

# Discovering statistically significant pathways in expression profiling studies

Lu Tian<sup>†</sup>, Steven A. Greenberg<sup>‡§</sup>, Sek Won Kong<sup>¶||</sup>, Josiah Altschuler<sup>¶</sup>, Isaac S. Kohane<sup>§††</sup>, and Peter J. Park<sup>§†††</sup>

<sup>†</sup>Department of Preventive Medicine, Feinberg School of Medicine, Northwestern University, 680 North Lake Shore Drive, Chicago, IL 60611;

<sup>‡</sup>Department of Neurology, Brigham and Women's Hospital, 75 Francis Street, Boston, MA 02115; <sup>§</sup>Children's Hospital Informatics Program, 300 Longwood Avenue, Boston, MA 02115; <sup>¶</sup>Bauer Center for Genomics Research, Harvard University, 7 Divinity Avenue, Cambridge, MA 02138;

<sup>||</sup>Molecular Medicine, Beth Israel Deaconess Medical Center, 330 Brookline Avenue, Boston, MA 02215; and <sup>††</sup>Harvard-Partners Center for Genetics and Genomics, 77 Avenue Louis Pasteur, Boston, MA 02115

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**Accurate and rapid identification of perturbed pathways through the analysis of genome-wide expression profiles facilitates the generation of biological hypotheses. We propose a statistical framework for determining whether a specified group of genes for a pathway has a coordinated association with a phenotype of interest. Several issues on proper hypothesis-testing procedures are clarified. In particular, it is shown that the differences in the correlation structure of each set of genes can lead to a biased comparison among gene sets unless a normalization procedure is applied. We propose statistical tests for two important but different aspects of association for each group of genes. This approach has more statistical power than currently available methods and can result in the discovery of statistically significant pathways that are not detected by other methods. This method is applied to data sets involving diabetes, inflammatory myopathies, and Alzheimer's disease, using gene sets we compiled from various public databases. In the case of inflammatory myopathies, we have correctly identified the known cytotoxic T lymphocyte-mediated autoimmunity in inclusion body myositis. Furthermore, we predicted the presence of dendritic cells in inclusion body myositis and of an IFN- $\alpha/\beta$  response in dermatomyositis, neither of which was previously described. These predictions have been subsequently corroborated by immunohistochemistry.**

microarrays | gene ontology | normalization | correlated data | inflammatory myopathies

Extracting clear and coherent hypotheses from genome-wide expression data remains an important challenge. Much of the initial work has focused on the development of techniques for accurate identification of differentially expressed genes and their statistical significance in a variety of experimental designs (1). However, the main difficulty in analysis lies not in the identification of differentially expressed genes but in their interpretation. Attempting to understand individual genes on a list of significant genes is demanding and laborious. Also, a comparison of gene lists from random subsets of a data set in simulation studies clearly shows that the gene list based on a small number of samples can be highly variable and that studying each gene separately may be ineffective in many cases (2, 3). The problem is compounded when the pathway of interest involves moderate effects that are not captured by the genes near the top of the list. Therefore, recent efforts have focused on the discovery of biological pathways rather than individual gene function, with the development of methods that are robust to the inaccuracies of specific gene estimates and provide a more expansive view of the underlying processes.

In the most common approach, genes are first ordered according to their evidence for differential expression, by one of many statistical methods available. Then, a short list of specified length containing the top genes is examined against each of the predefined sets of genes representing different pathways, to determine whether any set is overrepresented in the short list compared with the whole list. Suppose there are  $B_0$  differentially expressed genes from the total of  $B$  genes, and

$m_0$  genes of the pathway that involves  $m$  genes are among the differentially expressed genes. To examine the evidence of association in this case, Fisher's exact test based on the hypergeometric distribution or its large-sample approximation  $\chi^2$  test is typically used. Given its simplicity, numerous software and web sites provide this capability, most often by using Gene Ontology as the source of gene sets. Examples include GENMAPP (4), CHIPINFO (5), GOMINER (6), ONTO-TOOLS (7), and FUNCASSOCIATE (8).

This approach is reasonable but has at least three shortcomings, some of which are pointed out in ref. 9. First, only the most significant portion of the gene list is used to compute the statistic, treating the less-relevant genes as irrelevant. Second, the order of genes on the significant gene list is not taken into consideration. Simply counting the number of gene set members contained in the short list leads to loss of information, especially if the list is long and the difference between the more significant and the less significant is substantial. Third, the correlation structure of gene sets is not considered at all. This last issue is perhaps not as conspicuous as the first two, but it is an important aspect to consider in assessing statistical significance. We discuss this issue extensively in the present work.

An alternative and more successful technique should consider the distribution of pathway genes in the entire list of genes (9–12) as well as adjust for the correlation structure. In the innovative Gene Set Enrichment Analysis (GSEA) method (13), the following steps are applied: (i) all genes are ranked by using a signal-to-noise ratio; (ii) for each gene set, the distribution of gene ranks from the gene set is compared against the distribution for the rest of the gene set by using the enrichment score (ES) based on a one-sided Kolmogorov–Smirnov statistic; (iii) class labels are permuted to generate a null distribution of ES; and (iv) statistical significance of the observed score is assessed for the top-ranking gene set by comparison with the null distribution of maximum scores from each permutation. By considering the distribution of the gene ranks belonging to each gene set over the entire list, this method is a clear improvement over previous ones. However, the effect of the gene-set size and the influence of other gene sets not under consideration can be counterintuitive in some instances (14). Its normalization and permutation procedures also may lead to inaccurate assessment of statistical significance.

A successful approach for finding significant pathways depends on two components: (i) an accurate and powerful statistical method to discover significant patterns for a group of genes and (ii) a comprehensive and well-characterized pathway information mapped to microarray probes. In this work, we introduce a previ-

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Abbreviations: GSEA, Gene Set Enrichment Analysis; ES, enrichment score; NES, normalized ES; IBM, inclusion body myositis; AD, Alzheimer's disease; MMSE, Mini Mental Status Examination.

<sup>††</sup>To whom correspondence should be addressed. E-mail: peter.park@harvard.edu.

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hypothesis  $Q_1$  results in loss of power. Furthermore, to test  $Q_2$ , it seems counterintuitive to use the expression levels of genes outside the gene set as done in GSEA. All of the genes of interest are within the gene set, and the test result should not be influenced by genes outside the set.

**Normalization for Comparing Gene Set Scores.** After the test statistics  $T_k$  and  $E_k$  are computed for testing hypotheses  $Q_1$  and  $Q_2$ , respectively, we rank the  $K$  gene sets in order of their significance and control for the inflated Type I error due to multiple comparisons of gene sets. It is tempting to use a permutation-type procedure as in Significance Analysis of Microarrays (16), where a regularized  $t$  statistic is computed for each gene, and its significance is determined by how each observed order statistic compares with the mean of the same order statistic in permuted samples. The difficulty, however, is that unlike in the Significance Analysis of Microarrays procedure for regular microarray data, the null distributions of the test statistics ( $T_k$  or  $E_k$ ) for different gene sets are not the same. It is therefore unfair to rank the gene sets simply by the observed raw test statistics. For example, when we test hypothesis  $Q_1$ , the null distribution of  $T_1, \dots, T_K$  could be very different because of different gene set sizes and correlation structure. This effect is a subtle but critical issue.

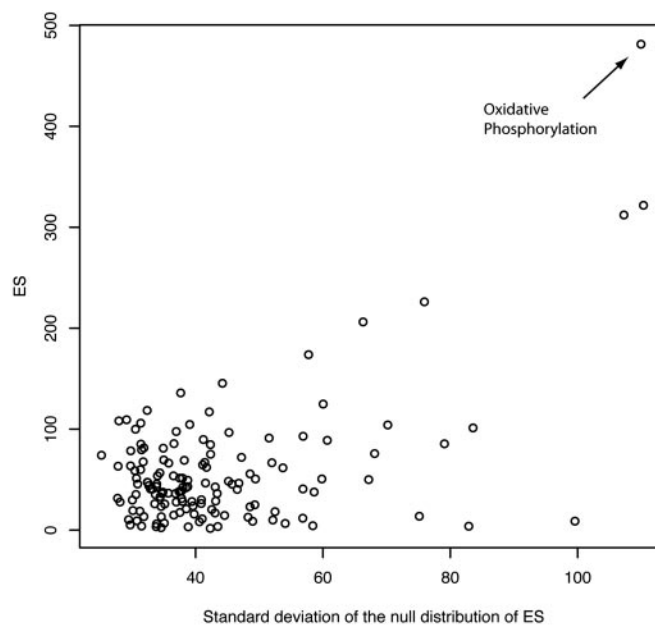
This phenomenon is observed, for example, in the application of GSEA to a diabetes data set (13). Focusing on the difference between the 17 normal glucose tolerance and 18 Type 2 diabetes mellitus subjects, we repeated the analysis with the same preprocessing steps and the same gene sets. When we simulated the null distribution of raw ES for each gene set by permuting the group labels with 1,000 permutations, we indeed found that the null distributions are markedly different, with their standard deviations (SDs) ranging from 25 to 110. This result implies that the same ES for different gene sets could suggest evidence of different strengths for association of interest and that the raw ES across different gene sets should not be compared directly. The marked difference in distributions is due to the complex correlation structure of genes within different gene sets. The highest ranked gene set representing oxidative phosphorylation, for example, contains genes that are tightly regulated and hence highly correlated. When we plot the SDs of the approximated null distribution for ES vs. the observed ES (Fig. 2), we see a clear positive correlation. In fact, the three highest gene sets by ES are the same three with the largest variance in the null distribution.

To remedy this problem, we suggest a simple standardization that results in normalized statistics  $NT_k$  and  $NE_k$ , which have the same null distributions for all gene sets. We then can rank the gene sets by  $NT_k$ , and a resampling procedure similar to the one in Significance Analysis of Microarrays can be carried out to approximate the joint null distribution of ordered  $\{NT_1, \dots, NT_K\}$ . See *Appendix* for a mathematical description.

## Results

**Example I: Reanalysis of Diabetes Data.** We carry out a more comprehensive analysis of the data set described above to illustrate the properties of the method, especially in relation to GSEA. To be sure that the differences observed are only due to the main feature of the algorithm, we make a couple of adjustments. First, the original GSEA was a one-sided approach to identify gene sets containing down-regulated genes in Type 2 diabetes mellitus subjects, but we implement a two-sided test. Second, we use the  $t$  statistic as the difference metric for individual genes.

For the measure of significance, we estimated the  $q$  value from the permutation procedure for each gene set, resulting in the identification of eight gene sets significant at the 0.05 level. As discussed in *Appendix*, the  $q$  value is the counterpart of the  $p$  value in the multiple testing scenario. Some of the test statistics and their corresponding ranks for 26 gene sets, including the five top-ranked gene sets for each procedure, are listed in Table 1. One statistic



**Fig. 2.** A scatterplot of the SDs of null distributions for the ES vs. the observed ES for the diabetes data. Each point represents a gene set. The Pearson correlation coefficient is 0.55. Without proper normalization among different gene sets, a high score may be due to its wide null distribution, which depends on the size and correlation structure of the gene set.

shown is the normalized ES (NES), applying the normalization step described above to ES. Interestingly, the oxidative phosphorylation gene set is still ranked first, but the rest of the rankings for ES and NES are substantially different, confirming the necessity of standardization. Overall, even when the various test statistics produced similar rankings, only some of them yielded statistically significant findings. In particular, we find that none of the NES based  $q$  values are  $<0.1$ . This loss in power is not surprising: In GSEA we tested the hypothesis  $Q_2$ , from which we generated the null distribution, by using the Kolmogorov–Smirnov test, which is designed to test  $Q_1$  and hence is less powerful.

The final interpretation requires consideration of both  $NT_k$  and  $NE_k$ . As described earlier, the correlation structure in gene sets can give false positives in  $NT_k$ ; conversely,  $NE_k$  can be influenced by the gene set size. Therefore, the gene sets that rank high in both categories are the best candidates. It appears that all procedures point to gene set OXPPOS (oxidative phosphorylation), whose members tend to be expressed relatively higher in normal glucose tolerance subjects. This finding is consistent with the previous conclusion (13) and also is supported by another gene set (MAP00190) and the mitochondria gene sets. Of particular interest are two gene sets that are significant by  $NT_k$  and  $NE_k$  criteria ( $q$  value  $<0.01$ ), even though their rankings by ES are not as high. MAP00910 group has 19 genes related to amino acid metabolism that are up-regulated in Type 2 diabetes mellitus patients, which has been repeatedly reported (17). *c22-U133* is more difficult to interpret because it refers to a cluster in ref. 18 consisting of heterogeneous set of genes. It contains many mitochondrial genes as well as those related to protein and carbohydrate metabolism and transcription. Further investigation is needed to identify targets of interest.

**Example II: Inflammatory Myopathies.** We examined 49 muscle samples consisting of 23 from patients with inclusion body myositis (IBM), 13 from patients with dermatomyositis, and 13 from normal subjects (NORM). After a global normalization, we eliminated those genes whose expression levels were below the



interferon- $\alpha/\beta$ -inducible genes, not predicted by the current model of this disease. The same finding also was made based on separate analyses of this data set, and subsequent immunohistochemical studies of muscle tissue confirmed a key role in the pathogenesis of proteins encoded by these genes (20).

IBM has been modeled as having cytotoxic T lymphocyte (CTL)-mediated destruction of MHC class I antigen expressing myofibers (19). Our analysis predicts that this model is largely correct, with enrichment of genes encoding MHC class I antigen presentation and the category "CTL-mediated immune response against target cells." Additionally, the analysis predicts the presence of dendritic cells in IBM muscle, which was not previously described. These results have been subsequently corroborated by immunohistochemistry, which showed a substantial number of dendritic cells infiltrating IBM muscle. The details of this observation will be reported separately (S.A.G., unpublished data). We emphasize that this finding is not evident from the list of differentially expressed genes but was found by the proposed method.

**Example III: AD Data.** Recently, the pathogenesis of AD was studied based on gene expression of hippocampal specimens, with 22 AD subjects and 9 controls (21). For all subjects, Mini Mental Status Examination (MMSE) scores as well as neurofibrillary tangle scores were obtained. We applied our method to this data set, concentrating on the MMSE score as the phenotype and excluding the control group. In the two previous examples, the phenotype was a class label, and the  $t$  statistic was used to measure the strength of association between the expression values and the phenotype. In this example, because the MMSE score is a continuous variable, Fisher's  $z$ ,  $1/2 \log\{(1 - \rho)/(1 + \rho)\}$ , is used as a metric for association, where  $\rho$  is the Pearson correlation coefficient between expression level and MMSE. The same filtering procedure used in the previous example was applied.

Strikingly, according to our analysis, MMSE score showed a strong positive correlation with calcium ion transport and calcium channel activity. More than 80% of the genes in each group were in fact up-regulated in the subjects with high MMSE scores. Destabilization of calcium signaling has been shown to be central to the pathogenesis of AD (22). Calcium ion transport group also was found to be significant by the authors of ref. 21, but only by marginal significance ( $p$  value = 0.0482). The second most significant group was "signal transduction in cancer," which contains numerous genes related to apoptosis, such as TP53, BAX, BCL2, AKT, and TNF. This group showed negative correlation with MMSE score or, equivalently, positive correlation with severity of AD. The third category "Tumor metastasis" also contained a number of genes implicated in AD including matrix metalloproteinase 2, 3, and 9 (MMP9), MAP2K4, TGFB1, and ERBB2; previously, MMP9 concentration was found to be elevated in cerebrospinal fluid of AD patients (23). Others on the list included several classes of genes related to energy metabolism including mitochondrial electron transport pathways, which showed positive correlation with MMSE score. This finding supports the mitochondria-mediated pathophysiology of AD (24). The table containing the top 10 gene sets in  $NT_k$  and  $NE_k$  (ordered by their average ranks) and more information on the three data sets in this section can be found in *Supporting Text* and Tables 3 and 4, which are published as supporting information on the PNAS web site.

## Discussion

The proposed method allows for the detection of subtle processes that are not likely to be revealed by examining a small list of highly significant genes. No technique for identifying differentially expressed genes can circumvent the problem of small sample sizes that arises in nearly all microarray studies, but by examining the pattern for a group of genes, it is possible to mitigate the effect of errors on individual gene estimates. By applying proper normalization and considering both  $Q_1$  and  $Q_2$ , the proposed approach selects those

gene sets that are likely to be relevant, with good statistical power. Valid statistical tests have been previously described (10, 25), but we emphasize the need to test both aspects: a gene set with tightly correlated genes, but otherwise unimportant, can appear significant if only  $Q_1$  is tested; when a high fraction of genes are associated with the phenotype, a large gene set can appear significant by chance if only  $Q_2$  is tested. We have found that ordering by the average rank of the two statistics can be a useful heuristic in ranking gene sets.

For this approach to be successful, a large collection of carefully curated information on pathways must be available. Although Gene Ontology has been a useful source in this regard, pathways involving multiple processes and functions are not well represented. In this work, we have collected several hundred pathways from public databases and demonstrated their utility. In the future, a coordinated effort to define the pathways and to map the gene identifiers of each pathway to the target sequence IDs of each array type will be essential. Defining the relationships among the gene sets themselves and organizing them also would facilitate interpretation, especially given the hierarchical structure in Gene Ontology.

We have considered three examples in which the phenotype of interest was a class label or a continuous variable, but the same approach also can be used for more complicated phenotypes. For example, for multiclass comparisons, we can use the  $F$ -statistic from ANOVA-type comparisons. If the phenotype is the right censored survival time, the standardized log-rank test statistic can be used.

## Appendix

**Testing Procedure for  $Q_1$ .** For this hypothesis, we can test whether the observed associations of genes in a gene set is a random sample from the background distribution of all observed associations. Because we have multiple gene sets under consideration, once we perform a statistical test for a specific gene set, we can rank the gene sets according to the strength of the statistical evidence against the null hypothesis  $Q_1$ .

We first introduce some notations. Let the indices  $i$  and  $j$  denote the  $i$ th gene and  $j$ th sample, with  $i = 1, \dots, B$  and  $j = 1, \dots, n$  for  $B$  genes and  $n$  subjects. We assume that the phenotype of interest is measured by  $\{z_1, \dots, z_n\}$  for the  $n$  subjects, with the resulting association measure  $t_i$  between the  $i$ th gene and the phenotype of interest.

We also assume that  $G_{ki}$ ,  $k = 1, \dots, K$  and  $i = 1, \dots, B$ , indexes the corresponding  $K$  gene sets of interest, i.e.,  $G_{ki} = 1$  if the  $k$ th gene set contains  $i$ th gene and 0 otherwise. With the prespecified gene set information, the data can be represented as the following matrix:

$$\begin{pmatrix} t_1 & t_2 & \cdots & t_B \\ G_{11} & G_{12} & \cdots & G_{1B} \\ \cdots & \cdots & \cdots & \cdots \\ G_{K1} & G_{K2} & \cdots & G_{KB} \end{pmatrix}.$$

If we view  $G_{i1}, \dots, G_{iB}$  and  $t_1, \dots, t_B$  as  $B$  independent and identically distributed copies of random variable  $G_i$  and  $t$ , respectively, then testing whether the observed associations of genes in the  $k$ th gene set is a random sample from the background distribution is equivalent to testing the independence between  $G_i$  and  $t$ . Various statistical tests can be used here.

To detect possibly moderate but coordinated associations for genes in a gene set, the specific alternative is likely to be a location (mean) shift from the background distribution. Therefore, a test against the omnibus alternative (any type of deviation from the reference distribution) such as the Kolmogorov–Smirnov test, which is used in GSEA, is not the most appropriate candidate in terms of power. Instead, we suggest the  $t$  test or the Wilcoxon rank test, both of which are more powerful for detecting location difference between two distributions. If we use the  $t$  test, the test statistics for  $k$ th gene set can be written as

$$T_k = \frac{1}{m_k} \sum_{i=1}^B G_{ki} t_i,$$

where  $m_k = \sum_{i=1}^B G_{ki}$ , the number of genes in the  $k$ th gene set. Under the null hypothesis,  $T_k$  should be centered at  $\hat{E}(t) = B^{-1} \sum_{i=1}^B t_i$ . Because different gene sets may or may not share the same genes,  $T_k$ ,  $k = 1, \dots, K$  are dependent. Their null distributions can be generated by permuting  $\{t_1, \dots, t_B\}$ . To be more specific, under the null hypothesis that  $t$  is independent with  $(G_1, \dots, G_K)$ , the null distribution of  $(T_1, \dots, T_K)$  can be approximated by the empirical distribution of  $(T_1^*, \dots, T_K^*)$ , where

$$T_k^* = \frac{1}{m_k} \sum_{i=1}^B G_{ki} t_i^*, \quad i = 1, \dots, K,$$

and  $\{t_1^*, \dots, t_B^*\}$  is permuted  $\{t_1, \dots, t_B\}$ .

This procedure is therefore different from GSEA in two respects. First, we favor the  $t$  test in view of the analysis objective. More importantly, permuting the phenotype  $\{z_1, \dots, z_n\}$  does not give the correct null distribution for  $Q_1$ , and therefore we propose to permute the association metric  $\{t_1, \dots, t_B\}$ .

**Testing Procedure for  $Q_2$ .** We propose a test for  $Q_2$  based on expression levels of genes within the gene set. One simple test statistic is the average of association metric  $t_i$  of genes in the gene set

$$E_k = \frac{1}{m_k} \sum_{i=1}^B G_{ki} t_i.$$

It is important to note that although the formula for  $E_k$  is the same as that of  $T_k$  for testing  $Q_1$ , their probability interpretations and hence their testing procedures are quite different. In  $T_k$ ,  $t_i$  is deterministic and the gene set structure is random; in  $E_k$ , the opposite is true.

Because  $t_i$  approximately follows  $N(0, 1)$  when the expression is independent of phenotype, it is tempting to conduct a test by using the approximation  $\sqrt{m_k} E_k \sim N(0, 1)$ , under hypothesis  $Q_2$ . However, the approximation is not valid even under the null hypothesis because of the potential correlations among  $t_i$ . Because the genes in the same gene set are functionally related, their expression levels and association metric  $t_i$  are likely to be dependent. Therefore, permutation methods should be used to approximate the null distribution of  $(E_1, \dots, E_K)$ , where phenotypes  $\{z_1, \dots, z_n\}$  are permuted, as was done in the original GSEA.

The power of the test against a certain alternative could be improved by using a more general linear combination of the form

$(1/m_k) \sum_{i=1}^B G_{ki} w_{ki} t_i$ , where  $w_{ki}$  are appropriate weights used to combine  $m_k$  test statistics while accounting for the correlations in  $t_i$ . This procedure is described in *Supporting Text*.

**Standardization of Gene Set Scores.** Assuming  $F_1(\cdot), \dots, F_K(\cdot)$  are the estimated null distributions of  $T_1, \dots, T_K$  by permutation, we first find the corresponding transformations  $\phi_k(\cdot) = \Phi^{-1}\{F_k(\cdot)\}$ ,  $k = 1, \dots, K$ , where  $\Phi(\cdot)$  is the cumulative distribution function for standard normal. This transformation results in the null distribution of  $NT_k = \phi_k(T_k)$  being  $N(0, 1)$  for all  $k$ .

**Multiple Testing Adjustment.** Because the testing procedure is carried out for hundreds of gene sets, it is critical to apply a proper adjustment to control for type I error. In our analysis, we use the  $q$  value, which is a counterpart of the  $p$  value in the context of false discovery rate, to assess the statistical significance of associations for each gene set (15). Family-wise error rates, such as those obtained by the Bonferroni or the Westfall–Young method, are too stringent. A simple version of the  $q$  value for the  $k$ th gene set is

$$\hat{p}_0 \frac{\sum_{m=1}^M \sum_{i=1}^B I_{\{|S_m^*| > |S_k|\}}}{M \sum_{i=1}^B I_{\{|S_i| > |S_k|\}}},$$

where  $\hat{p}_0$  is an estimated upper bound for the proportion of null hypotheses,  $S_i$  is the observed test statistic for the  $i$ th gene set,  $S_m^*$  is the permuted test statistic for the  $i$ th gene set in the  $m$ th permuted sample,  $m = 1, \dots, M$ , and  $I_{\{\cdot\}}$  is the indicator function giving 1 if the argument is true and 0 otherwise.

There are different ways to estimate  $\hat{p}_0$  in the literature, most involving a subjectively chosen smoothing parameter. Here, we adopt a previously undescribed, objective approach. We first compute  $\{p_1, \dots, p_B\}$ ,  $p$  values testing the association for all gene sets. Because the marginal density function  $f_0(p)$  for  $p$  values is nonincreasing,  $f_0(1 - \alpha)$  is an upper bound for the proportion of null hypotheses, and its estimator can be used to replace  $\hat{p}_0$ . We propose to estimate  $f_0(p)$  by the left derivative of the smallest concave function greater than the empirical distribution function of  $\{p_1, \dots, p_B\}$  (least concave majorant). This value is the nonparametric maximum likelihood estimator (NPMLE) of  $f_0(p)$ . Therefore  $\hat{p}_0$  can be replaced by  $\hat{f}_0(1 - \alpha)$  for a prespecified small  $\alpha$ , e.g., 0.05, where  $\hat{f}_0(p)$  is the aforementioned NPMLE of  $f_0(p)$ .

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