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Research Progress and Challenges of Machine Learning Algorithms in the Prediction Model of Perioperative Nausea and Vomiting

Lantian Li[1*], Haidong Zhou[2*#], Jihua Wei[2*#], Jinghao Huang[3*#], Dinggui Lu[2*#]

[1]Department of Gynecology, Affiliated Hospital of Youjiang Medical University for Nationalities, Baise, China
[2]Department of Orthopedic Surgery, Affiliated Hospital of Youjiang Medical University for Nationalities, Baise, China
[3]Department of Pathology, Baise Maternal and Child Health Hospital, Baise, China
Email: #1695573477@qq.com, #1261290953@qq.com, #1395747432@qq.com, #ludinggui@163.com

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Abstract

Postoperative nausea and vomiting (PONV) is a common complication after anesthesia and surgery. Traditional predictive models, such as Apfel scores, rely on linear assumptions and limited risk factors, and predictive efficacy is difficult to meet the needs of precision medicine. Machine learning (ML) significantly improves prediction accuracy through high-dimensional data processing and nonlinear modeling and reveals new risk factors. Supervised learning (random forest, support vector machine), ensemble learning (XGBoost, LightGBM) and deep learning have performed outstandingly in dynamic prediction and multimodal data fusion, improving the accuracy of risk warning. However, ML clinical transformation faces data heterogeneity, model interpretability controversy, and ethical compliance challenges. Federated learning, interpretability tools and causal inference frameworks (Bayesian networks) have become the key to breaking the deadlock. In the future, we need to promote the integration of multi-omics data, real-time biosensing technology and "enhanced intelligence" model, which refers to a human-AI collaborative system that continuously learns from clinician feedback and real-time patient data to adaptively refine predictions and interventions to achieve closed-loop management from prediction to prevention. This paper systematically reviews the algorithm innovation and clinical verification progress of ML in PONV prediction, providing theoretical and practical references for precise treatment and postoperative management.

Keywords

Machine Learning, Prediction, Perioperative Nausea and Vomiting

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*All authors contribute equally.

#Corresponding author.

1. Introduction

PONV is one of the most common complications after anesthesia and surgery, and about 20% - 30% of high-risk patients are troubled [1]. PONV not only causes subjective discomfort in patients, extends hospitalization time, and increases medical costs, but may also induce serious clinical consequences such as wound cleavage and aspiration. Traditional prediction models, such as Apfel scores (**Figure 1**) and Koivuranta scores, are constructed based on linear regression and rely on limited static risk factors (such as women, non-smoking history, etc.). Although they are clinically operable, their prediction efficacy is difficult to meet the needs of individualized precision medicine [2]. In contrast, ML models require high-dimensional, dynamic data inputs—such as real-time physiological signals, genomic markers, and multimodal clinical records—to capture complex nonlinear relationships and enable individualized risk stratification. In recent years, ML has provided a new path for innovation in PONV prediction paradigm with its high-dimensional data processing capabilities, nonlinear relationship modeling advantages and dynamic timing analysis potential (**Figure 2**). Research shows that the ML model can increase the predicted receiver characteristic Area under the curve (AUC) by integrating intraoperative physiological signals, multiomic data and unstructured text 0.85 or above, and potential risk markers not paid attention to by traditional methods [3]. However, ML faces multiple challenges such as data heterogeneity, controversy in model interpretability, and ethical compliance in clinical transformation. This article systematically reviews the value of ML in medical prediction, the clinical needs and clinical characteristics of PONV prediction models, the progress of ML in PONV prediction research, the discovery of key factors and clinical verification, and in-depth analysis of its technical bottlenecks and implementation barriers, aiming to provide theoretical reference and practical direction for future research (**Figure 3**).

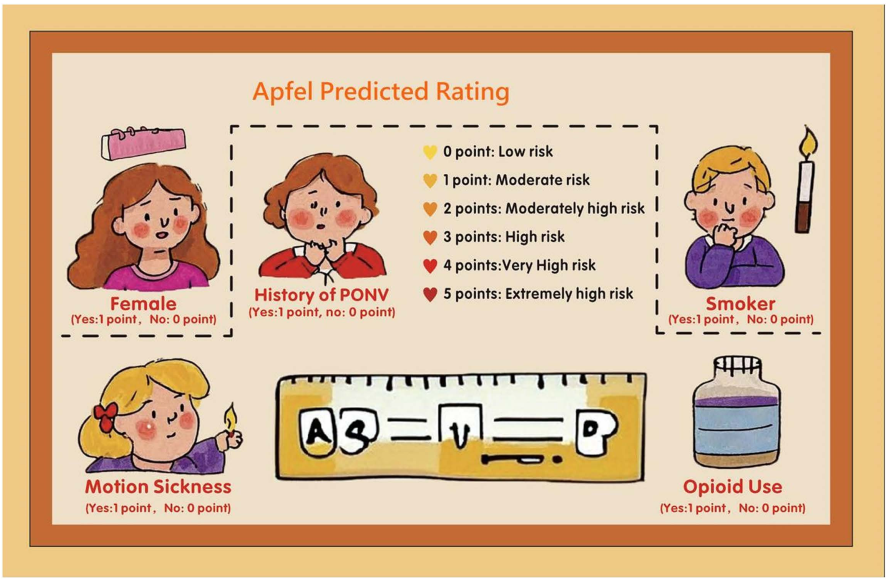

Figure 1. Schematic breakdown of apfel predicted rating.

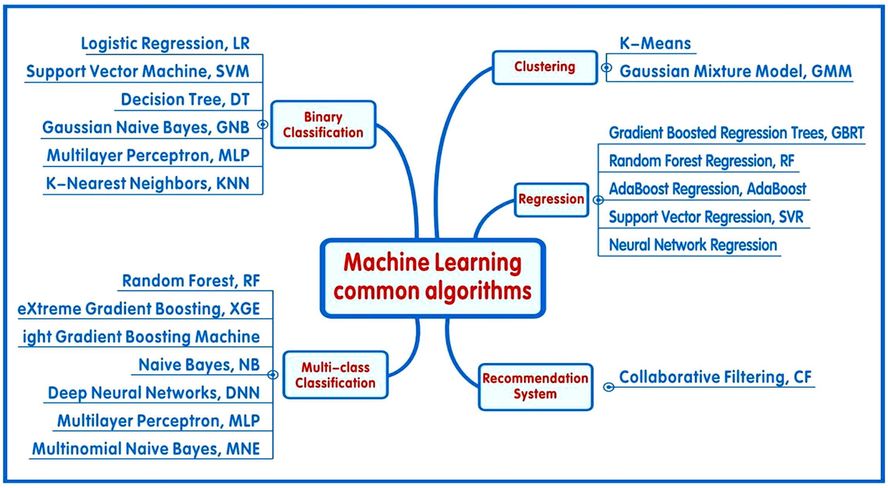

Figure 2. Summary of commonly used machine learning methods.

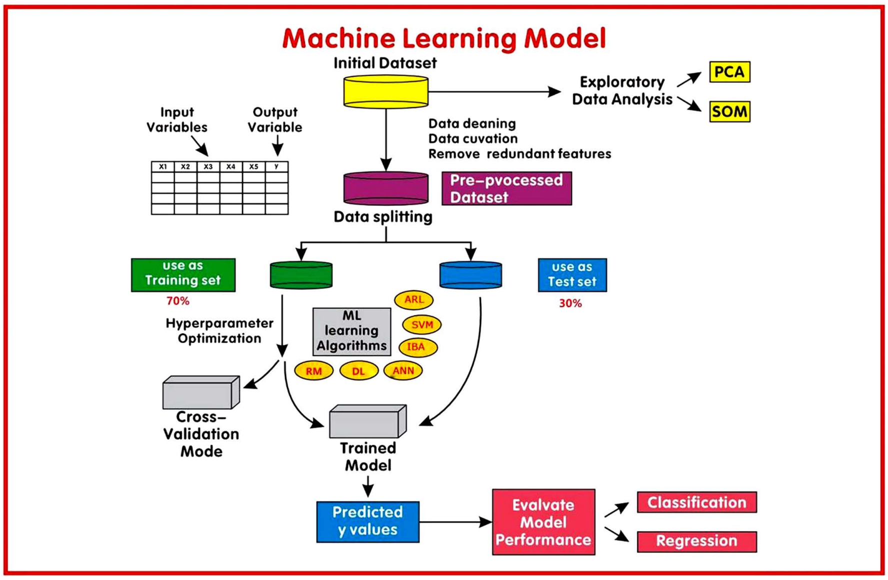

Figure 3. Initial Data: Gather historical risk data from PCA/SOM sources. Preprocessing: dataset (input and output missing values) and perform feature engineering. Date splitting; Model Training: Train ML algorithms (e.g., lerning regression, ARL, SVM, IBA, ANN, DL, RM) on labeled risk data, Hyperparameter optimization, Feature Selection. Trained model : A trained model is a mathematical representation learned from labeled training set. Predictted values: capable of making predictions or Evalvate model performance on new, unseen data. Classification: Predicts discrete class labels by learning decision boundaries from labeled data. Regression: Predicts continuous numerical values by modeling relationships between input features and target variables.

2. The Value of ML in Medical Predictions

Traditional medical prediction models (such as Logistic regression, score scale) are limited by linear assumptions and static characteristics, and are difficult to cope with the complexity and dynamicity of medical data [4]. Through breakthroughs in algorithm innovation and data processing capabilities, ML provides multi-dimensional value improvement for disease prediction, which is reflected in the following five major directions:

1) High-dimensional data processing and nonlinear summation mining, medical data usually include multi-dimensional variables such as patient demographic characteristics, laboratory indicators, imaging data, genomic information, etc. Traditional models are prone to failure due to "dimensional disasters" [5]. ML algorithms (such as random forests, neural networks) significantly improve prediction accuracy by automatically screening key features and capturing nonlinear interactions [6]. In the molecular pathophysiological risk prediction of alcoholic liver disease, ML found that these biomarker panels were accurate in predicting future liver-related events and all-cause mortality, increasing the predicted AUC from 0.79 to 0.90 in traditional models by analyzing more than 596 clinical and plasma proteomics [7]. In developing and validating predicting the incidence of type 2 diabetes in populations, the ML method accurately predicts the incidence of health management data in the population using routinely collected. This result suggests that this model can be used to inform population health planning and decision-making in diabetes prevention [8].

2) Dynamic prediction and real-time decision-making support. Traditional models are mostly static risk assessment (such as one-time score before surgery), which cannot reflect the real-time changes in the patient's status. ML combines time series data processing technology to dynamically update risk levels and provide time-sensitive guidance for clinical intervention [9].

3) Personalized medical care and precise intervention. ML promotes the transformation of the "one-size-fits-all" treatment model to precision medicine by segmenting patient subgroups and quantifying individual risk differences. Using ML, key differentially expressed genes associated with lung adenocarcinoma were identified. Based on these genes, the cell death index was programmed in the lung adenocarcinoma population and integrated with relevant clinical features to develop multiple prognostic column maps, a significant correlation between cell death index and immune characteristics in lung adenocarcinoma was observed, and patients with higher index scores may show resistance to immunotherapy and standard adjuvant chemotherapy regimens. Indexes can promote personalized treatment in patients with lung adenocarcinoma [10].

4) Multimodal data fusion improves comprehensive prediction capabilities, ML breaks through the limitations of a single data type, and realizes collaborative analysis of multimodal data such as images, texts, and signals. Data from 204 patients with Alzheimer's disease in the UK and 19,458 patients with Alzheimer's disease in France were extracted from the Health Improvement Network database in France. For each Alzheimer's disease case, random assignment was performed. Ten health conditions were significantly associated with an increased risk of Alzheimer's disease in the 2 - 10-year exposure window before Alzheimer's disease diagnosis by running conditional logistic regression to illustrate case and control match. Additionally, it occurred at least 9 years before the first clinical diagnosis, followed by anxiety, constipation and abnormal

weight loss. Results from two independent primary care databases provide new evidence on the temporality of risk factors and early signs of Alzheimer's disease, which can guide the implementation of new primary and secondary prevention policies [11].

5) Potential biomarkers and mechanisms were discovered. The causes of many diseases are unknown. Due to the lack of effective early diagnosis and prognosis tools, high mortality and limited treatment options make the disease prognosis poor. ML is used to identify biomarkers of idiopathic pulmonary fibrosis and to evaluate the role of immune infiltration in the disease. FHL2, HPCAL1, RNF182, and SLAIN1 were identified as biomarkers of idiopathic pulmonary fibrosis using Lasso Logistic regression, random forest algorithm and support vector machine recovery feature elimination algorithm. The Receiver Operating Characteristic (ROC) curves confirm the prediction accuracy of these biomarkers in the training set and test set. Immune cell infiltration analysis showed that patients with idiopathic pulmonary fibrosis had higher levels of B-cell memory, plasma cells, T-cell CD8, T-cell follicle helper, T-cell regulation, macrophage M0 and MAST cells. Correlation analysis showed that FHL2 was significantly associated with infiltrated immune cells. Four potential biomarkers (FHL2, HPCAL1, RNF182 and SLAIN1) were identified and the potential pathogenic effect of Slain1 in idiopathic pulmonary fibrosis was evaluated. These findings may be of great significance in guiding the understanding of disease mechanisms and potential therapeutic targets in idiopathic pulmonary fibrosis. ML is of great significance in exploring the mechanisms of disease occurrence and understanding of potential therapeutic targets [12]. Machine learning reconstructs the paradigm of medical prediction through high-dimensional modeling, dynamic analysis, personalized recommendation and multimodal fusion. Its core value lies not only in improving prediction accuracy, but also in promoting the leap of clinical decision-making from "group experience" to "individual data-driven" and providing a new perspective for disease mechanism research [13]. However, data quality, model interpretability and clinical transformation barriers are still challenges that need to be broken through. In the future, the deep integration of ML and evidence-based medicine will accelerate the arrival of the era of precision medicine.

3. Clinical Needs and Data Characteristics of PONV Prediction Model

Traditional PONV prediction models (such as Apfel scores, **Figure 1**) rely on finite linear factors, while ML reveals more complex risk associations through high-dimensional data mining and nonlinear modeling. Notably, traditional models utilize limited, static data inputs (e.g., patient demographics, smoking status), whereas ML models leverage high-dimensional and dynamic data sources such as intraoperative vital signs, genomic profiles, and real-time sensor data. The following analysis is carried out from four aspects: factor type, discovery method and clinical significance:

3.1. Deepening and Verification of Traditional Predictors

Patient PONV is a key driver of unplanned hospital admissions and patient satisfaction after surgery. Because traditional risk factors cannot fully explain the variability of risk. Assuming that genetics may contribute to the overall risk of this complication, a genome-wide association study of PONV was conducted to obtain a polygenic risk score for PONV, and to evaluate and verify the association between the polygenic risk score and PONV. The researchers determined genetic variations associated with PONV by conducting multigenomic association studies. Based on this study, they created a polygenic risk score for the PONV-derived cohort. The polygenic risk score only moderately enhances the prediction of PONV. When added to traditional risk factors, the use of this polygenic risk score did not lead to clinically significant improvements in PONV prediction [14].

3.2. New Predictors Revealed by Machine Learning

The prediction accuracy of traditional PONV models is not high. It is well known that the area under AUC is used as an evaluation index for judging the quality of the model, and a higher AUC value indicates that the model has better prediction accuracy. However, the AUC value of most models in the past did not exceed 0.70 [15]. Therefore, in addition to the predictors proposed by traditional models, there are other important factors that lead to PONV development in patients not yet identified. In recent years, with the rise of artificial intelligence (AI), ML has been increasingly used to develop predictive models [16]. Developing a model that predicts PONV based on ML and evaluating the predictive performance of the model using regions under AUC (accuracy, recall, F1 value, F1 value and precision curve) helps guide treatment and reduce the incidence of PONV [17].

3.3. Breakthrough Factors in Multimodal Data Fusion

Today's digital health revolution aims to increase the efficiency of healthcare and make care more personalized and timely. Data sources for digital health tools include multiple modes such as electronic medical records (EMR), radiological images, and genetic repositories. ML enables these data sources to be integrated to generate multimodal insights. Data fusion uses ML technology to integrate data from multiple models and is expected to form a breakthrough factor. With these data fusion capabilities, both clinicians and researchers will improve the diagnosis and treatment of the disease to provide more timely, accurate and precise patient care [18].

3.4. Research Challenges and Future Directions

Through multidimensional data integration and nonlinear modeling, machine learning not only verifies traditional PONV risk factors, but also reveals new predictors such as intraoperative physiological dynamics, molecular markers and psychological behavior. These findings drive the transformation of predictive models from "static scoring" to "dynamic individualization", but they need to solve the barriers to data acquisition timeliness, causal interpretation and clinical transformation [19]. In the future, the combination of multiomics technology and wearable devices will further improve the PONV risk panoramic map [20].

4. The Application Progress of ML Algorithm in PONV Prediction

PONV is a common postoperative complication. Traditional prediction models (such as Apfel scores) rely on linear assumptions and limited risk factors, making it difficult to meet the needs of individualized and accurate predictions. In recent years, ML has significantly improved the accuracy and practicality of PONV prediction through high-dimensional data processing, nonlinear relationship mining and dynamic modeling. Its core progress is reflected in the following five major directions:

4.1. Supervised Learning Model: From Basic Algorithms to Clinical Optimization

Improvement and comparison of logistic regression. Traditional logistic regression (LR) is still used in PONV prediction baseline model because of its strong interpretability. Its ability to capture nonlinear relationships is limited, which prompts the exploration of more complex algorithms [21]. Random Forest (RF) reveals risk factors that are not focused on in traditional models through character importance sorting [22]. RF is particularly suited for high-dimensional data with complex interactions, making it ideal for identifying non-linear risk patterns in PONV. For the small sample adaptability of support vector machines, in studies with limited data volume (such as pediatric surgery), high-dimensional space is mapped through kernel functions, showing strong classification capabilities. SVM's kernel trick allows it to handle small-sample, high-dimensional datasets common in pediatric PONV studies, enhancing classification performance where traditional models fail. A study on tonsillectomy in children showed that combined with preoperative PONV history and surgical duration, the predicted sensitivity reached 89%, which was better than 76% of the Apfel score [23].

4.2. Integrated Learning and Dynamic Performance Improvement

XGBoost's generalization advantages are outstanding in cross-medical institutions data verification through gradient enhancement and regularization strategies. ML developed from multi-institutional clinicopathological data reduces the number of cervical analyses of pathological lymph nodes and can also accurately identify patients with the highest risk of lymph node metastasis in patients with early oral squamous cell carcinoma [24]. The real-time prediction potential of Light GBM, due to its efficient computing characteristics, is used for intraoperative real-time risk monitoring updates [25].

4.3. Deep Learning and Multimodal Data Fusion

Complex relationship modeling of deep neural networks (DNNs), DNN captures complex interactions with patients' physiological states through hidden layer structures, exceeding all the latest algorithms tested. This method can solve large multidimensional optimization problems [26]. Dynamic prediction of timing models can process continuous physiological signals, and paroxysmal atrial fibrillation is usually diagnosed using long-term dynamic electrocardiogram monitoring. Identifying atrial fibrillation episodes from long-term electrocardiogram data will put a heavy burden on clinicians. Automatic detection method based on ML to solve this problem. A novel semi-supervised learning method was developed to train deep learning models to automatically detect paroxysmal atrial fibrillation in 24-h monitoring data, with sensitivity of 97.8%, specificity of 97.9%, and accuracy of 97.9% in five-fold cross-validation, can effectively reduce the need for data annotation and can improve the clinical utility of automatic atrial fibrillation detection [27].

Natural language processing (NLP) is a field of AI that simulates human languages, in the field of medicine, to automate diagnosis, detection of adverse events, support decision-making and predict clinical outcomes. NLP has been applied in the clinic to facilitate literature synthesis, data extraction, patient identification, automatic clinical reporting and outcome prediction. The application of NLP enhances research and practice in clinical science [28].

5. Clinical Validation and Translational Challenges

ML's potential in medical predictions has been widely recognized, but its transformation from laboratory to clinical still faces multiple barriers [29]. These challenges not only involve technical performance optimization, but also need to deal with the complexity of medical ethics, data ecology and medical behavior patterns. They can be summarized into the following six dimensions. These challenges align with the "deadlock" highlighted in the Summary, which can be addressed through targeted strategies: federated learning for data heterogeneity, interpretability tools for model transparency, and causal inference for confounding control.

5.1. Data Quality and Standardization Dilemma

Multicenter data heterogeneity, the mixed use of data structures, acquisition standards and diagnostic codes in different medical institutions leads to a decrease in model generalization ability [30]. Adopt the federated learning framework to achieve cross-institutional joint modeling, or follow the common data model for data mapping. Marking noise and missing values, clinical data labeling often relies on manual recording. These subjective symptoms are susceptible to nurse evaluation bias, and need to introduce semi-supervised learning combined with expert review, or use multiple interpolation techniques to fill missing values [31].

5.2. The Medical Specialty of Model Verification

The evaluation indicators are mismatched with clinical needs, and high AUC values cannot guarantee clinical effectiveness. For example, PONV prediction model

AUC = 0.85 But the positive predictive value is only 40%, which may lead to excessive prevention medication. Using clinical net benefit index and decision curve analysis, the clinical benefit of the model under different risk thresholds was quantified. In prospective trials, the sensitivity of ML decreased by 22% compared with retrospective tests [32]. Therefore, in practice, application reporting specifications are followed and prospective verification and intervention effect evaluation are mandatory.

5.3. Interpretability and Clinical Trust Crisis

The black box model conflicts with evidence-based medicine, and doctors refuse to believe unexplained predictions. Apply interpretability tools to generate local interpretations, or develop endogenous interpretable models (such as a hybrid architecture for decision trees and rule lists). Moreover, false correlation misleads clinical decision-making, and the model may learn non-causal characteristics, and it is necessary to introduce causal discovery algorithms and counterfactual analysis to distinguish causal factors from confounding signals [33].

5.4. Ethics and Regulatory Compliance Risks

ML involves patient privacy and data security, and medical data breaches are expensive. Although federated learning can mitigate privacy risks, model reverse attacks may still expose sensitive information (such as genomic data). Differential privacy technology is used to enable the collected data to be de-identified and firmly stored, or use homomorphic encryption to achieve the data “available and invisible” [34].

5.5. Doctor and Patient Acceptance Disorders

Clinical cognitive inertia, doctors rely on traditional experience to make decisions and are skeptical about AI suggestions. Research shows that when model predictions conflict with physician intuition, only 12% of cases adopt AI recommendations [35]. Design a Human-in-the-loop system, allowing doctors to correct model output and feedback to the training process. Patients have informed consent and psychological resistance, and patients have high requirements for transparency and controllability of AI decisions. The survey shows that 61% of patients refuse to develop treatment plans entirely by AI, and the solution is to visually demonstrate the confidence and uncertainty range of the model, providing the “veto” option to enhance the sense of control [36].

6. Future Research Methods and Directions of ML in PONV Prediction

With the initial success of ML in perioperative PONV prediction, its future research needs to focus on breakthroughs in technological innovation and clinical transformation bottlenecks, and through multidisciplinary intersection and data ecological reconstruction, the prediction model will leap from “superior laboratory performance" to "clinical practicality and reliability" [37]. The following explains the core methods of future research from five major directions:

6.1. Deep Integration and Standardization of Multimodal Data

Heterogeneous data fusion technology, through the development of a framework based on graph neural network, unified processing of structured data, unstructured text and multi-omic information. For instance, integrating real-time data from wearable sensors (e.g., heart rate variability, electrodermal activity) and specific genomic markers (e.g., polymorphisms in neurotransmitter receptors) could significantly enhance PONV risk stratification. Promote the general data model, establish a cross-institutional PONV database, combine federated learning to realize data sharing under privacy protection, and solve the problems of insufficient sample size and distribution deviation. By using multimodal data combined with AI, research can improve early diagnosis, personalized treatment, and more accurately predict disease outcomes, ultimately improving patients' quality of life [38].

6.2. Real-Time and Lightweight of Dynamic Prediction Models

Incremental learning strategy: Using online learning technology to dynamically incorporate real-time data to avoid prediction lag caused by changes in the treatment process, it is crucial to the success and safety of clinical prediction models. Over time, the dynamic nature of the response to the clinical environment will change over time. For data-driven model update strategies, methods are developed to maintain dynamic calibration curves through optimized online stochastic gradient descent and detect the increase in error through an adaptive sliding window [39].

6.3. Enhanced Interpretability Driven by Causal Inference

Use Bayesian networks to distinguish confounding variables from real causal factors and generate decision-making basis that conforms to clinical pathological mechanisms. Develop a hybrid architecture to output visual rule chains while maintaining high precision. It can not only speed up the data process, but also modify decision rules to better meet user needs. Model evaluation visual effects are created in interactive visualization tools, allowing users to evaluate the performance of risk models, monitor performance and allow users to be confident in the development of model quality [40].

6.4. Development and Verification of Closed-Loop Prevention System

Prediction-intervention linkage, build a closed-loop system of ML models and intelligent infusion pumps, and automatically adjust the amount of drugs used according to the real-time risk level. Dynamically optimize prevention plans to reduce side effects caused by excessive medication. Insulin pumps, as a continuous glucose monitoring and automatic insulin delivery system, insulin pumps evolved from early large equipment to modern sensor-enhanced pumps with automatic shutdown and hybrid closed-loop systems, requiring minimal user input. The second generation system demonstrates outstanding results, demonstrating very effective in diabetes management through biotech-enabled tools such as customized design insulin hybrid molecules, ML algorithms to control peptide release and engineered cells for optimal peptide production and secretion [41].

6.5. Ethical Compliance and Health Equity Guarantee

Adversarial debias module is embedded in model training to eliminate the interference of sensitive attributes such as race and gender on the prediction results. Develop a dynamic consent platform supported by blockchain, allowing patients to control data usage permissions in real time and ensure compliance. In recent years, data on medical system production has increased exponentially. The processing and knowledge extraction from this data helps to develop what is called big data. Compound big data of medicine is crucial to decision-making and generating new knowledge. Physicians can integrate ML technology to analyze and assist in decision-making. But ML methods applied to health systems can also be attacked and suffer from privacy risks [42]. Regarding privacy, many governments have defined regulations to formalize organizational data processing as more and more data leaks lead to reduced system confidence. The EU proposed general data protection regulations to establish rules and rights to manage sensitive data, and in 1996 the United States proposed a regulation to process medical data called the Health Insurance Portability and Accountability Act [43].

7. Conclusions

Machine learning pushes PONV prediction from static scoring to the era of dynamic individualization through algorithm innovation and data-driven strategies. Its core progress is reflected in nonlinear relationship modeling, multimodal data fusion and real-time early warning capabilities. However, clinical transformation still needs to solve the problems of data standardization, model lightweighting and ethical compliance. In the future, the deep integration of ML with wearable devices and intraoperative monitoring systems is expected to achieve closed-loop management from prediction to prevention.

ML needs to cross the triple gap of “technical superiority-medical practicality-social acceptance” in clinical implementation [44]. In the short term, we should focus on data standardization, interpretability improvement and forward-looking verification. In the long term, we should build a “medical and industrial cross-border” collaboration ecosystem to promote legal innovation and ethical consensus. Future research needs to use “accurate prediction-real-time intervention-mechanism exploration” as a closed loop, and through deep coupling of technological innovation and clinical scenes, we will crack the triple barriers of data, algorithms and ethics [45]. Key directions include: dynamic lightweight model deployment, enhanced causal interpretability, mining of multiple groups of biomarkers and building compliance guarantee system [46]. Only in this way can ML truly empower perioperative management and realize the paradigm revolution from "risk warning" to "precise prevention" [47].

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Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

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