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Consideration of Directional Hypotheses in Pairs for Making a Decision with Given Reliability

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The problem of testing directional hypotheses is examined using the consideration of the basic and alternative hypotheses in pairs, allowing implementing computation easily and faster with guaranteed reliability. The concept of mixed directional false discovery rate ($mdFDR$) is used for the decision rule optimality. The fact of guaranteeing the quality of a decision (in the developed approach) at the desired level is proved theoretically and is demonstrated practically by applied examples. The developed method is enhanced for testing multiple hypotheses that guarantees the restriction of the total $mdFDR$ on the desired level. It is also shown that the proposed method can be used for solving the problems of testing intersection-union and union-intersection hypotheses also. The proposed method is adapted to testing large numbers of the subsets of individual hypotheses in testing multiple hypotheses that saves computational time and resources. Reliability and convenience of the developed method for big data are also demonstrated.

Keywords: Directional Hypotheses, constrained Bayesian method, mixed directional false discovery rate, risk function, decision making regions.

AMS Subject Classification: 62F15, 62F03.

1. Introduction

The consideration of directional hypotheses was started in the fifties of the last century [1, 25]. Since that period, many investigations were dedicated to the solu-

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tion of this problem (see, for example, [4, 9, 10, 23, 26, 32]). The authors of the present work started developing a new approach of statistical hypotheses testing called Constrained Bayesian Method (CBM) in the mid-seventies of the last century [11–14, 18, 20]. Application of CBM to different types of hypotheses showed its advantage in comparison to other known classical methods [14]. Superiority of CBM over other methods is related not only with the minimality of the number of observations necessary for making decisions with the guaranteed reliability, but also with the simplicity, clarity and elegance of accommodating the restrictions of all possible criteria of optimality. In particular, for testing directional hypotheses, CBM allows us to provide very simple and clear restrictions on the desired levels of such criteria of quality of making decisions as: pure directional false discovery rate ($pdFDR$), mixed directional false discovery rate ($mdFDR$), Type III error rates and false acceptance rate (FAR) [2, 5, 6, 17, 32]. Decision making regions in CBM are formally similar to the regions of classical Bayesian approach except for Lagrange multipliers included as multiplication coefficients in the appropriate expressions. The existence of Lagrange multipliers in decision making regions of CBM cardinally changes their properties, giving them a unique character. In particular, unlike existing methods, it allows us to make a decision if the available information is sufficient to make a decision at the required level of confidence. Otherwise, we can increase the information if possible. If it is not possible to increase the information, make a decision based on the available information and indicate the probability of confidence in the decision made. If the information can be increased, move on to sequential analysis, where for each additional piece of information, the ability to make a decision with proper confidence is checked and a decision is made when it becomes possible.

When testing more than two hypotheses, in many statements of CBM, determination of vectors of Lagrange multipliers is necessary. This is quite problematic and a time consuming procedure because it is related to the solution of nonlinear equations. When testing multiple hypotheses, especially for a big number of the subsets of individual hypotheses in multiple hypotheses, this problem becomes more formidable. For overcoming this problem, consideration of hypotheses "two-by-two" for testing both a simple set of directional hypotheses and of multiple directional hypotheses is proposed below. Similar approach for testing a large number of simple hypotheses were previously developed in [11, 19, 28]. The idea to define the critical region of a statistical test as the union of separate critical regions was developed in [28] and later was considered, in e.g., [7, 8]. Analytical Determination of the Decision Making Regions of testing directional hypotheses, developed below, can be considered as a generalization of Roy's principle that was used for simple hypotheses, especially as here the offered rule is based on CBM.

General statement of the problem is given in Section 2. Analytical approaches of testing the individual and multiple directional hypotheses are given in Sections 3 and 4, respectively. Consideration of the normally distributed directional hypotheses constitutes Section 5. Computation results for practical examples are presented in Section 6. Discussion of the obtained results is offered in Section 7 and conclusion is presented in Section 8.

2. Statement of the problem

For parametric models, the problem of testing directional hypotheses can be stated as

$$H_0 : \theta = \theta_0 \text{ vs. } H_- : \theta < \theta_0 \text{ or } H_+ : \theta > \theta_0, \tag{2.1}$$

where θ is the parameter of the model and θ_0 is known. These alternatives will be termed directional alternatives.

In many applications such as Biology, Medicine, Genetics, Epidemiology, Defense, Environment, Economics, Communication, Radio Astronomy, Video Signals, Computers and Networks and more, the case of multiple directional hypotheses is considered, i.e. the hypotheses of interest are the following [2, 3, 5, 9, 32]:

$$H_i^{(0)} : \theta_i = \theta_i^{(0)} \text{ vs. } H_i^{(-)} : \theta_i < \theta_i^{(0)} \text{ or } H_i^{(+)} : \theta_i > \theta_i^{(0)}, \quad i = 1, \ldots, m, \tag{2.2}$$

where m is the number of individual hypotheses about parameters $\theta_1, \ldots, \theta_m$ that must be tested by test statistics $\mathbf{X} = (X_1, \ldots, X_m)$, where $X_i \sim f(x_i \mid \theta_i)$.

Let us introduce the following notations for our testing of hypotheses problem [14]. Let the sample $x^T = (x_1, \ldots, x_n)$ be generated from $p(x, \theta)$, and the problem of interest is to test $H_i : \theta_i \in \Theta_i$, $i = 1, \ldots, S$, where $\Theta_i \subset \mathbb{R}^m$, $i = 1, \ldots, S$, are disjoint subsets contained in $\mathbb{R}^m$. The number of hypotheses to be tested is S. Let the prior on θ be denoted by $\sum\limits_{i=1}^{S} \pi(\theta \mid H_i)p(H_i)$, where for each $i = 1, \ldots, S$, $p(H_i)$ is the a priori probability of hypothesis H_i and $\pi(\theta \mid H_i)$ is a prior density with support Θ_i; $p(x \mid H_i)$ denotes the marginal density of x given H_i, i.e., $p(x \mid H_i) = \int\limits_{\Theta_i} p(x \mid \theta)\pi(\theta \mid H_i)\, d\theta$ and $D = \{d\}$ is the set of solutions, where $d = \{d_1, \ldots, d_S\}$, it being so that

$$d_i = \begin{cases} 1, & \text{if hypothesis } H_i \text{ is accepted,} \\ 0, & \text{otherwise,} \end{cases}$$

$\delta(x) = \{\delta_1(x), \ldots, \delta_S(x)\}$ is the decision function that associates each observation vector x with a certain decision

$$x \xrightarrow{\delta(x)} d \in D;$$

Γ_j is the region of acceptance of hypothesis H_j, i.e. $\Gamma_j = \{x : \delta_j(x) = 1\}$. It is obvious that $\delta(x)$ is completely determined by the Γ_j regions, i.e. $\delta(x) = \{\Gamma_1, \ldots, \Gamma_S\}$. Let $L_1(H_i, \delta_j(x) = 1)$ and let $L_2(H_i, \delta_j(x) = 1)$ be the losses of incorrectly accepted and incorrectly rejected hypotheses. Then the total loss of incorrectly accepted and incorrectly rejected hypotheses $L(H_i, \delta(x))$ is the following:

$$L(H_i, \delta(x)) = \sum_{j=1}^{S} L_1(H_i, \delta_j(x) = 1) + \sum_{j=1}^{S} L_2(H_i, \delta_j(x) = 0).$$

In many cases, testing of hypotheses (2.1), especially (2.2), requires making a decision so that all possible errors of incorrect conclusions are restricted to the desired levels. Unfortunately, the existing classical methods do not have such opportunities. Contrary to this, CBM allows us to make such decisions. But, when the number of hypotheses surpasses two, in many statements of CBM, the determination of vectors of Lagrange multipliers is necessary. This is quite a difficult and time consuming procedure, as it requires the solution of nonlinear equations concerning Lagrange multipliers. These problems thus necessitate the simplification of the computation process with the reduction of necessary time at the expense of the determination of scalar Lagrange multipliers and, consequently, increase the accuracy of the obtained results. We propose to mitigate the above problems and achieve these goals by considering the hypotheses (2.1) in pairs as presented below.

Let us, instead of simultaneous consideration of the three hypotheses competing among themselves as is done in (2.1), consider them in pairs as follows:

$$\begin{aligned} &H_0:\ \theta=\theta_0\ \text{ vs. }\ H_-:\ \theta<\theta_0,\\ &H_0:\ \theta=\theta_0\ \text{ vs. }\ H_+:\ \theta>\theta_0, \end{aligned} \tag{2.3}$$

$$\begin{aligned} &H_-:\ \theta<\theta_0\ \text{ vs. }\ H_0:\ \theta=\theta_0,\\ &H_-:\ \theta<\theta_0\ \text{ vs. }\ H_+:\ \theta>\theta_0, \end{aligned} \tag{2.4}$$

$$\begin{aligned} &H_+:\ \theta>\theta_0\ \text{ vs. }\ H_0:\ \theta=\theta_0,\\ &H_+:\ \theta>\theta_0\ \text{ vs. }\ H_-:\ \theta<\theta_0, \end{aligned} \tag{2.5}$$

Let us denote: E_{0j}, E_{-j} and let E_{+j} be the regions of acceptance of testing the hypotheses H_0, H_- and H_+ versus hypotheses H_j, $j\in(-,+)$, $j\in(0,+)$ and $j\in(0,+)$ accordingly (see (2.3), (2.4) and (2.5), respectively). Then hypothesis H_i, $i\in(-,0,+)$ is accepted if an observation results $x\in E_{ij}$, $\forall\, j\in\{-,0,+\}$, $j\neq i$. For finding the regions E_{ij}, $i,j\in\{-,0,+\}$, $i\neq j$, let us consider one of the possible statements of CBM [14]:

$$\max_{\{E_{ij}\}}\int\limits_{E_{ij}} p(H_i)p(x\mid H_i)\,dx, \tag{2.6}$$

subject to

$$\int\limits_{E_{ij}} p(H_j)p(x\mid H_j)\,dx\le\gamma_{ij},\quad i\in(-,0,+),\quad j\in(-,0,+),\quad j\neq i. \tag{2.7}$$

Here γ_{ij}, $i,j\in\{-,0,+\}$, $i\neq j$, are real numbers (close to zero) in the interval $(0,1)$.

Following [19], let us call our proposed method of determination of regions E_{ij}, $i,j\in\{-,0,+\}$, $i\neq j$, using statements (2.6) and (2.7) as Quasi-Optimal Constrained Bayesian Method (QOCBM) for testing directional hypotheses.

Finally, let us note that the hypotheses (2.1), as well as the hypotheses (2.2), can be presented as a case of intersection-union and of union-intersection hypotheses, see e.g., [15, 28, 29]. For applications, see e.g., [27, 30, 31]. Therefore, an approach

developed below can be used for solving the problems of intersection-union and of union-intersection hypotheses also.

3. Analytical determination of the decision making regions of testing the hypotheses

The solution of the constrained optimization problems (2.6) and (2.7) is the following [14, 16]

$$E_{ij} = \Big\{x : \frac{p(H_j)p(x \mid H_j)}{p(H_i)p(x \mid H_i)} < \frac{1}{\lambda_{ij}}\Big\}, \tag{3.1}$$

where the Lagrange multiplier λ_{ij} is determined so that the equality takes place in (2.7).

Let $\Gamma_0 = E_{0-} \cap E_{0+}$, $\Gamma_- = E_{-0} \cap E_{-+}$ and let $\Gamma_+ = E_{+0} \cap E_{+-}$ be the regions of acceptance of hypotheses H_0, H_- and H_+, respectively in the initial problem (2.1); Then the decision making rule is defined by the following procedure:

Procedure A

- if $x \in \Gamma_- = E_{-0} \cap E_{-+}$ only, accept the hypothesis H_-,
- if $x \in \Gamma_0 = E_{0-} \cap E_{0+}$ only, accept the hypothesis H_0,
- if $x \in \Gamma_+ = E_{+0} \cap E_{+-}$ only, accept the hypothesis H_+.

Here it must be noted that because of the property of the decision making rule of CBM, along with the hypotheses acceptance regions there exist the regions of impossibility of making a decision [16, 21]. Therefore, instead of the condition

$$P(x \in \Gamma_- \mid H_i) + P(x \in \Gamma_0 \mid H_i) + P(x \in \Gamma_+ \mid H_i) = 1, \;\; i \in \{-, 0, +\},$$

of the classical decision making procedures, the following condition is fulfilled in CBM

$$P(x \in \Gamma_- \mid H_i) + P(x \in \Gamma_0 \mid H_i) + P(x \in \Gamma_+ \mid H_i) + P(imd \mid H_i) = 1, \;\; i \in \{-, 0, +\}, \tag{3.2}$$

where imd is the abbreviation of the impossibility of making a decision.

The averaged risk function of incorrect acceptance of the tested directional hypotheses is computed by the formula

$$\begin{aligned} r^Q_{CBM} = {} & p(H_-)\Big[\int\limits_{\Gamma_0} p(x \mid H_-)\,dx + \int\limits_{\Gamma_+} p(x \mid H_-)\,dx\Big] \\ & + p(H_0)\Big[\int\limits_{\Gamma-} p(x \mid H_0)\,dx + \int\limits_{\Gamma_+} p(x \mid H_0)\,dx\Big] \\ & + p(H_+)\Big[\int\limits_{\Gamma_-} p(x \mid H_+)\,dx + \int\limits_{\Gamma_0} p(x \mid H_+)\,dx\Big] \end{aligned}$$

$$= p(H_-)\Big[P\big(x \in E_{0-} \cap E_{0+} \mid H_-\big) + P\big(x \in E_{+0} \cap E_{+-} \mid H_-\big)\Big]$$
$$+ p(H_0)\Big[P\big(x \in E_{-0} \cap E_{-+} \mid H_0\big) + P\big(x \in E_{+0} \cap E_{+-} \mid H_0\big)\Big]$$
$$+ p(H_+)\Big[P\big(x \in E_{-0} \cap E_{-+} \mid H_+\big) + P\big(x \in E_{0-} \cap E_{0+} \mid H_+\big)\Big]. \quad (3.3)$$

One of the basic criteria of optimality of testing directional hypotheses is $mdFDR$ [5, 6] that has the following form for our present case [2, 18]:

$$mdFDR = P(x \in \Gamma_- \mid H_+)$$
$$+ P(x \in \Gamma_- \mid H_0) + P(x \in \Gamma_+ \mid H_-) + P(x \in \Gamma_+ \mid H_0). \quad (3.4)$$

Another criteria of optimality of testing directional hypotheses is *Type* III *error rate* [5, 6, 26, 32]. As is shown in [18, 22] there exists the relation $mdFDR = SERR_{\text{III}}$ between $mdFDR$ and the summary *Type* III *error rate* ($SERR_{\text{III}}$).

Taking into account our above notations, for $mdFDR$ we have

$$mdFDR = P\big(x \in E_{-0} \cap E_{-+} \mid H_+\big) + P\big(x \in E_{-0} \cap E_{-+} \mid H_0\big)$$
$$+ P\big(x \in E_{+0} \cap E_{+-} \mid H_-\big) + P\big(x \in E_{+0} \cap E_{+-} \mid H_0\big)$$
$$= P\big(x \in E_{-+} \mid H_+\big)P\big(x \in E_{-0} \mid x \in E_{-+}, H_+\big)$$
$$+ P\big(x \in E_{-0} \mid H_0\big)P\big(x \in E_{-+} \mid x \in E_{-0}, H_0\big)$$
$$+ P\big(x \in E_{+-} \mid H_+\big)P\big(x \in E_{+0} \mid x \in E_{+-}, H_-\big)$$
$$+ P\big(x \in E_{+0} \mid H_0\big)P\big(x \in E_{+-} \mid x \in E_{+0}, H_0\big). \quad (3.5)$$

Recalling the condition of determination of Lagrange multipliers, restrictions (2.7) can be rewritten as follows

$$P(x \in E_{-+} \mid H_+) = \frac{\gamma_{-+}}{p(H_+)}, \quad P(x \in E_{-0} \mid H_0) = \frac{\gamma_{-0}}{p(H_0)},$$
$$P(x \in E_{0-} \mid H_-) = \frac{\gamma_{0-}}{p(H_-)}, \quad P(x \in E_{0+} \mid H_+) = \frac{\gamma_{0+}}{p(H_+)}, \quad (3.6)$$
$$P(x \in E_{+-} \mid H_-) = \frac{\gamma_{+-}}{p(H_-)}, \quad P(x \in E_{+0} \mid H_0) = \frac{\gamma_{+0}}{p(H_0)}.$$

Theorem 3.1: *QOCBM with restriction levels* (2.7) (*that is* (3.6)), *at satisfying a condition*

$$\frac{\gamma_{-+}}{p(H_+)} + \frac{\gamma_{-0}}{p(H_0)} + \frac{\gamma_{+-}}{p(H_-)} + \frac{\gamma_{+0}}{p(H_0)} = q,$$

where $0 < q < 1$, *ensures a decision rule with* $mdFDR$ (*that is with* $SERR_{\text{III}}$) *less or equal to* q, *i.e. with the condition* $mdFDR = SERR_{\text{III}} \le q$.

Proof: Because the second multipliers in (3.5) are less than 1 and taking into account conditions (3.6), we can write

$$mdFDR \le P(x \in E_{-+} \mid H_+) + P(x \in E_{-0} \mid H_0) + P(x \in E_{+-} \mid H_-) + P(x \in E_{+0} \mid H_0) = \frac{\gamma_{-+}}{p(H_+)} + \frac{\gamma_{-0}}{p(H_0)} + \frac{\gamma_{+-}}{p(H_-)} + \frac{\gamma_{+0}}{p(H_0)} = q. \quad (3.7)$$

This theorem is proved. □

Theorem 3.2: *QOCBM with restriction levels* (2.7) (*that is* (3.6)), *at satisfying the condition*

$$\sum_{i\in\{-,0,+\}} \sum_{\substack{j\in\{-,0,+\}\\ j\neq i}} \gamma_{ij} = q,$$

where $0 < q < 1$, *ensures a decision rule with the averaged risk function* (3.3) *of incorrect acceptance of tested directional hypotheses of at most less or equal* q, *i.e. with the condition* $r^Q_{CBM} \le q$.

Proof: Let us rewrite the risk function (3.3) as follows

$$\begin{aligned} r^Q_{CBM} = {} & p(H_-)\Big[P(x \in E_{0-} \mid H_-) \cdot P\big(x \in E_{0+} \mid x \in E_{0-}, H_-\big) \\ & + P(x \in E_{+-} \mid H_-) \cdot P\big(x \in E_{+0} \mid x \in E_{+-}, H_-\big)\Big] \\ & + p(H_0)\Big[P(x \in E_{-0} \mid H_0) \cdot P\big(x \in E_{-+} \mid x \in E_{-0}, H_0\big) \\ & + P(x \in E_{+0} \mid H_0) \cdot P\big(x \in E_{+-} \mid x \in E_{+0}, H_0\big)\Big] \\ & + p(H_+)\Big[P(x \in E_{-+} \mid H_+) \cdot P\big(x \in E_{-0} \mid x \in E_{-+}, H_+\big) \\ & + P(x \in E_{0+} \mid H_+) \cdot P\big(x \in E_{0-} \mid x \in E_{0+}, H_+\big)\Big] \\ \le {} & p(H_-)\big[P(x \in E_{0-} \mid H_-) + P(x \in E_{+-} \mid H_-)\big] \\ & + p(H_0)\big[P(x \in E_{-0} \mid H_0) + P(x \in E_{+0} \mid H_0)\big] \\ & + p(H_+)\big[P(x \in E_{-+} \mid H_+) + P(x \in E_{0+} \mid H_+)\big] \\ = {} & p(H_-)\,\frac{\gamma_{0-} + \gamma_{+-}}{p(H_-)} + p(H_0)\,\frac{\gamma_{-0} + \gamma_{+0}}{p(H_0)} + p(H_+)\,\frac{\gamma_{-+} + \gamma_{0+}}{p(H_+)} \\ = {} & \sum_{i\in\{-,0,+\}} \sum_{\substack{j\in\{-,0,+\}\\ j\neq i}} \gamma_{ij} = q. \end{aligned} \quad (3.8)$$

This theorem is proved. □

Theorem 3.3: *For given restriction levels in* (2.7) *when minimum value of the Kullback–Leibler divergence between hypotheses* H_i *and* H_j *tends to infinity, i.e.* $\min\limits_{\{i,j\}} J(H_i, H_j) \to \infty$, $i, j \in \{-, 0+\}$, $i \neq j$, *both the risk function* (r^Q_{CBM}) *and* $mdFDR$, *for fixed Lagrange multipliers defined by formulae* (2.7) *satisfying* (3.7)

and (3.8)*, respectively, tend to zero.*

Proof: It is not difficult to see that when minimum value of the Kullback–Leibler divergence between hypotheses H_i and H_j,

$$\min_{\{i,j\}} J(H_i, H_j) \to \infty, \quad i, j \in \{-, 0+\}, \quad i \neq j$$

(see [24]), the second multipliers in (3.5) and (3.8) as well tend to zero and the values of the first multipliers are determined by condition (2.7). Therefore, their product tends to zero and, accordingly, the values of r^Q_{CBM} and $mdFDR$ tend to zero too. □

In general, it is impossible to determine the relation between r^Q_{CBM} and $mdFDR$, even when the values of both r^Q_{CBM} and $mdFDR$ are restricted on one and the same level because the value of r^Q_{CBM} depends on a priori probabilities whereas $mdFDR$ does not.

Because of the specific nature of the acceptance regions of CBM (see formula (3.2) of [14]), in testing directional hypotheses using Procedure A it can so happen that making a simple decision becomes impossible, e.g. when the test statistic belongs to the intersection areas of the acceptance regions or does not belong to any of these regions. In such a situation, it becomes impossible to make a simple decision with a specified confidence level on the basis of the existing information and more information is required to achieve this. If acquiring more information is impossible, then the restriction levels in (2.7) must be changed until a simple decision can be made. When acquiring more information is possible, we appeal to the sequential experiment, i.e. to increase a sample size, and apply Procedure A to all the observations until a decision can be made. The appropriate sequential procedure of making a decision in such a manner is given in Procedure B.

Procedure B

Let us denote the existing sample by $x = (x_1, \ldots, x_n)$ and the test statistic on the basis of n observations by $\overline{x}_n$. Then the sequential procedure is as follows:

Step 1

- if $\overline{x}_n$ belongs to only region $\Gamma_- = E_{-0} \cap E_{-+}$, accept hypothesis H_-,
- if $\overline{x}_n$ belongs to only region $\Gamma_0 = E_{0-} \cap E_{0+}$, accept hypothesis H_0,
- if $\overline{x}_n$ belongs to only region $\Gamma_+ = E_{+0} \cap E_{+-}$, accept hypothesis H_+,
- otherwise continue sampling; collect x_{n+1} and compute new test statistics $\overline{x}_{n+1}$;

Step 2

- if $\overline{x}_{n+1}$ belongs to only region $\Gamma_- = E_{-0} \cap E_{-+}$, accept hypothesis H_-,
- if $\overline{x}_{n+1}$ belongs to only region $\Gamma_0 = E_{0-} \cap E_{0+}$, accept hypothesis H_0,
- if $\overline{x}_{n+1}$ belongs to only region $\Gamma_+ = E_{+0} \cap E_{+-}$, accept hypothesis H_+,
- otherwise continue sampling; collect x_{n+2} and compute new test statistics $\overline{x}_{n+2}$;

etc.

The sampling continues until the test statistic does not belong to only one acceptance region.

Note 3.1. It is clear that in the beginning of the sequential test a sample size can be equal to one, i.e. $n = 1$ and this corresponds to the parallel experiment on which the testing process finishes if the desired level of reliability of making a decision is achievable for this amount of information. Otherwise sampling continues, i.e. the parallel experiment generalizes to the sequential experiment naturally.

4. Testing multiple directional hypotheses

For testing multiple directional hypotheses (2.2), let us introduce the concept of the total mixed directional false discovery rate ($tmdFDR$) [2, 3, 18], defined as

$$tmdFDR = \sum_{i=1}^{m} mdFDR_i. \tag{4.1}$$

For guaranteeing the level q, in testing hypotheses (2.2), we have to consider m subsets of directional hypotheses. Then for each of them, we use the Procedure B described above for providing level of q_i for the subset of hypotheses, so that $\sum_{i=1}^{m} q_i = q$ is achieved.

We act similarly to provide a level q for the total averaged risk function. Namely, we provide q_i, the level of the appropriate averaged risk function for the ith subset of the individual directional hypotheses. As a result, we have

$$r^{Q}_{CBM} = \sum_{i=1}^{m} r^{Q}_{i,CBM} \tag{4.2}$$

for the total averaged risk function, where $r^{Q}_{i,CBM}$ is the averaged risk function of the ith subset of directional hypotheses [18].

The values of q_i in both cases (for $tmdFDR$ and for r^{Q}_{CBM}) can be chosen to be equal, i.e. $q_i = q/m$ or different, e.g. inversely proportional to the informational distances between the tested hypotheses in the subsets of directional hypotheses [18].

In both the cases with restriction of $tmdFDR$ and of r^{Q}_{CBM} on the desired levels, we use the above described sequential Procedure B where the sampling continues until a simple decision is not made for all the subsets of multiple hypotheses (2.2). The stopping rules remain the same as in [18] and we choose one of them depending on whether the components of the vector $\mathbf{X} = (X_1, \ldots . X_m)$ are observed independently or dependently. The Theorems 5 and 6 of the work [18], proving the appropriateness of stopping rules for both the cases, are in force for the considered directional hypotheses as well.

Currently, in many real-life applications, we indeed encounter situations where the number of individual hypotheses in the set of multiple hypotheses (2.2) is very big, i.e. when data is big [2, 3]. In such a situation, determination of Lagrange multipliers for each subset of an individual hypothesis requires a long time for computation. Though the computation of Lagrange multipliers is completed in the preparatory stage before making a decision, still the reduction of computation time is important for many practical applications from the operational and cost

considerations. For this purpose, the following theorem is provided.

Theorem 4.1 : *Let individual hypotheses in the set of multiple hypotheses* (2.2) *be stated concerning values of parameters* $\theta_1, \ldots, \theta_m$ *when distribution laws* $f(x \mid \theta_i)$ *of test statistics* X_i $(i = 1, \ldots, m)$ *are similar in the form for all of subsets of individual hypotheses. Then, if for testing for all of subsets of individual hypotheses, we use one and the same Lagrange multipliers, determined for a subset of individual hypothesis with lowest divergence among directional hypotheses at the level* $q_i = q/m$, *satisfying condition* $\sum_{i=1}^{m} q_i = q$, *the total mixed directional false discovery rate* (4.1) *and the total risk function* (4.2) *will be restricted to the level* q.

Proof : Theorem 4.1 follows from Theorem 3.3 according to which $mdFDR$ and $r^{Q}_{i,CBM}$ $(i = 1, \ldots, m)$ tend to zero when the Kullback–Leibler divergence among directional hypotheses tends to infinity. □

5. Consideration of the directional hypotheses in the case of normal distributions

For illustrating the theoretical results presented above, let us consider the following example. Let sample $X_1, \ldots, X_n$ be derived from $N(\theta, \sigma^2)$ with known σ^2 at H_0, $p(x \mid H_-)$ and let $p(x \mid H_+)$ be the truncated normal densities $N(0, \omega_0^{-1}\sigma^2)$ (ω_0 known) over $(-\infty, 0)$ and $(0, +\infty)$, respectively [3, 4]. Let us use $\overline{x}$ as a test statistic. Then, for the density of $\overline{x}$ given H_i, $i \in \{-, 0, +\}$, we have

$$
\begin{aligned}
p(\overline{x} \mid H_0) &= \frac{\sqrt{n}}{\sqrt{2\pi}\cdot\sigma} \cdot \exp\Big\{ -\frac{n\overline{x}^{\,2}}{2\sigma^2}\Big\},\\
p(\overline{x} \mid H_-) &= \int_{-\infty}^{0} \frac{\sqrt{n}}{\sqrt{2\pi}\cdot\sigma} \cdot \exp\Big\{ -\frac{n(\overline{x}-\theta)^2}{2\sigma^2}\Big\}\\
&\qquad \times \frac{2\sqrt{\omega_0}}{\sqrt{2\pi}\cdot\sigma} \cdot \exp\Big\{ -\frac{\omega_0^2\theta^2}{2\sigma^2}\Big\}\, d\theta, \qquad (5.1)\\
p(\overline{x} \mid H_+) &= \int_{0}^{+\infty} \frac{\sqrt{n}}{\sqrt{2\pi}\cdot\sigma} \cdot \exp\Big\{ -\frac{n(\overline{x}-\theta)^2}{2\sigma^2}\Big\}\\
&\qquad \times \frac{2\sqrt{\omega_0}}{\sqrt{2\pi}\cdot\sigma} \cdot \exp\Big\{ -\frac{\omega_0^2\theta^2}{2\sigma^2}\Big\}\, d\theta.
\end{aligned}
$$

After routine transformation, we have

$$
\begin{aligned}
p(u \mid H_0) &= \frac{\sqrt{n}}{\sqrt{2\pi}\cdot\sigma} \cdot \exp\Big\{ -\frac{u^2}{2}\Big\} \cdot \exp\Big\{ -\frac{\omega_0 u^2}{2n}\Big\},\\
p(u \mid H_-) &= \frac{2\sqrt{\omega_0}}{\sqrt{n+\omega_0}} \cdot \frac{\sqrt{n}}{\sqrt{2\pi}\cdot\sigma} \cdot (1-\Phi(u)) \cdot \exp\Big\{ -\frac{\omega_0 u^2}{2n}\Big\}, \qquad (5.2)\\
p(x \mid H_+) &= \frac{2\sqrt{\omega_0}}{\sqrt{n+\omega_0}} \cdot \frac{\sqrt{n}}{\sqrt{2\pi}\cdot\sigma} \cdot \Phi(u) \cdot \exp\Big\{ -\frac{\omega_0 u^2}{2n}\Big\},
\end{aligned}
$$

where $u = n\overline{x}/(\sigma\sqrt{n+\omega_0})$ and $\Phi(\,\cdot\,)$ is the standard normal distribution function.

Putting these values into (3.1), we will obtain the following ratios for acceptance regions

$$E_{0-} = \left\{u: \ \frac{p(H_-)\cdot 2\cdot\sqrt{\omega_0}\cdot(1-\Phi(u))}{p(H_0)\cdot\sqrt{n+\omega_0}\cdot\exp\{-\frac{u^2}{2}\}} < \frac{1}{\lambda_{0-}}\right\},$$

$$E_{0+} = \left\{u: \ \frac{p(H_+)\cdot 2\cdot\sqrt{\omega_0}\cdot\Phi(u)}{p(H_0)\cdot\sqrt{n+\omega_0}\cdot\exp\{-\frac{u^2}{2}\}} < \frac{1}{\lambda_{0+}}\right\},$$

$$E_{-0} = \left\{u: \ \frac{p(H_0)\cdot\sqrt{n+\omega_0}\cdot\exp\{-\frac{u^2}{2}\}}{p(H_-)\cdot 2\cdot\sqrt{\omega_0}\cdot(1-\Phi(u))} < \frac{1}{\lambda_{-0}}\right\},$$

$$E_{-+} = \left\{u: \ \frac{p(H_+)\cdot\Phi(u)}{p(H_-)\cdot(1-\Phi(u))} < \frac{1}{\lambda_{-+}}\right\},$$

$$E_{+0} = \left\{u: \ \frac{p(H_0)\cdot\sqrt{n+\omega_0}\cdot\exp\{-\frac{u^2}{2}\}}{p(H_+)\cdot 2\cdot\sqrt{\omega_0}\cdot\Phi(u)} < \frac{1}{\lambda_{+0}}\right\},$$

$$E_{+-} = \left\{u: \ \frac{p(H_-)\cdot(1-\Phi(u))}{p(H_+)\cdot\Phi(u)} < \frac{1}{\lambda_{+-}}\right\}.$$

The Lagrange multipliers are determined so that in the conditions (2.7) the equalities hold. For the solution of the relevant equations, the suitable probability integrals are computed by the Monte-Carlo method (see, for example, [14, 18]).

6. Computation results

Example 6.1 Testing individual directional hypotheses

Let us consider a concrete example with the initial data from [4] and [18]: the values of the loss functions $K_0 = K_1 = 1$; coefficient $\omega_0 = 1$; variance $\sigma^2 = 1$; the restricted levels for both $mdFDR$ and risk function r^Q_{CBM} are the same as $q = 0.05$. Let us consider the case when a priori probabilities $p_- = p_0 = p_+ = 1/3$ and restriction levels in (2.7) $\gamma_{-0} = \gamma_{-+} = \gamma_{0-} = \gamma_{0+} = \gamma_{+-} = \gamma_{+0} = \gamma$; for keeping restriction levels of both $mdFDR$ and r^Q_{CBM} on the level of 0.05, we have to choose $\gamma = 0.00416(6)$ for $mdFDR$ and $\gamma = 0.0083(3)$ for r^Q_{CBM}.

Example 6.2 Testing multiple directional hypotheses

As multiple directional hypotheses (2.2), let us consider the case when the number of individual hypotheses $m = 3$. Let sample $\mathbf{X}_1, \ldots, \mathbf{X}_n$ of independent observations with the independently observed components $\mathbf{X}_i = (X_1^i, X_2^i, X_3^i)$ $(i = 1, \ldots, n)$ of the test statistics be derived from $N(\theta, \sigma^2)$ with known σ^2 at H_0 and from the truncated normal densities $N(\mu, \omega_0^{-1}\sigma^2)$ (ω_0 known) over $(-\infty, 0)$ and $(0, +\infty)$ at H_- and H_+, respectively. Let us consider a case when a priori probabilities $p_- = p_0 = p_+ = 1/3$ and restriction levels in (2.7) $\gamma_{-0} = \gamma_{-+} = \gamma_{0-} = \gamma_{0+} = \gamma_{+-} = \gamma_{+0} = \gamma$ for each subset of individual hypotheses. If for each set of individual hypotheses, we choose $\gamma = 0.00416(6)$ for $mdFDR$ and $\gamma = 0.0083(3)$ for r^Q_{CBM}, then, in accordance with (4.1) and (4.2), restriction levels of both $tmdFDR$ and total averaged risk function r^Q_{CBM} will be on the level of 0.15.

For testing directional hypotheses in both the cases, of individual and multiple directional hypotheses, we used Procedure B. The probability integrals from the restriction conditions (2.7) at determination of Lagrange multipliers were computed by Monte–Carlo method, simulating the samples with 10,000 observations from the appropriate distributions. Computed values of Lagrange multipliers for different n are given in Table 6.1. Computation results at testing individual directional hypotheses (2.1) are given in Tables 6.2 and 6.3. Computation results at testing multiple directional hypotheses (2.2) when the number of individual hypotheses $m = 3$, are given in Table 6.4. The values of $mdFDR$ and $Risk$ function computed by samples with different sizes in parallel experiments are given in Table A1. The values of $mdFDR$ and of r^{Q}_{CBM} are computed by simulation of random sequences with 10.000 observations at consideration of both individual and multiple directional hypotheses.

It is well known that the results of hypotheses testing depend on the Kullback–Leibler divergence between test hypotheses (see also above Theorems 3.3 and 4.1). For demonstration of this fact, let us calculate the mean information for discrimination of the considered hypotheses in Examples 6.1 and 6.2. Because hypotheses H_- and H_+ are symmetrical in relation to H_0, the divergences between couples of hypotheses (H_-, H_0) and (H_0, H_+) are identical. Therefore, only the mean information for discrimination in favor of H_0 against H_+ is considered below.

The mean information for discrimination in favor of H_0 against H_+ per observation from $p(u \mid H_0)$ is

$$I(H_0, H_+) = \int\limits_{-\infty}^{+\infty} \log \frac{p(u \mid H_0)}{p(u \mid H_+)} \cdot p(u \mid H_0)\, du. \tag{6.1}$$

This definition was introduced in [24] for absolutely continuous measures with respect to one another; that means that there exists no set where one density is equal to zero and another differs from zero. In the considered case $p(u \mid H_+)$ is determined on the region $[0, +\infty)$ but $p(u \mid H_0)$ is determined on the region $(-\infty, +\infty)$. Therefore, as the mean information for discrimination of considering hypotheses, instead of (6.1), let us use the following expression

$$I(H_0, H_+) = 0.5 + \int\limits_{0}^{+\infty} \log \frac{p(u \mid H_0)}{p(u \mid H_+)} \cdot p(u \mid H_0)\, du. \tag{6.2}$$

Taking into account formulae (5.2), expression (6.2) becomes

$$\begin{aligned} I(H_0, H_+) = {} & \frac{n}{2 \cdot \sqrt{n + \omega_0} \cdot \sigma} - \frac{\sqrt{n}}{\sqrt{2\pi} \cdot \sigma} \cdot \log \left(\frac{2\sqrt{\omega_0}}{\sqrt{n + \omega_0}} \cdot \frac{\sqrt{n}}{\sqrt{2\pi} \cdot \sigma} \right) \\ & \times \left[\int\limits_{0}^{+\infty} \log \Phi(u) \cdot \exp\Big(- \frac{n + \omega_0}{2n}\, u^2 \Big)\, du - \frac{\sqrt{\pi} \cdot \omega_0 \cdot \sqrt{n}}{2^{3/2} \cdot (n + \omega_0)^{3/2}} \right] \\ & - \frac{n}{2^2 \cdot \sigma \cdot \sqrt{n + \omega_0}} \cdot \log \left(\frac{\sqrt{n}}{\sqrt{2\pi} \cdot \sigma} \right), \end{aligned} \tag{6.3}$$

Table 6.1. Lagrange multipliers for different n and σ^2.

$n,\ \sigma^2$	For $mdFDR$ [1]						For r^{Q}_{CBM} [1]					
	λ_{0-}	λ_{+-}	λ_{-0}	λ_{+0}	λ_{-+}	λ_{0+}	λ_{0-}	λ_{+-}	λ_{-0}	λ_{+0}	λ_{-+}	λ_{0+}
$n=1$ [2] $\sigma^2=1$	0.1576995	0.0412280	7.4998712	7.7889060	0.0411605	0.1577064	0.157165	0.0411224	5.312420	6.0937595	0.0410127	0.1571846
$n=1$ $\sigma^2=2$	0.210693	0.058876	7.7056884	7.8125	0.058862	0.2106079	0.2099327	0.0586670	5.6426568	5.41015625	0.0586694	0.2099488
$n=1$ $\sigma^2=5$	0.3079820	0.09554	7.48046	8.1347751	0.095449	0.307861	0.3066263	0.09511	5.625	5.5859375	0.0950875	0.306982
$n=5$ $\sigma^2=1$	1.56182738	2.71014869	13.75	14.2833863	2.86078453	1.56245231	1.53942108	2.67748112	9.0625	9.29726229	2.0538330	1.54582023

1) Sample size $N = 10,000$ for computation of probabilities integrals; absolute values of the errors of the solution of equations (2.7) are less than or equal to 0.0001.

2) See Note 3.1

where $\Phi(\,\cdot\,)$ is the standard normal distribution function. Computed values of (6.3), depending on n, are given in Figure 1. The code for computation of (6.3), as well as all other necessary codes, were written on MATLAB.

From here it is seen that the mean information for discrimination in favor of H_0 against H_+ increases with increasing n. Computed values for some n are the following:

$$n=1,\ \ I=0.717797042647688; \quad n=2,\ \ I=1.045859242626548;$$
$$n=3,\ \ I=1.256701156104494; \quad n=5,\ \ I=1.539416780111406;$$
$$n=7,\ \ I=1.736014441439005; \quad n=10,\ \ I=1.953347963317561;$$
$$n=50,\ \ I=2.989780557332991; \quad n=100,\ \ I=3.359592492397021.$$

Computed values of (6.3), depending on σ^2, are given on Figure 2. The mean information for discrimination of hypotheses are computed for the values $\sigma^2 = \frac{1}{200}, \frac{2}{200}, \ldots, 1, 2, \ldots, 200$ at $n=1$.

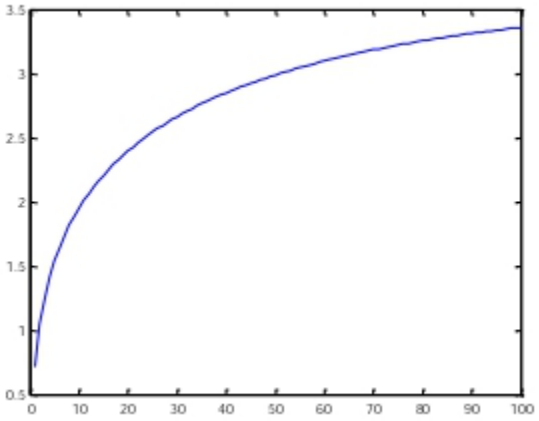

Figure 1. Dependence of the mean information for discrimination in favor of H_0 against H_+ on the sample size n at $\sigma^2 = 1$.).

From here it is seen that the mean information for discrimination in favor of H_0 against H_+ is maximum for $\sigma^2 = 1/2$ and it decreases in both cases when σ^2 is decreasing or increasing. Computed values for some σ^2 at $n=1$ are the following:

$$\sigma^2=1,\ \ I=0.717797042647688; \quad \sigma^2=\frac{1}{2},\ \ I=0.755671797836857;$$
$$\sigma^2=\frac{1}{3},\ \ I=0.739629938177342; \quad \sigma^2=\frac{1}{4},\ \ I=0.701768525112110;$$
$$\sigma^2=\frac{1}{5},\ \ I=0.652539411480660; \quad \sigma^2=2,\ \ I=0.637282413825231;$$
$$\sigma^2=3,\ \ I=0.582297318866539; \quad \sigma^2=4,\ \ I=0.542354911369660;$$
$$\sigma^2=5,\ \ I=0.511509310267286; \quad \sigma^2=10,\ \ I=0.419705706315754.$$

When σ^2 changes from $1/100$ to $1/2$ the mean information for discrimination in fa-

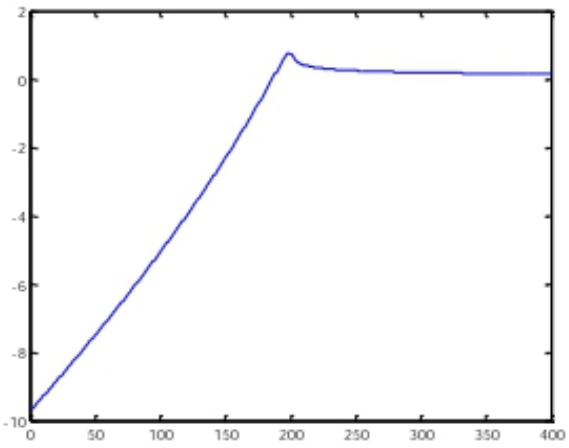

Figure 2. Dependence of the mean information for discrimination in favor of H_0 against H_+ on the sample variance σ^2 at $n = 1$.

vor of H_0 against H_+ increases from -5.010608299119358 up to 0.755671797836857 and after, at increasing σ^2 from $1/2$ up to 100, it decreases from 0.755671797836857 up to 0.193665491520731. When $\sigma^2 = 200$ the mean information for discrimination in favour of H_0 against H_+ is equal to 0.149914508081475.

Computational results given in tables of Appendix A confirm the fact that when we use Lagrange multipliers computed for minimal divergence between hypotheses for testing hypotheses with greater divergence, both $mdFDR$ and $Risk$ function remain restricted on the desired levels (see Table A1). If for testing hypotheses with less divergence, we use Lagrange multipliers computed for greater divergence, both or one of $mdFDR$ or $Risk$ function may be not restricted on the desired levels (see Lines for $n = 1$, $\sigma^2 = 3$ and $n = 1$, $\sigma^2 = 5$ of Table A1). When for testing hypotheses we use optimal Lagrange multipliers then the bigger is the divergence between hypotheses, the less are $mdFDR$ and $Risk$ function (see Tables 6.2 and 6.3).

Note 6.1. For keeping restriction levels of $mdFDR$ and $Risk$ function on one and the same level q, restrictions in (2.7) are different. For $mdFDR$ they are less than for $Risk$ function. Therefore, Lagrange multipliers, defined for $mdFDR$ supporting the level q, provide the same restriction level for $Risk$ function whereas Lagrange multipliers defined for $Risk$ function supporting the level q do not guarantee the same restriction level for $mdFDR$.

The results of testing multiple directional hypotheses when the number of individual hypotheses $m = 3$ for different scenarios are given in Table 6.4.

Table 6.2. The results of testing individual directional hypotheses at restriction of $mdFDR$ in sequential experiments.
Probabilities are computed by a sample of size $10,000$. Lagrange Multipliers computed at restrictions of $mdFDR$ accordingly for $n = 1$ and $n = 5$ at $\sigma^2 = 1$ are used here.

#	At H_0						At H_1						At H_2						$mdFDR$	$Risk$
$n=1$	AN	ND	AV	$P_{0,0}$	$P_{1,0}$	$P_{2,0}$	AN	ND	AV	$P_{0,1}$	$P_{1,1}$	$P_{2,1}$	AN	ND	AV	$P_{0,2}$	$P_{1,2}$	$P_{2,2}$		
Exp. 1	2.0010	10,000	20,010	1	0	0	2	10,000	20,000	0	1	0	2	10,000	20,000	0	0	1	0	0
Exp. 2	2.0012	10,000	20,012	1	0	0	2	10,000	20,000	0	1	0	2	10,000	20,000	0	0	1	0	0
Exp. 3	2.0013	10,000	20,013	1	0	0	2	10,000	20,000	0	1	0	2	10,000	20,000	0	0	1	0	0
Exp. 4	2.0015	10,000	20,015	1	0	0	2	10,000	20,000	0	1	0	2	10,000	20,000	0	0	1	0	0
Exp. 5	2.0015	10,000	20,015	1	0	0	2	10,000	20,000	0	1	0	2	10,000	20,000	0	0	1	0	0
$n=5$	AN	ND	AV	$P_{0,0}$	$P_{1,0}$	$P_{2,0}$	AN	ND	AV	$P_{0,1}$	$P_{1,1}$	$P_{2,1}$	AN	ND	AV	$P_{0,2}$	$P_{1,2}$	$P_{2,2}$		
Exp. 1	2.0071	10,000	20,071	1	0	0	2	10,000	20,000	0	1	0	2	9,912	19,824	0	0	1	0	0
Exp. 2	2.0073	10,000	20,073	1	0	0	2	10,000	20,000	0	1	0	2	9,909	19,818	0	0	1	0	0
Exp. 3	2.0085	10,000	20,085	1	0	0	2	10,000	20,000	0	1	0	2	9,908	19,816	0	0	1	0	0
Exp. 4	2.0074	10,000	20,074	1	0	0	2	10,000	20,000	0	1	0	2	9,900	19,800	0	0	1	0	0
Exp. 5	2.0088	10,000	20,088	1	0	0	2	10,000	20,000	0	1	0	2	9,916	19,832	0	0	1	0	0

Notations used in the table: # – number of experiments; AN – averaged number of observations for making a decision; ND – total number of made decisions; AV – averaged number of all made experiments; $P_{0,0} - P(x \in \Gamma_0 \mid H_0)$; $P_{1,0} - P(x \in \Gamma_- \mid H_0)$; $P_{2,0} - P(x \in \Gamma_+ \mid H_0)$; $P_{0,1} - P(x \in \Gamma_0 \mid H_1)$; $P_{1,1} - P(x \in \Gamma_- \mid H_1)$; $P_{2,1} - P(x \in \Gamma_+ \mid H_1)$; $P_{0,2} - P(x \in \Gamma_0 \mid H_2)$; $P_{1,2} - P(x \in \Gamma_- \mid H_2)$; $P_{2,2} - P(x \in \Gamma_+ \mid H_2)$.

Table 6.3. The results of testing individual directional hypotheses at restriction of *Risk* function in sequential experiments.
Probabilities are computed by a sample of size $10,000$. Lagrange Multipliers computed at restrictions of *Risk* function accordingly for $n = 1$ and $n = 5$ at $\sigma^2 = 1$ are used here.

#	At H_0						At H_1						At H_2						$mdFDR$	$Risk$
$n=1$	AN	ND	AV	$P_{0,0}$	$P_{1,0}$	$P_{2,0}$	AN	ND	AV	$P_{0,1}$	$P_{1,1}$	$P_{2,1}$	AN	ND	AV	$P_{0,2}$	$P_{1,2}$	$P_{2,2}$		
Exp. 1	2.0018	10,000	20,018	0.9923	0.0031	0.0046	2	10,000	20,000	0	1	0	2	10,000	20,000	0	0	1	0.0077	0.0025(6)
Exp. 2	2.0022	10,000	20,022	0.9924	0.0034	0.0042	2	10,000	20,000	0	1	0	2	10,000	20,000	0	0	1	0.0076	0.0025(3)
Exp. 3	2.0018	10,000	20,018	0.9903	0.0051	0.0046	2	10,000	20,000	0	1	0	2	10,000	20,000	0	0	1	0.0097	0.0032(3)
Exp. 4	2.0019	10,000	20,019	0.9917	0.0039	0.0044	2	10,000	20,000	0	1	0	2	10,000	20,000	0	0	1	0.0083	0.0027(6)
Exp. 5	2.0024	10,000	20,024	0.9925	0.0047	0.0028	2	10,000	20,000	0	1	0	2	10,000	20,000	0	0	1	0.0075	0.0025
$n=5$	AN	ND	AV	$P_{0,0}$	$P_{1,0}$	$P_{2,0}$	AN	ND	AV	$P_{0,1}$	$P_{1,1}$	$P_{2,1}$	AN	ND	AV	$P_{0,2}$	$P_{1,2}$	$P_{2,2}$		
Exp. 1	2.0134	10,000	20,134	1	0	0	2	10,000	20,000	0	1	0	2	9,834	19,668	0	0	1	0	0
Exp. 2	2.0146	10,000	20,146	1	0	0	2	10,000	20,000	0	1	0	2	9,841	19,682	0	0	1	0	0
Exp. 3	2.0133	10,000	20,133	1	0	0	2	10,000	20,000	0	1	0	2	9,814	19,628	0	0	1	0	0
Exp. 4	2.0117	10,000	20,117	1	0	0	2	10,000	20,000	0	1	0	2	9,844	19,688	0	0	1	0	0
Exp. 5	2.0147	10,000	20,147	1	0	0	2	10,000	20,000	0	1	0	2	9,824	19,648	0	0	1	0	0

Notations used in the table: # – number of experiments; AN – averaged number of observations for making a decision; ND – total number of made decisions; AV – averaged number of all made experiments; $P_{0,0} - P(x \in \Gamma_0 \mid H_0)$; $P_{1,0} - P(x \in \Gamma_- \mid H_0)$; $P_{2,0} - P(x \in \Gamma_+ \mid H_0)$; $P_{0,1} - P(x \in \Gamma_0 \mid H_1)$; $P_{1,1} - P(x \in \Gamma_- \mid H_1)$; $P_{2,1} - P(x \in \Gamma_+ \mid H_1)$; $P_{0,2} - P(x \in \Gamma_0 \mid H_2)$; $P_{1,2} - P(x \in \Gamma_- \mid H_2)$; $P_{2,2} - P(x \in \Gamma_+ \mid H_2)$.

Table 6.4. The results of testing multiple directional hypotheses when the number of individual hypotheses $m = 3$.

1. True hypotheses in three subsets of the considered below examples are: $H_0^{(1)}$, $H_1^{(2)}$, $H_2^{(3)}$.

Scenario: three set of skewed hypotheses; in each of a set to H_0 correspond normal distribution, to H_1 and H_2 – truncated normal distributions; in all of the sets $\sigma_1^2 = 1$, $\sigma_2^2 = 1/2$, $\sigma_3^2 = 1/2$.

Lagrange multipliers computed for $mdFDR$ at $n = 1$ and $\sigma_1^2 = 1$ are used.

#	At H_0							At H_-							At H_+							TND	TAV	$tmdFDR$	$TRisk$
	$P_{1,0}$	$P_{0,0}$	$P_{2,0}$	ND	AV	$mdFDR$	$Risk$	$P_{1,1}$	$P_{0,1}$	$P_{2,1}$	ND	AV	$mdFDR$	$Risk$	$P_{1,2}$	$P_{0,2}$	$P_{2,2}$	ND	AV	$mdFDR$	$Risk$				
Exp. 1	0.004121	0.991858	0.004021	9949	1.005126	0.008142	0.002714	1	0	0	9966	1	0	0	0	0	1	9949	1	0	0	9949	1.005126	0.00814	0.002714
Exp. 2	0.004415	0.990568	0.005017	9966	1.003412	0.009432	0.0031447	1	0	0	9966	1	0	0	0	0	1	9966	1	0	0	9966	1.003412	0.009432	0.003144
Exp. 3	0.004216	0.991268	0.004517	9963	1.003714	0.008732	0.002911	1	0	0	9963	1	0	0	0	0	1	9963	1	0	0	9963	1.003714	0.00873	0.002911
Exp. 4	0.004415	0.992575	0.003010	9966	1.003412	0.007425	0.002475	1	0	0	9966	1	0	0	0	0	1	9966	1	0	0	9966	1.003412	0.007425	0.002475
Exp. 5	0.004415	0.990568	0.005017	9966	1.003412	0.009432	0.003144	1	0	0	9966	1	0	0	0	0	1	9966	1	0	0	9966	1.003412	0.009432	0.003144
Average	0.004316	0.991367	0.004316	9962	1.003815	0.008633	0.002878	1	0	0	9962	1	0	0	0	0	1	9962	1	0	0	9962	1.00381	0.008633	0.002878

2. True hypotheses in three subsets of the considered below examples are: $H_0^{(1)}$, $H_1^{(2)}$, $H_0^{(3)}$.

Scenario: three set of skewed hypotheses; in each of a set to H_0 correspond normal distribution, to H_1 – truncated normal distributions; in all of the sets $\sigma_1^2 = 1$, $\sigma_2^2 = 1/2$, $\sigma_3^2 = 1/2$.

Lagrange multipliers computed for $mdFDR$ at $n = 1$ and $\sigma_1^2 = 1$ are used.

#	At H_0							At H_-							At H_0							TND	TAV	$tmdFDR$	$TRisk$
	$P_{1,0}$	$P_{0,0}$	$P_{2,0}$	ND	AV	$mdFDR$	$Risk$	$P_{1,1}$	$P_{0,1}$	$P_{2,1}$	ND	AV	$mdFDR$	$Risk$	$P_{1,0}$	$P_{0,0}$	$P_{2,0}$	ND	AV	$mdFDR$	$Risk$				
Exp. 1	0.003824	0.99165	0.004529	9936	1.003221	0.008353	0.002784	1	0	0	9936	1	0	0	0.003321	0.992452	0.004227	9936	1.003221	0.007548	0.002516	9936	1.006441	0.015902	0.005301
Exp. 2	0.004735	0.991639	0.003626	9927	1.003324	0.008361	0.002787	1	0	0	9927	1	0	0	0.004432	0.989926	0.005641	9927	1.004029	0.010074	0.003358	9927	1.007354	0.018435	0.006145
Exp. 3	0.003832	0.992437	0.003731	9917	1.004437	0.007563	0.002521	1	0	0	9917	1	0	0	0.004538	0.991832	0.003630	9917	1.003933	0.008168	0.002723	9917	1.008369	0.015731	0.005244
Exp. 4	0.004136	0.990820	0.005044	9913	1.003934	0.009180	0.003060	1	0	0	9913	1	0	0	0.0040351	0.992232	0.003732	9913	1.004842	0.007768	0.002589	9913	1.008776	0.016947	0.005649
Exp. 5	0.003824	0.991647	0.004530	9936	1.003221	0.008353	0.002784	1	0	0	9936	1	0	0	0.003321	0.992452	0.004227	9936	1.003221	0.007548	0.002516	9936	1.006441	0.015902	0.005301
Average	0.00400703	0.991638	0.004292	9926	1.003627	0.008362	0.002787	1	0	0	9926	1	0	0	0.00392	0.991779	0.004292	9926	1.003849	0.008221	0.002740	9926	1.007476	0.0166 583	0.005528

3. True hypotheses in three subsets of the considered below examples are: $H_1^{(1)}$, $H_1^{(2)}$, $H_2^{(3)}$.

Scenario: three set of skewed hypotheses; in each of a subset to H_1 and H_2 correspond normal distribution; in all of the sets $\sigma_1^2 = 1$, $\sigma_2^2 = 1/2$, $\sigma_3^2 = 1/2$.

Lagrange multipliers computed for $mdFDR$ at $n = 1$ and $\sigma_1^2 = 1$ are used.

#	At H_-							At H_0							At H_+							TND	TAV	$tmdFDR$	$TRisk$
	$P_{1,1}$	$P_{0,1}$	$P_{2,1}$	ND	AV	$mdFDR$	$Risk$	$P_{1,1}$	$P_{0,1}$	$P_{2,1}$	ND	AV	$mdFDR$	$Risk$	$P_{1,2}$	$P_{0,2}$	$P_{2,2}$	ND	AV	$mdFDR$	$Risk$				
Exp. 1	0.996 567	0.003 433	0	8448	1.183 594	0	0.001 144	1	0	0	8449	1	0	0	0	0	1	8449	1	0	0	8448	1.183 594	0	0.001 144
Exp. 2	0.996 339	0.003 660	0	8469	1.183 594	0	0.001 220	1	0	0	8470	1	0	0	0	0	1	8470	1	0	0	8469	1.180 659	0	0.001 220
Exp. 3	0.995 292	0.004 708	0	8496	1.177 024	0	0.001 569	1	0	0	8496	1	0	0	0	0	1	8496	1	0	0	8446	1.177 0245	0	0.001 569
Exp. 4	0.995 382	0.004 618	0	8446	1.183 874	0	0.001 539	1	0	0	8447	1	0	0	0	0	1	8447	1	0	0	8446	1.183 874	0	0.001 539
Exp. 5	0.996 112	0.003 888	0	8487	1.178 273	0	0.00 1296	1	0	0	8487	1	0	0	0	0	1	8487	1	0	0	8487	1.178	0	0.001 296
Average	0.995 938	0.004 061	0	8469	1.181 272	0	0.001 354	1	0	0	8470	1	0	0	0	0	1	8470	1	0	0	8470	1.180 685	0	0.001 354

4. True hypotheses in three subsets of the considered below examples are: $H_0^{(1)}$, $H_0^{(2)}$, $H_0^{(3)}$.

Scenario: three subsets of skewed hypotheses; in each of a subset to H_0 correspond normal distribution, where $\sigma_1^2 = 5$, $\sigma_2^2 = 2$, $\sigma_3^2 = 3$.

Lagrange multipliers computed for $mdFDR$ at $n = 1$ and $\sigma_1^2 = 5$ are used in computation.

#	At H_0							At H_-							At H_0							TND	TAV	$tmdFDR$	$TRisk$
	$P_{1,0}$	$P_{0,0}$	$P_{2,0}$	ND	AV	$mdFDR$	$Risk$	$P_{1,1}$	$P_{0,1}$	$P_{2,1}$	ND	AV	$mdFDR$	$Risk$	$P_{1,0}$	$P_{0,0}$	$P_{2,0}$	ND	AV	$mdFDR$	$Risk$				
Exp. 1	0.003 882	0.992 026	0.004 092	9531	1.049 208	0.007 974	0.002 658	0.000 105	0.999 790	0.000 105	9531	1.001 574	0.000 210	0.000 070	0.000 210	0.999 475	0.000 315	9531	1.00 209	0.000 525	0.000 175	9531	1.049 208	0.008 708	0.002 903
Exp. 2	0.005 547	0.991 103	0.003 349	9554	1.046 682	0.008 897	0.002 966	0.000 3148	0.999 686	0.0	9554	1.003 245	0.000 314	0.000 105	0.000 105	0.999 791	0.000 1047	9554	1.001 989	0.000 209	0.000 070	9554	1.046 682	0.009 420	0.003 140
Exp. 3	0.005 761	0.990 573	0.003 666	9547	1.047 449	0.009 427	0.003 142	0.000 209	0.999 372	0.000 419	9547	1.002 199	0.000 628	0.000 209	0.000 210	0.999 791	0.0	9547	1.001 990	0.000 209	0.000 070	9547	1.047 449	0.010 265	0.003 422
Exp. 4	0.004 104	0.991 055	0.004 841	9503	1.052 299	0.008 945	0.002 982	0.0	0.999 684	0.000 316	9503	1.001 789	0.000 316	0.000 105	0.000 210	0.999 579	0.000 210	9503	1.003 999	0.000 421	0.000 140	9503	1.052 299	0.009 681	0.003 227
Exp. 5	0.005 027	0.990 574	0.004 399	9548	1.047 340	0.009 426	0.003 142	0.000 419	0.999 267	0.000 314	9548	1.001 152	0.000 733	0.000 144	0.000 209	0.999 476	0.000 314	9548	1.002 828	0.000 524	0.000 175	9548	1.047 340	0.010 683	0.003 561
Average	0.004 864	0.991 066	0.004 069	9537	1.048 596	0.008 934	0.002 978	0.000 209	0.999 560	0.000 231	9537	1.001 992	0.000 440	0.000 127	0.000 189	0.999 622	0.000 189	9537	1.002 581	0.000 378	0.000 126	9537	1.048 957	0.009 596	0.003 752	0.003 251

5. True hypotheses in three subsets of the considered below examples are: $H_0^{(1)}$, $H_0^{(2)}$, $H_0^{(3)}$.

Scenario: three subsets of skewed hypotheses; in each of a subset to H_0 correspond normal distribution, where $\sigma_1^2 = 5$, $\sigma_2^2 = 2$, $\sigma_3^2 = 3$.
Lagrange multipliers computed for $mdFDR$ at $n = 1$ and $\sigma_1^2 = 5$ are used in computation.

#	At H_0							At H_-							At H_0							TND	TAV	$tmdFDR$	$TRisk$
	$P_{1,0}$	$P_{0,0}$	$P_{2,0}$	ND	AV	$mdFDR$	$Risk$	$P_{1,1}$	$P_{0,1}$	$P_{2,1}$	ND	AV	$mdFDR$	$Risk$	$P_{1,0}$	$P_{0,0}$	$P_{2,0}$	ND	AV	$mdFDR$	$Risk$				
Exp. 1	0.003 777	0.991 921	0.004 302	9531	1.049 208	0.008 079	0.002 693	0.000 105	0.999 790	0.000 105	9531	1.001 784	0.000 210	0.000 070	0.000 210	0.999 475	0.000 315	9531	1.002 308	0.000 0 525	0.000 175	9531	1.049 208	0.008 813	0.002 938
Exp. 2	0.005 549	0.991 101	0.003 350	9552	1.046 901	0.008 899	0.002 967	0.000 314	0.999 686	0.0	9552	1.003 350	0.000 314	0.000 105	0.000 105	0.999 791	0.000 105	9552	1.001 989	0.000 209	0.000 070	9552	1.046 901	0.009 422	0.003 141
Exp. 3	0.004 206	0.990 958	0.004 837	9511	1.051 414	0.009 042	0.003 014	0.0	0.999 685	0.000 315	9511	1.001 893	0.000 315	0.000 105	0.000 210	0.999 579	0.000 210	9511	1.003 890	0.000 421	0.000 140	9511	1.051 414	0.009 778	0.003 259
Exp. 4	0.004 926	0.990 673	0.004 402	9542	1.047 998	0.009 327	0.003 109	0.000 419	0.999 162	0.000 419	9542	1.001 258	0.000 838	0.000 279	0.000 210	0.999 476	0.000 314	9542	1.00 283	0.000 524	0.000 1750	9542	1.047 998	0.010 690	0.003 563
Exp. 5	0.004 297	0.991 720	0.003 983	9541	1.048 108	0.008 280	0.002 760	0.0	0.999 790	0.000 210	9541	1.002 620	0.000 210	0.000 070	0.000 210	0.999 371	0.000 419	9541 1	1.001 991	0.000 629	0.000 210	9541	1.048 108	0.009 119	0.003 040
Average	0.004 551	0.991 275	0.004 175	9535	1.048 726	0.008 725	0.002 908	0.000 168	0.999 623	0.000 210	9535	1.002 181	0.000 377	0.000 252	0.000 188	0.999 539	0.000 273	9535	1.002 602	0.000 462	0.000 154	9535	1.048 726	0.009 564	0.003 188

Notations used in the table: # – number of experiments; AN – averaged number of observations for making a decision; ND – number of made decisions; AV – averaged number of experiments; TND – total number of made decisions; TAV – total averaged number of observations for making a decision; $P_{0,0} - P(x \in \Gamma_0 \mid H_0)$; $P_{1,0} - P(x \in \Gamma_- \mid H_0)$; $P_{2,0} - P(x \in \Gamma_+ \mid H_0)$; $P_{0,1} - P(x \in \Gamma_0 \mid H_1)$; $P_{1,1} - P(x \in \Gamma_- \mid H_1)$; $P_{2,1} - P(x \in \Gamma_+ \mid H_1)$; $P_{0,2} - P(x \in \Gamma_0 \mid H_2)$; $P_{1,2} - P(x \in \Gamma_- \mid H_2)$; $P_{2,2} - P(x \in \Gamma_+ \mid H_2)$.

7. Discussions

On the basis of the computational results, given in Tables 6.2, 6.3 and 6.4, the following are obvious.

1. The larger is the divergence between hypotheses, the smaller are $mdFDR$ and $Risk$ functions (see Tables 6.2 and 6.3; also cases 4 and 5 of Table 6.4) as a result of making decision in sequential experiments.
2. Statements of Theorems 3.1 and 3.2 are confirmed by the computational results given in Tables A1, 6.2 and 6.3.
3. Statement of Theorem 3.3 is confirmed by computational results given in Tables 6.2 and 6.3.
4. Statement of Theorem 4.1 is confirmed by computational results given in Table 6.4.
5. When for ith $(i = 1, \ldots, m)$ subset of individual directional hypotheses appropriate $mdFDR$ (as well as appropriate $Risk$ function) are restricted on the level q_i and the following condition $\sum_{i=1}^{m} q_i = q$ are satisfied, then $tmdFDR$ (as well as r^{Q}_{CBM}) is restricted on the level q (see Table 6.4).
6. At testing multiple hypotheses the values of $tmdFDR$ and r^{Q}_{CBM} are basically determined by true basic hypotheses H_0 in the subsets of individual hypotheses, i.e. the larger is the number of true basic hypotheses in the subsets of tested individual hypotheses, the larger are the values of $tmdFDR$ and r^{Q}_{CBM} (see Table 6.4).
7. The use of Lagrange multipliers computed for only one subset of individual hypotheses with less divergence among them, gives significant savings of computational time and resources for testing multiple hypotheses with a large number of subsets of individual hypotheses (see Table 6.4).

8. Conclusions

Consideration of the basic and alternative hypotheses in pairs is offered for testing individual and multiple directional hypotheses. The concepts of $mdFDR$ and $Risk$ function are used as criteria of testing. Theorems proving restrictions of $mdFDR$ and $Risk$ function on the desired levels at the suitably chosen restriction levels in CBM for testing individual and multiple directional hypotheses are presented. Reliability and convenience of the developed method for testing a big number of the subsets of individual hypotheses at testing multiple hypotheses allowing significant reduction of the necessary computation time for obtaining the final results are established. Computational results for concrete examples validate the theoretical results. The advantage of the presented method against classical methods (Bayes and frequentist) lies in the opportunities to restrict criteria of testing such as $mdFDR$ and $Risk$ function. There is no difference between the proposed method and the Bayes method in terms of the computations required to make a direct decision, except that at the preparatory stage, which is not executed in real time, it is necessary to compute the Lagrange multipliers for further use. Another positive side of the proposed approach is that in the case of a large number of hypotheses to be tested, it allows to perform calculations in parallel, that is, to perform calcu-

lations for each pair of hypotheses on parallel processors and combine the results to make a final decision.

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References

[1] R.R. Bahadur. *A property of the t-statistic*, Sankhyā **12** (1952), 79–88
[2] N.K. Bansal, G.G. Hamedani, M. Maadooliat. *Testing multiple hypotheses with skewed alternatives*, Biometrics **72**, 2 (2016), 494–502
[3] N.K. Bansal, K.J. Miesc. *A Bayesian decision theoretic approach to directional multiple hypotheses problems*, J. Multivariate Anal., **120** (2013), 205–215
[4] N.K. Bansal, R. Sheng. *Bayesian decision theoretic approach to hypothesis problems with skewed alternatives*, J. Statist. Plann. Inference, **140**, 10 (2010), 2894–2903
[5] Y. Benjamini, Y. Hochberg. *Controlling the false discovery rate: a practical and powerful approach to multiple testing*, J. Roy. Statist. Soc. Ser. B, **57**, 1 (1995), 289–300
[6] Y. Benjamini, D. Yekutieli. *False discovery rate-adjusted multiple confidence intervals for selected parameters With comments and a rejoinder by the authors*, J. Amer. Statist. Assoc., **100**, 469 (2005), 71–93
[7] G. Casella, R.L. Berger. *Statistical Inference*, The Wadsworth & Brooks/Cole Statistics/Probability Series. Wadsworth & Brooks/Cole Advanced Books & Software, Pacific Grove, CA, 1990
[8] P.K. Choudhary, H.N. Nagaraja. *Measuring agreement in method comparison studies-review*, Advances in ranking and selection, multiple comparisons, and reliability, 215–244, Stat. Ind. Technol., Birkhäuser Boston, Boston, MA, 2005
[9] H. Finner. *Stepwise multiple test procedures and control of directional errors*, Ann. Statist., **27**, 1 (1999), 274–289
[10] L.V. Jones, J.W. Tuke. *A sensible formulation of the significance test*, Psychological Methods **5**, 4 (2000), 411–414
[11] K.J. Kachiashvili. *Bayesian Algorithms of Many Hypothesis Testing*, Ganatleba, Tbilisi, 1989
[12] K.J. Kachiashvili. *Generalization of Bayesian rule of many simple hypotheses testing*, Int. J. Inf. Technol. Decis. Mak., **2**, 1 (2003), 41–70
[13] K.J. Kachiashvili. *The methods of sequential analysis of Bayesian type for the multiple testing problem*, Sequential Anal., **33** 1 (2014), 23–38
[14] K.J. Kachiashvili. *Constrained Bayesian Methods of Hypotheses Testing: A New Philosophy of Hypotheses Testing in Parallel and Sequential Experiments*, Nova Science Publishers, Inc., New York, 2018
[15] K.J. Kachiashvili. *An example of application of cbm to intersection-union hypotheses testing*, Biomed. J. Sci. & Tech. Res., **19**, 3 (2019), 14345–14346
[16] G.K. Kachiashvili, K.J. Kachiashvili, A. Mueed. *Specific features of regions of acceptance of hypotheses in conditional Bayesian problems of statistical hypotheses testing*, Sankhya A **74**, 1 (2012), 112–125
[17] K.J. Kachiashvili, N.K. Bansal, I.A. Prangishvili. *Constrained Bayesian method for testing the directional hypotheses*, Journal of Mathematics and System Science, **8**, 4 (2018), 96–118
[18] K.J. Kachiashvili, J.K. Kachiashvili, I.A. Prangishvili, *CBM for testing multiple hypotheses with directional alternatives in sequential experiments.*, Sequential Anal., **39**, 1 (2020), 115–131
[19] K.J. Kachiashvili, M.A. Hashmi, A. Mueed. *Quasi-optimal Bayesian procedures of many hypotheses testing*, J. Appl. Stat., **40**, 1 (2013), 103–122
[20] K.J. Kachiashvili, Sh.S. Lobjanidze. *Computation of the average risk by expansion of the density by Chebyshev-Hermite orthogonal polynomials in particular Bayesian problem of testing many hypotheses*, Technical Cybernetics: Proceedings of Georgian Technical Institute **7**, 198 (1977), 59–66
[21] K.J. Kachiashvili, A. Mueed. *Conditional Bayesian task of testing many hypotheses* Statistics, **47**, 2 (2013), 274–293
[22] K.J. Kachiashvili1, I.A. Prangishvili1, J.K. Kachiashvili. *Constrained Bayesian methods for testing directional hypotheses restricted false discovery rates*, Biostat. Biometrics Open Acc. J., **9**, 3 (2019), 001–010
[23] K. Kaiser. *Zur Theorie algorithmisch abgeschlossener Modellklassen* (German), Math. Systems Theory, **4** (1970), 160–167

[24] S. Kullback. *Information Theory and Statistics*, Reprint of the second (1968) edition. Dover Publications, Inc., Mineola, NY, 1997
[25] E.L. Lehmann. *Some principles of the theory of testing hypotheses*, Ann. Math. Statistics, **21** (1950), 1–26
[26] L. Leventhal, C.L. Huynh. *Directional decisions for two-tailed tests: Power, error rates, and sample size*, Psychological Methods, **1**, 3 (1996), 278–292
[27] S.T. Rachev, A. SenGupta. *Laplace-Weibull mixtures for modeling price changes*, Manage. Sci., **39**, 8 (1993), 915–1038
[28] S.N. Roy. *On a heuristic method of test construction and its use in multivariate analysis*, Ann. Math. Statistics, **24** (1953), 220–238
[29] A. SenGupta. *P^3 approach to intersection-union testing of hypotheses*, J. Statist. Plann. Inference, **137**, 11 (2007), 3753–3766
[30] A. SenGupta, C. Pal. *Optimal tests for no contamination in symmetric multivariate normal mixtures*, Ann. Inst. Statist. Math., **45**, 1 (1993), 137–146
[31] A. SenGupta, C. Pal. *On optimal tests for isotropy against the symmetric wrapped stable-circular uniform mixture family*, J. Appl. Stat., **28**, 1 (2001), 129–143
[32] J.P. Shaffer. *Multiplicity, directional (Type III) errors, and the Null Hypothesis*, Psychological Methods **7**, 3 (2002), 356–369

Appendix

Table A1. The values of $mdFDR$ and $Risk$ function computed for different number of observations in parallel experiments (in each case decisions are made on the basis of only one averaged value of n observations).
Probabilities are computed by a sample of size $10,000$. Computations are realized for Lagrange multipliers computed for $n = 1$ and $\sigma^2 = 1$.

Changing of n	The values of probability integrals for $mdFDR$				The values of probability integrals for $Risk$							
$\sigma^2 = 1$	Accept H_+ at H_-	Accept H_- at H_0	Accept H_+ at H_0	Accept H_- at H_2	Accept H_+ at H_-	Accept H_0 at H_-	Accept H_- at H_0	Accept H_+ at H_0	Accept H_- at H_2	Accept H_0 at H_2	$mdFDR$	$Risk$
1	2	3	4	5	6	7	8	9	10	11	12	13
$n = 1$	0	0.0042	0.0044	0	0	0	0.0058	0.006	0	0	0.0086	0.00393(3)
$n = 2$	0	0.008	0.0068	0	0	0	0.0109	0.0101	0	0	0.0148	0.007
$n = 3$	0	0.0103	0.00776	0	0	0	0.0117	0.0107	0	0	0.0179	0.00746(6)
$n = 4$	0	0.01	0.0091	0	0	0	0.0129	0.0125	0	0	0.0191	0.00846(6)
$n = 5$	0	0.0117	0.0096	0	0	0	0.0141	0.0124	0	0	0.0213	0.00883(3)
$n = 6$	0	0.0095	0.0085	0	0	0	0.0122	0.0113	0	0	0.0180	0.00783(3)
$n = 7$	0	0.0084	0.0083	0	0	0	0.0102	0.0104	0	0	0.0167	0.00686(6)
$n = 10$	0	0.0087	0.0074	0	0	0	0.0108	0.0100	0	0	0.0161	0.00693(3)
$n = 20$	0	0.0067	0.0072	0	0	0	0.0079	0.0092	0	0	0.0139	0.0057
$n = 50$	0	0.0042	0.0039	0	0	0	0.0053	0.0047	0	0	0.0081	0.003(3)
$n = 100$	0	0.0031	0.0029	0	0	0	0.0034	0.0039	0	0	0.0060	0.00243(3)
Changing of σ^2 $n = 1$	2	3	4	5	6	7	8	9	10	11	12	13
$\sigma^2 = 1/2$	0	0.0042	0.0037	0	0	0	0.0057	0.0053	0	0	0.0079	0.0036(6)
$\sigma^2 = 1/3$	0	0.0042	0.0044	0	0	0	0.0058	0.006	0	0	0.0086	0.00393(3)
$\sigma^2 = 3$	0	0.0044	0.0040	0	0	0.2892	0.0061	0.0057	0.3941	0	0.0084	0.2317
$\sigma^2 = 5$	0	0.0044	0.004	0	0	0.4514	0.0061	0.0057	0.5302	0	0.0084	0.33113(3)