Enrichment or depletion of a GO category within a class of genes: which test?

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ABSTRACT

Motivation: A number of available program packages determine the significant enrichments and/or depletions of GO categories among a class of genes of interest. Whereas a correct formulation of the problem leads to a single exact null distribution, these GO tools use a large variety of statistical tests whose denotations often do not clarify the underlying P-value computations.

Summary: We review the different formulations of the problem and the tests they lead to: the binomial, χ², equality of two probabilities, Fisher’s exact and hypergeometric tests. We clarify the relationships existing between these tests, in particular the equivalence between the hypergeometric test and Fisher’s exact test. We recall that the other tests are valid only for large samples, the test of equality of two probabilities and the χ²-test being equivalent. We discuss the appropriateness of one- and two-sided P-values, as well as some discreteness and conservatism issues.

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Supplementary information: Supplementary data are available at Bioinformatics online.

1 INTRODUCTION

A common problem in functional genomic studies is to detect significant enrichments and/or depletions of Gene Ontology (GO) categories within a class of genes of interest, typically the class of significantly differentially expressed (DE) genes. Many GO processing tools perform this task using various statistical tests referred to as: the binomial test, the χ²-test, the equality of two probabilities test, Fisher’s exact test and the hypergeometric test (see Table 1). The authors of some packages claim the advantages of the test(s) they propose, often seemingly contradicting each other. For example, Zeeberg et al. (2003) favor Fisher’s exact test: ‘Unlike the Z-statistics with the hypergeometric distribution, and tests based on it, Fisher’s exact test is appropriate even for categories containing a small number of genes’, whereas for Martin et al. (2004) the hypergeometric test is most appropriate: ‘On the average, the hypergeometric distribution seems to be both the most adapted model and the most powerful test’. Moreover, even though the most recent review papers use a number of criteria to exhaustively compare the different existing tools (Khatri and Draghici, 2005), they do not discuss in detail the identity and approximation relationships existing between the different tests. This is precisely the aim of the present paper.

2 PROBLEM STATEMENT

We consider a total population of genes, e.g. the genes expressed in a microarray experiment, and we are interested in the property of a gene to belong to a specific GO category. The aim is to establish whether the class of the DE genes presents an enrichment and/or a depletion of the GO category of interest with respect to the total gene population.

3 CANDIDATE FORMULATIONS

Let H₀ denote the null hypothesis that the property for a gene to belong to the GO category of interest and that to be DE are independent, or equivalently that the DE genes are picked at random from the total gene population. We consider successively the hypergeometric, the comparison of two probabilities, and the 2 × 2 contingency table formulations of the above problem, and introduce the exact or approximate null distributions they lead to.

Notations (see Table 2): the total number of genes is denoted by n, the total number of genes belonging to the GO category of interest by n₁, the number of DE genes by n₁⁺, n₁⁻ and n₁⁻⁺ are hence fixed by the experiment. The number of DE genes belonging to the GO category is denoted by n₁⁺.

3.1 Hypergeometric formulation

The hypergeometric formulation is directly derived from the problem statement.

3.1.1 Exact null distribution If H₀ is true, the random variable N₁⁺ whose realization is the observed value n₁⁺, has a hypergeometric distribution with parameters n, n₁⁺, and n₁⁺, which we denote by N₁⁺ ~ Hyper(n, n₁⁺, n₁⁻⁺), with:

\[ P(N_{1+} = x) = \binom{n_{1+}}{x} \binom{n - n_{1+}}{n_{1+} - x} \binom{n}{x} \binom{n_{1+} + n_{1-}}{n_{1+} + n_{1-}}. \] (1)

Note that Hyper(n, n₁⁺, n₁⁻⁺) ≡ Hyper(n, n₁⁺, n₁⁻⁺).

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Table 1. Reviewed GO processing tools

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<thead>
<tr>
<th>GO tool</th>
<th>Statistical tests</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>BINGO</td>
<td>Hypergeometric</td>
<td>Maere et al., 2005</td>
</tr>
<tr>
<td>CLENCH</td>
<td>Hypergeometric, binomial, $\chi^2$</td>
<td>Shah and Fedorov, 2004</td>
</tr>
<tr>
<td>DAVID</td>
<td>Fisher</td>
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</tr>
<tr>
<td>EASEonline</td>
<td>Fisher</td>
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<td>eGOn</td>
<td>Fisher</td>
<td><a href="http://www.genetools.microarray.ntnu.no/help/help_egon.php?egon=1#intro">http://www.genetools.microarray.ntnu.no/help/help_egon.php?egon=1#intro</a></td>
</tr>
<tr>
<td>FatiGO</td>
<td>Fisher</td>
<td>Al-Sharoar et al., 2004</td>
</tr>
<tr>
<td>FuncAssociate</td>
<td>Fisher</td>
<td><a href="http://llama.med.harvard.edu/cgi/func/funcassociate">http://llama.med.harvard.edu/cgi/func/funcassociate</a></td>
</tr>
<tr>
<td>FunSpec</td>
<td>Hypergeometric</td>
<td>Robinson et al., 2002</td>
</tr>
<tr>
<td>GeneMerge</td>
<td>Hypergeometric</td>
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<tr>
<td>GFINDer</td>
<td>Hypergeometric, binomial, Fisher $^a$</td>
<td>Masseroli et al., 2004</td>
</tr>
<tr>
<td>GoMiner</td>
<td>Fisher</td>
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<td>GOstat</td>
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<td>GoSurfer</td>
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<td>GO TermFinder (CPAN)</td>
<td>Hypergeometric</td>
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<tr>
<td>GO TermFinder (SGD)</td>
<td>Binomial</td>
<td><a href="http://www.yeastgenome.org/help/goTermFinder.html">http://www.yeastgenome.org/help/goTermFinder.html</a></td>
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<td>GOTM</td>
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<tr>
<td>GOTOolBox</td>
<td>Hypergeometric, binomial, Fisher</td>
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<td>NetAffx GO Mining Tool</td>
<td>$\chi^2$</td>
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<td>Onto-Express</td>
<td>Binomial, $\chi^2$, Fisher</td>
<td>Khatri et al., 2002; Draghici et al., 2003</td>
</tr>
<tr>
<td>Ontology Traverser</td>
<td>Hypergeometric</td>
<td>Young et al., 2005</td>
</tr>
<tr>
<td>STEM</td>
<td>Hypergeometric</td>
<td>Ernst et al., 2005</td>
</tr>
<tr>
<td>THEA</td>
<td>Hypergeometric, binomial</td>
<td>Pasquier et al., 2004</td>
</tr>
</tbody>
</table>

$^a$The website now proposes 3 additional tests, but they are not documented.

Table 2. Classification of the genes expressed in a microarray experiment

<table>
<thead>
<tr>
<th></th>
<th>Category 1 (GO category)</th>
<th>Category 2 (GO category)</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Class 1 (DE)</td>
<td>$n_{11}$</td>
<td>$n_{12}$</td>
<td>$n_{1+}$</td>
</tr>
<tr>
<td>Class 2 (not DE)</td>
<td>$n_{21}$</td>
<td>$n_{22}$</td>
<td>$n_{2+}$</td>
</tr>
<tr>
<td>Total</td>
<td>$n_{11}$</td>
<td>$n_{12}$</td>
<td>$n_{21}$</td>
</tr>
</tbody>
</table>

3.1.2 Approximate null distribution For a large sample, $N_{11}$ has approximately a binomial distribution with parameters $n_{1+}$ and $n_{1+}/n$: $N_{11} \sim Bi(n_{1+}, n_{1+}/n)$. Note that if $n_{1+} n_{1+}/n$ is also large, the binomial approximation can further be approximated by a Gaussian distribution.

3.2 Comparison of two probabilities formulation

In a second formulation, we consider two samples, that of the DE genes of size $n_{1+}$, among which $n_{11}$ genes belong to the GO category of interest, and that of the not DE genes of size $n_{2+}$, among which $n_{21}$ genes belong to the GO category. The proportions of genes belonging to the GO category in the two samples are thus $f_1 = n_{11}/n_{1+}$ (DE genes) and $f_2 = n_{21}/n_{2+}$ (not DE genes). Let $p_1$ and $p_2$ denote the probabilities to belong to the GO category in the two samples; then $N_{11} \sim Bi(n_{1+}, p_1)$ and $N_{21} \sim Bi(n_{2+}, p_2)$. In this formulation, the null hypothesis $H_0$ is the equality of the two probabilities $p_1 = p_2 = p$, i.e. there is neither enrichment nor depletion in the sample of DE genes with respect to that of the not DE genes.

3.2.1 Approximate null distribution The case of large samples arises frequently. Then, the binomial distributions can be approximated with Gaussian distributions. Under $H_0$, $n_{1+}$ and $n_{2+}$ being large, the probability $p$ can be correctly estimated with $f = (n_{11} + n_{21})/(n_{1+} + n_{2+}) = n_{1+}/n$, leading to the approximately normally distributed variable:

$$Z = \frac{F_1 - F_2}{\sqrt{F(1-F)\left(\frac{1}{n_{1+}} + \frac{1}{n_{2+}}\right)}} \sim N(0,1).$$

This distribution is approximate for two reasons: (1) the replacement of the binomial distributions by Gaussian distributions holds only for large samples (both $n_{1+}$ and $n_{2+}$ must be large), and (2) it has not been taken into account that, according to our problem statement, the sum $N_{11} + N_{21}$, the total number of genes belonging to the GO category, is fixed and equal to $n_{1+}$.

3.2.2 Exact null distribution Without approximating the binomial distribution, and taking into account that $N_{11} + N_{21} = n_{1+}$, we naturally obtain $N_{11} \sim \text{Hyper}(n, n_{1+}, n_{1+})$ (see (Fisher, 1935; Lehman, 1986) for the complete computation with the binomial distribution conditionally on $N_{11} + N_{21} = n_{1+}$). Hence, the exact distribution of $N_{11}$ under $H_0$ is as before the hypergeometric distribution.

3.3 Contingency table formulation

A third formulation is based on Table 2 seen as a 2 × 2 contingency table. Let again $H_0$ denote the hypothesis that the property to belong to the GO category of interest and that to be DE are independent.
3.3.1 Approximate null distribution  The case of a large sample is frequently considered where, if H₀ is true, the following variable is asymptotically \( \chi^2 \) distributed with one degree of freedom (Mood et al., 1974):

\[
D^2 = \sum_{i=1}^{n_1} \sum_{j=1}^{n_2} \left( \frac{N_{ij} - \frac{n_{ij} n_{i+} n_{j+}}{n}}{} \right)^2 \sim \chi^2(1). \tag{3}
\]

Note that \( D^2 \) is the square of the realization of the random variable \( Z \) given by Equation (2):

\[
d^2 = \frac{n(n_1 n_2 - n_12 n_21)^2}{n_1 n_2 n_12 n_21} = z^2. \tag{4}
\]

3.3.2 Exact null distribution  Whatever the sample size, Fisher’s formula gives the probability of the observed configuration of the contingency table under H₀ (Fisher, 1935; Mood et al., 1974; Agresti, 2002):

\[
P(\{N_{ij} = n_{ij}\}) = \frac{n! n_{i+!} n_{j+!} n_{+!}}{n_{i+!}! n_{j+!}! n_{+!}!} \frac{n_{ij}}{n_{i+}}! \frac{n_{ij}}{n_{j+}}! \frac{n_{ij}}{n_{+}}!. \tag{5}
\]

It is easy to show that \( N_{11} \sim \text{Hyper}(n, n_{i+}, n_{j+}) \):

\[
P(N_{11} = x | N_{i+} = n_{i+}, N_{j+} = n_{j+}) = \frac{n_{i+!} n_{j+!} n_{+!}}{n_{i+!}! n_{j+!}! n_{+!}!} \frac{n_x}{n_{i+}}! \frac{n_{x}}{n_{j+}}! \frac{n_{n-x}}{n_{+}}! \tag{6}
\]

As expected, the exact distribution of \( N_{11} \) under H₀ is again the hypergeometric distribution, see Equation (1).

3.4 Summary  Under H₀, i.e. assuming the independence of the property to belong to the GO category of interest and of the property to be DE, or equivalently assuming \( p_1 = p_2 \) where \( p_1 \) is the probability of the DE genes to belong to the GO category, and \( p_2 \) the probability of the not DE genes to belong to the GO category, the exact distribution of \( N_{11} \) is the hypergeometric distribution \( N_{11} \sim \text{Hyper}(n, n_{i+}, n_{j+}) \) which, if \( n \) is large, can be approximated with the binomial distribution \( B(n_{i+}, n_{i+}/n) \). If the two samples are large, it is also possible to exhibit an approximately normal variable \( Z \) or its square \( D^2 = Z^2 \), the latter being hence approximately \( \chi^2 \) distributed with one degree of freedom.

4 TESTS AND P-VALUES  Generally, when performing the test of a null hypothesis H₀ against some alternative hypothesis Hₐ, one disposes of a realization \( x \) of a random variable \( X \) with known distribution under H₀, the null distribution. One chooses \textit{a priori} a probability \( \alpha \) of type I error (the error to reject H₀ whereas it is true) that must not be exceeded, also called significance level, the decision to reject H₀ being taken when \( x \) falls in the critical region. In this context, the \( P \)-value is the minimum significance level for which H₀ would be rejected, or equivalently, it is the probability, under H₀, of the minimal critical region containing \( x \).

The choice of a critical region in order to maximize the power of the test, and hence the choice of the corresponding \( P \)-value, depends on the alternative hypothesis Hₐ, which may be ‘enrichment’ (\( p_1 > p_2 \), one-sided test, critical region right), ‘depletion’ (\( p_1 < p_2 \) ‘one-sided’ test, critical region left), or ‘enrichment or depletion’ (\( p_1 \neq p_2 \), two-sided test, critical region left and right). Enrichment, depletion and enrichment or depletion are later denoted by E, D, and E/D, respectively.

4.1 One-sided tests  The one-sided \( P \)-value is defined as:

\[
\begin{cases} 
\text{if } H₀ = E, P_{\text{one}}(n_{11}) = P(N_{11} \geq n_{11}) \\
\text{if } H₀ = D, P_{\text{one}}(n_{11}) = P(N_{11} \leq n_{11}).
\end{cases} \tag{7}
\]

If the case of a discrete distribution, like the exact hypergeometric distribution or the approximate binomial distribution, it is not possible to guaranty any value of the significance level with the rule ‘reject H₀ if \( p_{\text{one}}(n_{11}) \leq \alpha' \). Due to the discreteness, the actual significance level (or size of the test) is generally smaller than the nominal (desired) significance level \( \alpha \), which results in a loss of power.

To minimize this loss, a good remedy is the use of mid-\( P \)-values (Agresti and Min, 2001; Agresti, 2002). The one-sided mid-\( P \)-value, which we denote by \( P_{\text{one}} \), is defined as:

\[
\begin{cases} 
\text{if } H₀ = E, P_{\text{one}}(n_{11}) = P(N_{11} > n_{11}) + \frac{1}{2}P(N_{11} = n_{11}) \\
\text{if } H₀ = D, P_{\text{one}}(n_{11}) = P(N_{11} < n_{11}) + \frac{1}{2}P(N_{11} = n_{11}).
\end{cases} \tag{8}
\]

It must be noted that the actual significance level, i.e. the actual probability of type I error, is no longer guaranteed to be smaller than the nominal significance level. However, it is rarely much greater (Agresti, 2002).

Another remedy is randomization, with which any desired significance level can be achieved. However in practice, randomization having nothing to do with the data does not make much sense (Lehmann, 1986; Agresti, 2002).

If the approximately normal variable \( Z \) is considered, we have:

\[
\begin{cases} 
\text{if } H₀ = E, P_{\text{one}}(z) = P(Z > z) \\
\text{if } H₀ = D, P_{\text{one}}(z) = P(Z < z).
\end{cases} \tag{9}
\]

If the approximately \( \chi^2 \) distributed variable \( D^2 \) is used, a one-sided test cannot be performed, since both enrichment (large observed \( n_{11} \)) and depletion (small observed \( n_{11} \)) lead to a large value of \( D^2 \), i.e. there is a single critical region.

4.2 Two-sided tests  In the case of a two-sided test i.e. \( H₀ = E/D \), and of a discrete null distribution, there are several popular definitions of the \( P \)-value, see (Agresti, 1992, 2002). A first approach defines the two-sided \( P \)-value as twice the one-sided \( P \)-value:

\[
P_{\text{two}}(n_{11}) = 2 \times \min[P(N_{11} \geq n_{11}), P(N_{11} \leq n_{11})]. \tag{10}
\]

Yates and Fisher himself were in favor of this ‘doubling’ approach (Yates, 1984). A second approach, which after Gibbons and Pratt (1975) we name the ‘minimum-likelihood’ approach, defines the \( P \)-value as the sum of the probabilities of the values of \( N_{11} \) that are
smaller or equal to that of the observed value \( n_{11} \), as recommended for example in (Mehta and Patel, 1998):

\[
p_{\text{two}}^{\text{min lik}}(n_{11}) = \sum_{P(N_{11} = m) < P(n_{11})} P(N_{11} = m).
\]

The minimum-likelihood approach is the only one we have encountered in the GO tools of Table 1. A third approach defines the \( P \)-value as the sum of the probabilities that are smaller than \( n_{11} \) that are at least as or more extreme (with respect to the \( P \)-value of the hypergeometric distribution. The problem is also that these \( P \)-values do not correspond to any well-defined two-sided test. This issue is discussed for example in (Dunne et al., 1996), where a two-sided \( P \)-value based on an uniformly most powerful unbiased test is proposed. However, this \( P \)-value is obtained with an iterative procedure, which makes this approach inadequate for the screening of hundreds of different GO categories.

Thus, if a single simple and computationally light (see subsection 6.3) procedure were to be recommended, we would advice the doubling approach, against which there is no strong argument, and using the mid-\( P \)-value, in order to reduce the discreteness and conservatism effects:

\[
p_{\text{two}}^{\text{double}}(n_{11}) = 2 \times \min\{P(N_{11} > n_{11}) + P(N_{11} = n_{11}), P(N_{11} < n_{11}) + P(N_{11} = n_{11})\}.
\]

A mid-\( P \)-value can also be defined for the minimum-likelihood approach, as the sum of the probabilities that are smaller than the probability of the observed value \( n_{11} \), plus half the sum of the probabilities equal to it:

\[
p_{\text{two}}^{\text{min lik}}(n_{11}) = \sum_{P(N_{11} = m) < P(n_{11})} P(N_{11} = m) + \frac{1}{2} \sum_{P(N_{11} = m) = P(n_{11})} P(N_{11} = m).
\]

However, we must again emphasize that the actual probability of type I error may exceed the nominal significance level.

If the approximately normal variable \( Z \) is considered (a continuously and symmetrically distributed variable), we have:

\[
p_{\text{two}}(z) = 2 \times \min\{P(Z > z), P(Z < z)\}.
\]

If the approximately \( \chi^2 \) distributed variable \( D^2 \) is considered, the \( P \)-value is computed as:

\[
p_{\text{two}}(d^2) = P(D^2 > d^2) = p_{\text{two}}(z).
\]

### 4.3 One versus two-sided tests?

Consider a dataset consisting of tissues in a pathological condition and of normal tissues, and a GO category whose genes are directly affected by the condition, i.e. the genes belonging to this GO category are DE (either over- or under-expressed). Such a GO category is likely to be over-represented among the DE genes, i.e. an enrichment is expected. Thus, detecting an enrichment is desirable. On the other hand, consider a GO category such that the normal expression of the corresponding genes is necessary for the condition to develop, i.e. the genes belonging to this GO category are not DE. Such a GO category is likely to be under-represented among the DE genes, i.e. a depletion is expected. Thus, detecting a depletion is also desirable, even if there is a risk to detect the depletion of a GO category corresponding to genes whose normal expression is necessary to the mere survival of the species.

Thus, both enrichments and depletions of GO categories are potentially of interest. Hence, unless there is a specific reason not to consider enrichment or depletion, the adequate alternative hypothesis is \( H_a = E/D \), i.e. two-sided tests are appropriate.

### 5 SUMMARY AND DISCUSSION

To summarize, there is a single exact null distribution of \( N_{11} \), the hypergeometric distribution, but different exact tests (exact in the sense that they are based on the exact null distribution), one or two-sided, and with several definitions of the \( P \)-value in the latter case. These tests can equally be called hypergeometric or Fisher’s exact tests. Thus, it is not justified to claim, as Masseroli et al. (2004) do, that ‘the \( \chi^2 \) and Fisher’s exact tests have less power than the hypergeometric and binomial distribution tests’. GFINDER and GOToolBox propose the hypergeometric test and Fisher’s exact test as two alternative options: GFINDER indeed provides the same results for the two options (one-sided tests), but strangely enough, GOToolBox gives different results, whereas they should be identical for the same choice of a \( P \)-value (incorrect results given by some GO tools are detailed in the Appendix, which is available as supplementary data).

The available GO tools often do not explicitly state which \( P \)-value is computed. For example, BINGO calls the test it performs ‘hypergeometric test’ (Maere et al. 2005), without saying that it is two-sided with the minimum-likelihood approach. According to both references and websites, we could establish that FuncAssociate, GFINDER and THEA provide only one-sided tests in both directions, while FuncSpec, EASEonline, GO Term Finder (CPAN), Term Finder (SGD), GOTM, L2L, Ontology Traverser and STEM only one-sided enrichment tests and that BINGO, DAVID, eGOn, 2004 FatiGo, GeneMerge, GoMiner, GOSTat, GoSurfer, NetAffx and Onto-Express provide two-sided tests, the \( P \)-values being computed according to the minimum-likelihood approach when a discrete distribution is used.

As discussed in section 4.3, two-sided tests are usually most appropriate. Be it with the doubling or the minimum-likelihood approach to the \( P \)-value, the discreteness and conservatism effects can be efficiently dealt with using mid-\( P \)-values, a possibility that is not offered by any of the GO tools of Table 1.

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As a matter of fact, (Fisher, 1935) describes a one-sided test in the direction of the observed departure of the null hypothesis.
6 NUMERICAL ILLUSTRATIONS

6.1 Small sample

We consider a small sample with \( n = 20, n_{1a} = 7, n_{a1} = 6 \) and \( n_{11} = 4 \), i.e. \( f_1 = 0.57 \) and \( f_2 = 0.15 \). The null distribution of \( N_{11} \sim \text{Hyper}(n, n_{1a}, n_{a1}) \) is shown in Figure 1. The sample being very small, we consider only the tests based on this exact distribution.

6.1.1 One-sided test

For illustration purposes, let us first consider a one-sided test (suppose one is interested in enrichments only). The corresponding one-sided \( P \)-value equals:

\[
p_{\text{one}}(4) = P(N_{11} \geq 4) = P(4) + P(5) + P(6) = 7.04 \times 10^{-2} + 7.04 \times 10^{-3} + 1.81 \times 10^{-4} = 7.77 \times 10^{-2}.
\]

The one-sided mid-\( P \)-value is:

\[
\pi_{\text{one}}(4) = P(N_{11} > 4) + P(4)/2 = 7.04 \times 10^{-3} + 1.81 \times 10^{-4} + 7.04 \times 10^{-2}/2 = 4.24 \times 10^{-2}.
\]

There is a substantial difference between the \( P \)-value and the mid-\( P \)-value. With a significance level \( \alpha = 5\% \), the mid-\( P \)-value leads to reject \( H_0 \); whereas the \( P \)-value does not: the use of a mid-\( P \)-value corresponds to a less conservative test. However, the actual significance level is no longer guaranteed to be smaller than the nominal significance level 5\%.

6.1.2 Two-sided tests

The two-sided doubling \( P \)-value equals:

\[
p_{\text{doubling}}(4) = 2 \times \min (P(N_{11} \leq 4), P(N_{11} \geq 4)) = 2 \times P(N_{11} \geq 4) = 2 \times P_{\text{one}}(4) = 1.55 \times 10^{-1}.
\]

The two-sided doubling mid-\( P \)-value equals:

\[
\pi_{\text{doubling}}(4) = 2 \times \min (P(N_{11} < 4) + P(N_{11} = 4)/2, P(N_{11} > 4) + P(N_{11} = 4)/2) = 2 \times P(N_{11} > 4) + P(4)/2 = 2 \times \pi_{\text{one}}(4) = 8.49 \times 10^{-2}.
\]

As for the one-sided test, there is a substantial difference between the two values. Also, with a significance level \( \alpha = 5\% \), a two-sided test does not reject \( H_0 \).

The two-sided minimum-likelihood \( P \)-value equals:

\[
p_{\text{two}}^{\text{min lk}}(4) = \sum_{P(N_{11} - m) \geq P(4)} P(N_{11} = m) = P(0) + P(4) + P(5) + P(6) = 4.43 \times 10^{-2} + 7.04 \times 10^{-2} + 7.04 \times 10^{-3} + 1.81 \times 10^{-4} = 1.22 \times 10^{-1}.
\]

The hypergeometric distribution being here asymmetric, the doubling and minimum-likelihood \( P \)-values are quite different.

The two-sided minimum-likelihood mid-\( P \)-value equals:

\[
\pi_{\text{two}}^{\text{min lk}}(4) = \sum_{P(N_{11} - m) \geq P(4)} P(N_{11} = m) + P(N_{11} = 4)/2 = P(0) + P(5) + P(6) + P(4)/2 = 8.67 \times 10^{-2}.
\]

It is always smaller than the \( P \)-value, and hence corresponds to a less conservative test.

6.2 Large sample

We now consider a sample whose size is analogous to that of samples encountered when testing enrichment of GO categories among DE genes on dedicated microarrays. We have \( n = 800, n_{1a} = 40, n_{a1} = 100, \) and observe \( n_{11} = 10 \), i.e. \( f_1 = 0.25 \) and \( f_2 = 0.12 \). The alternative hypothesis is \( H_a = E/D \) (two-sided test).

- The exact two-sided doubling \( P \)-value obtained with the hypergeometric distribution is \( p_{\text{doubling}}^{\text{hyper}}(n_{11}) = 3.95 \times 10^{-2} \), and the two-sided mid-\( P \)-value is \( \pi_{\text{doubling}}(n_{11}) = 2.66 \times 10^{-2} \). With the minimum-likelihood approach, \( p_{\text{two}}^{\text{min lk}}(n_{11}) = 2.39 \times 10^{-2} \), and the two-sided mid-\( P \)-value is \( \pi_{\text{two}}^{\text{min lk}}(n_{11}) = 1.74 \times 10^{-2} \). Note that, the null distribution being asymmetric, there is a noticeable difference between the two approaches, and, though the sample is quite large, between the \( P \)-values and the corresponding mid-\( P \)-values.

- The approximate binomial test leads to a doubling \( P \)-value of \( 4.54 \times 10^{-2} \), and to a doubling mid-\( P \)-value of \( 3.11 \times 10^{-2} \), to a minimum-likelihood \( P \)-value of \( 2.75 \times 10^{-2} \), and to a minimum-likelihood mid-\( P \)-value of \( 2.03 \times 10^{-2} \). Note that though the sample is not small, there is quite a difference with the exact distribution.

- The approximate test of equality of two probabilities leads to the value of an approximately normal statistic \( z = 2.45 \), and to a two-sided \( P \)-value of \( p_{\text{two}}(x) = 1.42 \times 10^{-2} \). This value is even less accurate than that obtained with the binomial approximation, because the DE sample is too small (\( n_{1a} = 40 \)).

- The \( \chi^2 \)-test indeed leads to a statistic value \( d^2 = 6.015 = z^2 \), and hence to the same two-sided \( P \)-value.

In the case of larger samples, obtained with mouse or human pangenomic microarrays, typically with \( n \) of the order of 25,000:

- The approximate binomial test leads to (mid-) \( P \)-values that are very close to those of the exact hypergeometric test. However, with today’s computing means, there is no decisive advantage in performing this approximation (see next section).

- The approximate test of equality of two probabilities becomes closer to the exact one only if the number of DE genes is large,
which is not necessarily the case. There is thus no reason to use this test.

- This is hence also true for the equivalent χ² test.

6.3 Implementation with R and computational issues

All the exact tests can be implemented ‘by hand’ with the hypergeometric cumulative distribution function ‘phyper’ and the distribution function ‘dhyper’, and the binomial approximations with ‘pbinom’ and ‘dbinom’.

The default implementation of the exact test with R provides the two-sided minimum-likelihood P-value. The corresponding instruction is ‘fisher.test(c)’, where the matrix c is the 2 × 2 contingency table [n₁₁ n₁₂; n₂₁ n₂₂]. The one-sided enrichment test is obtained with ‘fisher.test(c, alternative = “greater”)’, the one-sided depletion test with ‘fisher.test(c, alternative = “less”)’.

In order to evaluate the computation time of the two-sided tests, let us consider the case of a microarray with n = 25 000 genes, n₁ = 1000 DE genes, and 500 different GO categories. We take n₁₁ uniformly distributed in [0,n], and n₁₁ uniformly distributed in [max(0, n₁1+ n₁-n), min(n₁, n₁1)]. With R 2.1.0 running under Mac OS X on a 2 GHz two processor Macintosh (PowerPC 970 2.2), we obtain the following total elapsed times (mean and standard error on 20 runs) for the doubling approach:

- hypergeometric doubling P-values, computed with the functions ‘dhyper’ and ‘phyper’: 0.17 ± 0.02 s, and 0.20 ± 0.02 s for the mid-P-values.
- binomial doubling P-values, computed with the functions ‘dbinom’ and ‘pbinom’: 0.16 ± 0.02 s, and 0.19 ± 0.02 s for the mid-P-values.

Hence, the gain in time obtained by using the binomial approximation to the hypergeometric distribution is negligible.

For the minimum-likelihood approach, the R function ‘fisher.test’, (which does not only compute a P-value) is much slower than a computation ‘by hand’:

- hypergeometric minimum-likelihood P-values, computed with the function ‘fisher.test’: 17.15 ± 0.21 s.
- hypergeometric minimum-likelihood P-values, computed with the functions ‘dhyper’ and ‘phyper’: 1.83 ± 0.04 s and 2.10 ± 0.05 s for the mid-P-values.

The computation time is hence an argument in favor of the doubling approach to the two-sided P-value.

7 CONCLUSION

The correct statement of the enrichment and/or depletion testing problem leads to a unique exact null distribution of the number of DE genes belonging to the GO category of interest, given the total gene number and the total number of genes belonging to the GO category. This distribution is the hypergeometric one, whose values are equivalently given by Fisher’s formula for a 2 × 2 contingency table. Since both enrichments and depletions of GO categories are potentially of interest, two-sided tests are generally most appropriate. With the doubling or the popular minimum-likelihood definitions of the P-value, a loss of power due to the discreteness of the hypergeometric distribution is efficiently dealt with using mid-P-values, the doubling P-value involving lighter computations than the minimum-likelihood P-value. Finally, since many dedicated microarrays involve small data sets, and given the currently available algorithms and computing means, there is no strong argument in favor of the approximate large sample tests.

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REFERENCES


The code of the R functions can be found at the R project site https://svn.r-project.org/R/trunk/src/nmath/. The best known and most complete software for contingency table methods in general is StatXact (Agresti, 2006).


