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Review

Review of the Problems Solved Using the Constrained Bayesian Methods

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Abstract

A new philosophy of hypothesis testing - the constrained Bayesian method (CBM) and its application for testing different types of statistical hypotheses such as: simple, composite, asymmetric, multiple hypotheses, are considered in the work. The advantage of the CBM over existing classical methods is theoretically proven in the form of theorems and practically demonstrated by the results of numerous example computations. Examples of the use of CBM to solve some practically important problems are presented, which confirm the flexibility of the method and its great ability to deal with difficult problems.

Keywords: hypothesis; constrained Bayesian method; simple; composite and multiple hypotheses; parallel methods; sequential methods; equi-correlation coefficient; ANOVA

MSC: 62F15, 62F03

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1. Introduction

As is known, there are four main approaches (philosophies) to statistical hypothesis testing, which differ from each other in the formalization of the problem, the metrics introduced, and the characteristics of the information used. These approaches are: Fisher's [1], Neyman-Pearson's [2], Jeffrey's (so-called Bayesian) [3] (so-called parallel methods) and Wald's (so-called sequential method) [4]. Based on these ideas, many methods have been developed and successfully used to solve various problems.

Since the late 1970s, we have been developing a new approach (philosophy) for testing hypotheses, which we have called the Constrained Bayesian Method (CBM).

As is known, two types of errors can be made when testing hypotheses: rejecting the true hypothesis (decision) and accepting the false hypothesis (decision). The measures of the possibility of making these decisions, i.e. probabilities, are called the levels of the first type (Type I) and second type (Type II) errors, respectively.

Unlike the classical Bayesian method, where an unconstrained optimization problem is solved, namely, the general loss function containing type I and type II errors is minimized, in CBM the minimization is performed of one type of error under the condition of imposing restrictions on another type of errors.

Depending on the constraints, it is possible to formulate seven different tasks, which allows us to very flexibly choose the appropriate task based on the characteristics of the problem to be solved [5]. In three of them, the levels of type I errors are limited and the levels of type II errors are minimized. In the following four, Type II error rates are limited and Type I error rates are minimized.

For clarity, let us give one formulation for each of these two groups.

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2. Constrained Bayesian Method

Let us introduce the following notations: $x \in R^n$ is n dimensional random variable with distribution density $p(x;\theta)$; $H_i : \theta_i \in \Theta_i$, $i = 1,2,...,S$, are S quantity testable hypotheses, where $\Theta_i \subset \Omega^m$, $i = 1,2,...,S$; Θ_i are non-intersecting subsets $\bigcup \Theta_i = \Omega^m$; Ω^m is m dimensional parameter space; $p(H_i)$ is a priori probability of H_i hypothesis; $p(x \mid H_i)$ is the density of the distribution of x under the fairness of H_i hypothesis; Γ_j is the area of acceptance of H_j hypothesis; $L_1(H_i, \delta_j(x) = 1)$ and $L_2(H_i, \delta_j(x) = 0)$ are losses caused by wrongly accepting and wrongly rejecting hypotheses.

2.1. Restrictions on the Conditional Probabilities of Accepting True Hypotheses (CBM 2)

The average loss caused by incorrectly accepting hypotheses is minimizing

$$r_\delta = \min_{\{\Gamma_j\}} \left\{ \sum_{i=1}^{S} p(H_i) \sum_{j=1}^{S} \int_{\Gamma_j} L_1(H_i, \delta_j(x) = 1) p(x \mid H_i) dx \right\}, \quad (1)$$

subject to

$$\sum_{j=1}^{S} \int_{R^n - \Gamma_j} L_2(H_i, \delta_j(x) = 0) p(x \mid H_i) dx \le r_2, \quad i = 1,...,S. \quad (2)$$

The solution of this problem gives

$$\Gamma_j = \left\{ x : \sum_{i=1}^{S} p(H_i) L_1(H_i, \delta_j(x) = 1) p(x \mid H_i) < \sum_{i=1}^{S} \lambda_i L_2(H_i, \delta_j(x) = 0) p(x \mid H_i) \right\}, \quad (3)$$

where the Lagrange multipliers λ_i, $i = 1,...,S$, are determined so that the equalities in (2) hold.

2.2. Restrictions on Posterior Probabilities of Rejecting True Hypotheses (CBM 7)

In this case, we are looking for the maximum of the average probability of accepting true hypotheses (let us call it the average power of the criterion)

$$G_\delta = \max_{\{\Gamma_j\}} \left\{ \sum_{i=1}^{S} p(H_i) \sum_{j=1}^{S} \int_{\Gamma_j} L_2(H_i, \delta_j(x) = 0) p(x \mid H_i) dx \right\}, \quad (4)$$

at the following restrictions

$$\sum_{i=1}^{S} p(H_i) \int_{\Gamma_j} L_1(H_i, \delta_j(x) = 1) p(x \mid H_i) dx \le r_7, \quad j = 1,...,S. \quad (5)$$

Lagrange's method gives us

$$\Gamma_j = \left\{ x : \sum_{i=1}^{S} p(H_i) L_2(H_i, \delta_j(x) = 0) p(x \mid H_i) > \lambda_j \sum_{i=1}^{S} p(H_i) L_1(H_i, \delta_j(x) = 1) p(x \mid H_i) \right\},$$
$$j = 1,...,S, \quad (6)$$

where, λ_j are determined so that the equalities in (5) hold.

3. General Characterization of the CBM

CBM turned out to be a generalization of existing methodologies, which gives unique results in terms of the optimality of the obtained decisions under the conditions of the minimum number of observations. Constrained Bayesian methodology surpasses in existing methodologies in that: 1) it uses all the information that existing methodologies use; 2) at formalization, all features of formalization of existing methodologies are taken into account.

In particular, the constrained Bayesian methodology uses not only the loss function and a priori probabilities to make decisions, as the classical Bayesian methodology does, but also the significance level of the criterion, as the frequentist (Neiman-Pearson) methodology does, and it is data-dependent like the Fisher methodology. The combination of these capabilities has increased the quality of the decisions made in the Constrained Bayesian methodology compared to other methodologies.

Constrained Bayes methodology has been used to test various types of hypotheses, such as simple, composite, asymmetric, multiple hypotheses, for which the superiority of CBMs compared to existing methods has been theoretically proven in the form of theorems and practically demonstrated by the results of many example calculations [5,6]. When testing the mentioned hypotheses, the constrained Bayesian methodology allows to obtain such decision rules, which, without any coercion, naturally allow to minimize practically all existing criteria of optimality of the decision, such as: type I, II and III error rates; false acceptance rate (FAR); pure directional false discovery rate ($pdFDR$); mixed directional false discovery rate ($mdFDR$); Family-wise error rates of type I and type II ($FWERI$, $FWERII$) and others.

To illustrate what has been said, let us quote some results obtained using the mentioned methodology.

Let us define the summary risk (*SR*) of making an incorrect decision when testing hypotheses as a weighted sum of the probabilities of making incorrect decisions, i.e.

$$r_S(\Gamma)=\sum\nolimits_{i=1}^{S}\sum\nolimits_{j=1,\, j\neq i}^{S} L(H_i,H_j)p(H_i)\int_{\Gamma_j} p(x\,|\,H_i)dx \quad (7)$$

Here $L(H_i,H_j)$ is the sum function of losses caused by both types of errors.

It is clear that for given losses and probabilities, SR depends on decision areas. Let us note: Γ^{CBM} and Γ^{B} are the regions of acceptance of hypotheses, respectively, in constrained Bayesian (CBM) and Bayesian (B) methods; $r_S(\Gamma^{CBM})$ and $r_S(\Gamma^{B})$ are, respectively, the summary risks (SR) in constrained Bayesian and Bayesian methods.

The following theorem is equitable [5,7].

Theorem 1. *For given losses and probabilities, SR of making incorrect decision in CBM is a convex function of* λ *with a maximum at* $\lambda=1$. *By increasing or decreasing* λ *, SR decreases, and in the limit,* i.e., *at* $\lambda\to\infty$ *or* $\lambda\to 0$, *SR tends to zero.*

From the theorem directly follows the following.

Corollary 1. *At the same conditions SR of making the incorrect decision in CBM is less or equal to SR of the Bayesian decision rule,* i.e., $r_S(\Gamma^{CBM})\le r_S(\Gamma^{B})$.

Similar to Corollary 1, it is not difficult to be convinced that SR of making an incorrect decision in the CBM does not exceed the SR of the frequentist method, that is, $r_S(\Gamma^{CBM})\le r_S(\Gamma^{f})$, *where* $r_S(\Gamma^{f})$ *is the SR of the frequentist method.*

The following theorem is equitable [8].

Theorem 2. *Let us assume that probability distributions* $p(x\,|\,H_i)$, $i=1,\ldots,S$, *are such that, at increasing number of repeated observations* n, *the entropy concerning distribution parameter* θ, *in relation to which the hypotheses are formulated, decrease. In such a case, for all given values* $0<\alpha_1<1$ *and* $0<\beta_1<1$ *there can always be found such a finite, positive integer number* n^* *that inequalities* $\alpha(\bar{x}_n)<\alpha_1$ *and* $\beta(\bar{x}_n)<\beta_1$, *where the number of repeated observations is* $n>n^*$, *take place.*

Here $\alpha(\bar{x}_n)$ and $\beta(\bar{x}_n)$ are the probabilities of errors of the first and the second types, respectively, in constrained Bayesian task when the decision is made on the basis of arithmetic mean of the observation results $\bar{x}_n$ calculated by n repeated observations. That is, the CBM allows us to make a decision by increasing information so that the levels of possible first and second type errors are restricted to any desired level.

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Let us bring examples of the use of the CBM in cases of different types of hypotheses (simple, composite, asymmetric, multiple) and show its advantage over existing methods.

4. Simple Hypotheses

4.1. Parallel Methods

Example 1 [9]**.** Suppose that $X_1, X_2, \ldots, X_n$ are independent identically distributed (i.i.d.) random variables with distribution law $N(x;\theta,1)$. Let us test the basic hypothesis $H_0:\theta=-1$ against the alternative $H_A:\theta=1$.

Below, when discussing examples, we assume that the hypotheses are a priori equally probable.

Table 1 presents the results of testing hypotheses using various criteria for various $\bar{x}$ calculated from $n=4$ observations.

The results of the computation show that the Berger (T^C and T^* criteria), Bayesian, and Neyman-Pearson methods accept the alternative hypothesis on the basis of $\bar{x}=0$, i.e. $B(x)=1$, when there is no basis for such a decision [9]. Both hypotheses are equally likely to be true or false.

In this respect, Fisher's p-value test is better because it rejects the hypothesis H_0 but says nothing about H_A. However, the probability value p does not provide any information about the existence of another possible hypothesis instead of H_0. In this situation, CBM gives the most logical answer, because it confirms that both hypotheses are equally true or equally false, that is, an unambiguous decision cannot be made in this case. For other values of the statistic $\bar{x}$, all the considered methods make correct decisions with different error probabilities. But even in these cases, the advantage of CBM is obvious, because it gives us the error levels of Type I and Type II for which one of the testable hypotheses can be accepted according to the given statistic $\bar{x}$.

Table 1. Results of hypothesis testing for different values of $\bar{x}$.

$\bar{x}$	$B(x)$	For tests T^C, T^* and Bayes			For N-P test			For *p-value* test		For constrained Bayes test (CBM)			
		CEP $\alpha(B)$	CEP $\beta(B)$	AH*)	α	β	AH*)	*p-value*	AH*)	γ	$\alpha(\gamma,B)$	$\beta(\gamma,B)$	AH*)
0	1	0.5	0.5	H_A	0.02275	0.02275	H_A	0.02275	Reject H_0	$\gamma\le 0.0455$ $\gamma>0.0455$	$\alpha\le 0.02275$ $\alpha>0.02275$	$\beta\le 0.02275$ $\beta>0.02275$	None1) Both2)
0.028	0.8	0.444(4)	0.555(5)	H_A	0.02275	0.02275	H_A	0.01989	Reject H_0	$\gamma\in[0.02,0.025]$ $\gamma>0.025$ $\gamma<0.02$	$\alpha\in[0.02,0.025]$ $\alpha<0.02$ $\alpha>0.025$	$\beta\in[0.02,0.025]$ $\beta>0.025$ $\beta<0.02$	H_A Both None
0.25	0.14	0.1228	0.8772	H_A	0.02275	0.02275	H_A	0.00621	Reject H_0	$\gamma\in[0.007,0.05]$ $\gamma>0.05$ $\gamma<0.007$	$\alpha\in[0.009,0.06]$ $\alpha<0.009$ $\alpha>0.06$	$\beta\in[0.007,0.05]$ $\beta>0.05$ $\beta<0.007$	H_A Both None

1	0.00034	0.00034	0.99966	H_A	0.02275	0.02275	H_A	0.00003	Reject H_0	$\gamma \in [0.0001, 0.5)$ $\gamma \geq 0.5$	$\alpha \in (0.00003, 0.38936]$ $\alpha \leq 0.00003$ | $\beta \in [0.0001, 0.5)$ $\beta \geq 0.5$	H_A Both e
-0.25	7.389	0.88	0.1192	H_0	0.02275	0.02275	H_0	0.06681	Accept H_0	$\gamma \in [0.007, 0.05]$ $\gamma > 0.05$ $\gamma < 0.007$	$\alpha \in [0.00920, 0.06145]$ $\alpha < 0.00926$ $\alpha > 0.06145$	$\beta \in [0.007, 0.05]$ $\beta > 0.05$ $\beta < 0.007$	H_0 Both e No one
-1	2980.958	0.99966	0.00034	H_0	0.02275	0.02275	H_0	0.5	Accept H_0	$\gamma \in [0.0001, 0.5)$ $\gamma \geq 0.5$	$\alpha \in (0.00003, 0.38936]$ $\alpha \leq 0.00003$ | $\beta \in [0.0001, 0.5)$ $\beta \geq 0.5$	H_0 Both e

*) Accepted hypothesis 1) Both hypotheses are equally impossible to be true. 2) Both hypotheses are equally likely to be true.

4.2. Sequential Methods

Example 2 [9]**.** Let us consider the scenario of Example 1, but assume that the data is obtained sequentially.

The results of the computation of 17 random samples generated by $N(x;1,1)$ sequentially processed are given in Table 2, where the arithmetic mean of the observations $x_k,\ldots,x_m$ is indicated by $\bar{x}_{k,m}$.

Table 2. Results of hypothesis testing for normal sampling.

n	Observation results x_i	$\bar{x}_{k,m}$	The Berger's test	The Wald's test	$\bar{x}_{k,m}$ for sequential test of Bayesian type	The sequential teat of Bayesian type
1	1.201596	$\bar{x}_{1,3} = 0.6347$	H_A, $\alpha = 0.0217$, $\beta = 0.9783$.	H_A	$\bar{x}_1 = 1.2016$	H_A
2	0.043484					
3	0.658932				$\bar{x}_{2,3} = 0.3512$	H_A
4	0.039022	$\bar{x}_{4,6} = 0.8942$	H_A, $\alpha = 0.0047$, $\beta = 0.9953$.	H_A	$\bar{x}_{4,5} = 0.3280$	H_A
5	0.616960					
6	2.026540				$\bar{x}_6 = 2.02654$	H_A
		$\bar{x}_{7,11} = 0.2992$	H_A, $\alpha = 0.0478$, $\beta = 0.9522$.		$\bar{x}_{7,9} = 0.1643$	H_A
7	-0.422764			H_A		
8	0.562569				$\bar{x}_{10,11} = 0.5015$	H_A
9	0.353047					
10	-0.123311					
11	1.126263				$\bar{x}_{12} = 1.521061$	

12	1.521061	$\bar{x}_{12}=1.521061$	H_A, $\alpha=0.0456$, $\beta=0.9544$.	H_A		H_A
13	1.486411	$\bar{x}_{13}=1.4864$	H_A, $\alpha=0.0487$, $\beta=0.9513$.	H_A	$\bar{x}_{13}=1.486411$	H_A
14	-0.578935	$\bar{x}_{14,16}=0.5536$	H_A, $\alpha=0.0348$, $\beta=0.9652$.	H_A	$\bar{x}_{14,16}=0.55362$	H_A
15	0.623006					
16	1.616669					
17	1.754413	$\bar{x}_{17}=1.7544$	H_A, $\alpha=0.0291$, $\beta=0.9709$.	H_A	$\bar{x}_{17}=1.754413$	H_A
$\bar{n}$			2.43	2.43		1.7

4.3. Sequential Methods

Example 3 [9]. Let us consider the scenario of Example 1, but assume that the data is obtained sequentially.

The results of the computation of 17 random samples generated by $N(x;1,1)$ sequentially processed are given in Table 3, where the arithmetic mean of the observations $x_k,\ldots,x_m$ is indicated by $\bar{x}_{k,m}$.

Table 3. Results of hypothesis testing for normal sampling.

n	Observation results x_i	$\bar{x}_{k,m}$	The Berger's test	The Wald's test	$\bar{x}_{k,m}$ for sequential test of Bayesian type	The sequential teat of Bayesian type
1		$\bar{x}_{1,3}=0.6347$	H_A, $\alpha=0.0217$, $\beta=0.9783$.	H_A	$\bar{x}_1=1.2016$	H_A
2	1.201596					
3	0.043484				$\bar{x}_{2,3}=0.3512$	H_A
	0.658932					
4		$\bar{x}_{4,6}=0.8942$	H_A, $\alpha=0.0047$, $\beta=0.9953$.	H_A	$\bar{x}_{4,5}=0.3280$	H_A
5	0.039022					
6	0.616960				$\bar{x}_6=2.02654$	H_A

	2.026540					
		$\bar{x}_{7,11}=0.2992$	H_A,		$\bar{x}_{7,9}=0.1643$	H_A
7			$\alpha=0.0478$,	H_A		
8	-0.422764		$\beta=0.9522$.		$\bar{x}_{10,11}=0.5015$	H_A
9	0.562569					
10	0.353047					
11	-0.123311				$\bar{x}_{12}=1.521061$	
	1.126263		H_A,			H_A
		$\bar{x}_{12}=1.521061$	$\alpha=0.0456$,	H_A		
12			$\beta=0.9544$.			
	1.521061					
					$\bar{x}_{13}=1.486411$	
			H_A,			H_A
		$\bar{x}_{13}=1.4864$	$\alpha=0.0487$,			
			$\beta=0.9513$.	H_A		
13						
	1.486411		H_A,			
			$\alpha=0.0348$,		$\bar{x}_{14,16}=0.55362$	
			$\beta=0.9652$.			H_A
		$\bar{x}_{14,16}=0.5536$				
				H_A		
14			H_A,			
15	-0.578935		$\alpha=0.0291$,		$\bar{x}_{17}=1.754413$	
16	0.623006		$\beta=0.9709$.			H_A
	1.616669	$\bar{x}_{17}=1.7544$				
				H_A		
17						
	1.754413					
$\bar{n}$			2.43	2.43		1.7

The table shows that the Wald and Berger T^* tests give the same results, although the error probabilities in the Berger test are slightly lower than in the Wald test due to the fact that Berger calculated the error probabilities with a given value of the statistic. In the Wald criterion, they are determined by the decision thresholds. Out of 17 observations, correct decisions were made 7 times based on 3, 3, 5, 1, 1, 3, and 1 observations in both tests, and all decisions were correct. The average number of observations in making a decision is equal to 2.43. With the Bayesian-type sequential method, correct decisions for the same sample were made 10 times based on 1, 2, 2, 1, 3, 2, 1, 1, 3, and 1 observations, and all decisions were also correct. The average number of observations in making a decision is equal to 1.7.

5. Composite Hypotheses

Similar to the cases above, where CBM is optimal for testing simple hypotheses in parallel and sequential experiments, it retains optimal properties when testing composite hypotheses. Also, it easily, without much effort, overcomes Lindley's paradox, which arises when testing a simple hypothesis against a composite hypothesis. These facts are shown theoretically and based on the computation of specific examples in the work [10].

6. Testing Multiple Hypotheses

For several last decades, multiple hypotheses testing problems have attracted significant attention because of their huge applications in many fields (see, for example, [11–17 and so on]).

CBM maintains optimal properties when testing multiple hypotheses. For example, in [18] were considered d individual hypotheses about parameters $\theta_1,...,\theta_d$ of sequentially observed vectors $\mathbf{X_1}, \mathbf{X}_2,...$

$$H_0^{(1)}:\theta_1 \in \Theta_{01} \quad vs \quad H_A^{(1)}:\theta_1 \in \Theta_{11},$$

$$H_0^{(2)}:\theta_2 \in \Theta_{02} \quad vs \quad H_A^{(2)}:\theta_2 \in \Theta_{12},$$

$$H_0^{(d)}:\theta_k \in \Theta_{0d} \quad vs \quad H_A^{(d)}:\theta_k \in \Theta_{1d}. \quad (8)$$

The following stopping rule in the sequential test was developed

$$T = \inf\left\{m:\bigcap_{j=1}^{d}\left\{\Lambda_m^{(j)} \notin \left(\lambda_{*j},\lambda_j^*\right)\right\}\right\}, \quad (9)$$

where λ_{*j} and λ_j^* are Lagrange multipliers obtained in CBM; $\Lambda_m^{(j)}$ is the likelihood ratio (10) for the j th parameter ($j=1,...,d$) calculated on the basis of m sequentially obtained observation results

$$\Lambda_m = \frac{p(\mathbf{x}^1 \mid H_1)\cdots p(\mathbf{x}^m \mid H_1)}{p(\mathbf{x}^1 \mid H_0)\cdots p(\mathbf{x}^m \mid H_0)}, \quad m=1,2,... \quad (10)$$

The following theorem was proved [18]

Theorem 3. A *sequential Bonferroni procedure for testing multiple hypotheses (8) with stopping rule (9), rejection regions* $\Lambda_T^{(j)} > \lambda_j^*$, *and acceptance regions* $\Lambda_T^{(j)} < \lambda_{*j}$, *where* λ_j^* *and* λ_{*j} *are defined in CBM for* $\beta_j = \beta / d$ *and* $\alpha_j = \alpha / d$, *controls both error rates at levels* $FWER_I \le \alpha$ *and* $FWER_{II} \le \beta$.

The computed results (given in [18]) clearly demonstrate the validity and optimality of the developed scheme in comparison with the existing methods.

7. Testing Multiple Hypotheses with Directional Alternatives in Sequential Experiments

Testing a simple basic hypothesis versus composite alternative is a common, well-studied problem in many scientific works [19–26]. In many problems, whether to make a decision in favor of the alternative hypothesis as well as making sense of the direction of difference between parameter values, defined by basic and alternative hypotheses, is important; that is, making a decision whether the parameter outstrips or falls behind the value defined by the basic hypothesis is meaningful [27–33]. Such problems occur, for example, in microarray data analysis, imaging analysis, biological applications and genetic research [32,34] and many others.

For parametrical models, this problem can be stated as

$$H_0:\theta=\theta_0 \quad \text{vs.} \quad H_-:\theta<\theta_0 \quad \text{or} \quad H_+:\theta>\theta_0, \quad (11)$$

where θ is the parameter of the model, θ_0 is known. These alternatives are called skewed or directional alternatives.

In many applications, the case of multiple directional hypotheses is considered, i.e. the testing hypotheses are the following [29,31,33–35]

$$H_i^{(0)}: \theta_i = 0 \;\; vs \;\; H_i^{(-)}: \theta_i < 0 \;\; or \;\; H_i^{(+)}: \theta_i > 0, \;\; i = 1,...,m. \quad (12)$$

where m is the number of individual hypotheses about parameters $\theta_1,...,\theta_m$ *that must be tested by test statistics* $\mathbf{X} = (X_1, X_2,..., X_m)$, *where* $X_i \approx f(x_i \mid \theta_i)$.

The following theorem for hypotheses (11) is proved in [36].

Theorem 4. *Let us assume that the probability distributions* $p(x \mid H_i)$, $i \in \Psi$, *where* $\Psi \equiv \{-,0,+\}$, *are such that, at increasing number of observations* n *in the sample, the entropy concerning distribution parameter* θ*, in relation to which the hypotheses are formulated, decreases. In such case, for given set of hypotheses* H_0, H_- *and* H_+, *there always exists such sample of size* n *on the basis of which decision concerning tested hypotheses can be made with given reliability when Lagrange multipliers are determined for* $n=1$ *in decision making regions and the condition* $mdFDR \le q$ *is satisfied.*

For multiple directional hypotheses (12) the stopping rule is as follows:

$$T = \inf\left\{ n : \bigcap_{i=1}^{m} \left[t_i\left(\mathbf{X^{(1)}}, \mathbf{X^{(2)}},..., \mathbf{X^{(n)}}\right) \in only \;\; one \right] of \;\; \Gamma_j^i, j \in \mathbf{\Psi} \right\},$$

where $\mathbf{X}^{(i)}$, $i = 1,...,n$, are independent m-dimensional observation vectors with correlated parameters; Γ_j^i is j-th hypothesis acceptance region for i-th sub-set of hypothesis.

The following theorem is proved in [36].

Theorem 5. *Let's for each sub-set of directional hypotheses of multiple hypotheses (12) one of the possible stated task of CBM is used with the restriction levels providing the condition* $mdFDR_i \le q_i$, $i = 1,...,m$. *Then, if* q_i, $i = 1,...,m$, *are taken so that* $\sum_{i=1}^{m} q_i = q$, *the following condition* $tmdFDR \le q$ *is fulfilled.*

Here $tmdFDR$ is the total mixed directional false discovery rate that was introduced in [36].

8. Testing Composite Hypotheses Concerning Normal Distribution with Equal Parameters

In a large variety of practical situations, a normal distribution with equal parameters, that is $N(\theta,\theta)$, may be postulated as a useful model for data [37–39].

Let us consider a random variable X distributed as $N(\theta,\theta)$. The problem is to test the hypotheses

$$H_0: \theta = \theta_0, \;\; \theta_0 > 0 \;\; \text{vs.} \;\; H_-: 0 < \theta < \theta_0 \;\; \text{or} \;\; H_+: \theta > \theta_0, \quad (13)$$

on the basis of *independent identically distributed* (i.i.d.) random variables $X_1, X_2,..., X_n$.

The following theorems for directional alternatives were proved in [36].

Theorem 6. *CBM 7, at satisfying a condition* $\dfrac{r_7^- + r_7^+}{K_1 \cdot P_{\min}} = q$ (i.e. $r_7^- + r_7^+ = q \cdot K_1 \cdot P_{\min}$), *where* $0 < q < 1$, $P_{\min} = \min\{p(H_-), p(H_0), p(H_+)\}$, *ensures a decision rule with* $mdFDR$ (i.e. *with* $SERR_{III}$) *less or equal to* q, i.e. *with the condition* $mdFDR = SERR_{III} \le q$.

Theorem 7. *CBM 7, at satisfying a condition* $\dfrac{r_7^- + r_7^0 + r_7^+}{K_1 \cdot P_{\min}} = q$ (i.e. $r_7^- + r_7^0 + r_7^+ = q \cdot K_1 \cdot P_{\min}$), *where* $0 < q < 1$, $P_{\min} = \min\{p(H_-), p(H_0), p(H_+)\}$, *ensures a decision rule with* $mdFDR + FAR$ *less or equal to* q, i.e. *with the condition* $mdFDR + FAR \le q$.

Here, we have: $FAR = P(x \in \Gamma_0 \mid H_-) + P(x \in \Gamma_0 \mid H_+)$ as the false acceptance rate; r_7^-, r_7^0, r_7^+ are restriction levels in CBM 7; K_1 is the loss for incorrect acceptance of hypothesis.

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Moreover, the following theorems are proven in [39].

Theorem 8. *CBM 2, for hypotheses (12), ensures a decision rule with the error rates of the Type-I and Type-II restricted by the following inequalities*

$$\alpha \le \frac{r_2^0}{K_0 \cdot p(H_0)},$$

$$\beta \le \frac{r_2^-}{K_0 \cdot p(H_-)} + \frac{r_2^+}{K_0 \cdot p(H_+)}. \quad (14)$$

Theorem 9. *CBM 2, for hypotheses (12), ensures a decision rule with r_δ the averaged loss of incorrectly accepted hypotheses and α_s the averaged loss of incorrectly rejected hypotheses restricted by the following inequalities*

$$r_\delta \le \frac{K_1}{K_0}\left[r_2^- + r_2^0 + r_2^+\right],$$

$$\alpha_s \le r_2^- + r_2^0 + r_2^+. \quad (15)$$

Correctness of these theorems and superiority of CBM over Bayes method are clearly demonstrated by computation results.

9. Testing Equi-Correlation Coefficient

Symmetric Multivariate Normal Distribution (SMND) is widely used in many applications of different spheres of human activities such as psychology, education, genetics and so on [40]. It is also used extensively in statistical inference procedures, e.g., in analysis of variance (ANOVA) for modeling of the error part [41].

Let the k-dimensional random vector X follow the k-variate normal distribution with zero mean vector and correlation matrix W of the following structure:

$$W = (1-\rho)\cdot I_{k\times k} + \rho \cdot J_{k\times k}, \quad (16)$$

where $I_{k\times k}$ is an identity matrix and $J_{k\times k}$ is matrix of ones.

The support of ρ, $(-1/(k-1),1)$ assures the non-singularity of the correlation matrix W [41].

The problem, we want to solve, can be formulated as follows: to test

$$H_0 : \rho = \rho_0 \text{ vs. } H_- : -1/(k-1) < \rho < \rho_0 \text{ or } H_+ : \rho_0 < \rho < 1, \quad (17)$$

$$\rho, \rho_0 \in \left(-1/(k-1),1\right).$$

on the basis of the sample $Y_1,\dots,Y_n$. Here Y_i is the Helmert orthogonal transformation $Y_1, Y_2, \dots$ on uncorrelated multivariate normal vectors sequence $X_1, X_2, \dots$, i.e. $Y_i = H \cdot X_i$, $i = 1,2,\dots,$ where H is the Helmert matrix given as [41]

$$H=\begin{bmatrix} \frac{1}{\sqrt{k}} & \frac{1}{\sqrt{k}} & \frac{1}{\sqrt{k}} & & \cdots & \frac{1}{\sqrt{k}} \\ \frac{1}{\sqrt{2}} & -\frac{1}{\sqrt{2}} & 0 & & \cdots & 0 \\ \frac{1}{\sqrt{6}} & \frac{1}{\sqrt{6}} & -\frac{2}{\sqrt{6}} & 0 & \cdots & 0 \\ \cdots\cdots & \cdots\cdots & \cdots\cdots & \cdots\cdots & \cdots\cdots & \cdots\cdots \\ \frac{1}{\sqrt{k(k-1)}} & \cdots & \frac{1}{\sqrt{k(k-1)}} & & & -\frac{(k-1)}{\sqrt{k(k-1)}} \end{bmatrix}. \quad (18)$$

i.e. Y_i is k-dimensional random vector with independent components each of which has zero mean and variances determined by

$$v_1=1+(k-1)\rho \text{ and } v_2=\ldots=v_k=1-\rho. \quad (19)$$

The probability density function (pdf) of Y_i is

$$p(Y_i\mid\rho)=(2\pi)^{-\frac{k}{2}}|V|^{-\frac{1}{2}}\cdot\exp\left\{-\frac{1}{2}Y_i\cdot V^{-1}\cdot Y_i^T\right\},\quad i=1,\ldots,n. \quad (20)$$

The joint pdf of the sample $Y_1,\ldots,Y_n$ has the following form [42]

$$p(Y_1,\ldots,Y_n\mid\rho)=(2\pi)^{-kn/2}\cdot|V|^{-\frac{n}{2}}\cdot\exp\left\{-\frac{1}{2}\sum_{i=1}^{n}Y_i\cdot V^{-1}\cdot Y_i^T\right\}=$$

$$=(2\pi)^{-kn/2}(1+(k-1)\rho)^{-\frac{n}{2}}(1-\rho)^{-\frac{n(k-1)}{2}}\cdot\exp\left\{-\frac{1}{2}\left(\frac{V_{1n}}{1+(k-1)\rho}+\frac{V_{2n}}{1-\rho}\right)\right\}, \quad (21)$$

where V_{1n} and V_{2n} are defined by ratio

$$V_{1n}=\sum\nolimits_{i=1}^{n}y_{i1}^2 \text{ and } V_{2n}=\sum\nolimits_{i=1}^{n}\sum\nolimits_{j=2}^{k}y_{ij}^2, \quad (22)$$

where $Y_i=(y_{i1},y_{i2},\ldots,y_{ik})$, $i=1,\ldots,n$.

To test hypotheses (17) were applied CBM using the maximum likelihood estimation and Stein's approach [43]. Simulation results showed that CBM using Stein's approach gives opportunities to make decisions with higher reliability for testing (17) hypotheses then Bayes method (see Figure 1).

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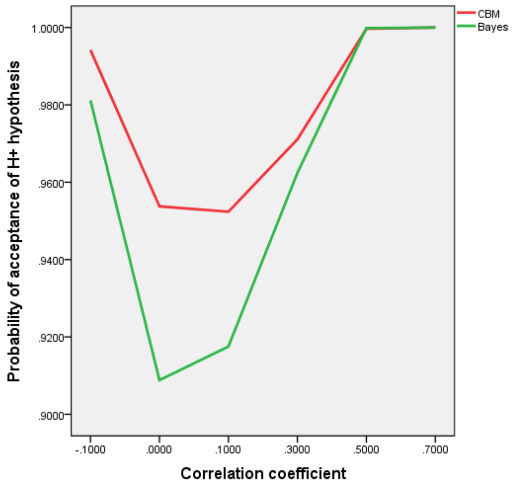

Figure 1. Dependence of true Hypothesis H_+ acceptance probability on correlation coefficient.

The samples for making decisions are generated by (21) with $\rho \in (\rho_0, 1)$ for the size $m = 5000$.

10. Solving ANOVA Problem with Restricted Type I and Type II Error Rates

The problem of comparing the means of several normally distributed random variables attracted researchers' attention from the middle of last century. Such problems arise in many practical applications. For example, at comparing treatment effects in clinical trials, or experimental studies at comparing effects of different experiments, or at comparing the failure rate of a machine with its ages [44]. Also, an important question in many applications is whether the nonparametric time trends are all the same [45]. In the framework of ANOVA, the problem can be formulated as follows [46]. Let's consider k normal populations $N(\mu_i, \sigma_i^2)$, $i = 1, \ldots, k$. Let $X_{i1}, \ldots, X_{in_i}$ be a random sample from $N(\mu_i, \sigma_i^2)$, independent from each other. The problem is to test hypotheses

$$H_0 : \mu_1 = \ldots = \mu_k \quad \text{vs.} \quad H_a : \mu_i \neq \mu_j \quad \text{for some} \quad i \neq j. \quad (23)$$

In some studies the researcher may believe before observing the data that the true means are simply ordered ($\mu_1 \leq \ldots \leq \mu_k$). For example, the treatment means may be a sequences of increasing dose levels of a drug. In this case ANOVA takes the form

$$H_0 : \mu_1 = \ldots = \mu_k \quad \text{vs.} \quad H_a : \mu_1 \leq \ldots \leq \mu_k, \quad (24)$$

with at least one strict inequality. This statement has received considerable attention in the statistical literature (see, for example, [46–50]).

The simplest case $k = 2$, i.e. the case with only two normal populations, called as the Behrens-Fisher problem, is well studied. For its solution, at the statement (23), a simple and accurate method is introduced in [51,52] which gives good results in both cases when variances are equal or are not. For arbitrary case, when $k > 2$ a compact but quite good review of the existed methods of solving the problem (23) is given in [53], on the basis of which there is concluded that a procedure that gives satisfactory results by Type I error rate for all sample sizes, large k and parameters configurations does not exist [53,54].

For the statement (24), a one-sided studentized range test is offered in Hayter [48]. It provides simultaneous one-sided lower confidence bounds for the ordered pairwise comparisons $\mu_i - \mu_j$, $1 \leq j < i \leq k$. Similar inference procedures are discussed in many works.

Without loss of generality, we can suppose that all μ_i ($i=1,...,k$) are positive, because if this condition is not fulfilled, we can always achieve it by moving the origin.

Let us rewrite hypotheses (23) as follows

$H_0:\theta_1=\theta_2=...=\theta_{k-1}=0$ vs. $H_a:\theta_i\neq 0$, for some $i\in(1,...,k-1)$, (25)

where $\theta_i=\mu_{i+1}-\mu_i$, $i=1,...,k-1$. In this case, hypotheses (24) take the form

$H_0:\theta_1=\theta_2=...=\theta_{k-1}=0$ vs. $H_a:\theta_i\geq 0$, with at least one strict inequality, (26)

Using the concept of directional hypotheses [5], hypotheses (25) can be considered as a set of directional hypotheses

$$H_0^i:\theta_i=0 \text{ vs. } H_-^i:\theta_i<0 \text{ or } H_+^i:\theta_i>0,\ i=1,...,k-1. \quad (27)$$

Statement (27) allows us to test hypotheses (23) and (24) (which are the same as hypotheses (25) and (26)) simultaneously, using techniques developed in [6,36]. In particular: after testing hypotheses (27), if for even one value of i, left sided hypothesis is accepted among accepted alternatives, accept alternative hypothesis in (25), if all the accepted alternative hypotheses are right sided – accept alternative hypothesis in (26), otherwise accept the null hypothesis.

To test a subset of individual hypotheses of (27) the following hypothesis was proven.

Theorem 10. *CBM 7, at satisfying a condition* $(r_7^-+r_7^+)/(K_1\cdot p(H_0))=q$, *where* $0<q<1$, *ensures a decision rule with Type I error rate less or equal to* q, i.e. *with the condition* $TIER\leq q$.

For testing multiple directional hypotheses (27), the concept of the $tmdFDR$ was used

$$tmdFDR=\sum\nolimits_{i=1}^{k-1} mdFDR_i. \quad (28)$$

To provide a level q for the total Type I error rate ($TTIER$) and for the total Type II error rate ($TTIIER$), we provide q_i, the level of the appropriate criteria for the i th subset of the individual directional hypotheses. As a result, we have

$$TTIER=\sum\nolimits_{i=1}^{k-1} TIER_i \text{ and } TTIIER=\sum\nolimits_{i=1}^{k-1} TIIER_i \quad (29)$$

where $TIER_i$ and $TIIER_i$ are the Type I error rate and the Type II error rate, respectively, of the i th subset of directional hypotheses [18,36].

The values of q_i in all three cases (for $tmdFDR$, for $TTIER$ and for $TTIIER$) can be chosen to be equal, i.e. $q_i=q/(k-1)$ or different, e.g. inversely proportional to the informational distances between the tested hypotheses in the subsets of directional hypotheses [36].

The offered method of solving ANOVA problem, for known and unknown variances of observation results, with restricted Type I and Type II error rates based on CBM gives very reliable results that surpass the existing methods for today. The latter is confirmed by the calculation results of practical examples by simulating different scenarios [44].

The offered method is a sequential one that requires a set of observations to make a decision.

11. Conclusion

A brief review of the application of CBM to test different types of statistical hypotheses arising in many practical problems are considered above. It confirms the advantage of the CBM over existing classical methods at testing simple, composite, asymmetric, multiple hypotheses of different kinds. Obtained results, published in many important scientific publication, confirm the flexibility of the method and its great ability to deal with difficult problems.

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Abbreviations

The following abbreviations are used in this manuscript:

CBM	Constrained Bayesian method
FAR	False acceptance rate
pdFAR	Pure directional false discovery rate
mdFAR	Mixed directional false discovery rate
FWERI	Family-wise error rates of type I
FWERII	Family-wise error rates of type II
SR	Summary risk
tmdFAR	Total mixed directional false discovery rate
i.i.d.	Independent identically distributed
SMND	Symmetric Multivariate Normal Distribution
ANOVA	Analysis of variance
TTIER	Total Type I error rate
TTIIER	Total Type II error rate

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