# **Automatic Diagnosis of Lung Diseases (Pneumonia, Cancer) with given Reliabilities on the Basis of an Irradiation Images of Patients**

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**Abstract:** The article proposes algorithms for the automatic diagnosis of human lung diseases pneumonia and cancer, based on images obtained by radiation irradiation, which allow us to make decisions with the necessary reliability, that is, to restrict the probabilities of making possible errors to a pre-planned level. Since the information obtained from the observation is random, Wald's sequential analysis method and Constrained Bayesian Method (CBM) of statistical hypothesis testing are used for making a decision, which allow us to restrict both types of possible errors. Both methods have been investigated using statistical simulation and real data, which fully confirmed the correctness of theoretical reasoning and the ability to make decisions with the required reliability using artificial intelligence. The advantage of CBM compared to Wald's method is shown, which is expressed in the relative scarcity of observation results needed to make a decision with the same reliability. The possibility of implementing the proposed method in modern computerized X-ray equipment due to its simplicity and promptness of decision-making is also shown.

**Keywords:** Automatic diagnosis, lung diseases, pneumonia, cancer, making decision, simulation, artificial intelligence.

## **1. INTRODUCTION**

Making a diagnosis of the disease is the initial and very important stage of the treatment of a sick person, the correctness of which greatly depends on the successful completion of the subsequent stages of treatment. Accurate and timely diagnosis practically (with high probability) ensures the cure of the patient's disease. The diagnosis is made based on the examination of the patient's condition by the doctor. Examination of the condition involves blood, urine and other analyzes of the patient, as well as observation of various organs, which can be done by many different methods, including the use of X-rays and radiation. Based on the results of the observation, the doctor of the relevant profile makes a decision about the presence or absence of the disease. The correctness of the decision depends greatly on the qualification and experience of the doctor. Different doctors can make different decisions on the same data. A misdiagnosis can lead to a disastrous outcome with high probability. In order to avoid such subjective errors and to improve the quality of diagnosis, in recent decades, attempts have been made to use modern computers for diagnosis through machine learning and artificial

intelligence methods (see, for example, [1]). While diagnosing, as well as when making any decision, two types of errors are possible: mistaking a sick person for healthy, and mistaking a healthy person for sick. The correctness of the decision depends greatly on the qualification and experience of the doctor. The results caused by such errors are diametrically (significantly) different from each other. In the second case, after some stress experienced by the patient, on the basis of additional examinations, the real condition of the patient will be established, and in the first case, the result will be fatally disastrous with a high probability. Based on what has been said, the requirements for automatic diagnosis methods are clearly visible. They should minimize possible errors of both types, especially the possibility of errors of the first type.

Among the diseases that exist today, human lung diseases with pneumonia and cancer occupy an important place. "Pneumonia is a form of acute respiratory infection that affects the lungs. The lungs are made up of small sacs called alveoli, which fill with air when a healthy person breathes. When an individual has pneumonia, the alveoli are filled with pus and fluid, which makes breathing painful and limits oxygen intake that can cause the death  $[2]$ . "Cancer is a generic term for a large group of diseases that can affect any part of the body and cause the death. One defining feature of cancer is the rapid creation of

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abnormal cells that grow beyond their usual boundaries, and which can then invade adjoining parts of the body and spread to other organs; the latter process is referred to as metastasis. Widespread metastases are the primary cause of death from cancer" [3]. According to the World Health Organization "Pneumonia is the single largest infectious cause of death in children worldwide. Pneumonia killed 740 180 children under the age of 5 in 2019, accounting for 14% of all deaths of children under 5 years old but 22% of all deaths in children aged 1 to 5 years" [4]. Also "Cancer is a leading cause of death worldwide, accounting for nearly 10 million deaths in 2020, or nearly one in six deaths. The most common cancers are breast, lung, colon and rectum and prostate cancers. Each year, approximately 400 000 children develop cancer. Cancer mortality is reduced when cases are detected and treated early" [5]. Thus, timely correct diagnosis of the presence of the mentioned diseases is a very necessary and important problem.

The article proposes methods of automatic diagnosis of pneumonia and lung cancer, which allow to reduce both types of errors mentioned above to the desired levels. Besides their widespread, these diseases are interrelated as mentioned in the paper [6]: "We found a positive association between incident cancer and risk of death pneumonia in this study. These results imply the possibility that the immunocompromised status and respiratory failure due to antitumor treatment."

Two types of lung cancer are discussed in the paper: adenocarcinoma and carcinoma. "Carcinoma is the most common form of cancer. It starts in the epithelial tissue of your skin or internal organs. Adenocarcinoma is a subtype of carcinoma. It grows in the glands that line the insides of your organs" [7].

To make a decision about the diagnosis of the disease, the observation results extracted from the images obtained by radiation irradiation are used, which, like most of the observation results, contain a random component and, therefore, has a random character. Therefore, statistical hypothesis testing methods are used to make decisions, which allow restricting both types of possible errors. Such methods are Wald's sequential analysis method and constrained Bayesian method [8-10]. It is shown that both methods provide the opportunity to solve the given problem. It is also shown that the constrained Bayesian method, as a rule, requires a relatively small number of observations to make a decision with a given reliability than the Wald method, which is completely consistent with the results obtained earlier by the author of CBM and is its advantage [10-12].

The results of the investigation are distributed in the paper as follows. Materials and Methods are presented in Section 2. The results of the investigation of the applied methods using simulation and real data are given in Section 3. Short discussion and conclusion are offered in Sections 4 and 5, respectively. In Appendices A-I attached to the paper are given the results of processing of experimental data. In particular, Appendices A-E show the results of statistical processing of the data of lung diseases by pneumonia, adenocarcinoma and carcinoma, as well as the results of combined data of both kinds of the cancer. In Appendices F-I are given the results of diagnosis on the basis of the data of pneumonia, adenocarcinoma, carcinoma and the combined data of both kinds of cancer.

## **2. MATERIALS AND METHODS**

## **2.1. Disease Data Acquisition and Preprocessing Results**

Data from lung pneumonia and lung cancer patients, as well as from healthy patients examined by the same method, were obtained from the Internet at the following web addresses under the appropriate names:

- Chest X-Ray Images (Pneumonia) (https://www.kaggle.com/datasets/paultimothymo oney /chest-xray-pneumonia)
- RSNA Pneumonia Detection Challenge (https://www.kaggle.com/competitions/rsnapneumonia-detection-challenge/overview)
- VinBigData Chest X-ray Abnormalities Detection (https://www.kaggle.com/competitions/ vinbigdata-chest-xray-abnormalitiesdetection/data)
- Viral Pneumonia, Normal (https://www.kaggle. com/datasets/pranavraikokte/covid19-imagedataset)
- Chest CT-Scan images Dataset (Cancer) (https://www.kaggle.com/datasets/mohamedh anyyy/chest-ctscan-images)

As it is clear from the indicated addresses, the examination of pneumonia patients was carried out on the basis of X-ray images, and cancer patients - on the

basis of computer tomography (CT) Scan images. At the mentioned addresses, photographs showing the condition of the lungs of the examined patients obtained by appropriate methods are provided. Photos are in black and white format. For the digital representation of visual images, for their further processing, a code was written using the Python programming language, which read the photo using the OpenCV library and displayed the image (information) on it in an Excel file with a certain number of lines and columns, in each cell a number between 0-255 is recorded, which represents the intensity of the corresponding point of the photo image, i.e. pixel intensity value. In order to make a decision about the health status of the patient, the data given under the name Chest X-Ray Images (Pneumonia) of patients suffering from pneumonia were processed using a convolutional neural network (CNN) method [13, 14], which is realized in the programing language Python, under the framework Pytorch. The CNN is a class of artificial neural networks most commonly applied to analyze visual imagery. CNNs use a mathematical operation called convolution in place of general matrix multiplication in at least one of their layers [15]*.* They are specifically designed to process pixel data and are used in image recognition and processing. For learning the network model, the data was distributed as follows: 3900 photos were used for model training, 300 photos for model validation, and 300 photos for model testing. The dimensions of all the photographs used in the practically acceptable time period to make a decision about the final result or the patient's condition were reduced to the standard size  $384$  *pixel*  $\times$  384 *pixel* . Processing such data (training, validation, testing) took about 25 minutes. 93.91% accuracy was achieved on the validation data, and 95% accuracy on the test data. Using the mentioned method, the processing of photo images with initial sizes (the sizes of which, in the case of pneumonia, are significantly larger than 1000 *pixel* !1000 *pixel* for both healthy and diseased patients) is practically impossible without powerful computing resources, because network models take up a lot of space in the computer's RAM, and when a highdimensional photo is added to it, the problem becomes even worse. As a rule, the processing of photos larger than 800 *pixel* × 800 *pixel* dimensions requires quite powerful computing resources, in the absence of which, models of small dimensions are used, which greatly reduces the accuracy of the obtained results.

 It is clear that the level of 95% accuracy of the diagnosis is unacceptable for modern medicine.

Therefore, in order to increase the reliability of the diagnosis, as well as to develop a simple, fast method that can be implemented in modern, computerized Xray equipment, it was decided to use statistical hypothesis testing methods for decision-making, which allow to simultaneously restrict both types of possible errors when making a decision. Such methods are Wald's sequential analysis method and CBM, the essence of which is briefly described in the next paragraph. In order to use the mentioned methods, it is necessary to define a vector representing the state of the objects under investigation (about the state of which a decision must be made), which takes different values depending on the state of the object under investigation. In our case, such a vector turned out to be the dimensions of the patient's photo image represented in pixels, which are equal to the number of rows and columns of the corresponding Excel files. It was found that they take different values for healthy and sick patients and vary randomly from patient to patient.

Appendices A, B, C, and D show the results obtained by processing of the data of pneumonia, adenocarcinoma, carcinoma, and combined data of both types of cancer with the help of statistical package SPSS, while Appendix E shows the results of statistical processing of lung examination data of healthy patients, obtained by CT Scan method. Based on these results, we conclude that for each of these diseases, the two-dimensional random vector corresponding to the dimensions of the patient's state photo is a normally distributed vector with correlated parameters. In particular, in the case of pneumonia, the parameters of the normal distribution for healthy patients, the vector of mathematical expectation and the covariance matrix, are given as

$$
\mu = (\mu_1, \mu_2) = (1811.1923, 1412.9308),
$$
\n
$$
W = \begin{pmatrix} w_{11}, w_{12} \\ w_{21}, w_{22} \end{pmatrix} = \begin{pmatrix} 120850.699, 114569.20 \\ 114569.20, 144827.429 \end{pmatrix},
$$

and for patients suffering from pneumonia –

$$
\mu = (\mu_1, \mu_2) = (1144.60, 788.1538),
$$
\n
$$
W = \begin{pmatrix} w_{11}, w_{12} \\ w_{21}, w_{22} \end{pmatrix} = \begin{pmatrix} 51120.211, 45821.4796 \\ 45821.4796, 51735.682 \end{pmatrix}.
$$

For patients with carcinoma, we have:

$$
\mu = (407.4846, 269.6385), \ W = \begin{pmatrix} 667.911, 384.875 \\ 384.875, 1673.861 \end{pmatrix}.
$$

For the combined data of both types of cancer, we have:

$$
\mu = (401.0615, 265.1538), \ W = \begin{pmatrix} 818.382, 171.3007 \\ 171.3007, 1349.544 \end{pmatrix}.
$$

For healthy patients examined by computer tomography method, we have:

$$
\mu = (632.6, 476.2857), W = \begin{pmatrix} 33007.718, 18500.7969 \\ 18500.7969, 14801.798 \end{pmatrix}.
$$

The number of observation results used for computations for each case are given in the corresponding tables of descriptive statistics results (see appropriate appendices).

#### **2.2. The Methods Used for Making a Decision**

On the basis of the investigation results given in the previous paragraph, the problem of making a decision about the condition of a patient can be formulated as follows. On the basis of the observed values of a random vector  $\xi = (\xi_1, \xi_2) \sim N(\mu, W)$ , where  $\mu$  is the vector of mathematical expectation and *W* is the covariance matrix, must be tested basic hypothesis  $H_0: \mu = \mu_0$ ,  $W = W_0$  vs. alternative one  $H_1: \mu = \mu_A$ ,  $W = W_A$ . Here  $\mu_0$  and  $W_0$  correspond to the supposition that a patient is healthy while  $\mu_A$  and  $W_A$ correspond to a diseased patient. Let us consider the set of sequentially obtained i.i.d. observation results  $x_1, x_2, \ldots, x_n, \ldots$  of a patient concerning of which a decision must be made. A decision must be made in such a way that the probabilities of incorrectly rejected or incorrectly accepted hypotheses, i.e. the Type I and Type II error rates were restricted on the desired levels. For this purpose, let us consider the Wald's test and the method of sequential analysis of Bayesian type (MSABT) [8-10, 12].

#### *2.2.1. The Wald's Test*

The essence of the Wald's sequential test consists in the following [8, 9]: compute the likelihood ratio  $B(x) = p(x_1, x_2, ..., x_n | H_0) / p(x_1, x_2, ..., x_n | H_0)$  for *n* sequentially obtained observation results, and, if

 $B < B(x) < A$ ,

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

 $B(x) \ge A$ ,

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

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

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

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

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

It is proved [8, 9] 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.

## *2.2.2. The Method of Sequential Analysis of Bayesian Type*

Let us consider a set of hypotheses  $H_i$ ,  $i = 1,...,S$  ( $S \ge 2$ ), involving that the random vector *X* is distributed by the law  $p(x, \theta)$ , i.e.  $H_i: X \sim p(x, \theta_i) = p(x | H_i)$ ;  $p(H_i)$  is a priori probability of hypothesis  $H_i$ ;  $\Gamma_i$  is the region of acceptance of  $H_i$  $(\Gamma_i$  belongs to the observation space of random variable *X*, i.e.  $\Gamma_i \in \mathbb{R}^n$ , where *n* is the dimension of the observation vector). The decision is made on the basis of  $\mathbf{x}^T = (x_1, ..., x_n)$ , the measured value of the random vector **X** . It is possible to formulate different constrained tasks of testing the considered hypotheses [10, 12]. Here we consider only one of them, namely the task with restrictions on the averaged probability of rejection of true hypotheses for stepwise loss function with two possible values 0 and 1. The essence of this method is the minimization of the averaged probability of incorrect acceptance of hypotheses at restriction of the averaged probability of rejection of true hypotheses, i.e.

$$
\min_{\{T_i\}} \left\{ 1 - \sum_{i=1}^s p(H_i) P(\mathbf{X} \in \Gamma_i \mid H_i) \right\},\tag{1}
$$

subject to

$$
p(H_i) \sum_{j=1, j \neq i}^{S} P(\mathbf{X} \in \Gamma_j \mid H_i) \le \gamma_i, \ i = 1, ..., S. \tag{2}
$$

Solution of task (1) and (2) is [5]

$$
\Gamma_j = \{ \mathbf{x} : \lambda_j p(H_j) p(\mathbf{x} | H_j) > \sum_{i=1, i \neq j}^{S} p(H_i) p(\mathbf{x} | H_i) \},
$$
  
 
$$
j = 1, ..., S .
$$
 (3)

Coefficient  $\lambda_i$  are determined so that in (2) the equality takes place.

 $B(x) \leq B$ ,

The sequential test developed on the basis of CBM consists in the following [10, 12]. Let  $\varGamma_i^n$  be the  $H_i$ hypothesis acceptance region (3) on the basis of *n* sequentially obtained repeated observation results;  $R_n^m$ is the decision-making space in the sequential method;  $m$  is the dimensionality of the observation vector;  $I_i^n$  is the population of sub-regions of intersections of hypotheses  $H_i$  acceptance regions  $\Gamma_i^n$   $(i=1,...,S)$  with the regions of acceptance of other hypotheses  $H_i$ ,  $j = 1,...,S$ ,  $j \neq i$ ;  $E_n^m = R_n^m - \bigcup_{i=1}^s \Gamma_i^n$ *i*=1  $\bigcup_{i=1}^S \varGamma^n_i$  is the population of regions of space  $R_n^m$  which do not belong to any of hypotheses acceptance regions.

The *Hi* hypotheses acceptance regions for *n* sequentially obtained observation results in the sequential method are:

$$
R_{n,i}^m = \Gamma_i^n / I_i^n, \ i = 1, ..., S ; \qquad (4)
$$

the no-decision region is:

$$
R_{n,S+1}^m = \left(\bigcup_{i=1}^S I_i^n\right) \bigcup E_n^m \tag{5}
$$

where  $\Gamma_i^n$ ,  $i = 1,...,n$ , are defined by (3) on the basis of *n* sequentially obtained observation results.

This test is called *the sequential test of Bayesian type* [10]. Such tests could be considered for all constrained Bayesian methods offered in [10, 12] and differing from each other in restrictions.

When the number of hypotheses is equal to two and their a priori probabilities are equal to  $1/2$ , solution (3) can be rewritten using the Bayes factor:

$$
\Gamma_0: \frac{p(x|H_0)}{p(x|H_A)} > \frac{1}{\lambda_0}, \ \Gamma_A: \frac{p(x|H_0)}{p(x|H_A)} < \lambda_A,
$$

where  $\lambda_0$  and  $\lambda_A$  are determined so that in the conditions (2) equalities take place.

It is worth noting the shortcoming of Wald's method: 1) it is optimal for normal distribution in the limit case when  $n \rightarrow \infty$ ; 2) it is developed for the case of two hypotheses; 3) its generalization for more than two hypotheses is quite problematic. Although this is done using the Bayes approach, its practical implementation is very difficult.

CBM is free from all these drawbacks. It works for hypotheses of any number and dimension (both continuous and discrete distributions), and the complexity of its implementation practically does not changes.

#### **3. RESULTS**

Appendix F presents the results of the diagnosis of lung pneumonia by sequential methods of testing the hypotheses described in the previous paragraph based on the data. Appendices G, H, and I present the results of the sequential methods of testing the hypotheses described in the previous paragraph based on lung cancer disease data. In particular, the results of diagnosis by sequential methods are presented: adenocarcinoma - in Appendix G, carcinoma - in Appendix H, and combined data of adenoma and adenocarcinoma - in Appendix I. The Bayesian decision-making method for all these diseases used the same values of Lagrange multipliers, which are given in Table **1** and calculated for the pneumonia data for different levels of type I and type II errors. In this case, the Kullback-Leibler divergence between the hypotheses to be tested is minimal compared to the cancer diseases discussed in the paper (see Table **2**). The Kullback–Leibler divergence between two multivariate Gaussian distributions is [16]

$$
D_{KL}(p \parallel q) = \frac{1}{2} \left[ \log \frac{|W_q|}{|W_p|} - n + (\mu_p - \mu_q)^T \right] \cdot \left[ W_q^{-1} (\mu_p - \mu_q) + tr \{ W_q^{-1} W_p \} \right].
$$

#### **Table 1: Dependence of Lagrange Multipliers on Type 1 and Type II Error Rates**





It has been proved and shown in papers [10-12] that the Lagrange multipliers in CBM that are calculated to ensure decision making with given reliability for hypotheses with minimum Kullback-Leibler distance, ensure making correct decision with higher reliability when the Kullback-Leibler distance between hypotheses increases.

#### **3.1. Statistical Analysis**

The first tables in Appendices G, H and I show the results obtained with 200,000 data points generated by the distribution parameters corresponding to the observations of healthy and diseased patients given in paragraph 2. The calculation results show that the reliability of diagnosis for healthy and sick patients for each considered case, that is, for each considered restriction of the first and second type error levels, is satisfied both by the Wald criterion and for the decisions made by the MSABT. However, Wald's criterion requires a larger number of observations for each considered case (see Tables **G.2**, **H.2**, **I.2**). Tables **3** and **4** of the same appendices, respectively, show the results of decisions made with real data of sick and healthy patients, which completely match the results obtained by modeling and assure us that with the proposed methods it is possible to automatically diagnose the considered diseases with a predetermined reliability.

The results given in Tables **3** and **4** of the appendices F-I are obtained with real data of different numbers of sick and healthy patients for different diseases. This is due to the limited possibilities of obtaining them from the Internet and in general as well.

For the visibility of the calculation results, the graphical representation of the data of Tables **F.1** and **F.2** are given on Figure **1** and Figure **2** respectively as an example.



**Figure 1:** Dependencies of the reliabilities of made decisions on Type I and Type II error rates.

 $pG0H0 - P(x \in \Gamma_0 | H_0)$ ,  $pGAH0 - P(x \in \Gamma_A | H_0)$ ,  $pG0HA P(x \in \Gamma_0 | H_A)$ , pGAHA -  $P(x \in \Gamma_A | H_A)$ .

#### **4. DISCUSSION**

Both sequential analysis methods of Wald and of Bayesian type give opportunities to diagnose lung pneumonia and lung cancer with given reliabilities. Sequential analysis method of Bayesian type needs comparatively small quantity of observations for diagnosis with given reliability in comparison with Wald's method. It is especially important to emphasize the fact that both sequential analysis methods (of Wald and CBM) require practically negligible time (less than one second) and memory for their implementation in modern computerized X-ray equipment (in contrast to the methods based on modern neural networks mentioned in paragraph 2), which allows their widespread implementation in serial equipment.

## **5. CONCLUSION**

A method of automatic diagnosis of pneumonia and lung cancer with computerized X-ray equipment is proposed, which requires very little memory and time to make a decision. At the same time, both types of possible errors can be limited to predetermined levels with guarantee. The method is based on the method of sequential analysis of Bayesian type of statistical hypothesis testing. The results of the experimental investigation, both on modeled and real data, showed the ease of implementation, high reliability and accuracy of the proposed method of automatic diagnosis. In our opinion, the implementation of the mentioned method in serially produced relevant



**Figure 2:** Percentage distribution of the number of observations necessary for making a decision at different Type I and Type II error rates.

CBM\_H0 - Hypothesis  $H_0$  is true at applying CBM, CBM\_HA - Hypothesis  $H_A$  is true at applying CBM, W\_H0 - Hypothesis  $H_0$ is true at applying Wald's test, W\_HA - Hypothesis  $H_A$  is true at applying Wald's test.

equipment will significantly increase the quality of the diagnosis, which in turn will play a decisive role in the final recovery of the patient. It should be noted here that the implementation of this method in serially produced modern relevant equipment, provided with microprocessor equipment, requires insignificant time and material costs. If necessary, we can provide the relevant computer program implemented on MATLAB to the interested party.

#### **ABBREVIATIONS**

- CBM = Constrained Bayesian Method
- CT = computer tomography
- CNN = convolutional neural network
- MSABT = the method of sequential analysis of Bayesian type

#### **ETHICS APPROVAL**

Not applicable.

### **CONSENT TO PARTICIPATE**

All authors participated in the development of the paper.

#### **HUMAN AND ANIMAL RIGHTS**

All Human and Animal Rights are Reserved.

#### **CONFLICT OF INTEREST**

Not applicable.

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## **APPENDIX A. RESULTS OF STATISTICAL PROCESSING OF DATA SHOWING LUNG PNEUMONIA.**



## Descriptive statistics results

*Note 1*. The first two columns contain the results of processing the quantities of columns (x\_nor\_R) and rows (x\_nor\_L) of the Excel files of healthy patients, and the next two rows contain the same data for patients with pneumonia. The same type of designations are used for other diseases.

## The results of correlation analysis.



\*\*. Correlation is significant at the 0.01 level (2-tailed).



Based on the results of the research, we conclude that the vector representing the patient's condition is distributed according to the two-dimensional normal distribution law with different values of the parameters of healthy and sick patients. From the results of statistical processing presented in Appendices 2, 3 and 4, it is clear that the same conclusion is correct for other cases discussed in the article.

## **APPENDIX B. RESULTS OF STATISTICAL PROCESSING OF DATA SHOWING LUNG ADENOCARCINOMA DISEASE.**

Descriptive statistics results.



The results of correlation analysis.



\*\*Correlation is significant at the 0.01 level (2-tailed).



## **APPENDIX C. RESULTS OF STATISTICAL PROCESSING OF DATA SHOWING LUNG CARCINOMA.**

Descriptive statistics results.



The results of correlation analysis.





## **APPENDIX D. RESULTS OF STATISTICAL PROCESSING OF DISEASE WITH COMBINED DATA OF BOTH TYPES OF LUNG CANCER.**

Descriptive statistics results.



The results of correlation analysis.



\*\*Correlation is significant at the 0.01 level (2-tailed).



## **APPENDIX E. RESULTS OF STATISTICAL PROCESSING OF LUNG EXAMINATION DATA OF HEALTHY PATIENTS BY COMPUTER TOMOGRAPHY OR CT SCAN METHOD.**

Descriptive statistics results.



## The results of correlation analysis



\*\*Correlation is significant at the 0.01 level (2-tailed).



## **APPENDIX F. RESULTS OF DIAGNOSIS BASED ON LUNG PNEUMONIA DATA.**

Results obtained by simulation

## **Table F.1:Decisions Made on the Basis of Simulated Data**













## **Table F.3:Decisions made on the basis of real data of sick patients.**



## **Table F.4:Decisions Made on the Basis of Real Data of Healthy Patients**

## APPENDIX G. **RESULTS OF LUNG ADENOCARCINOMA DIAGNOSIS BASED ON DATA.**







## **Table G.2: Percentage Distribution of the Number of Observations Necessary for Making a Decision**





Ex. 5		82.1430	0	77.6215	U
	2	16.7680	0	20.4780	
	3	1.0610	0	1.8395	0
		0.0280	73.9405	0.0610	
	5	0	25.9510	0	34.6780
	6	0	0.1085	0	63.8665
		0	0	0	1.4555
	8		0	0	

**Table G.3: Decisions Made on the Basis of Real Data of Sick Patients**

Number of patients	Type I error rate	Type II error rate	<b>CBM</b>				Wald			
			Average number of observations necessary for making a decision when $H_A$ is true	Probability οf acceptance of basic hypothesis when alternative hypothesis is true	Probability οf acceptance οf alternative hypothesis when it is true	<b>Number</b> of made decisions	Average number of observations necessary for making a decision when $H_A$ is true	Probability οf acceptance of basic hypothesis when alternative hypothesis is true	Probability οf acceptance οf alternative hypothesis when it is true	<b>Number</b> of made decisions
$\boldsymbol{m}$	$\alpha$	$\beta$	AN	$P(x \in$	$P(x \in$	N	AN	$P(x \in$	$P(x \in$	$\mathbf N$
				$\Gamma_0$   $H_A$ )	$\Gamma_A H_A)$			$\Gamma_0 H_A)$	$\Gamma_A H_A)$	
100	0.05	0.05	$\mathbf{1}$	$\mathbf 0$	$\mathbf{1}$	100	$\mathbf{1}$	$\mathbf 0$	$\mathbf{1}$	100
	0.01	0.01	$\mathbf{1}$	$\mathbf 0$	$\mathbf{1}$	100	$\mathbf{1}$	$\mathbf 0$	$\mathbf{1}$	100
	0.001	0.001	$\overline{2}$	0	$\mathbf{1}$	50	3	0	$\mathbf{1}$	33
	0.0001	0.0001	$\overline{4}$	$\mathbf 0$	$\mathbf{1}$	25	4	0	$\mathbf{1}$	25
	0.00001	0.00001	5	0	$\mathbf{1}$	20	5	0	$\mathbf{1}$	20
196	0.05	0.05	$\mathbf{1}$	$\mathbf 0$	$\mathbf{1}$	196	2	$\mathbf 0$	$\mathbf{1}$	98
	0.01	0.01	$\mathbf{1}$	$\Omega$	$\mathbf{1}$	196	$\overline{c}$	$\Omega$	$\mathbf{1}$	98
	0.001	0.001	$\overline{2}$	$\mathbf 0$	$\mathbf{1}$	98	4	$\mathbf 0$	$\mathbf{1}$	49
	0.0001	0.0001	$\overline{4}$	$\mathbf 0$	$\mathbf{1}$	49	5	$\mathbf 0$	$\mathbf{1}$	39
	0.00001	0.00001	5	$\mathbf 0$	$\mathbf{1}$	39	$\overline{7}$	$\mathbf 0$	$\mathbf{1}$	28
196 (the sequence of observations is changed)	0.05	0.05	$\mathbf{1}$	$\mathbf 0$	$\mathbf{1}$	196	2	0	$\mathbf{1}$	98
	0.01	0.01	$\mathbf{1}$	$\mathbf 0$	$\mathbf{1}$	196	$\overline{2}$	$\mathbf 0$	$\mathbf{1}$	98
	0.001	0.001	$\overline{2}$	0	$\mathbf{1}$	98	3	$\mathbf 0$	$\mathbf{1}$	65
	0.0001	0.0001	3	$\mathbf 0$	$\mathbf{1}$	65	4	$\mathbf 0$	$\mathbf{1}$	49
	0.00001	0.00001	$\overline{4}$	$\mathbf 0$	$\mathbf{1}$	49	5	0	$\mathbf{1}$	39

**Table G.4: Decisions Made on the Basis of Real Data of Healthy Patients**





## **APPENDIX H. RESULTS OF LUNG CARCINOMA DIAGNOSIS BASED ON DATA.**

#### **Table H.1: Decisions Made on the Basis of Simulated Data**

















#### **Table H.3: Decisions Made on the Basis of Real Data of Sick Patients**









## **APPENDIX I. RESULTS OF LUNG ADENOMA AND ADENOCARCINOMA DIAGNOSIS BASED ON COMBINED DATA.**

#### **Table I.1: Decisions Made on the Basis of Simulated Data**



## **Table I.2: Percentage Distribution of the Number of Observations Necessary for Making a Decision**













## **Table I.3: Decisions Made on the Basis of Real Data of Sick Patients**

## **Table I.4: Decisions Made on the Basis of Real Data of Healthy Patients**



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