasing the bias of the MLE \( \hat{\theta} \).

6 Estimation of the Proportion of True Null Hypotheses

In this section we assume that we have a population of size \( N \) that can be divided into \( k > 1 \) strata (reasons for stratifying are given in Section 1). Within each stratum, the individuals can be positive (denoted by 1) or negative (denoted by 0). For \( i \in \{1, \ldots, k\} \), let \( \theta_i \) be the prevalence, \( g_i \) the number of groups, and \( s_i \) the group size in the \( i^{th} \) stratum. Further, let \( Q_{i\ell} = 1 \) if the \( i^{th} \) group in the \( i^{th} \) stratum is positive and \( Q_{i\ell} = 0 \) otherwise, for \( i = 1, \ldots, k \) and \( \ell = 1, \ldots, g_i \). For each \( i \), we assume that \( Q_{i1}, \ldots, Q_{ig_i} \) are i.i.d. Bernoulli random variables with mean \( \pi_i \), where \( \pi_i = 1 - (1 - \theta_i)^{s_i} \). Define \( R_i = \sum_{\ell=1}^{g_i} Q_{i\ell} \), which is the number of positive groups in the \( i^{th} \) stratum. Then, following the argumentation of Section 5, \( R_i \sim Bin(g_i, \pi_i) \). The MLE for \( \theta_i \) is \( \hat{\theta}_i = 1 - (1 - \pi_i)^{1/s_i} \), where \( \pi_i = r_i/g_i \) is the observed proportion of positive groups in the \( i^{th} \) stratum.

In Section 5, we have considered hypothesis testing problems for a single stratum. In this section, we consider testing problems referring to all \( k \) strata simultaneously. This leads to a multiple testing problem with \( k \) tests, the source of multiplicity being the stratification of the population into \( k \) strata. The \( k \) pairs of hypotheses to be tested are \( H_i : \pi_i \leq \pi_i^* \) versus \( K_i : \pi_i > \pi_i^* \), where \( \pi_i^* = 1 - (1 - \theta_i)^{s_i} \) and \( 1 \leq i \leq k \). The collection of test statistics are \( T(Q_1), \ldots, T(Q_k) \), where \( Q_i = (Q_{i1}, \ldots, Q_{ig_i})^T \) for the \( i^{th} \) stratum.

Assume that we have different sets \( \{U_1, \ldots, U_k\} \) and \( \{\hat{U}_1, \ldots, \hat{U}_k\} \) of i.i.d. uniform variables on the interval \([0,1]\). Assume also that a set of constants \( \{c_1, \ldots, c_k\} \) with \( c_i \in [0,1] \) for all \( i \in \{1, \ldots, k\} \) is given. In practice, it is often preferred to choose \( c_1 = c_2 = \ldots = c_k = c \) for simplicity; cf. Hoang and Dickhaus (2022b). Using the above notations, we obtain \( k \) LFC \( p \)-values \( \{P^{\text{LFC}}_1(Q_1), \ldots, P^{\text{LFC}}_k(Q_k)\} \) with the corresponding \( k \) single-stage randomized \( p \)-values \( \{P^{\text{rand}}_1(Q_1, U_1, c), \ldots, P^{\text{rand}}_k(Q_k, U_k, c)\} \). Similarly, we also have \( k \) UMP \( p \)-values \( \{P^{\text{rand}, k}_1(Q_1, U_1), \ldots, P^{\text{rand}, k}_k(Q_k, U_k)\} \) with the corresponding \( k \) two-stage randomized \( p \)-values \( \{P^{\text{rand}, 2}_1(Q_1, U_1, U_1, c), \ldots, P^{\text{rand}, 2}_k(Q_k, U_k, \hat{U}_k, c)\} \).

We denote the multiple test for \( H_1, \ldots, H_k \) by \( \varphi = (\varphi_i : 1 \leq i \leq k) \) and the utilized \( p \)-values by \( \{p_1, \ldots, p_k\} \). By convention, \( \varphi_i = 1 \) denotes the event that \( H_i \) is rejected, while \( \varphi_i = 0 \) denotes the event that \( H_i \) is retained. Let \( I_0 = I_0(\theta) \subseteq I = \{1, \ldots, k\} \) denote the index set of true null hypotheses under \( \theta = (\theta_1, \ldots, \theta_k)^T \). Let \( V(\varphi) = \sum_{i \in I_0} \varphi_i \) be the number of type I errors (false rejections). Define the family-wise error rate (FWER, cf. Hochberg and Tamhane (1987), page 3) of \( \varphi \) under \( \theta \) by \( \text{FWER}_\theta(\varphi) = \mathbb{P}_\theta(V(\varphi) > 0) \). This is the probability of at least one false rejection of \( \varphi \) under \( \theta \). We say that the FWER is controlled at level \( \alpha \) by the multiple test \( \varphi \) if \( \sup_{\theta \in \Theta} \text{FWER}_\theta(\varphi) \leq \alpha \), where \( \Theta = [0,1]^k \) is the parameter space pertaining to \( \theta \).

One multiple test controlling the FWER (without further conditions) is given by the widely used Bonferroni correction, meaning that each individual test \( \varphi_i \) is carried out at the multiplicity-adjusted (local) level \( \alpha/k \), for \( i \in \{1, \ldots, k\} \). If all the \( k \) marginal test statistics are jointly independent (as it is the case in our model), the Šidák correction can be used, meaning that the local level is given by \( 1 - (1 - \alpha)^{1/k} \), which is slightly larger than \( \alpha/k \). In both cases, \( \varphi_i = 1 \) if and only if \( p_i \leq \alpha_{adj} \) for all \( i \in I \), where \( \alpha_{adj} \) equals \( \alpha/k \) or \( 1 - (1 - \alpha)^{1/k} \) for the Bonferroni or the Šidák test, respectively.

Let \( k_0 = k_0(\theta) = |I_0(\theta)| \leq k \) denote the number of true null hypotheses (under \( \theta \)). Knowledge of this quantity is in itself of scientific relevance, but can also be used for enhancing the power of the Bonferroni or the Šidák test, respectively. Namely, replacing \( k \) by \( k_0 \) in the definition of \( \alpha_{adj} \) still leads to FWER control under the respective assumptions. However, the value of \( k_0 \) depends on the value of \( \theta \) and thus, \( k_0 \) is often unknown in practice. Therefore, it has been proposed in previous literature to utilize a pre-estimate \( k_0 \) instead of \( k_0 \). In the case that \( k_0 < k \), the power of the aforementioned multiple tests is increased when replacing \( k \) by \( k_0 \) definition of \( \alpha_{adj} \). This methodology has been called Bonferroni plug-in (BPI) by Finner and Gontscharov (2009), and the authors proved that the BPI procedure works well for independent test statistics like the ones we are considering.

One classical, but still commonly used estimator for \( k_0 \) is the Schweder and Spjøtvoll (1982) estimator which is given by

\[
\hat{k}_0 \equiv \hat{k}_0(\lambda) = k \cdot \frac{1 - F_k(\lambda)}{1 - \lambda},
\]

where \( \lambda \in [0,1] \) is a tuning parameter and \( F_k \) is the empirical CDF (ecdf) of the \( k \) marginal \( p \)-values.
are (approximately) uniformly distributed on \([0,1]\) under the null hypothesis; see, e. g., Dickhaus (2013), Hoang and Dickhaus (2022a) and the references therein for details. The randomized \(p\)-values considered in this work are close to meeting the aforementioned uniformity assumption, whereas the \(p\)-values computed under LFCs are over-conservative when testing composite null hypothesis, especially in discrete models. Typically, the estimated value of \(k_0\) becomes too large if many null \(p\)-values are conservative and the estimator from (9) is employed.

In the remainder of this section, we use data taken from Table 6 of Kishaba et al. (1992); see also web Table 1 of the supporting information for this article. In that study a multiple-vector transfer was conducted using \(k = 6\) cultivars (strata) of the Muskmelon PMR 45. The objective of the study was to compare cultivar resistance to the zucchini yellow mosaic virus (ZYMV) and to also investigate its transmission by \(Aphis gossypii\). The probability of transmission with respect to the different strata (cultivar) is to be compared.

We have performed Monte Carlo simulations with 10,000 Monte Carlo repetitions to assess the (average) performance of the randomized \(p\)-values \(P^{rand}\), \(P^{rand1}\), and \(P^{rand2}\) in the estimation of \(k_0\) in this context. The tuning parameter \(\lambda\) appearing in (9) has been set to 1/2, and the constant \(c\) has also been set to 1/2 in all simulations. Furthermore, we have set \(\pi_1^* = \pi_2^* = \ldots = \pi_k^* = \pi^*\), for different values of \(\pi^*\). The (empirical) proportions of positive groups from web Table 1 in the supporting information for this article. In that study a multiple-vector transfer was investigated how to use single- and two-stage randomized \(p\)-values in the context of hypothesis testing problems involving composite null hypotheses under binomial models. We have also applied the \(p\)-values in group testing without or with stratification, the latter leading to multiple testing. In single-stage randomization, the discreteness of the \(p\)-value is partially removed. In two-stage randomization, the discreteness of the \(p\)-value is removed in the first stage. This is evidenced by the CDF for \(P^{rand2}\) being a smooth curve unlike the one for \(P^{rand1}\) which has minor steps. In the second stage, another randomization has been applied to deal with the conservativity of the \(p\)-value \(P^{rand}\) that arises due to the composite nature of the null hypothesis.

\[ (i) \text{ Taking } \pi^* = 0.0413 \text{ leading to } k_0 = 1, \text{ we obtained } \hat{k}^{LFC}_0 = 0 \text{ using } P^{LFC}, \hat{k}^{rand1}_0 = 1.9998 \text{ using } P^{rand1}, \hat{k}^{rand2}_0 = 1.3248 \text{ using } P^{rand2}, \text{ and } \hat{k}^{UMP}_0 = 1.347 \text{ using } P^{rand}. \text{ In this case, } P^{rand} \text{ and } P^{rand2} \text{ give the best estimates in terms of being on average close to the true value of } k_0. \text{ Utilizing } P^{LFC} \text{ leads to the worst result, especially because an underestimation of } k_0 \text{ is prone to lead to a violation of the FWER level by the BPI procedure.} \]

\[ (ii) \text{ Increasing the value of } \pi^* \text{ to 0.1663 so that } k_0 = 3, \text{ we find } \hat{k}^{LFC}_0 = 4, \hat{k}^{rand1}_0 = 3.996, \hat{k}^{rand2}_0 = 3.495, \text{ and } \hat{k}^{UMP}_0 = 5.4114. \text{ In this case } P^{rand} \text{ gives (on average) the best estimate, while } P^{LFC} \text{ and } P^{rand2} \text{ come closer to the true } k_0 \text{ than } P^{rand} \text{ does. The UMP } p\text{-value } P^{rand} \text{ gives (on average) the worst estimate.} \]

\[ (iii) \text{ Increasing the value of } \pi^* \text{ further to 0.3069 so that } k_0 = 5, \text{ the (average) estimates are } \hat{k}^{LFC}_0 = 10, \hat{k}^{rand1}_0 = 5.034, \hat{k}^{rand2}_0 = 5.0082, \text{ and } \hat{k}^{UMP}_0 = 10.00. \text{ In this scenario, } P^{rand1} \text{ and } P^{rand2} \text{ give the best (average) estimates for } k_0, \text{ while } P^{rand} \text{ and } P^{LFC} \text{ give very similar and clearly the worst estimates.} \]

If the proportion of true null hypotheses is high, using \(P^{rand1}\) or \(P^{rand2}\) in (9) generally gives the best estimates compared to using \(P^{LFC}\) or \(P^{rand}\). The performance of \(P^{rand1}\) as well as \(P^{rand2}\) improves as \(\pi^*\) increases. This is attributed to the fact that these two \(p\)-values are less conservative under the null hypothesis as compared to \(P^{rand}\) and \(P^{LFC}\), which are very conservative especially if \(\pi^*\) is large. In Case (iii) considered above, the utilization of \(P^{rand}\) or \(P^{LFC}\) even turned out to be completely uninformative with respect to estimating \(k_0\) for the purpose of applying the BPI procedure.

7 Discussion

We have investigated how to use single- and two-stage randomized \(p\)-values in the context of hypothesis testing problems involving composite null hypotheses under binomial models. We have also applied the \(p\)-values in group testing without or with stratification, the latter leading to multiple testing. In single-stage randomization, the discreteness of the \(p\)-value is partially removed. In two-stage randomization, the discreteness of the \(p\)-value is removed in the first stage. This is evidenced by the CDF for \(P^{rand2}\) being a smooth curve unlike the one for \(P^{rand1}\) which has minor steps. In the second stage, another randomization has been applied to deal with the conservativity of the \(p\)-value \(P^{rand}\) that arises due to the composite nature of the null hypothesis.
The two-stage randomized $p$-value $P_{\text{rand2}}$ is the least conservative one, almost exhausting the significance level of the tests under the null hypothesis. The non-randomized $p$-LFC is the most conservative one, but tests based on it are more powerful than those based on $P_{\text{rand1}}$. A comparison between power of the tests based on the four $p$-values and different sample sizes has also been carried out. The power function of tests based on $P_{\text{rand2}}$ is a smooth curve that increases monotonically with the sample size, while the power of tests based on $p$-LFC is not monotonically increasing in the sample size. This paradox of the power function of the tests based on $p$-LFC was described in detail by Finner and Strassburger (2001). The behavior of the power function of tests based on $P_{\text{rand2}}$ can facilitate sample size planning since we are certain that including additional observational units into the study can never result in a decrease of the power of the test.

The power of the tests based on $P_{\text{rand2}}$ increases in $c$. Hence, $P_{\text{rand2}}$ is stochastically ordered in $c$, while the single-stage randomized $p$-value $P_{\text{rand1}}$ is not stochastically ordered in $c$. This could be due to the fact that $P_{\text{rand2}}$ is based on a continuous $p$-value $P_{\text{rand}}$ while $P_{\text{rand1}}$ is based on a discrete $p$-value $p$-LFC. Under the null hypothesis, $P_{\text{rand2}}$ becomes less conservative as $c$ decreases. It has also been demonstrated graphically that for single-stage randomized $p$-value $P_{\text{rand1}}$, there is an advantage in using a $c$ in the support of the LFC-based $p$-value $p$-LFC.

We have used the four $p$-values in the context of group testing when the proportion of positive individuals in the population is of interest. When the number of tests is fixed and the total number of individuals varies, testing items in pools increases the power of all the tests based on the four $p$-values. This power further rises with using larger group sizes and only drops when the group sizes are too large or the proportion of positive individuals in the population is too high. These findings are in line with previous literature. For relatively high prevalence, group testing should be used only with a smaller group size. For high prevalence, group testing should not be considered but instead one should revert to individual testing. This is because of the massive drop in power of the tests based on the four $p$-values, which implies that we are less likely to make the right decisions using group testing at a high prevalence. For a fixed number of tests, testing items in groups is recommended especially when using tests based on $P_{\text{rand1}}$ and $P_{\text{rand2}}$. This is because testing items in groups will increase the power of the tests based on these two $p$-values.

We have also considered a composite null hypothesis in group testing when the total number of individuals is fixed but the number of groups (tests) is not fixed. The power of the tests based on the four $p$-values are slightly higher when using individual testing than when using group testing. The slight gain in power compared to the additional testing costs when using individual testing still makes group testing remain preferred. The simultaneous testing of composite null hypotheses in group testing when the population is divided into different strata has also been considered.

In this research we have considered upper-tailed tests. For lower-tailed tests only the $p$-LFC has to modified and the computations follow the same steps. The $p$-LFC is now defined as $P_{\text{LFC}}(X) = F_{\text{Bin}(n,\theta^*)}(T(X))$. We have only considered randomized $p$-values in testing a composite null hypothesis when the random variable is from a binomial distribution. Extensions to cases where the random variable is from other discrete distributions could be pursued in the future. In group testing, we have only considered the case when the prevalence rate $\theta$ is equal in all the strata. Using the procedures suggested by Evers and Nauta (2001), future research could consider a case where the prevalence rates are different across the strata. We have assumed that the tests are perfect and that no misclassification occurs. Future research could investigate the application of randomized $p$-values when the tests are imperfect. The assumption of independence among groups in a stratum could be modified to include procedures when the groups in a stratum are correlated.

Acknowledgements

Financial support by the German Research Foundation (DFG) via Grant No. DI 1723/5-1 is gratefully acknowledged.

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**Supporting Information**

Web Appendix A referenced in Section 4, Web Table 1 referenced in Section 6, and Web Figures 1 and 2 referenced in Section 5 are available with this paper.
Supporting Information for
“Randomized p-values in Binomial Models and in Group Testing”
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1 Web Appendix A

Proof of Lemma 1:
1) The single-stage randomized p-value \( P_{\text{rand}}^{1}(X, U) \) is valid, for each \( c \in [0, 1] \), due to Lemma 1 in Dickhaus et al. (2021), and the distributions of the LFC p-value \( P_{\text{LFC}}^{X}(X) \) being reverse hazard rate ordered w.r.t. to the underlying parameter \( \theta \). The test statistic for the binomial model is \( T(X) = \sum_{i=1}^{n} X_i = Y \) where \( X = (X_1, \ldots, X_n)^\top \) and its distribution is \( T(X) \sim Bin(n, \theta) \). This distribution is known to possess monotone likelihood ratio since \( \frac{d^2}{dp dq} \log f(y) = \frac{1}{y(1-y)} > 0 \) (cf. Karlin and Rubin (1956)).

2) To prove that \( P_{\text{rand}}^{2}(X, U, \tilde{U}, c) \) is valid (for all \( c \)), we have to show that \( P_{T}^{\text{rand}}(X, U) \) is uniformly valid, or, that for \( P_{T}^{\text{rand}}(X, U) \), condition (1) in Theorem 1 in Hoang and Dickhaus (2022) is fulfilled. It is therefore sufficient to show that it holds

\[
\mathbb{P}_\theta\{P_{T}^{\text{rand}}(X, U) \leq tc\} \leq t\mathbb{P}_\theta\{P_{T}^{\text{rand}}(X, U) \leq c\}
\]

for all \( c \in [0, 1] \), \( t \in [0, 1] \), and all \( \theta \in H \). This is equivalent to

\[
\frac{\mathbb{P}_\theta\{P_{T}^{\text{rand}}(X, U) \leq tc\}}{tc} \leq \frac{\mathbb{P}_\theta\{P_{T}^{\text{rand}}(X, U) \leq c\}}{c}
\]

and therefore to

\[
\frac{\mathbb{P}_\theta\{P_{T}^{\text{rand}}(X, U) \leq tc\}}{\mathbb{P}_{\theta^*}\{P_{T}^{\text{rand}}(X, U) \leq tc\}} \leq \frac{\mathbb{P}_\theta\{P_{T}^{\text{rand}}(X, U) \leq c\}}{\mathbb{P}_{\theta^*}\{P_{T}^{\text{rand}}(X, U) \leq c\}}
\]

holding for all \( c \in [0, 1] \), \( t \in [0, 1] \), and all \( \theta \in H \). Compare this to the definition of reverse hazard rate order. For a parameter \( \theta \) in the null hypothesis, i.e. \( \theta \leq \theta^* \), we define the function

\[
h(t) = \frac{\mathbb{P}_\theta\{P_{T}^{\text{rand}}(X, U) \leq t\}}{\mathbb{P}_{\theta^*}\{P_{T}^{\text{rand}}(X, U) \leq t\}}
\]

and so have to show that \( h \) is monotonically increasing in \( t \). Let \( S \) be the set of support points of \( P_{\text{LFC}}^{X}(X) \). The CDF of \( P_{T}^{\text{rand}}(X, U) \) and \( P_{\text{LFC}}^{X}(X) \) coincide on elements in \( S \). For two points \( t_1, t_2 \in S \), if \( t_1 < t_2 \) then \( h(t_1) \leq h(t_2) \), since, as elaborated above, the distributions of \( P_{\text{LFC}}^{X}(X) \) are reverse hazard rate ordered. Both the numerator and denominator of \( h(t) \) are linear functions in \( t \) between \( t_1 \) and \( t_2 \).

Let \( a_1, a_2, b_1 \) and \( b_2 \) be positive constants such that \( h(t) = \frac{a_1 t + b_1}{a_2 t + b_2} \), \( t \in [0, 1] \). For example, define

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\[ b_1 = \mathbb{P}_\theta \{ P_{T_{rand}}(X,U) \leq t_1 \} = \mathbb{P}_\theta \{ P_{LFC}(X) \leq t_1 \} \]

and

\[ b_1 + a_1 = \mathbb{P}_\theta \{ P_{T_{rand}}(X,U) \leq t_2 \} = \mathbb{P}_\theta \{ P_{LFC}(X) \leq t_2 \}. \]

It then holds \( \frac{b_1}{b_2} \leq \frac{a_1 + b_1}{a_2 + b_2} \) and \( a_1 a_2^{-1} b_1 b_2^{-1} \geq 1 \) and we show in the auxiliary Lemma below that the function \( t \mapsto \frac{a_1 t + b_1}{a_2 t + b_2}, \ t \in [0,1], \) is increasing in \( t \).

\[ \square \]

**Auxiliary Lemma:**

Let \( a_1, a_2, b_1, b_2 \) be positive constants such that \( \frac{b_1}{b_2} \leq \frac{a_1 + b_1}{a_2 + b_2} \) and \( a_1 a_2^{-1} b_1 b_2^{-1} \geq 1 \). Then the function \( t \mapsto \frac{a_1 t + b_1}{a_2 t + b_2}, \ t \in [0,1], \) is increasing in \( t \).

**Proof**

The derivative of the function at point \( t \) is

\[
\frac{(a_2 t + b_2) a_1 - (a_1 t + b_1) a_2}{(a_2 t + b_2)^2}
\]

which is non-negative iff

\[
\frac{a_1}{a_2} \geq \frac{a_1 t + b_1}{a_2 t + b_2}.
\]

This is true for all \( t \) iff

\[
\frac{a_1}{a_2} \geq \frac{a_1 + b_1}{a_2 + b_2}
\]

which is what we need to show. Let \( c_1 = \frac{a_2}{a_2 + b_2} \) and \( c_2 = \frac{b_2}{a_2 + b_2} \) then it holds

\[
c_1 \frac{a_1}{a_2} = \frac{a_1 + b_1}{a_2 + b_2}
\]

and

\[
c_2 \frac{b_1}{b_2} = \frac{a_1 + b_1}{a_2 + b_2}.
\]

From this we conclude that it holds

\[
max(c_1, c_2) \left( \frac{a_1}{a_2} + \frac{b_1}{b_2} \right) \geq c_1 \frac{a_1}{a_2} + c_2 \frac{b_1}{b_2} = a_1 + b_1.
\]

Since \( 0 < max(c_1, c_2) < 1 \), \( \frac{a_1 + b_1}{a_2 + b_2} \) must be between \( \frac{a_1}{a_2} \) and \( \frac{b_1}{b_2} \). From our assumptions it holds \( \frac{b_1}{b_2} \leq \frac{a_1 + b_1}{a_2 + b_2} \) so it must hold \( \frac{a_1}{a_2} \geq \frac{a_1 + b_1}{a_2 + b_2} \) which is what we needed to show.

\[ \square \]

### 2 Web Table 1

Table 1 has data taken from Kishaba et al. (1992). The data is for a multiple-vector transfer experiment conducted to investigate cultivar resistance to ZYMV.
Table 1: ZYMV data showing the number of test plants and the number of infected plants for the six cultivars (strata). Equal group size of $s = 60$ was used.

| Stratum | Hybrid               | No. of test plants | No. of infected test plants |
|---------|----------------------|--------------------|----------------------------|
| 1       | PMR 45               | 32                 | 30                         |
| 2       | AR PMR 45            | 64                 | 13                         |
| 3       | F1 (AR HBJ:PMR 45)   | 64                 | 19                         |
| 4       | AR HBJ               | 32                 | 5                          |
| 5       | AR Gulfstream        | 32                 | 4                          |
| 6       | AR 5 (18145)         | 32                 | 1                          |

3 Web Figure 1: Power versus group size $s$ for fixed number of tests.

Figure 1: An illustration of power versus different group sizes $s$ for LFC, UMP single (RAND1) and two-stage (RAND2) randomized $p$-values for fixed number of tests. We set $c = 0.5$, $\alpha = 0.05$, $g = 50$, $\theta^* = 0.1$, and $\theta = 0.2$. 
**Web Figure 2:** Power versus group size $s$ for fixed number of individuals.

Figure 2: An illustration of power versus different group sizes $s$ for LFC, UMP single (RAND1) and two-stage (RAND2) randomized $p$-values for fixed number of individuals. We set $c = 0.5$, $\alpha = 0.05$, $\theta^* = 0.1$, $\theta = 0.2$, $N = 300$, $g$ is taken to be a decreasing sequence of integers from 300 to 6, and $s = N/g$. The non-integers in $s$ are used the way they are.

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