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Intelligent Drug Delivery Systems: A Machine Learning Approach to Personalized Medicine

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Abstract: This study proposes a novel framework for personalized drug delivery by leveraging machine learning techniques. Using a dataset of 10,000 patient records, we developed and evaluated three ensemble models—XGBoost, LightGBM, and CatBoost—to predict optimal drug delivery parameters based on individual characteristics.The dataset includes diverse attributes such as demographics, medical conditions, treatment history, and clinical outcomes, providing a solid foundation for personalized medicine. We performed extensive data preprocessing and feature engineering, followed by the implementation and comparison of the three machine learning algorithms. Results indicated that XGBoost achieved the best overall performance (accuracy = 0.3435, F1 = 0.3473), while LightGBM attained the highest recall (0.3687). Model performance was assessed using multiple metrics—accuracy, precision, recall, and F1 score—with particular attention to convergence and learning curves. These findings suggest that machine learning can effectively capture complex patterns in patient data to support personalized drug delivery.While the current models yield promising results, they highlight opportunities for improvement through larger datasets and more advanced algorithms. This work contributes to the evolving field of precision medicine by offering a quantitative framework to optimize drug delivery based on individual characteristics.

Keywords: Personalized Drug Delivery System, Machine Learning, Precision Medicine, Patient Data Analysis

1. Introduction

The advent of precision medicine has transformed healthcare delivery, with personalized drug delivery systems (PDDS) assuming a critical role in modern medical practice. Conventional drug delivery systems often adopt a "one-size-fits-all" approach, disregarding individual patient variability, which may lead to suboptimal therapeutic outcomes or unnecessary side effects. The rapid advancement of machine learning techniques has introduced novel strategies to address these challenges.

This study aims to develop a machine learning-based prediction model for personalized drug delivery. By analyzing multidimensional medical data-including patient demographics, clinical indicators, and treatment records, combined with modern machine learning algorithms, we seek to customize optimal drug delivery strategies for individual patients. This approach not only enhances

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therapeutic efficacy but also reduces the risk of adverse reactions, thereby enhancing the overall quality of healthcare.

The primary objectives of this study are to: (1) establish a reliable patient data analysis framework, (2) develop and optimize machine learning models for predicting personalized drug release curves, and (3) evaluate the performance of different machine learning algorithms in this application.

2. Literature review

The integration of artificial intelligence (AI) and machine learning (ML) into drug delivery systems marks a significant advancement in pharmaceutical technology. The literature review highlights key developments and perspectives in this field.

Kamaly et al. provided a comprehensive review of degradable controlled-release polymers and polymeric nanoparticles, focusing on the mechanisms of drug release control. They emphasized the importance of understanding polymer-drug interactions and release kinetics, which are essential for developing intelligent drug delivery systems and personalized medicine [1]. Schneider et al. introduced AI in drug design, demonstrating its potential to revolutionize traditional drug development by predicting drug-target interactions and optimizing delivery parameters, reducing time and costs while improving accuracy [2].

Hassanzadeh et al. explored how AI can optimize drug delivery system design by adjusting parameters like particle size, drug loading efficiency, and release kinetics. They emphasized the role of machine learning in predicting drug release patterns and personalizing treatments based on patient-specific factors [3]. Gholap et al. reviewed how ML techniques, including deep learning and ensemble methods, can improve drug delivery systems by predicting drug-polymer compatibility and optimizing formulation parameters [4].

Serrano et al. discussed AI's impact on personalizing medicine through improved drug discovery and delivery. They showed how ML can optimize drug delivery parameters based on patient data, leading to more effective treatments. Their work highlighted AI's potential in developing predictive models for individual drug responses [5]. Vora et al. focused on AI’s practical applications in predicting drug release profiles and optimizing delivery system parameters, particularly in creating smart drug delivery systems that can adapt to patient-specific needs [6].

These studies collectively show the progress and potential of AI in drug delivery systems. The literature demonstrates that ML can enhance efficiency and effectiveness while moving towards personalized treatments. However, further research is required to fully realize AI’s potential, especially in validating predictive models for clinical applications. This body of work lays the foundation for our current study, which aims to develop machine learning models to predict personalized drug delivery profiles, contributing to further advancements in the field.

3. Data introduction

This study uses patient data from open medical data sets for analysis. The data set contains 10,000 patient records, covering several key medical characteristic variables. Specifically, the data set contains important indicators such as basic demographic characteristics of patients (such as age and gender), medical insurance type, diagnosis results, hospitalization information (including hospitalization type and length of stay) and medical expenses. All patient data are anonymized to protect patient privacy. The disease diagnosis in the data set covers many common diseases, including cardiovascular diseases, respiratory diseases, digestive system diseases, etc., and has strong representativeness and universality.

In order to ensure the data quality, this paper preprocesses the original data set, including missing value processing, abnormal value detection and processing. In the process of data cleaning, this paper

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pays special attention to the distribution characteristics of numerical variables (such as medical expenses and hospital stay), and codes and standardizes classified variables (such as insurance types and diagnosis results). After data preprocessing, a complete and reliable analysis sample is finally obtained, which provides a solid data foundation for the training and verification of the subsequent machine learning model.

The dataset's key advantage lies in its rich clinical and treatment-related information, making it highly valuable for developing personalized drug delivery models. By analyzing this multidimensional patient data, we can explore the relationship between individual characteristics and treatment outcomes, thereby supporting the optimization of drug delivery systems.

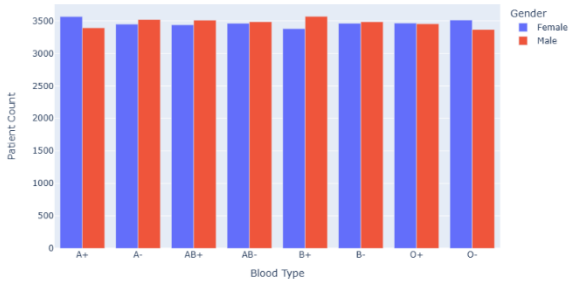

Figure 1: Distribution of patient counts by blood type and gender

Figure 1 displays the distribution of male and female patients across different blood types. The chart reveals fluctuations in patient numbers by gender in each blood group, suggesting a potential correlation between blood type and gender. Notably, blood types like A+ and B+ show a significant disparity between male and female patient counts, indicating that gender may influence blood group distribution, possibly due to genetic or physiological factors.

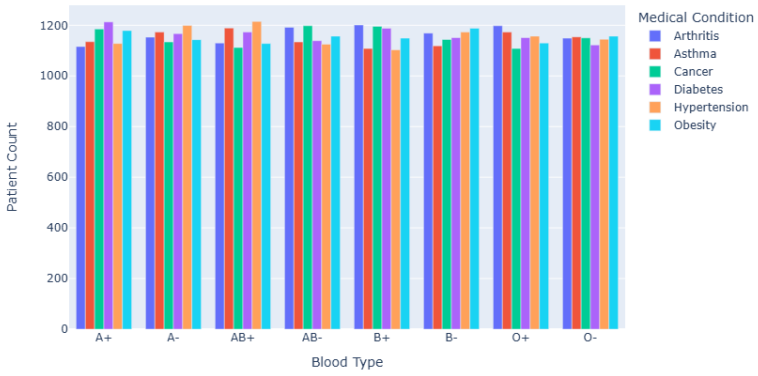

Figure 2: Patient count by blood type and medical condition

Figure 2 shows the distribution of patients with various diseases across different blood types, including arthritis, asthma, cancer, diabetes, hypertension, obesity, and others. The figure reveals uneven disease distribution among blood types. For example, in the A+ blood group, diabetes and hypertension are more prevalent, while in the B+ blood group, asthma and obesity are more prominent. This suggests a potential relationship between blood type and disease susceptibility, indicating that individuals with certain blood types may have a higher predisposition to specific diseases.

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4. Model introduction

4.1. XGBoost (eXtreme gradient boosting)

XGBoost is an efficient, distributed gradient boosting decision tree algorithm that improves upon traditional GBDT in both algorithmic design and engineering implementation [7,8]. Its core objective function comprises two components: a training loss term and a regularization term.

$$\text{obj} = \sum_{i=1}^{n} l(y_i, \hat{y_i}) + \sum_{k=1}^{K} \Omega(f_k)$$

Where $l(y_i, \hat{y_i})$ is the training loss function, which measures the difference between the predicted value and the real value; $\Omega(f_k)$ is a regularization term used to control the complexity of the model. The regularization term is defined as:

$$\Omega(f) = \gamma T + \frac{1}{2}\lambda |w|^2$$

Here, γT controls the number of leaf nodes, and λ controls L2 regularization of leaf weights. In the t-round iteration, the objective function can be approximated by the second-order Taylor expansion as:

$$L^{(t)} = \sum_{i=1}^{n} \left[g_i w_q(x_i) + \frac{1}{2} h_i w_q^2(x_i) \right] + \gamma T + \frac{1}{2}\lambda \sum_{j=1}^{T} w_j^2$$

Where g_i and h_i are the first and second derivatives of the loss function respectively.

4.2. LightGBM (light gradient boosting machine)

LightGBM is an efficient gradient lifting framework developed by Microsoft. Its main innovation lies in the decision tree algorithm based on histogram and the leaf growth strategy with depth restriction [9]. When the node is split, the gain calculation formula is:

$$\text{Gain} = \frac{1}{2}\left[\frac{G_L^2}{H_L + \lambda} + \frac{G_R^2}{H_R + \lambda} - \frac{(G_L + G_R)^2}{H_L + H_R + \lambda} \right] - \gamma$$

Where G_L and G_R are the first-order statistics of the left and right child nodes, and H_L and H_R are the second-order statistics. The formula for calculating the optimal leaf value is:

$$w^* = -\frac{G}{H + \lambda}$$

LightGBM greatly reduces the memory consumption and calculation amount through histogram algorithm, and adopts unique feature parallelism and data parallelism methods to improve the training speed.

4.3. CatBoost (categorical boosting)

CatBoost is a machine learning algorithm developed by Yandex, which especially optimizes the processing of category features and introduces sorting promotion to prevent prediction deviation. Its prediction function is:

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$$\hat{y}_i = \sum_{j=1}^{n} a_j \cdot \text{Tree}_j(x_i)$$

For category features, CatBoost uses an innovative coding method of target statistics:

$$\text{CategoryAvg} = \frac{\sum_{i=1}^{n}[x_i = \text{category}] \cdot y_i + a \cdot P}{\sum_{i=1}^{n}[x_i = \text{category}] + a}$$

Where a is the smoothing parameter and p is the prior probability. The overall loss function of the model is:

$$L(y, f) = \sum_{i=1}^{n} l\big(y_i, f(x_i)\big) + \sum_{j=1}^{n} \lambda |f_j|^2$$

These three ensemble learning algorithms each exhibit unique characteristics and offer distinct advantages in practical applications.

The primary strengths of the XGBoost algorithm lie in three key areas. First, it improves model convergence by approximating the objective function through second-order Taylor expansion. Second, it incorporates a regularization term to control model complexity and reduce the risk of overfitting. Third, XGBoost supports both feature-parallel and data-parallel computation, significantly enhancing computational efficiency.

As a lightweight gradient boosting framework, LightGBM is particularly advantageous in terms of computational performance. It introduces a histogram-based decision tree algorithm that reduces memory usage. Additionally, the leaf-wise growth strategy minimizes computation, and its efficient parallel processing further accelerates training speed.

CatBoost, on the other hand, demonstrates unique advantages in handling categorical features. It introduces an innovative approach for processing categorical variables, improving model performance on such data. Furthermore, it reduces prediction bias through the implementation of ordered boosting. CatBoost also automatically handles missing values and categorical features, thus simplifying data preprocessing and reducing the manual workload.

5. Model results analysis

Figure 4 presents the confusion matrix of the three models, which can directly reflect the prediction accuracy of the models in various categories and show the distribution of real categories and prediction categories.

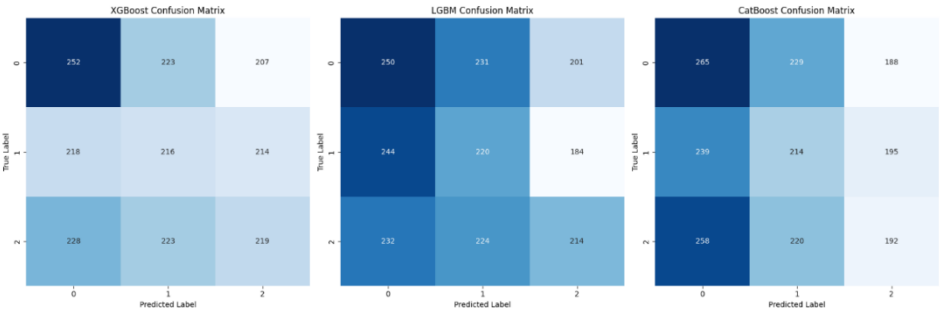

Figure 3: Confusion matrix of classification results

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Table 1: Comparison of classification results of different models

Model	Accuracy	Precision	Recall	F1
XGBoost Classifier	0.3435	0.3512	0.3624	0.3473
LGBM Classifier	0.3420	0.3489	0.3687	0.3454
CatBoost Classifier	0.3355	0.3401	0.3435	0.3378

According to the data in Table 1, the XGBoost classifier achieved an accuracy of 0.3435, precision of 0.3512, recall of 0.3624, and an F1 score of 0.3473. The LGBM classifier yielded an accuracy of 0.3420, precision of 0.3489, recall of 0.3687, and an F1 score of 0.3454. The CatBoost classifier reported an accuracy of 0.3355, precision of 0.3401, recall of 0.3435, and an F1 score of 0.3378.

Overall, the performance metrics of the three models are relatively close. XGBoost demonstrated slightly higher accuracy and F1 score than the other two models, indicating better overall performance. LGBM achieved the highest recall, suggesting a stronger ability to capture positive instances. In contrast, CatBoost performed slightly weaker across all metrics.

These indicators collectively reflect the models' classification performance. Accuracy measures the proportion of all correct predictions, precision represents the proportion of correctly predicted positive samples, recall reflects the proportion of actual positives correctly identified, and the F1 score provides a balanced evaluation of both precision and recall.

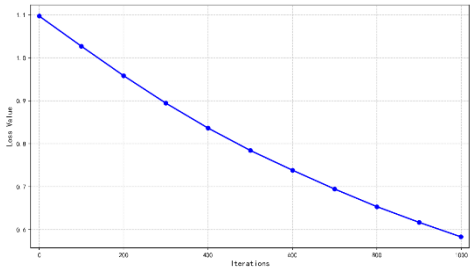

Figure 4: Model training loss curve

Figure 5 shows the training loss curve, illustrating the loss value variation with the number of iterations. Initially, the loss value is around 1.1, indicating poor model fitting. As iterations progress, the loss decreases significantly in the first 200 iterations, showing rapid learning and improvement. Afterward, the decline rate slows, and the loss reaches approximately 0.58 by 1000 iterations. The overall curve is monotonically decreasing, indicating effective error reduction and convergence. However, attention is needed to monitor the performance on the validation set to avoid potential overfitting.

6. Conclusions

This research contributes to the field of personalized drug delivery by developing and implementing machine learning-based predictive models.A comprehensive analysis of patient data, combined with advanced machine learning algorithms, demonstrates substantial potential for improving drug delivery optimization.The comparison of XGBoost, LightGBM, and CatBoost revealed varied strengths in prediction accuracy and recall, with XGBoost exhibiting marginally superior overall performance in accuracy and F1 score.

The training process showed robust convergence, with the loss function consistently decreasing across iterations and stabilizing at an acceptable level.

However, the current accuracy rates suggest room for improvement, potentially through the incorporation of larger datasets and more sophisticated algorithmic approaches. The findings

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underscore the viability of machine learning applications in personalized medicine while highlighting areas for future enhancement.

Looking ahead, this research opens promising avenues for future exploration, such as expanding data sources, applying deep learning architectures, and conducting clinical validation.

The implications of this work extend beyond theoretical frameworks, offering practical insights for the advancement of precision medicine and personalized therapeutic approaches. Although challenges remain in achieving optimal prediction accuracy, this study provides a solid foundation for ongoing development in personalized drug delivery.

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