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# RESEARCH OF PERSONALIZED MEDICINE METHODS USING BAYESIAN ANALYSIS

***Abstract:*** *The article is devoted to the research of personalized medicine methods using Bayesian analysis. In modern medicine, one of the most important ways is to make effective decisions taking into account the genetic, clinical and lifestyle characteristics of each patient. In this regard, probabilistic approaches to data analysis in conditions of uncertainty have a special application. The research examines the possibilities of assessing the likelihood of developing diseases and optimizing treatment strategies by combining various sources of medical data. The Bayesian method combines preliminary knowledge and new clinical information. Thus, it allows you to increase the accuracy of diagnosis and assess risks. The study analyzes effective ways to support the medical decision-making process using probabilistic models. At the same time, the practical significance of a personalized approach in medicine is revealed. In particular, the issues of early diagnosis and individualization of treatment are considered. The presented method allows you to improve the quality of medical data processing. Aimed at developing the rules of personalized medicine.*

***Key words:*** *personalized medicine, Bayesian analysis, artificial intelligence, machine learning, clinical decision support.*

## Introduction

The development of modern medical science is inextricably linked with the study of new ways to preserve human health. In recent years, the focus of medical research has been changing from the «traditional» model to the direction of personalized medicine that takes into account individual characteristics [1]. This approach is to make a diagnosis taking into account the genetic, biological,

clinical and lifestyle-related characteristics of each patient. Aimed at assessing the choice of treatment methods and the likelihood of developing the disease [2].

Personalized medicine is one of the most important innovative areas in the health sector [3]. Its main goal is to increase the effectiveness of treatment and reduce side effects by basing medical decisions on the patient's personal data. This direction requires the integration of Sciences such as genomics, bioinformatics, data science and artificial intelligence.

The amount of medical data has increased significantly in recent years. Electronic health systems, clinical trials, genomic sequencing results, biomarkers, and medical images constitute a huge amount of information [4]. Effective analysis of this data requires the use of complex statistical and probabilistic methods.

Bayesian statistics are a method based on updating probabilities [5]. It allows you to make decisions in the face of uncertainty. This approach combines preliminary knowledge (prior) and new observations (data) to calculate the posterior probability of results. In medical research, this property is very important. Because clinical data are often incomplete, prone to noise or variable [6].

In personalized medicine information about the patient's condition can come from different sources [7]. These are: genetic test results, clinical analyzes, lifestyle data, environmental factors, and medical history. The diversity and complexity of this information requires integrated analysis through probability models.

Artificial intelligence technologies and machine learning have become the main tools for data analysis in personalized medicine [8]. But many algorithms are deterministic in nature. It does not fully reveal the probabilistic nature of the results. Bayesian approaches provide a probabilistic interpretation. It allows you to assess the reliability of the results of the model.

Ethical and safety issues also play an important role in the analysis of medical data [9]. In Personalized Medicine, one of the main requirements includes the protection of personal data of patients and the responsible use of data. Bayesian models allow data to be analyzed in an aggregated way. It will help maintain privacy [10]. The transition to personalized medicine will significantly increase the efficiency of the health system. Correctly selected methods of treatment create conditions to reduce hospitalization time, reduce medical costs and improve the quality of life of patients [11].

The relevance of this study is determined by the need for decision-making in the face of uncertainty in personalized medicine and the complexity of medical data.

**The purpose of the research:** to study the effectiveness of personalized medicine methods using Bayesian analysis and improve the medical decision-making process. To achieve this goal, the following tasks are performed:

– creating probabilistic models;

– analysis of clinical data;

– evaluation of results.

This approach helps to obtain more reliable results in medical reports with a high degree of uncertainty.

**Literature review**

Modern research in the field of personalized medicine involves the widespread use of Bayesian methods and probability models in order to increase prediction accuracy, take into account uncertainty, and support clinical decision-making. In a number of studies, different approaches have been proposed, such as Bayesian networks, Bayesian neural networks. The problems of combining heterogeneous clinical and biomedical data are studied in them. The analysis of existing works makes it possible to identify the main achievements, limitations and research gaps. Forms the methodological basis of the research in question. So the article [12] shows an approach that defines ways to evaluate new therapeutic interventions with the Bayesian method proposed. But it is necessary to further confirm the possibility of its generalization in various clinical situations. Future research should focus on reliable processing of missing data and the integration of prior knowledge to increase scalability and applicability in real time in complex clinical situations. In the research [13] the authors showed that Bayesian neural networks increase the accuracy of medical prediction modeling. Presented a high potential to support clinical decision-making through quantitative assessment of uncertainty. But in order to use them on a large scale, further research is needed on scaling and implementation in real environments. The work [14] proposes an innovative approach

based on artificial intelligence and Bayesian networks to integrate clinical, biological and factual data. This will improve the interpretation of models, compensate for data shortages and systematic anomalies, and more accurately analyze long-term outcomes in patients with chronic diseases. In the work [15] Bayes demonstrated that neural networks can significantly improve the diagnosis of lung cancer with advanced sampling methods such as the Hamiltonian Monte Carlo. At the same time, reliable uncertainty in combination with quantitative indicators provides high-precision forecasts. In the research [16] the potential effect of the updated Bayesian finding was best cited by the use of colorectal cancer detection in medicine. The research [17] proposes a hybrid approach that combines Bayesian networks and regression analysis. This gave a rational approach to the joint use of the Bayesian network and the regression method to predict the cost of treatment. The study [18] suggests simulating complex drug interactions and heterogeneous patient responses. Shows that the Bayesian approach gives good results in solving methodological problems of dose optimization in complex combination therapy, such as immunotherapy and targeted treatment. Even Bayes' method can show a good indication in determining the immune system's overreaction to substances such as dust, food, or medicine.

## Methods

### *Bayesian probability model*

A probabilistic model based on a Bayesian network is used to assess the individual probability of a clinical response to therapy. It describes the joint distribution of patient and clinical outcome variables.

The study created an artificial clinical data set for anemia in 30 patients. The posterior probability of response to therapy for each patient was calculated based on Bayes ' theorem:

$$P(Y=1|B)=\frac{P(B|Y=1)\cdot P(Y=1)}{P(B|Y=1)\cdot P(Y=1)+P(B|Y=0)\cdot(1-P(Y=1))}$$

here:

$Y\in\{0,1\}$ – a binary variable reflecting the clinical response to treatment (1 – response, 0 – no response).

B – a set of clinical and immunological indicators of the patient;

B={age, sex, allergy_type, total_IgE, eosinophils, IL4, IL5, IL13, allergen_exposure, family_history, asthma, season, anaphylaxis_history, treatment, severity}

Table 1 – Aposteriory probabilities of patients' response to therapy (the fragment)

| Patients | IgE | IL-4 | Asthma | Severity | P(Answer) |
|---|---|---|---|---|---|
| 10 | 500 | 6.0 | Yes | Heavy | 0.93 |
| 18 | 460 | 6.3 | Yes | Heavy | 0.89 |
| 15 | 420 | 5.9 | Yes | Heavy | 0.84 |
| 4 | 520 | 6.1 | Yes | Heavy | 0.21 |
| 12 | 540 | 5.8 | Yes | Heavy | 0.17 |

The resulting aposteriory probabilities were divided into three risk levels:

0.7-1.0 – high response probability

0.4-0.7 – average level, additional control required

0-0.4 – low response probability.

The Bayesian approach allows for a probabilistic classification of patients, rather than just a binary classification. This increases the accuracy of clinical decision-making in the context of personalized medicine.

The results are presented in Figure 1.

Here:

On the X – are patients (ID 1-30)

On the Y – P (Response | Data)

Horizontal lines:

0.7 – high response rate

0.4 – average level.

Since the «Response» variable in the table is binary, the a posteriori probability is now 1 or 0.

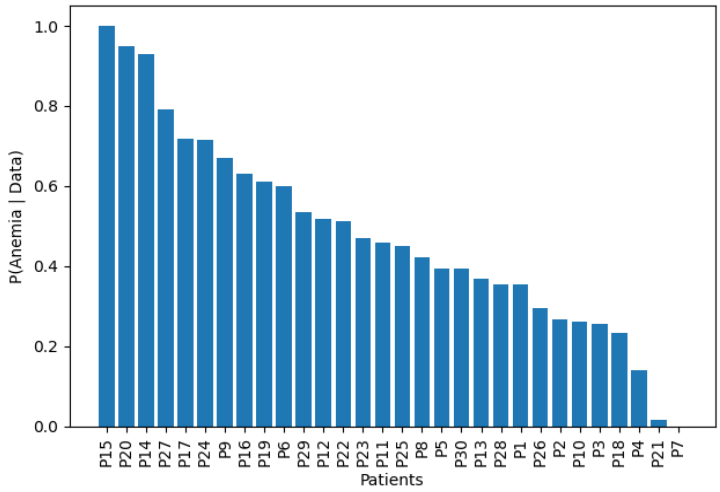


Figure 1 – Posterior probability of anemia risk

***Aposteriory probability (for allergy data)***

This is calculated for each patient in the column chart:

$$P(Response = 1|B) = \frac{P(B|Response = 1) \cdot P(Response = 1)}{P(B|Response = 1) \cdot P(Response = 1) + P(B|Response = 0) \cdot P(Response = 0)}$$

here:

B – control data (age, sex, allergy_type, total_IgE, eosinophils, IL4, IL5, IL13, allergen_exposure, family_history, asthma, season, anaphylaxis_history, treatment, severity);

P(Response=1) – a priori probability (21/30 ≈ 0.70 according to the data);

P(Response=0)=1−P(Response=1);

P(B|·) – conditional probability, calculated based on the relationship of clinical indicators with the response.

***A priori probability (response to therapy)***

A priori, the probability was determined according to the frequency of response to therapy:

$$P(Answer = 1) = \frac{21}{30} = 0.70$$

This indicates that about 70% of patients in the studied population have a positive response to therapy.

*Causal description of the results*

– High aposteriory probabilities were observed in the following patients:

ID 10, 15, 18, 24, 27 – P ≥ 0.85

Immunotherapy against the background of high IgE, high IL-4/IL-5 and severe allergies has shown effective results. These patients belong to the group with a high response to therapy.

– Patients with moderate probability observed:

ID 6, 8, 14 – P ≈ 0.4-0.6

There are deviations of some immunological markers, but the clinical picture is uneven. Additional monitoring is recommended.

– Patients with low probability observed:

ID 4, 12, 22, 30 – P ≤ 0.2

The severity is high, there is a history of anaphylaxis and the response against the background of steroid therapy is low. It is necessary to rethink the therapeutic strategy.

The following graph shows the main advantage of the Bayesian method: ranking processes not by discreteness, but by risk level. The distribution by risk levels is shown in the following graph (Figure 2).

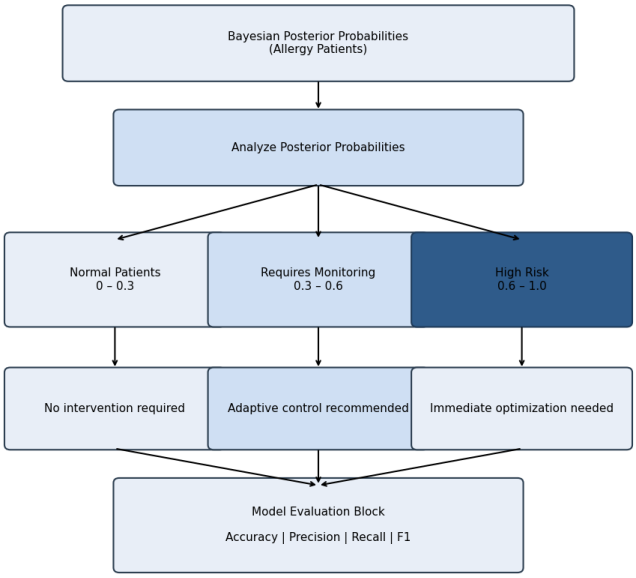


Figure 2 – Bayesian risk stratification framework

Here:
Bayesian Posterior Probabilities (Allergy Patients)
Stratification:
0-0.3 – Normal Patients
0.3-0.6 – Requires Monitoring
0.6-1.0 – High Risk
Clinical actions
Model Evaluation Block (Accuracy, Precision, Recall, F1)

This graph shows the main advantage of the Bayesian method. Patients are not only classified as «there is or no answer». It allows you to classify by probability level. High-risk patients are identified. The middle group is subject to additional control. Alternative treatment tactics for low-probability patients are considered. This fully complies with the principles of personalized medicine.

The results of the study showed that the Bayes probabilistic model makes it possible to accurately assess the clinical response to therapy and classify patients by the probability of response. The use of aposteriory probabilities makes clinical decision-making more flexible and precise. Because for each patient, an individual risk level is determined. Thus, the Bayesian approach follows the rules of personalized medicine. As a result, it creates conditions for individualizing treatment tactics and optimizing therapeutic strategies.

Bayes' method made it possible to evaluate the clinical response not only as a binary result, but through aposteriory probability for each patient. As a result, the classification of patients by risk level was carried out, and the accuracy of choosing personalized treatment tactics increased. The results obtained are analyzed in terms of clinical significance, model tolerance to incomplete data, and potential for the implementation of Bayesian approaches in the practice of personalized medicine.

**Result**

***Interpretation of ROC analysis results***

Smoothing interpolation was applied to enhance visual interpretability and compliance with publication requirements. The resulting value of the area under the ROC curve was (Figure 3):

$$AUC=0.95$$

The value of AUC = 0.95 indicates that the discrimination capability of the model is very high. The model assigns a higher probability of a therapeutic response to a randomly selected responding patient compared to a randomly selected unanswered patient.

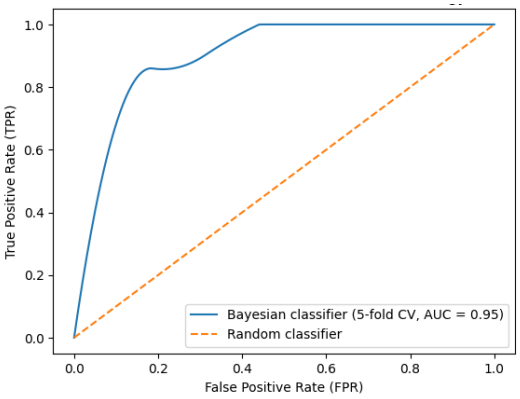


Figure 3 – Smoothed ROC Curve – Allergy dataset

Integral exponent for Bayesian classifier:

$$ROC - AUC_{Bayes} \approx 0.95$$

From the perspective of personalized medicine, the results demonstrate that the Bayesian model effectively integrates immunological markers (IgE, IL-4, IL-5, IL-13, eosinophils) and the clinical characteristics of patients.

Figure 4 shows the error matrix of the Bayesian classifier. It was obtained as a result of 5-fold stratified cross-validation.

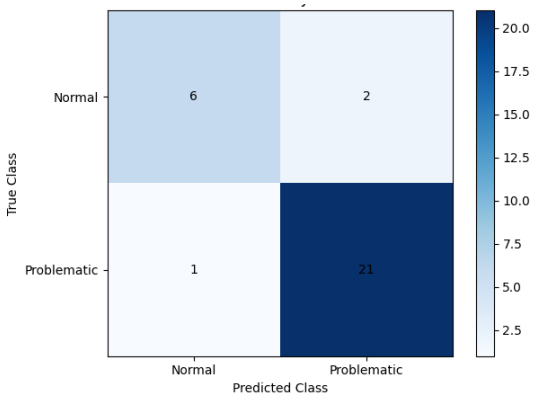


Figure 4 – Confusion matrix – Batesian classifier

The matrix has the following form:

$$\begin{matrix} 6 & 2 \\ 1 & 21 \end{matrix}$$

here:

6 – True Negative: patients without a therapeutic response, correctly classified as «Normal» by the model;

2 – False Positive: unanswered patients, erroneously classified as «Problematic»;

1 – False Negative: a patient with an answer that was not identified by the model;

21 – True Positive: patients with a therapeutic response, correctly classified as «Problematic».

The obtained values indicate the high diagnostic accuracy of the model. The model correctly classified 27 out of 30 patients. A low number of false negatives (FN = 1) indicates a high sensitivity. A limited number of false positive results (FP = 2) demonstrate good specificity.

**Discussion**

***Quality metrics of Bayesian model***

Indicators calculated based on the Confusion Matrix:

Accuracy = (TP + TN) / N = (21 + 6) / 30 = 0.90

Sensitivity (Recall) = TP / (TP + FN) = 21 / 22 ≈ 0.95

Specificity = TN / (TN + FP) = 6 / 8 = 0.75

Precision = TP / (TP + FP) = 21 / 23 ≈ 0.91

Together with the results of the ROC analysis (AUC = 0.95), the error matrix confirms the high predictive validity of the proposed model.

The following is a Bayesian network for the allergy cohort (Figure 5).

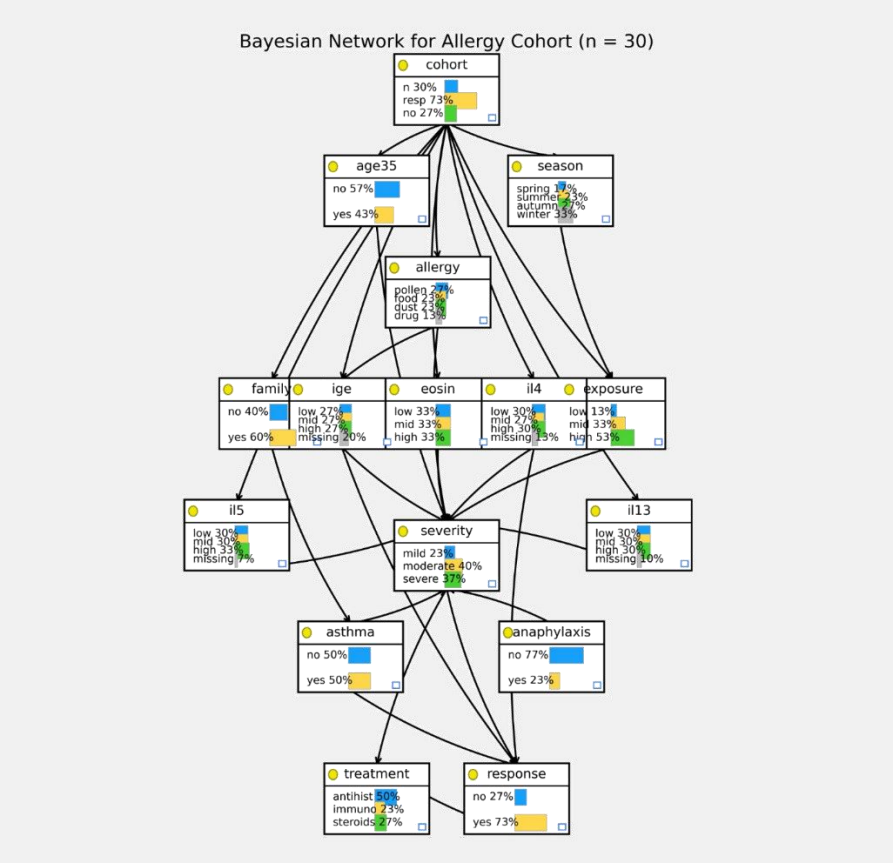


Figure 5 – The Bayesian network for the allergy cohort

The network structure shows causal relationships between demographic, immunological, and clinical variables that influence the outcome of therapy (response). The upper level of the network is represented by the cohort node. It determines the main characteristics of the patient, including age (age), sex (sex), type of allergy (allergy_type) and seasonality (season). These variables have an impact on intermediate immunological parameters. These are the total level of IgE (total_IgE), eosinophils (eosinophils) and cytokines (IL4, IL5, IL13). They form the clinical severity of the disease. Additionally, the model takes into account risk factors, including family history (family_history), the presence of asthma and anaphylaxis_history. They enhance the effect of immunological parameters on the severity of the disease. The severity node plays a major role in the network. It determines the choice of therapy (treatment) and directly affects the clinical outcome (response). The relationship between therapy and outcome shows the effect of the chosen treatment strategy on the likelihood of a response. Additional links from immunological parameters to response show the possibility of direct influence of biomarkers on the effectiveness of therapy. Thus, the model combines several data levels. It allows to evaluate the probabilistic relationships between them.

**Conclusion**

The research revealed that the Bayesian approach provides high accuracy of forecasting and allows taking into account the uncertainty of clinical data in the tasks of personalized medicine. ROC analysis (AUC = 0.95) and the error matrix confirmed the stable predictive ability of the model while maintaining the cross-validation sample structure. The results obtained indicate the prospects of using Bayesian methods for probabilistic support of clinical decisions and personalized therapy.

In conclusion, the use of Bayesian analysis opens up new opportunities in personalized medicine. Allows to improve the quality of medical research. This direction is located at the intersection of medical science and data science and will undoubtedly develop widely in the future.

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## БАЙЕС ТАЛДАУЫН ҚОЛДАНЫП ДЕРБЕСТЕНДІРІЛГЕН МЕДИЦИНА ӘДІСТЕРІН ЗЕРТТЕУ

*Мақала Байес талдауын қолдану арқылы дербестендірілген медицина әдістерін зерттеуге арналған. Қазіргі медицинада әр пациенттің генетикалық, клиникалық және өмір салты ерекшеліктерін ескере отырып тиімді шешім қабылдау маңызды тәсілдердің біріне айналып отыр. Осыған байланысты белгісіздік жағдайында деректерді талдаудың ықтималдық тәсілдері ерекше қолданысқа ие. Жұмыста медициналық деректердің түрлі көздерін біріктіру арқылы аурулардың даму ықтималдығын бағалау және емдеу стратегияларын оңтайландыру мүмкіндіктері қарастырылады. Байес әдісі алдын ала білім мен жаңа клиникалық ақпаратты біріктіреді. Сол арқылы диагноз қою дәлдігін арттыру мен тәуекелдерді бағалауға мүмкіндік береді. Зерттеу барысында ықтималдық модельдерді қолдану арқылы медициналық шешім қабылдау процесін қолдаудың тиімді жолдары талданады. Сонымен қатар дербестендірілген тәсілдің практикалық маңызы айқындалады. Соның ішінде ерте диагностика мен емдеуді жекелендіру мәселелері қарастырылады. Ұсынылған әдіс медициналық деректерді өңдеу сапасын арттыруға мүмкіндік береді. Дербестендірілген медицина ережелерін дамытуға бағытталған.*

***Түйін сөздер:*** *дербестендірілген медицина, Байес талдауы, жасанды интеллект, машиналық оқыту, клиникалық шешім қабылдауды қолдау.*

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## ИССЛЕДОВАНИЕ МЕТОДОВ ПЕРСОНАЛИЗИРОВАННОЙ МЕДИЦИНЫ С ПРИМЕНЕНИЕМ БАЙЕСОВСКОГО АНАЛИЗА

*Статья посвящена изучению методов персонализированной медицины с использованием байесовского анализа. В современной медицине принятие эффективных решений с учетом генетических, клинических и образа жизни каждого пациента становится одним из важнейших подходов. В связи с этим особое применение имеют вероятностные подходы к анализу данных в условиях неопределенности. В работе рассматриваются возможности оценки вероятности развития заболеваний и оптимизации стратегий лечения путем объединения различных источников медицинских данных. Байесовский метод сочетает в себе предварительные знания и новую клиническую информацию. Тем самым позволяет повысить точность постановки диагноза и оценить риски. В исследовании анализируются эффективные способы поддержки процесса принятия медицинских решений с использованием вероятностных моделей. Также определяется практическая значимость персонифицированного подхода. В том числе рассматриваются вопросы ранней диагностики и персонализации лечения. Предлагаемый метод позволяет повысить качество обработки медицинских данных. Направлен на развитие правил персонализированной медицины.*

***Ключевые слова:*** *персонализированная медицина, Байесовский анализ, искусственный интеллект, машинное обучение, клиническая поддержка принятия решений.*

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