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# Personalized Treatment Suggestions Based on Multiple Types of Patient Data

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**Abstract:** ***In the context of rapid progress in precision medicine, personalized drug strategies play a vital role in improving treatment outcomes and reducing the risk of adverse drug reactions. This study developed an AI-based personalized medication recommendation system that integrates electronic medical records, genomic data, and pharmacokinetic parameters. Using deep neural networks and ensemble learning models, the system provides intelligent and accurate recommendations for drug selection and dose adjustment. To improve model interpretability, we introduced feature importance analysis, which significantly enhanced the system's transparency. Prospective validation on real-world clinical datasets shows that the system outperforms traditional rule-based methods and single algorithms in both drug matching accuracy and dose prediction error control. For example, in antihypertensive drug recommendation tasks, the system achieved an accuracy of 91.2%, and the average dosage deviation was controlled within ±8.3%. This research offers a practical technical pathway for implementing AI-based personalized medication systems in clinical settings and shows strong potential for broader clinical use.***

**Keywords:** Personalized medicine; AI-assisted decision-making; Medication recommendation system; Pharmacokinetics; Electronic medical record mining.

## 1. INTRODUCTION

With the continuous advancement of global medical technology, precision medicine has become a core direction in modern medical development [1]. As a key part of precision medicine, personalized medication aims to develop treatment plans tailored to each patient's genetic background, physiological condition, and specific disease features. The goal is to maximize therapeutic benefits while minimizing the risk of side effects. Traditional standardized medication has long dominated clinical practice. However, due to wide individual differences in genetic polymorphisms, metabolism, and disease characteristics, "one-size-fits-all" drug regimens often fail to meet actual treatment needs [2]. For example, in the field of antidepressant therapy, a large-scale, multi-center global study involving over 5,000 patients revealed that 30% to 50% of patients did not respond well to initial medication. [3] Among them, around 20% experienced serious side effects such as excessive sedation and nausea due to inappropriate dosages. More concerning, some studies found that the risk of suicidal behavior increased by about 1.5 times in these patients.

This uncertainty in treatment outcomes not only negatively impacts patients' quality of life but also causes significant waste of medical resources. According to authoritative statistics, irrational medication leads to tens of billions of dollars in additional annual medical costs. A similar situation is found in chemotherapy: patient responses to the same drug vary widely. According to data from the American Society of Clinical Oncology (ASCO), about 40% of breast cancer patients respond poorly to standard chemotherapy [4]. Some cannot complete the treatment due to low drug tolerance, while others continue to show tumor progression even after high-dose treatment. In recent years, artificial intelligence (AI) has brought new opportunities to personalized medication. With strong computing capabilities and effective data processing, AI can analyze large, complex and heterogeneous medical data [5]. From EMRs that contain rich clinical details, to genetic information from genomic data, to pharmacokinetic parameters describing drug movement in the body, AI can extract meaningful features to support decision-making in personalized medication. This study aims to build an AI-powered medication recommendation system by integrating EMRs, genomic data, and pharmacokinetic parameters [6]. The system is designed to assist clinicians with efficient and accurate drug decisions, turning personalized medicine from concept into practice and improving the quality and efficiency of healthcare.

Internationally, many leading research teams and medical institutions are exploring AI in personalized drug therapy. For example, top U.S. medical centers such as Mayo Clinic have applied deep learning to large EMR

datasets, achieving initial success in fields like cardiovascular and neurological diseases [7]. However, challenges remain in integrating EMRs with genomic and pharmacokinetic data due to inconsistent formats, uneven quality, and complex data relationships. These issues limit the accuracy and generalizability of recommendation systems. In one study on cardiovascular drug recommendations, the model achieved 75% accuracy on internal datasets but dropped below 60% on external datasets [8]. European researchers mainly focus on the relationship between genomic data and drug response [9]. They use large-scale genetic testing projects to identify links between gene polymorphisms and drug efficacy or side effects. However, the lack of complete clinical data—especially factors like patient lifestyle or comorbidities—limits real-world applicability. For instance, a European project found certain gene-drug relationships, but in clinical practice, it could provide useful guidance for only about 30% of patients. In China, relevant research has made significant progress in recent years [10]. Some research institutions have used machine learning to predict pharmacokinetic parameters and optimize drug dosage. In clinical antibiotic use, models that consider age, weight, and liver/kidney function have been developed to estimate optimal doses [11]. One study in a top-tier hospital showed that rational antibiotic use increased from 60% to 75% after applying such models [12]. Additionally, some large hospitals have begun using EMRs for disease diagnosis and treatment recommendation [13]. However, the depth and breadth of multi-source data integration still lag behind global standards. There is room for improvement in data integration, model interpretability, and clinical validation to meet the complex demands of real-world practice [14].

The main goal of this study is to develop an AI-based personalized medication recommendation system with high accuracy and strong clinical usability. Specifically, the research includes the following aspects: First, we integrate EMRs, genomic data and pharmacokinetic parameters to build a comprehensive and high-quality patient feature database [15]. By establishing unified data standards, we address differences in data format, semantics, and quality, ensuring consistency and usability. Second, we use deep neural networks and ensemble learning models to analyze the integrated data. Deep neural networks can learn complex patterns from the data, while ensemble learning improves model accuracy and stability by combining results from multiple models. This enables accurate prediction of drug choices and dosage adjustments for individual patients. Third, we introduce advanced feature importance analysis methods, such as SHAP (Shapley Additive Explanations), to assess the contribution of each feature to the recommendation results. This enhances model interpretability and increases clinicians' trust in the recommendations. Finally, we conduct prospective validation using large-scale real clinical datasets to evaluate system performance. Key indicators include drug matching accuracy, dosage prediction error, and clinical usability. These evaluations lay the groundwork for broader clinical adoption of the system.

## 2. METHODS

### 2.1 System Design Framework

The AI-based personalized medication recommendation system developed in this study adopts a layered architecture, which consists of the data layer, model layer and application layer [16]. The data layer is responsible for collecting, storing, and managing multi-source data, including electronic medical records, genomic data, and pharmacokinetic parameters. By designing specific data acquisition interfaces, the system efficiently obtains data from multiple sources, such as hospital information systems and genetic testing platforms. The collected data undergo comprehensive cleaning, preprocessing and integration to ensure accuracy and consistency. The model layer serves as the core component of the system. It uses an innovative approach that combines deep neural networks with ensemble learning models. Deep neural networks have strong learning capabilities and can effectively capture complex patterns and features in the data [17]. Ensemble learning improves the accuracy and stability of predictions by integrating the outputs of multiple individual models. During model training, feature importance analysis is applied to accurately identify the features that significantly affect drug recommendation. This enhances the interpretability of the model. The application layer provides convenient and efficient medication recommendation services for clinicians. With a user-friendly interface, clinicians can input patient information, and the system quickly generates personalized medication recommendations, including drug choices and dosage suggestions [18]. The system also provides detailed explanations and supporting evidence for the recommendations to assist clinicians in making informed and rational decisions.

### 2.2 Data Collection and Preprocessing

The data collection and preprocessing in this study were extensive and carried out with careful attention to detail. Electronic medical record (EMR) data were obtained from the information systems of several partner hospitals. These data included comprehensive information such as patient demographics, disease diagnoses, treatment

records, and laboratory and examination results. Genomic data were acquired through close collaboration with professional genetic testing institutions, with a primary focus on genetic polymorphism data. Pharmacokinetic parameters were collected by systematically reviewing relevant literature, drug package inserts, and selected clinical trial data. Because there were significant differences in format, quality, and semantics across these heterogeneous data sources, strict cleaning and integration were required. For EMR data, denoising was performed by removing duplicate, erroneous, and incomplete entries. For genomic data, quality control of genotyping was conducted to exclude low-quality results. During the integration stage, a unified data standard and coding system was established. Data from different sources were linked and merged based on each patient's unique identifier. This process resulted in the construction of a complete and high-quality patient dataset, laying a solid foundation for subsequent research.

### 2.3 Feature Engineering and Importance Analysis

Clinical features—including disease diagnosis, disease progression, comorbidities and medication history—were thoroughly extracted from electronic medical record data. From the genomic data, genetic polymorphism sites related to drug metabolism and response were accurately identified. Key pharmacokinetic parameters such as half-life, peak plasma concentration and clearance rate were extracted from the pharmacokinetic data [19]. By deeply mining these multi-source data, a comprehensive and precise patient feature vector was constructed. Feature selection was carried out using advanced machine learning algorithms, including Random Forest and LightGBM, to identify variables that had a significant impact on medication recommendations. At the same time, SHAP (SHapley Additive exPlanations) value analysis was applied to accurately calculate the importance score of each feature, clearly illustrating the contribution of each variable to the recommendation outcome. For instance, the analysis revealed that certain genetic polymorphism sites were strongly associated with the therapeutic effects of specific drugs and played an important role in the recommendation process.

### 2.4 Model Construction and Training

A multilayer perceptron (MLP) was used as the basic structure of the deep neural network. The multi-source patient feature vector was taken as the input [20,21]. Through multiple hidden layers, the input data were subjected to nonlinear transformations to effectively learn complex patterns. After processing through these layers, the model generated drug recommendation results. By adjusting the number of hidden layer nodes, activation functions, and other parameters, the model's performance was optimized. The Stacking ensemble learning method was applied to integrate multiple different base models, such as logistic regression, decision trees, and support vector machines. First, each base model was used to make predictions on the training data. These prediction results were then used as new features and input into a second-level model (e.g., logistic regression) for secondary training. The final recommendation results were obtained from the output of the second-level model. This approach effectively combined the strengths of different models and significantly improved the accuracy and stability of the recommendation system. During training, a five-fold cross-validation method was used to divide the dataset into training and validation sets. The model was trained and evaluated multiple times to reduce the risk of overfitting. Mean squared error (MSE) and accuracy were selected as evaluation metrics. The model's performance was further improved by tuning parameters and using the Adam optimization algorithm. Deep learning frameworks such as TensorFlow and PyTorch were used to support efficient training and deployment of the model [22].

## 3. RESULTS

### 3.1 Accuracy of Drug Matching

The experimental results clearly showed that the AI-based personalized medication recommendation system developed in this study had a significant advantage in drug matching accuracy compared with traditional rule-based methods and single algorithm models. Among the 500 hypertensive patient samples included in the analysis, the system achieved a drug recommendation accuracy of 91.2%, meaning that 456 patients were accurately matched with appropriate antihypertensive medications. In contrast, the traditional rule-based method, which relies on standard clinical guidelines and physician experience, reached an accuracy of only 78.5%, with 393 patients correctly matched. The single algorithm model, using logistic regression as an example, achieved an accuracy of 82.3%, with 412 patients accurately matched. Subgroup analysis further revealed that, for patients with primary hypertension, the system achieved an accuracy of 93.5%. The corresponding accuracy rates for the rule-based method and the single algorithm model were 80.2% and 84.7%, respectively. For patients with secondary hypertension, the system's accuracy was 88.8%, while the traditional rule-based method and the single

algorithm model achieved 75.6% and 79.9%, respectively.

**Table 1:** Comparison of Overall Accuracy Across All Samples

| Method | Accuracy (%) | Number of Matched Patients (cases) |
|---|---|---|
| AI-Based Personalized Medication Recommendation System | 91.2 | 456/500 |
| Traditional Rule-Based Method | 78.5 | 393/500 |
| Single Algorithm Model (Logistic Regression) | 82.3 | 412/500 |

**Table 2:** Accuracy Comparison in Subgroup Analysis

| Patient Type | AI-Based Personalized Medication Recommendation System (%) | Traditional Rule-Based Method (%) | Single Algorithm Model (Logistic Regression) (%) |
|---|---|---|---|
| Primary Hypertension | 93.5 | 80.2 | 84.7 |
| Secondary Hypertension | 88.8 | 75.6 | 79.9 |

It can be clearly observed from Table 1 and Table 2 that, in both the overall hypertensive patient population and the subgroups of primary and secondary hypertension, the drug matching accuracy of the AI-based personalized medication recommendation system developed in this study is significantly higher than that of the traditional rule-based method and the single algorithm model. This clearly demonstrates the system's superior performance in accurate drug selection.

### 3.2 Dose Prediction Error

In dose prediction, the system developed in this study demonstrated outstanding control over prediction error. Taking nifedipine, a commonly used antihypertensive drug, as an example, among 200 patients receiving this medication, the system maintained the average dose deviation precisely within ±8.3%. Specifically, the difference between the actual average dose used and the system-recommended dose fluctuated within a minimal range. In contrast, the traditional rule-based method showed an average dose deviation of ±15.6%, indicating a larger gap between actual usage and the dose recommended by conventional methods. This may increase the risk of adverse effects in some patients due to overdosing, or reduce treatment efficacy due to underdosing. The single algorithm model showed an average deviation of ±12.4%, which was an improvement over the traditional method, but a noticeable difference remained when compared with the system developed in this study. Further analysis based on patient age showed that, among elderly patients aged ≥65 years, the system maintained a dose deviation of ±9.1%, while the traditional rule-based method and the single algorithm model showed deviations of ±17.3% and ±13.8%, respectively. Among patients aged <65 years, the system's dose deviation was ±7.8%, compared to ±14.5% for the traditional method and ±11.6% for the single algorithm model.

**Table 3:** Performance of Different Methods in Dose Prediction

| Method | Dose Deviation in Total Sample (%) | Dose Deviation in Elderly Patients (Age ≥65) (%) | Dose Deviation in Non-Elderly Patients (Age <65) (%) |
|---|---|---|---|
| AI-Based Personalized Medication Recommendation System | ±8.3 | ±9.1 | ±7.8 |
| Traditional Rule-Based Method | ±15.6 | ±17.3 | ±14.5 |
| Single Algorithm Model (Logistic Regression) | ±12.4 | ±13.8 | ±11.6 |

It can be clearly seen from Table 3, regardless of patient age, the dose deviation of the system developed in this study was consistently kept within a small range. In all age groups, the system significantly outperformed the traditional rule-based method and the single algorithm model. This strongly demonstrates that the system fully considers individual factors during the dose prediction process and can accurately provide dose recommendations that match the actual needs of patients [23,24].

### 3.3 Case Analysis

The effectiveness of the system was further verified through a specific clinical case. For example, a 62-year-old patient, Mr. Li, had hypertension and a specific genetic polymorphism (CYP2D6 poor metabolizer). The conventional treatment plan used a standard dose of metoprolol. After three months, blood pressure control did not meet expectations. The systolic pressure remained between 150–160 mmHg, and the diastolic pressure stayed between 95–100 mmHg. The patient also developed obvious adverse reactions such as bradycardia. Using the personalized medication plan recommended by this system, the influence of genetic polymorphisms on drug metabolism was fully considered [25,26]. The medication was changed to an angiotensin-converting enzyme inhibitor (ACEI), enalapril. The dosage was adjusted precisely based on the patient's renal function, body weight, and other relevant factors. After two months of treatment, the blood pressure was effectively controlled. The systolic pressure stabilized at 130–135 mmHg and the diastolic pressure at 80–85 mmHg. No significant adverse effects were observed. This case clearly demonstrates the significant value and potential of the system in clinical practice. It can provide more effective personalized medication plans based on individual physiological and genetic features, thus improving treatment outcomes and the patient's quality of life.

## 4. RESULTS AND DISCUSSION

### 4.1 System Performance Evaluation

According to the comprehensive experimental results, the AI-based personalized medication recommendation system developed in this study demonstrated excellent performance in terms of accuracy, stability and interpretability. For accuracy, the system achieved significant improvements in drug recommendation accuracy and dosage prediction precision by combining multi-source data with advanced modeling algorithms [27]. The multi-source data included detailed clinical information from electronic medical records, genetic characteristics from genomic data, and pharmacokinetic parameters that reflect drug behavior in the body. These data provided the model with comprehensive and detailed inputs, allowing it to accurately identify the complex relationships between individual patient features and medication selection and dosage. The deep neural network was able to learn complex patterns in the data automatically, while the ensemble learning model integrated the advantages of several individual models to ensure high accuracy in the recommendation results [28]. For stability, the ensemble model effectively reduced the uncertainty of individual models by combining their predictions. This significantly improved the overall stability of the system. For example, when dealing with clinical data from different sources and varying quality, the ensemble model could synthesize the outputs of each model to reduce errors caused by data fluctuations or outliers. This ensured that the system could still provide relatively stable and reliable results under different conditions. For interpretability, the system incorporated feature importance analysis mechanisms such as SHAP value analysis, which allowed doctors to clearly understand the reasoning behind the recommendations [29]. By intuitively showing how much each feature (such as genetic polymorphism sites, disease diagnosis, or disease course) contributed to the recommendation, the system helped physicians understand why certain drugs and dosages were suggested. This greatly increased their trust in the system and supported its broader use in clinical practice.

### 4.2 Clinical Application Value

From the perspective of clinical application, this system holds significant practical value. On one hand, it can provide doctors with accurate medication recommendations, assisting them in developing more scientific and reasonable treatment plans. This significantly improves treatment effectiveness and reduces the occurrence of adverse drug reactions. In busy clinical environments, physicians often face large patient volumes and complex conditions. It is difficult to fully and thoroughly consider all key factors affecting medication decisions within a limited time. This system can quickly integrate multi-source patient information and accurately recommend appropriate drugs and optimized dosages. It offers valuable decision support and helps doctors avoid irrational medication caused by subjective limitations or missing information. On the other hand, the system helps optimize the allocation of medical resources. It prevents unnecessary drug waste and overtreatment, thereby reducing medical costs. With its precise drug matching and dosage prediction capabilities, the system can reduce treatment failures and repeated treatments caused by improper drug selection or incorrect dosage. This leads to substantial savings in healthcare resources. At the same time, additional expenses caused by adverse drug reactions—such as prolonged hospital stays or treatment of complications—can also be reduced. For example, by reducing the number of extra hospitalization days due to adverse reactions, the system directly lowers related costs such as bed occupancy.

Moreover, personalized medication significantly improves patients’ adherence to treatment and enhances their

quality of life. When patients receive drugs and dosages that match their individual conditions, treatment outcomes improve and adverse effects are reduced. This strengthens their confidence in treatment and increases their willingness to follow medical advice and take medication on time. As a result, their condition is more likely to improve, creating a positive cycle that comprehensively enhances their quality of life. In the long term, as this system is widely applied in clinical practice, it is expected to have a positive and lasting impact on the overall quality of healthcare services. It will support the development of personalized medicine, promote more efficient and reasonable use of medical resources, and ultimately benefit a wide range of patients.

## 5. CONCLUSION

This study successfully constructed an AI-powered personalized medication recommendation system that integrates electronic medical records, genomic data and pharmacokinetic parameters. By combining multiple data sources and applying advanced algorithms, the system significantly outperformed traditional methods in both drug matching accuracy and dose prediction error control. For example, the recommendation accuracy for antihypertensive drugs reached 91.2%, and the dosage deviation was controlled within ±8.3%. The system showed strong performance in terms of accuracy, consistency, and interpretability. It can assist doctors in formulating precise medication plans, improve treatment outcomes, reduce adverse reactions, and help optimize the allocation of medical resources. These results demonstrate its considerable potential for clinical application and provide an effective path for applying AI in personalized medicine.

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