

# Testing Statistical Hypotheses with Given Reliability



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By

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# TABLE OF CONTENTS

Preface .....	ix
Introduction .....	1
Chapter 1 .....	6
Hypotheses Testing Methods	
1.1. Existed Basic Parallel Methods of Hypotheses Testing.....	6
1.1.1. The Fisher's $p$ -test.....	6
1.1.2. The Newman-Pearson's frequentist test .....	6
1.1.3. The Jeffreys Bayesian approach.....	7
1.1.3.1. General loss function .....	9
1.1.3.2. Stepwise loss function .....	10
1.1.4. The Berger's conditional test.....	12
1.2. Sequential Tests .....	14
1.2.1. The Wald's Method.....	14
1.2.2. The Bayes' Method .....	15
1.2.3. The Berger's Method.....	15
1.3. Constrained Bayesian Methods (CBM) of Hypotheses Testing...	16
1.4. The Method of Sequential Analysis of Bayesian Type.....	20
Chapter 2 .....	23
Constrained Bayesian Method for Testing Different Type of Hypotheses	
2.1. General Statement of Constrained Bayesian Method.....	23
2.1.1. Restrictions on the averaged probability of acceptance of true hypotheses (Task 1).....	23
2.1.2. Restrictions on the conditional probabilities of acceptance of true hypotheses (Task 2).....	25
2.1.3. Restrictions on the conditional probabilities of acceptance of each true hypothesis (Task 2 <sup>1</sup> ).....	27
2.1.4. Restrictions on posterior probabilities of acceptance of true hypotheses (Task 3).....	29
2.1.5. Restriction on the averaged probability of rejection of true hypotheses (Task 4).....	30
2.1.6. Restrictions on the conditional probabilities of rejection of each true hypothesis (Task 5).....	32

2.1.7. Restrictions on a posteriori probabilities of rejection of each true hypothesis (Task 6).....	33
2.1.8. Restrictions on probabilities of rejection of true hypothesis (Task 6 <sup>1</sup> ) .....	34
2.1.9. Restrictions on posterior probability of rejected true hypotheses (Task 7).....	35
2.2. Directional Hypotheses Testing Methods .....	36
2.3. CBM for Testing Directional Hypotheses Restricted False Discovery Rates .....	49
2.3.1. Restrictions on the averaged probability of acceptance of true hypotheses for testing directional hypotheses (Task 1) ....	50
2.3.2. Restrictions on the conditional probabilities of acceptance of each true hypothesis for testing directional hypotheses (Task 2).....	55
2.3.3. Restrictions on the averaged probability of rejection of true hypotheses for testing directional hypotheses (Task 4) .....	56
2.3.4. Restrictions on the conditional probabilities of rejection of each true hypothesis for testing directional hypotheses (Task 5).....	58
2.3.5. Restrictions on posterior probabilities of rejected true hypotheses for testing directional hypotheses (Task 7) .....	63
2.4. CBM for Testing Multiple Hypotheses with Directional Alternatives in Sequential Experiments .....	66
2.4.1. CBM for testing multiple directional hypotheses .....	68
2.4.1.1. A sequential test for multiple directional hypotheses ...	70
2.5. Application of CBM to Union-Intersection and Intersection-Union Hypotheses Testing Problems .....	75
2.5.1. Statement of the problem .....	77
2.5.2. General solution of the stated problem.....	79
2.5.2.1. Another loss function.....	83
2.5.3. Examples .....	86
2.6. Quasi-Optimal Rule of Testing Directional Hypotheses and Its Application to Big Data.....	92
2.6.1. Quasi-optimal approach of testing the hypotheses .....	94
2.6.2. Testing multiple directional hypotheses .....	100
2.7. CBM for Testing Hypotheses Concerning Parameters of Normal Distribution with Equal Mathematical Expectation and Variance ...	102
2.7.1. Statement of the problem .....	105
2.7.1.1. Estimation of the parameter .....	106
2.7.2. Testing Hypotheses (2.169).....	107
2.7.2.1. The maximum ratio test.....	107

2.7.2.2. Stein's method .....	108
2.7.3. CBM for testing hypotheses (2.169) at conditional distributions (2.189).....	113
2.7.4. Testing hypotheses (2.175) at conditional distributions (2.176) using CBM 2 .....	116
2.8. Constrained Bayesian Method for testing Equi-Correlation Coefficient of a Standard Symmetric Multivariate Normal Distribution .....	121
2.8.1. Introduction .....	121
2.8.2. Statement of the problem .....	123
2.8.3. Testing (2.221) hypotheses.....	126
2.8.3.1. The maximum ratio test.....	126
2.8.3.2. Stein's approach.....	127
2.8.4. CBM for testing (2.224) hypotheses .....	128
2.8.5. Evolution of CBM 2 for testing (2.224) hypotheses.....	132
2.8.5.1. Using the maximum ratio estimation.....	132
2.8.5.2. Using the Stein's approach .....	135
Chapter 3 .....	138
Comparison Analysis Hypotheses Testing Methods	
3.1. Comparison of CBM with the frequentist and the Bayes methods .....	138
3.2. Comparison of Hypotheses Testing in Parallel Experiments .....	140
3.3. Comparison of Hypotheses Testing in Sequential Experiments .....	165
3.4. Comparison of the Directional Hypotheses Testing Methods.....	178
3.4.1. CBM for the normally distributed directional hypotheses... ..	179
3.4.1.1. Determination of the Lagrange multiplier .....	181
3.4.2. Computation results.....	183
3.4.2.1. Discussion.....	189
Chapter 4 .....	195
Experimental Investigations	
4.1. Simulation results of Directional Hypotheses at Restriction of False Discovery Rates.....	195
4.1.1. Computation results for the normally distributed directional hypotheses .....	197
4.1.2. Discussion of the obtained results .....	203
4.2. Simulation results of Multiple Hypotheses with Directional Alternatives in Sequential Experiments .....	205
4.2.1. Computation results.....	206
4.2.2. Discussion of the obtained results .....	213

4.3. Simulation results of Union-Intersection and Intersection-Union Hypotheses .....	214
4.3.1. Calculations for concrete examples .....	214
4.3.2. Computational results.....	219
4.3.3. Discussion of the obtained results .....	237
4.4. Consideration of the normal distribution for Quasi-Optimal Rule of Testing directional hypotheses.....	238
4.4.1. Computation results.....	240
4.4.2. Discussion of the obtained results .....	264
4.5. Computation results for Testing Composite Hypotheses Concerning Normal Distribution with Equal Parameters .....	265
4.5.1. Maximum Likelihood method.....	265
4.5.2. Computation results obtained by Stein's Method.....	268
4.6. Simulation results of testing Equi-Correlation Coefficient of a Standard Symmetric Multivariate Normal Distribution .....	290
4.6.1. Computation results.....	290
4.6.2. Discussion of the obtained results .....	292
Appendix A1 .....	308
Algorithm of computation of (2.251) distribution function	
Appendix A2 .....	310
The Kullback–Leibler divergence between the distributions corresponding to the basic and alternative hypotheses	
References .....	313



## PREFACE

It is difficult to overestimate the role and place of one of the main fields of mathematical statistics, hypothesis testing, in both theoretical and applied statistics. There are many theoretical and applied works dedicated to solving this problem, the number of which is increasing every day. Among them, based on contemporary research, my 2018 book is worth noting, the logical continuation of which is this book (Kachiashvili, 2018a). In particular, the results of the further development of the CBM for many types of interesting and practically useful hypotheses and comparison results with the existing basic methods are given there (Fisher, 1925; Neyman and Pearson, 1928, 1933; Jeffreys, 1939; Wald, 1947a, b; Berger, 2003). A brief description of the discussed methods is given in the first chapter. The second chapter provides optimal and quasi-optimal methods for testing individual and multiple directional hypotheses for parallel and sequential experiments using CBM; Also, the general forms of presentation of statistical hypotheses in the form of their intersection-union and union-intersection and optimal decision-making methods for such formulation using CBM are discussed; hypothesis testing methods using CBM for normal distribution with equal parameters and for equi-correlation coefficient of standard symmetric multivariate normal distribution are considered. The next chapter shows the advantage of CBM compared to existing classical methods in terms of the reliability of the made decisions and the minimization of required information (sample size). The fourth chapter presents the results of the experimental investigation of the developed methods, which clearly

confirm the validity of the obtained theoretical results and the conclusions made on their basis.

In our opinion, the work will be interesting and useful for both professional and beginner researchers and practitioners of many fields, who are interested in the theoretical and practical issues of the considered direction of mathematical statistics, namely, in statistical hypothesis testing. It will also be very useful for specialists of different directions for solving suitable problems at the appropriate level, because the book discusses in detail many practically important problems and provides detailed algorithms for their solution, the direct use of which does not represent much difficulty.

# INTRODUCTION

A statistical hypothesis is a formalized record of properties of the investigated phenomenon and relevant assumptions. Statistical hypotheses are set when random factors affect the investigated phenomena, i.e., when the observation results of the investigated phenomena are random. The properties of the investigated phenomenon are completely defined by its probability distribution law. Therefore, the statistical hypothesis is an assumption concerning this or that property of the probability distribution law of a random variable. Mathematical statistics is the set of methods for studying the events caused by random variability and estimates the measures (the probabilities) of possibility of occurrence of these events. For this reason, parametrical methods of hypotheses testing directly use distribution laws and non-parametrical methods use not distribution laws but only the properties of these laws. Practically all methods of mathematical statistics one way or another, in different doses, use hypotheses testing techniques. Therefore, it is very difficult to overestimate the meaning of the methods of statistical hypotheses testing in the theory and practice of mathematical statistics (Kachiashvili, 2019, 2022).

A lot of investigations are dedicated to the statistical hypotheses testing theory and practice (see, for example, Berger, 1985, 2003; Berger et al., 1994; Bernardo and Rueda, 2002; Christensen, 2005; Hubbard and Bayarri, 2003; Lehmann, 1993, 1997; Moreno and Giron, 2006; Moreno and Martínez, 2022; Mei and Jiang, 2022; Wolpert, 1996; Zou et al., 2022) and their number increase steadily. But, despite this, there are only three

following basic ideas (philosophies) of hypotheses testing at parallel experiments: the Fisher, the Neyman-Pearson and the Jeffreys (Fisher, 1925; Neyman and Pearson, 1928, 1933; Jeffreys, 1939). They use different ideas for testing hypotheses but all of them are identical in one aspect: they all necessarily accept one of the stated hypotheses in making decisions, despite the existence or absence of enough information for decision making with given reliability. The considered methods have well known positive and negative sides (Kachiashvili, 2022). All other existing methods are the particular cases of these approaches taking into account the peculiarities of the concrete problems and adapting to these specificities for increasing the reliability of the decision (see, for example, Berger and Wolpert, 1988; Berger et al., 1994; Bernardo, 1980; Delampady and Berger, 1990; Kiefer, 1977; Bansal and Sheng, 2010; Bansal and Miescke, 2013; Bansal et al., 2016).

The essences of these methods are discussed below. Fisher considered only one hypothetical distribution and on the basis of the observation results was making a decision concerning its correctness (see Item 2.1). A question that Fisher did not raise was the origin of his test statistics: Why these rather than some others? This is the question that Neyman and Pearson considered (Neyman & Pearson, 1928, 1933). Their solution involved not only the hypothesis but also a class of possible alternatives and the probabilities of two kinds of errors (see Item 2.2): false rejection (Error I) and false acceptance (Error II) (Lehmann, 1993). The “best” test was the one that minimized the probability of an alternative at validity of the basic hypothesis (Error II) subject to a bound on probability of the basic hypothesis at validity of the alternative (Error I). The latter is the significance level of the test. To the requirements of the Neyman-Pearson experiment, Jeffrey added a priori probabilities and loss function, using

which he defined a risk function as averaged losses and by minimizing the risk function, hypotheses acceptance regions are defined (see Item 2.3).

An attempt to reconcile the different points of view of noted philosophies was made in (Berger, 2003), and as a result there was offered a new, compromise  $T^*$  method of testing (see Item 2.4). The method uses the Fisher's  $p$ -value criterion for making a decision, the Neyman-Pearson's statement (using basic and alternative hypotheses) and Jeffrey's formulae for computing the Type I and Type II conditional error probabilities for every observation result  $x$  on the basis of which the decision is made.

A new approach (philosophy) to the statistical hypotheses testing, called Constrained Bayesian Methods (CBM), was comparatively recently developed (Kachiashvili, 1989, 2003, 2011, 2014a, b, 2015, 2016, 2018a, b; Kachiashvili et al. 2012a, b, c; Kachiashvili and Mueed, 2013; Kachiashvili et al., 2018; Kachiashvili, 2021) (see Item 1.4). This method differs from the traditional Bayesian approach with a risk function split into two parts, reflecting risks for incorrect rejection and incorrect acceptance of hypotheses and stating the risk minimization problem as a constrained optimization problem when one of the risk components is restricted and the another one is minimized. It generates data-dependent measures of evidence with regard to the level of restriction. In spite of absolutely different motivations of introduction of  $T^*$  and CBM, they lead to the hypotheses acceptance regions with identical properties in principle. Namely, despite the classical cases when the observation space is divided into two complementary sub-spaces for acceptance and rejection of tested hypotheses, here the observation space contains the regions for making the decision and the regions for no-making the decision (see, for example, Berger, 2003; Kachiashvili et al., 2012a; Kachiashvili et al. 2012b;

Kachiashvili and Mueed, 2013; Kachiashvili, 2018a). Though, for CBM, the situation is more differentiated than for  $T^*$ . For CBM, the regions for not making the decision are divided into the regions of impossibility of making the decision and the regions of impossibility of making a unique decision. In the first case, the impossibility of making the decision is equivalent to the impossibility of making the decision with given probability of the error for a given observation result, and it becomes possible when the probability of the error decreases. In the second case, it is impossible to make a unique decision when the probability of the error is required to be small, and it is unattainable for the given observation result. By increasing the error probability, it becomes possible to make a decision.

In our opinion, these properties of  $T^*$  and CBM are very interesting and useful. They bring the statistical hypotheses testing rule much closer to the everyday decision-making rule when, at shortage of necessary information, acceptance of one of made suppositions is not compulsory.

The specific features of hypotheses testing regions of the Berger's  $T^*$  test and CBM, namely, the existence of the no-decision region in the  $T^*$  test and the existence of regions of impossibility of making a unique or any decision in CBM give the opportunities to develop the sequential tests on their basis (Berger et al., 1994; Kachiashvili and Hashmi, 2010; Kachiashvili, 2015, 2018a). The sequential test was introduced by Wald in the middle of forty of last century (Wald, 1947a, b). Since Wald's pioneering works, a lot of different investigations were dedicated to the sequential analysis problems (see, for example, Berger and Wolpert, 1984; Ghosh, 1970; Ghosh and Sen, 1991; Siegmund, 1985) and efforts to the development of this approach constantly increase as it has many important

advantages in comparison with the parallel methods (Tartakovsky et al., 2015).

Application of CBM to different types of hypotheses (two and many simple, composite, directional and multiple hypotheses) with parallel and sequential experiments showed the advantage and uniqueness of the method in comparison with existing ones (Kachiashvili, 2014a, b, 2015, 2016, 2018a, b; Kachiashvili et al., 2018). The advantage of the method is the optimality of made decisions with guaranteed reliability and minimality of necessary observations for given reliability. CBM uses not only loss functions and a priori probabilities for making decisions as the classical Bayesian rule does, but also a significance level as the frequentist method does. The combination of these opportunities improves the quality of made decisions in CBM in comparison with other methods. This fact has been confirmed many times by application of CBM to the solution of different practical problems (Kachiashvili, 2018a, 2019a, b; Kachiashvili et al., 2012c; Kachiashvili and Melikdzhanian, 2006; Kachiashvili et al., 2007; Kachiashvili et al., 2008; Kachiashvili et al., 2009; Kachiashvili et al., 2012b; Kachiashvili and Prangishvili, 2018; Kachiashvili et al., 2019; Kachiashvili et al., 2020).

# CHAPTER 1

## HYPOTHESES TESTING METHODS

### 1.1. Existed Basic Parallel Methods of Hypotheses Testing

#### 1.1.1. The Fisher's $p$ -test

Let us suppose that the observation result  $X \sim f(x|\theta)$ , where  $f(x|\theta)$  is the probability distribution density of  $X$  at hypothesis  $H$  and it is necessary to test hypothesis  $H_0:\theta=\theta_0$ . Let us choose the test statistics  $T=t(X)$  such that large values of  $T$  reflects evidence against  $H_0$ . After computing the  $p$ -value  $p=P(t(X)\geq t(x)|H_0)$ , where  $t(x)$  is a value of the statistics  $t(X)$ , computed by sample  $x$ , hypothesis  $H_0$  will be rejected if  $p$  is small (Kachiashvili, 2014b).

Some methods of generalization of this approach for multiple hypotheses can be found in (Kachiashvili, 2018a).

#### 1.1.2. The Newman-Pearson's frequentist test

For the Neyman-Pearson (N-P) criterion for testing a null hypothesis  $H_0:\theta=\theta_0$ , it is necessary to form some alternative hypothesis, for instance,  $H_A:\theta=\theta_A$ ,  $\theta_A>\theta_0$ . The null hypothesis rejection region has the form  $T\geq c$  and otherwise it is accepted. Here  $c$  is the critical value defined from the condition  $\alpha=P(T\geq c|H_0)$ . Quantity  $\alpha$  is the Type I error



probability, while the Type II error probability is calculated as  $\beta = P(T < c | H_A)$  (Kachiashvili, 2014b, 2018a).

Generalization of this method for many (more than two) hypotheses is given by generalized Neyman-Pearson lemma (Rao, 2006) but its application in practice is quite problematic.

### 1.1.3. The Jeffreys Bayesian approach

The general statement of the Bayes Method (the Jeffrey's Method) for arbitrary number of hypotheses is the following.

Let the sample  $x^T = (x_1, \dots, x_n)$  be generated from  $p(x; \theta)$ , and the problem of interest is to test  $H_i : \theta_i \in \Theta_i$ ,  $i = 1, 2, \dots, S$ , where  $\Theta_i \subset R^m$ ,  $i = 1, 2, \dots, S$ , are disjoint subsets with  $\bigcup \Theta_i = R^m$ . The number of tested hypotheses is  $S$ . Let the prior on  $\theta$  be denoted by  $\sum_{i=1}^S \pi(\theta | H_i) p(H_i)$ , where for each  $i = 1, 2, \dots, S$ ,  $p(H_i)$  is the a priori probability of hypothesis  $H_i$  and  $\pi(\theta | H_i)$  is a prior density with support  $\Theta_i$ ;  $p(x | H_i)$  denotes the marginal density of  $x$  given  $H_i$ , i.e.,  $p(x | H_i) = \int_{\Theta_i} p(x | \theta) \pi(\theta | H_i) d\theta$  and  $D = \{d\}$  is the set of solutions, where  $d = \{d_1, \dots, d_S\}$ , it being so that

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

$\delta(x) = \{\delta_1(x), \delta_2(x), \dots, \delta_S(x)\}$  is the decision function that associates each observation vector  $x$  with a certain decision

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

$\Gamma_j$  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  $\Gamma_j$  regions, i.e.

$$\delta(x) = \{\Gamma_1, \Gamma_2, \dots, \Gamma_S\}.$$

Let us introduce loss function  $L(H_i, \delta(x))$  which determines the value of loss in the case when the sample has the probability distribution corresponding to hypothesis  $H_i$ , but, because of random errors, decision  $\delta(x)$  is made.

Making the decision that hypothesis  $H_i$  is true, in reality true could be one of the hypotheses  $H_1, \dots, H_{i-1}, H_{i+1}, \dots, H_S$ , i.e. accepting one of the hypothesis, we risk to reject one of  $(S-1)$  really true hypotheses. This risk is called the risk corresponding to the hypothesis  $H_i$ , and is equal to (Berger, 1985; Kachiashvili, 2003)

$$\rho(H_i, \delta) = \int_{R^n} L(H_i, \delta(x)) p(x | H_i) dx.$$

A complete risk for any decision rule  $\delta(x)$ , i.e. the risk of making an incorrect decision, is characterized by the function:

$$r_\delta = \sum_{i=1}^S \rho(H_i, \delta) p(H_i) = \sum_{i=1}^S p(H_i) \int_{R^n} L(H_i, \delta(x)) p(x | H_i) dx, \quad (1.1)$$

which is called risk function.

Decision rule  $\delta^*(x)$  or, what is the same,  $\Gamma_i^*$ ,  $i = 1, \dots, S$  - the regions of acceptance of hypotheses  $H_i$ ,  $i = 1, \dots, S$ , is called a Bayes rule if there takes place:

$$r_{\delta^*} = \min_{\{\delta(x)\}} r_{\delta} \quad (1.2)$$

Its solutions for general and stepwise loss functions are given below.

### 1.1.3.1. General loss function

In the general case, the loss function  $L(H_i, \delta(x))$  consists of two components:

$$L(H_i, \delta(x)) = \sum_{j=1}^S L_1(H_i, \delta_j(x) = 1) + \sum_{j=1}^S L_2(H_i, \delta_j(x) = 0), \quad (1.3)$$

i.e. loss function  $L(H_i, \delta(x))$  is the total loss of incorrectly accepted and incorrectly rejected hypotheses.

Taking into account (1.3), the solution of the problem (1.2) can be written down in the following form (Berger, 1985; Kachiashvili, 2003):

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

$$j = 1, \dots, S. \quad (1.4)$$

Let us suppose that the losses are the same within the acceptance and rejection regions and introduce denotations  $L_1(H_i, H_j)$  and  $L_2(H_i, H_j)$  for incorrect acceptance of  $H_i$  when  $H_j$  is true and incorrect rejection of  $H_i$  in favor of  $H_j$ . Then it is possible to rewrite the risk function (1.1) as follows (Kachiashvili, 1989, 2003):

$$r_{\delta} = \sum_{j=1}^S \sum_{i=1, i \neq j}^S L(H_i, H_j) p(H_i) \int_{\Gamma_j} p(x | H_i) dx, \quad (1.5)$$

and condition (1.4) takes the form

$$\Gamma_j = \left\{ x : \sum_{i=1}^S L_1(H_i, H_j) p(H_i | x) < \sum_{i=1}^S L_2(H_i, H_k) p(H_i | x); \right. \\ \left. \forall k : k \in (1, \dots, j-1, j+1, \dots, S) \right\}, j = 1, \dots, S. \quad (1.6)$$

*Example 1.1.* Let us consider the case when the number of hypotheses equals two. Then risk function (1.5) is

$$r_\delta = L(H_1, H_2) p(H_1) \int_{\Gamma_2} p(x | H_1) dx + \\ L(H_2, H_1) p(H_2) \int_{\Gamma_1} p(x | H_2) dx, \quad (1.7)$$

and hypotheses acceptance regions (1.6) take the form

$$\Gamma_1 = \left\{ x : L_1(H_1, H_1) p(H_1) p(x | H_1) + \right. \\ \left. + L_1(H_2, H_1) p(H_2) p(x | H_2) < \right. \\ \left. < L_2(H_1, H_2) p(H_1) p(x | H_1) + L_2(H_2, H_2) p(H_2) p(x | H_2) \right\}, \\ \Gamma_2 = \left\{ x : L_1(H_1, H_2) p(H_1) p(x | H_1) + \right. \\ \left. + L_1(H_2, H_2) p(H_2) p(x | H_2) < \right. \\ \left. < L_2(H_1, H_1) p(H_1) p(x | H_1) + L_2(H_2, H_1) p(H_2) p(x | H_2) \right\}. \quad (1.8)$$

### 1.1.3.2. Stepwise loss function

Let us suppose that the losses for incorrectly accepted hypotheses are identical, while those for correctly-made decisions are equal to zero, i.e.

$$L(H_i, H_j) = \begin{cases} C & \text{at } i \neq j, \\ 0 & \text{at } i = j. \end{cases} \quad (1.9)$$

In this case, risk function (1.5) takes the form (Kachiashvili, 1989, 2003; Duda et al., 2006; Sage and Melse, 1972):

$$r_\delta = C \cdot \left( 1 - \sum_{i=1}^S p(H_i) \int_{\Gamma_i} p(x | H_i) dx \right). \quad (1.10)$$

The minimum in (1.10) is achieved by solving the problem:

$$\max_{\{\Gamma_i\}} \sum_{i=1}^S p(H_i) \int_{\Gamma_i} p(x | H_i) dx. \quad (1.11)$$

It is evident, that we can consider  $C = 1$  without limiting the generality.

It is not difficult to be persuaded that the solution of problem (1.11) has the following form:

$$\begin{aligned} \Gamma_i &= \{x : p(H_i)p(x | H_i) > p(H_j)p(x | H_j)\}; \\ \forall j : j &\in (1, \dots, i-1, i+1, \dots, S)\}. \end{aligned} \quad (1.12)$$

Let us denote:

$$\begin{aligned} \Gamma_{ij} &= \{x : p(H_i)p(x | H_i) > p(H_j)p(x | H_j)\} = \\ &= \left\{ x : \frac{p(x | H_i)}{p(H_i)} > \frac{p(x | H_j)}{p(H_j)} \right\}. \end{aligned} \quad (1.13)$$

Then

$$\Gamma_i = \bigcap_{j=1, j \neq i}^S \Gamma_{ij}.$$

*Example 1.2.* For stepwise loss functions (1.9), hypotheses acceptance regions (1.12) at testing two hypotheses are the following

$$\begin{aligned} \Gamma_1 &= \{x : p(H_1)p(x | H_1) > p(H_2)p(x | H_2)\}, \\ \Gamma_2 &= \{x : p(H_2)p(x | H_2) > p(H_1)p(x | H_1)\}. \end{aligned} \quad (1.14)$$

An attempt to reconcile the different points of view of noted philosophies was made in (Berger, 2003), and as a result there was offered a new, compromise  $T^*$  method of testing. The method uses the Fisher's  $p$ -value criterion for making a decision, the Neyman-Pearson's statement (using basic and alternative hypotheses) and Jeffrey's formulae for computing the Type I and Type II conditional error probabilities for every observation result  $x$  on the basis of which the decision is made.

#### 1.1.4. The Berger's conditional test

The conditional test  $T^C$  is the following

$$T^C = \begin{cases} \text{if } B(x) \leq c_0, \text{ reject } H_0 \text{ and report} \\ \text{conditional error probability (CEP)} \\ \alpha(x) = \frac{B(x)}{1+B(x)}, \\ \text{if } B(x) > c_0, \text{ accept } H_0 \text{ and} \\ \text{report CEP } \beta(x) = \frac{1}{1+B(x)}, \end{cases}$$

where  $B(x)$  is the likelihood ratio, and  $c_0$  is the minimax critical value defined as

$$P(B(x) < c | H_0) = 1 - P(B(x) < c | H_1). \quad (1.15)$$

The modified conditional test  $T^*$  consists in the following

$$T^* = \begin{cases} \text{if } B(x) \leq r, \text{ reject } H_0 \text{ and report} \\ \text{conditional error probability (CEP)} \\ \alpha(B(x)) = B(x)/(1+B(x)); \\ \text{if } r < B(x) < a \text{ make no decision,} \\ \text{if } B(x) \geq a, \text{ accept } H_0 \text{ and report} \\ \text{CEP } \beta(x) = 1/(1+B(x)), \end{cases}$$

where  $B(x) = p(x|H_0)/p(x|H_A)$  is the likelihood ratio and  $a$  and  $r$  are defined as follows

$$\begin{aligned} r &= 1 \text{ and } a = F_0^{-1}(1 - F_A(1)) \text{ if } F_0(1) \leq 1 - F_A(1), \\ r &= F_A^{-1}(1 - F_0(1)) \text{ and } a = 1 \text{ if } F_0(1) > 1 - F_A(1), \end{aligned} \quad (1.16)$$

where  $F_0$  and  $F_A$  are the cumulative distribution functions (c.d.f.) of  $B(X)$  under  $p(x|H_0)$  and  $p(x|H_A)$ , respectively.

As was mentioned in (Dass and Berger, 2003, p. 196), “ $T^*$  is an actual frequentist test; the reported CEPs,  $\alpha(B(\mathbf{x}))$  and  $\beta(B(\mathbf{x}))$ , are conditional frequentist Type I and Type II error probabilities, conditional on the statistic we use to measure strength of evidence in the data. Furthermore,  $\alpha(B(\mathbf{x}))$  and  $\beta(B(\mathbf{x}))$  will be seen to have the Bayesian interpretation of being (objective) posterior probabilities of  $H_0$  and  $H_A$ , respectively. Thus,  $T^*$  is simultaneously a conditional frequentist and a Bayesian test.” Generalization of the  $T^*$  test for any number of hypotheses seems quite problematic. For the general case, it is possible only by simulation because the definition of exact distribution of  $B(\mathbf{x})$  likelihood ratio for arbitrary hypothetical distributions is very difficult if not impossible.

## 1.2. Sequential Tests

### 1.2.1. The Wald's method

The sequential test was introduced by Wald in the mid-forties of last century (Wald, 1947a, b). The essence of the Wald's sequential test consists in the following: compute the likelihood ratio  $B(x) = p(x_1, x_2, \dots, x_n | H_0) / p(x_1, x_2, \dots, x_n | H_A)$  for  $n$  sequentially obtained observation results, and, if

$$B < B(x) < A,$$

do not make the decision and continue the observation of the random variable. If

$$B(x) \geq A,$$

accept the hypothesis  $H_0$  on the basis of  $n$  observation results. If

$$B(x) \leq B,$$

accept the hypothesis  $H_A$  on the basis of  $n$  observation results.

The thresholds  $A$  and  $B$  are chosen so that

$$A = \frac{1 - \beta}{\alpha} \quad \text{and} \quad B = \frac{\beta}{1 - \alpha}.$$

Here  $\alpha$  and  $\beta$  are the desirable values of the error probabilities of Types I and II, respectively.

It is proved (Wald, 1947a) that in this case the real values of the error probabilities of Types I and II are close enough to the desired values, but still are distinguished from them.

Since Wald's pioneer works, a lot of different investigations were dedicated to the sequential analysis problems (see, for example, Ghosh, 1970; Siegmund, 1985; Kachiashvili, 2018a) and efforts to the development of this approach constantly increase as it has many important advantages in



comparison with the parallel methods (see, for example, Tartakovsky et al., 2015).

### 1.2.2. The Bayes' method

Concerning the Bayesian sequential methods, the following is written in Berger (1985): “While Bayesian analysis in fixed sample size problems is straightforward (robustness consideration aside), Bayesian sequential analysis is very difficult” (p. 442). The idea of sequential Bayesian procedure consists in computation of the Bayes risk function for every stage of obtained observation result and its comparison with expected posterior Bayes risk that will be obtained if more observations are taken. If the posterior Bayes risk is greater than the Bayes risk function, to stop experimentation and to make decision, otherwise to continue experimentation.

The readers, interested in details of sequential Bayesian method, can refer to the following sources (Berger, 1985; Arrow et al., 1949; Ghosh and Sen, 1991).

### 1.2.3. The Berger's method

The sequential test developed on the basis of  $T^*$  test is as follows (Berger et al., 1994):

if the likelihood ratio  $B(x) \leq r$ , reject  $H_0$  and report the conditional error probability  $\alpha(B(x)) = B(x)/(1 + B(x))$ ;

if  $r < B(x) < a$ , make no decision and the observations continue;

if  $B(x) \geq a$ , accept  $H_0$  and report the conditional error probability  $\beta(B(x)) = 1/(1 + B(x))$ .

Here  $r$  and  $a$  are determined by ratios (1.16).

### 1.3. Constrained Bayesian Methods (CBM) of Hypotheses Testing

A new approach (philosophy) to the statistical hypotheses testing, called Constrained Bayesian Methods (CBM), was comparatively recently developed (Kachiashvili, 2003, 2011, 2014a,b, 2015, 2016, 2018a,b; Kachiashvili et al., 2012a,bc; Kachiashvili and Mueed, 2013; Kachiashvili et al., 2018). This method differs from the traditional Bayesian approach with a risk function split into two parts, reflecting risks for incorrect rejection and incorrect acceptance of hypotheses and stating the risk minimization problem as a constrained optimization problem when one of the risk components is restricted and the another one is minimized. It generates data-dependent measures of evidence with regard to the level of restriction. In spite of absolutely different motivations of introduction of  $T^*$  and CBM, they lead to the hypotheses acceptance regions with identical properties in principle. Namely, in despite of the classical cases when the observation space is divided into two complementary sub-spaces for acceptance and rejection of tested hypotheses, here the observation space contains the regions for making the decision and the regions for no-making the decision (see, for example, Berger, 2003; Kachiashvili, 2018a; Kachiashvili et al., 2012a; Kachiashvili et al., 2012b; Kachiashvili and Mueed, 2013). Though, for CBM, the situation is more differentiated than for  $T^*$ . For CBM the regions for no-making the decision are divided into the regions of impossibility of making the decision and the regions of impossibility of making unique decision. In the first case, the impossibility of making the decision is equivalent to the impossibility of making the

decision with given probability of the error for a given observation result, and it becomes possible when the probability of the error decreases. In the second case, it is impossible to make a unique decision when the probability of the error is required to be small, and it is unattainable for the given observation result. By increasing the error probability, it becomes possible to make a decision.

It is possible to formulate nine different statements of CBM depending on what type of restrictions is desired which is determined by the aim of the practical problem that must be solved (Kachiashvili, 2011, 2018a; Kachiashvili et al., 2012b). They are (see chapter 2): 1) Restrictions on the averaged probability of acceptance of true hypotheses (Task 1); 2) Restrictions on the conditional probabilities of acceptance of true hypotheses (Task 2); 3) Restrictions on the conditional probabilities of acceptance of each true hypothesis (Task 2<sup>1</sup>); 4) Restrictions on posterior probabilities of acceptance of true hypotheses (Task 3); 5) Restrictions on the averaged probability of rejection of true hypotheses (Task 4); 6) Restrictions on the conditional probabilities of rejection of each true hypothesis (Task 5); 7) Restrictions on a posteriori probabilities of rejection of each true hypothesis (Task 6); 8) Restrictions on probabilities of rejection of true hypothesis (Task 6<sup>1</sup>); 9) Restrictions on posterior probability of rejected true hypotheses (Task 7).

Let us introduce Task 1, as an example, for a demonstration of the specificity of CBM. In this case, we have to minimize the averaged loss of incorrectly accepted hypotheses

$$r_{\delta} = \min_{\{\Gamma_j\}} \left\{ \sum_{i=1}^S p(H_i) \sum_{j=1}^S \int_{\Gamma_j} L_1(H_i, \delta_j(x) = 1) p(x | H_i) dx \right\}, \quad (1.17)$$

subject to the averaged loss of incorrectly rejected hypotheses

$$\begin{aligned}
& \sum_{i=1}^S p(H_i) \sum_{j=1}^S \int_{R^n - \Gamma_j} L_2(H_i, \delta_j(x) = 0) p(x | H_i) dx = \\
& = \sum_{i=1}^S p(H_i) \sum_{j=1}^S \int_{R^n} L_2(H_i, \delta_j(x) = 0) p(x | H_i) dx - \\
& - \sum_{i=1}^S p(H_i) \sum_{j=1}^S \int_{\Gamma_j} L_2(H_i, \delta_j(x) = 0) p(x | H_i) dx \leq r_1. \quad (1.18)
\end{aligned}$$

where  $r_1$  is some real number determining the level of the averaged loss of incorrectly rejected hypotheses.

By solving problem (1.17), (1.18), we have

$$\begin{aligned}
\Gamma_j = & \left\{ x : \sum_{i=1}^S L_1(H_i, \delta_j(x) = 1) p(H_i) p(x | H_i) < \right. \\
& \left. < \lambda \sum_{i=1}^S L_2(H_i, \delta_j(x) = 0) p(H_i) p(x | H_i) \right\}, \\
& j = 1, \dots, S, \quad (1.19)
\end{aligned}$$

where Lagrange multiplier  $\lambda$  ( $\lambda > 0$ ) is defined so that in (1.18) the equality takes place.

*Example 1.3.* Let us consider stepwise losses

$$\begin{aligned}
L_1(H_i, \delta_j(x) = 1) & = \begin{cases} 0 & \text{at } i = j, \\ 1 & \text{at } i \neq j, \end{cases} \\
L_2(H_i, \delta_j(x) = 0) & = \begin{cases} 0 & \text{at } i \neq j, \\ 1 & \text{at } i = j. \end{cases} \quad (1.20)
\end{aligned}$$

Then problem (1.17), (1.18) transforms

$$r_\delta = \min_{\{\Gamma_j\}} \left\{ \sum_{i=1}^S p(H_i) \sum_{j=1, j \neq i}^S \int_{\Gamma_j} p(x | H_i) dx \right\}, \quad (1.21)$$

subject to

$$1 - \sum_{i=1}^S p(H_i) \int_{\Gamma_i} p(x | H_i) dx \leq r_1, \quad (1.22)$$

and hypotheses acceptance regions (1.19) take the form (Kachiashvili, 2013).

$$\Gamma_j = \left\{ x : \sum_{i=1, i \neq j}^S p(H_i) p(x | H_i) < \lambda p(H_j) p(x | H_j) \right\},$$

$$j = 1, \dots, S. \quad (1.23)$$

When number of hypotheses  $S=2$  statement of the problem and its solution are

$$r_\delta = \min_{\{\Gamma_1, \Gamma_2\}} \left\{ p(H_1) \int_{\Gamma_2} p(x | H_1) dx + p(H_2) \int_{\Gamma_1} p(x | H_2) dx \right\}, \quad (1.24)$$

$$p(H_1) \int_{\Gamma_1} p(x | H_1) dx + p(H_2) \int_{\Gamma_2} p(x | H_2) dx \geq 1 - r_1, \quad (1.25)$$

$$\Gamma_1 = \left\{ x : p(H_2) p(x | H_2) < \lambda p(H_1) p(x | H_1) \right\},$$

$$\Gamma_2 = \left\{ x : p(H_1) p(x | H_1) < \lambda p(H_2) p(x | H_2) \right\}, \quad (1.26)$$

In our opinion, the mentioned properties of  $T^*$  and CBM are very interesting and useful. They bring the statistical hypotheses testing rule much close to the everyday decision-making rule when, at shortage of necessary information, acceptance of one of made suppositions is not compulsory.

The specific features of hypotheses testing regions of the Berger's  $T^*$  test and CBM, namely, the existence of the no-decision region in the  $T^*$  test and the existence of regions of impossibility of making a unique or any decision in CBM give the opportunities to develop the sequential tests on

their basis (Berger et al., 1994; Kachiashvili, 2018a; Kachiashvili, 2015; Kachiashvili and Hashmi, 2010).

#### 1.4. The Method of Sequential Analysis of Bayesian Type

Let us suppose that there is an opportunity to obtain repeated observations. To introduce the method of sequential analysis for an arbitrary number of hypotheses on the basis of constrained Bayesian task, let us use the denotations introduced by (Wald, 1947a). Let  $R_m^n$  be the sampling space of all possible samples of  $m$  independent  $n$ -dimensional observation vectors  $\mathbf{x} = (x_1, \dots, x_n)$ . Let us split  $R_m^n$  into  $S+1$  disjoint sub-regions  $R_{m,1}^n, R_{m,2}^n, \dots, R_{m,S}^n, R_{m,S+1}^n$  such that  $R_m^n = \bigcup_{i=1}^{S+1} R_{m,i}^n$ . Let  $p(\mathbf{x}^1, \dots, \mathbf{x}^m | H_i)$  be the total probability distribution density of  $m$  independent  $n$ -dimensional observation vectors;  $m$  is the sample size. Then  $p(\mathbf{x}^1, \dots, \mathbf{x}^m | H_i) = p(\mathbf{x}^1 | H_i) \dots p(\mathbf{x}^m | H_i)$ .

Let us determine the following decision rule (Kachiashvili, 2014a, 2018a; Kachiashvili and Hashmi, 2010). If the matrix of observation results  $\mathbf{x} = (\mathbf{x}^1, \dots, \mathbf{x}^m)$  belongs to the sub-region  $R_{m,i}^n, i = 1, \dots, S$ , then hypothesis  $H_i$  is accepted and, if  $\mathbf{x} = (\mathbf{x}^1, \dots, \mathbf{x}^m)$  belongs to the sub-region  $R_{m,S+1}^n$ , the decision is not made and the observations continue until one of the tested hypotheses is accepted.

Regions  $R_{m,i}^n, i = 1, \dots, S+1$ , are determined in the following way:  $R_{m,i}^n, i = 1, \dots, S$ , is such a part of acceptance region  $\Gamma_i^m$  of hypothesis  $H_i$  that does not belong to any other region  $\Gamma_j^m, j = 1, \dots, i-1, i+1, \dots, S$ ;  $R_{m,S+1}^n$  is