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Improving Accuracy of Disease Prediction Models

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ABSTRACT

The accurate prediction of disease outcomes is a pivotal objective in the domain of computational healthcare, with significant implications for patient management, resource allocation, and clinical decision-making. This paper explores innovative methodologies aimed at enhancing the precision of disease prediction models, integrating advancements in machine learning algorithms, data preprocessing techniques, and feature selection strategies. By leveraging a comprehensive dataset encompassing diverse patient profiles, we address the challenges posed by heterogeneity in clinical data and the inherent complexity of disease pathology.

Our approach emphasizes the implementation of ensemble learning techniques, which amalgamate multiple predictive models to mitigate overfitting and improve generalization capabilities. We employ methods such as random forests and gradient boosting, demonstrating their efficacy in capturing non-linear relationships and interactions within the dataset. Furthermore, we introduce a novel hybrid feature selection framework that combines filter, wrapper, and embedded methods to identify the most salient predictors, thereby enhancing model interpretability and performance.

To address the issue of class imbalance, prevalent in medical datasets, we incorporate advanced resampling strategies alongside cost-sensitive learning to ensure robust model training and evaluation. Additionally, we utilize cross-validation and hyperparameter optimization techniques to fine-tune model parameters, ensuring optimal performance across various disease categories.

Results indicate a significant improvement in predictive accuracy and robustness when compared to traditional models. Our findings underscore the potential of integrating sophisticated machine learning methodologies with domain-specific insights to advance the field of disease prediction. This study not only contributes to the theoretical understanding of predictive modeling in healthcare but also provides practical insights for the development of next-generation diagnostic tools. Future work will focus on extending these models to incorporate real-time data streams and exploring their applicability across a broader spectrum of diseases.

1. Introduction

The accurate prediction of diseases is a critical component in the advancement of personalized medicine and public

health strategies. With the proliferation of electronic health records (EHRs) and the exponential increase in available health data, predictive modeling has emerged as a formidable tool in anticipating disease onset and progression. These models hold the promise of shifting healthcare paradigms from reactive to proactive, thereby improving patient outcomes and optimizing resource allocation. However, the reliability and precision of these models remain a pressing challenge. Enhancements in prediction accuracy are imperative to ensure that these models can be effectively integrated into clinical practice and policy-making.

Numerous methodologies have been developed to improve the accuracy of disease prediction models. These range from traditional statistical approaches to sophisticated machine learning algorithms. The integration of diverse data types—such as genomics, proteomics, lifestyle, and environmental factors—has also been explored to enrich the predictive power of these models. Despite these advancements, there remain significant obstacles in achieving high levels of accuracy and generalizability across different populations and healthcare settings [4, 5, 17].

1.1. Historical Background and Significance

Historically, disease prediction models have evolved from simple risk factor analysis to complex, multi-layered frameworks that incorporate machine learning and artificial intelligence (AI) techniques. The early models primarily relied on logistic regression and Cox proportional hazards models, focusing on a limited set of risk factors [1, 22]. These models laid the groundwork for more advanced approaches by highlighting the significance of variable selection and the handling of confounders in predictive accuracy.

The advent of AI and machine learning has revolutionized the landscape of disease prediction. Algorithms such as decision trees, random forests, support vector machines, and neural networks have been increasingly utilized to capture non-linear relationships and interactions among predictors [14, 21]. These methods have demonstrated remarkable potential in improving predictive performance, particularly in complex diseases with multifaceted etiologies [12].

1.2. Challenges in Current Models

Despite technological advances, several challenges persist in the development of accurate disease prediction models. One major issue is the quality and heterogeneity of data sources. Inconsistencies in data collection methods, missing values, and biases in datasets can significantly undermine model performance [2, 20]. Furthermore, the generalizability of models across diverse demographic

and geographic populations remains a critical concern. Models trained on specific cohorts may not perform well when applied to different populations, highlighting the need for robust external validation [7].

Another challenge is the interpretability of complex models. While machine learning algorithms can achieve high accuracy, their 'black-box' nature often complicates the interpretation of results, which is crucial for clinical decision-making [16, 18]. The balance between model complexity and interpretability is an ongoing area of research, with efforts focusing on developing explainable AI techniques that provide insights into model predictions without compromising accuracy [13].

1.3. Strategies for Improvement

To address these challenges, several strategies have been proposed. The integration of multi-omics data, including genomics, transcriptomics, and metabolomics, has shown promise in enhancing the predictive accuracy of disease models [8, 9]. Leveraging these comprehensive datasets can capture the underlying biological processes associated with disease development more effectively.

Another promising approach is the use of ensemble learning techniques, which combine multiple models to achieve superior predictive performance compared to individual models [15]. This method has been particularly effective in reducing overfitting and improving model robustness.

Moreover, advancements in computational power and algorithmic innovation have facilitated the development of real-time prediction models that can adapt to new data inputs continually. Such dynamic models hold the potential to significantly enhance the timeliness and accuracy of disease predictions [10, 19].

In conclusion, while significant progress has been made in the field of disease prediction modeling, ongoing research is essential to overcome existing limitations and harness the full potential of predictive analytics in healthcare [3, 6, 11]. This paper aims to explore the latest methodologies and innovations that can contribute to the improvement of model accuracy and their implementation in real-world settings.

2. Related Work

The field of disease prediction has witnessed significant advancements over recent years, largely driven by the integration of machine learning and deep learning methodologies. These computational models have become indispensable tools for predicting various diseases, offering enhanced accuracy and efficiency compared to traditional statistical methods. This section reviews the foundational and contemporary literature related to disease prediction models, emphasizing techniques,

challenges, and improvements made to enhance their predictive accuracy.

The literature primarily categorizes disease prediction models into two broad types: statistical models and machine learning models. Statistical models, such as logistic regression, have been extensively used due to their simplicity and interpretability. However, these models often struggle with complex, non-linear relationships inherent in medical data. As a response, machine learning models, including decision trees, support vector machines, and neural networks, have been increasingly adopted, demonstrating superior performance in handling high-dimensional datasets and capturing intricate patterns [4, 5].

2.1. Statistical Methods in Disease Prediction

Traditional statistical methods have laid the groundwork for understanding disease dynamics and prediction. Logistic regression and Cox proportional hazards models are among the most commonly used techniques for binary and survival data, respectively [1, 17]. These methods excel in situations where the relationship between predictors and outcome is well-defined and linear. However, their limitations become evident in the presence of non-linear interactions and when dealing with large volumes of data.

2.2. Machine Learning Models

With the advent of big data, machine learning models have emerged as powerful alternatives to traditional techniques. Algorithms such as Random Forests and Gradient Boosting Machines have been widely adopted for their ability to manage large datasets and model complex interactions without explicit feature engineering [14, 21, 22]. Neural networks, particularly deep learning architectures, have further pushed the boundaries by automatically learning hierarchical feature representations from raw data [12, 20].

2.3. Deep Learning and Neural Networks

Deep learning has revolutionized disease prediction by leveraging large-scale datasets and computational power to uncover patterns that are often imperceptible to human researchers. Convolutional Neural Networks (CNNs) and Recurrent Neural Networks (RNNs), including their variants such as Long Short-Term Memory (LSTM) networks, have been deployed for image and sequence data analysis in medical diagnosis [2, 7]. These models excel in capturing spatial and temporal dependencies, which are crucial for accurate disease prediction.

2.4. Hybrid and Ensemble Models

To further enhance predictive accuracy, researchers have explored hybrid and ensemble approaches that combine the strengths of multiple models. Techniques such as stacking, bagging, and boosting have been employed to improve robustness and reduce variance [16, 18]. Hybrid models often integrate machine learning algorithms with statistical methods or other domain-specific heuristics to leverage complementary strengths [8, 13].

2.5. Challenges and Future Directions

Despite considerable progress, several challenges persist in the development of disease prediction models. Issues such as data imbalance, feature selection, and generalization to diverse populations remain active areas of research [9, 15]. Moreover, the interpretability of complex models, particularly deep learning algorithms, poses a significant barrier to their clinical adoption [10, 19]. Future work is likely to focus on developing models that not only enhance predictive accuracy but also offer transparency and explainability [3, 11].

In summary, the evolution of disease prediction models reflects a trajectory from traditional statistical methodologies to advanced machine learning and deep learning techniques. Continued research and development in this area are essential for improving the precision and applicability of these models in real-world clinical settings [6].

3. Methodology

In this section, we delineate the methodology employed to enhance the accuracy of disease prediction models. Our approach integrates advanced machine learning algorithms with domain-specific insights to create a robust predictive framework. This framework is designed to address the inherent challenges in disease prediction, such as imbalanced datasets, feature selection, and model interpretability. By leveraging recent advancements in data science and computational biology, we aim to improve the predictive capabilities of existing models while ensuring their applicability in real-world clinical settings.

The efficacy of disease prediction models is contingent on various factors, including the quality of data, the selection of appropriate algorithms, and the calibration of these algorithms to specific disease characteristics [4, 5, 17]. Our methodology builds upon previous works [1, 14, 22] by incorporating both traditional statistical methods and contemporary machine learning techniques. Through a meticulous process of model development and validation, we strive to achieve superior predictive performance, as well as greater transparency and reliability in the models utilized by healthcare professionals.

3.1. Data Collection and Preprocessing

The foundation of any predictive model is the data upon which it is trained. We sourced our data from multiple healthcare databases, ensuring a diverse representation of patient demographics and medical histories [12, 21]. The datasets were meticulously curated to include a wide range of features pertinent to disease prediction, such as patient age, gender, genetic markers, and lifestyle factors.

Data preprocessing is a critical step that involves cleaning, normalizing, and transforming raw data into a format suitable for analysis. Missing values were addressed using imputation techniques, such as mean substitution and k-nearest neighbors (KNN) imputation [2, 20]. Additionally, categorical variables were encoded using one-hot encoding, and continuous variables were standardized to facilitate model training.

3.2. Feature Selection and Engineering

Feature selection plays a pivotal role in enhancing model accuracy by identifying the most relevant predictors of disease outcomes [7, 16]. We employed a combination of filter, wrapper, and embedded methods to select features that significantly contribute to the predictive performance. Techniques such as recursive feature elimination (RFE) and LASSO regularization were utilized to refine the feature set [13, 18].

Feature engineering further augmented the dataset by creating new variables that encapsulate complex interactions between existing features. This process involved the generation of polynomial features, interaction terms, and domain-specific indices that capture intricate patterns within the data [8, 9].

3.3. Model Selection and Training

The core of our methodology lies in the selection of appropriate machine learning algorithms. We experimented with a variety of models, including logistic regression, decision trees, random forests, and support vector machines (SVM) [15, 19]. To enhance predictive accuracy, we also explored ensemble methods such as boosting and bagging, which combine multiple models to produce a more robust prediction.

Model training was conducted using a stratified k-fold cross-validation approach to ensure that the model's performance is consistent across different subsets of the data [3, 10]. This technique helps mitigate overfitting and provides a more reliable assessment of the model's generalizability.

3.4. Model Evaluation and Validation

The evaluation of model performance was based on several metrics, including accuracy, precision, recall, F1-

score, and area under the receiver operating characteristic curve (AUC-ROC) [11]. These metrics provide a comprehensive understanding of the model's ability to predict disease outcomes accurately.

To validate the models, we employed both internal validation, using a hold-out test set, and external validation, using an independent dataset from a different population [6]. This rigorous validation process ensures that our models are not only accurate but also applicable across diverse clinical settings.

In conclusion, our methodology integrates advanced machine learning techniques with rigorous data preprocessing and feature engineering to improve the accuracy of disease prediction models. By addressing common challenges in model development and validation, we offer a robust framework that enhances the predictive capabilities of existing healthcare systems.

4. Results

In this section, we present the results of our investigation into improving the accuracy of disease prediction models. Through a combination of advanced statistical techniques and machine learning algorithms, our study seeks to enhance the predictive capabilities of existing models, thereby contributing to the broader field of medical informatics. Our results are organized into specific subsections that address key elements of the model development process, including data preprocessing, model selection, and performance evaluation.

Our research leverages a comprehensive dataset encompassing multiple disease categories, allowing for a robust analysis of model accuracy across diverse medical conditions. By incorporating both traditional statistical methods and state-of-the-art machine learning approaches, we aim to provide a comparative analysis that highlights the strengths and limitations of each method. The results presented herein are grounded in rigorous testing and validation procedures, ensuring their relevance and applicability to real-world scenarios.

4.1. Data Preprocessing and Feature Selection

The initial phase of our study focused on data preprocessing and feature selection, which are critical steps in improving model accuracy. Utilizing techniques such as normalization, imputation, and dimensionality reduction, we ensured that the data was clean and suitable for further analysis [4, 5]. Feature selection was conducted using a combination of algorithmic and statistical methods, including recursive feature elimination and principal component analysis, to identify the most relevant predictors [2, 17].

The implementation of these preprocessing techniques resulted in a significant reduction in data dimensionality without compromising the informational content, thus enhancing the computational efficiency of the predictive models [1]. Our approach was validated by observing improved model performance metrics compared to baseline models that did not employ these preprocessing strategies.

4.2. Model Development and Optimization

In the model development phase, we explored a variety of machine learning algorithms, including logistic regression, random forests, and neural networks, to ascertain their respective strengths in disease prediction [14, 21]. Each model was subjected to hyperparameter tuning using grid search and cross-validation techniques to optimize their predictive accuracy [12, 20].

Our findings indicate that ensemble methods such as random forests and gradient boosting machines consistently outperformed traditional models, achieving higher accuracy and AUC scores across multiple disease categories [22]. This aligns with existing literature that advocates for the use of ensemble techniques in complex prediction tasks [7, 16].

4.3. Performance Evaluation and Comparison

The performance of the developed models was evaluated using standard metrics, including accuracy, precision, recall, F1-score, and area under the receiver operating characteristic curve (AUC-ROC) [10, 19]. Our results demonstrate that the integration of advanced preprocessing and model optimization techniques led to substantial improvements in predictive performance.

Specifically, models incorporating feature selection and ensemble learning methods exhibited a marked increase in precision and recall, thereby reducing the incidence of false positives and false negatives [13, 18]. The comparative analysis revealed that these models consistently outperformed baseline models, which lacked such enhancements, reinforcing the efficacy of our approach [8, 9].

4.4. Discussion and Implications

The improved accuracy of disease prediction models achieved in this study has significant implications for clinical decision-making and patient outcomes [3, 15]. Enhanced models can lead to earlier and more accurate diagnoses, potentially improving treatment efficacy and reducing healthcare costs [6, 11]. Our findings underscore the importance of integrating cutting-edge data processing and machine learning techniques in

the development of predictive models, offering valuable insights for future research and application in the field of healthcare informatics [6, 16].

In conclusion, our study provides a comprehensive examination of methodologies to enhance disease prediction model accuracy, contributing to the ongoing discourse on innovative approaches in medical data analysis. The results serve as a foundation for future investigations aimed at further refining predictive models and expanding their applicability across diverse medical contexts [6, 19].

5. Discussion

The study of improving the accuracy of disease prediction models is an ever-evolving field that holds promise for significant advancements in public health. In recent years, there has been an exponential increase in the availability of medical data, which, when properly utilized, can enhance predictive capabilities and inform clinical decision-making. However, the challenge remains to refine these predictive models to ensure they are not only accurate but also robust and generalizable across diverse populations. This discussion explores the critical aspects that influence the accuracy of disease prediction models and examines how contemporary methodologies and technological advancements are shaping the future of predictive analytics in healthcare.

The discussion is structured into key subsections that address various dimensions of the problem and potential solutions. We analyze methodological innovations, the integration of multi-modality data sources, the role of machine learning and artificial intelligence, and the implications of ethical considerations in the deployment of these models. Additionally, we compare the effectiveness of different approaches and frameworks as evidenced in recent literature.

5.1. Methodological Innovations in Disease Prediction

The accuracy of disease prediction models is heavily dependent on the underlying methodologies employed. Traditional statistical models, such as logistic regression, have been widely used due to their interpretability, but they often fall short in capturing complex, non-linear relationships inherent in medical data [4, 5]. Recent innovations have witnessed the adoption of machine learning techniques, including decision trees, random forests, and neural networks, which offer enhanced flexibility and predictive power [14, 22]. These approaches allow for the modeling of intricate interactions and can accommodate large feature spaces, thereby improving prediction accuracy [20].

The development of ensemble methods, which combine

multiple models to improve overall performance, has been particularly noteworthy. Techniques such as boosting and bagging have demonstrated significant improvements in accuracy by reducing variance and bias in predictions [2, 21]. Furthermore, advancements in deep learning, particularly in the use of convolutional and recurrent neural networks, have shown promise in handling high-dimensional data, such as imaging and temporal sequences, with superior performance [12, 17].

5.2. Integration of Multi-Modality Data Sources

The integration of diverse data sources is crucial for enhancing the predictive accuracy of disease models. Multi-modality data, which includes genomic, proteomic, imaging, and electronic health records (EHR), provides a comprehensive view of patient health [1]. The fusion of these data types can uncover novel insights that are not apparent when each modality is analyzed in isolation [7, 16]. Integrative models that utilize heterogeneous data sources have been shown to improve prediction accuracy significantly [18].

Challenges remain in the standardization and preprocessing of multi-modality data, which can introduce noise and variability into models [13]. However, recent advances in data harmonization and feature extraction are addressing these issues, enabling more accurate and reliable predictions [19].

5.3. Role of Artificial Intelligence and Machine Learning

Artificial intelligence (AI) and machine learning (ML) are at the forefront of transforming disease prediction models. AI-driven approaches are particularly adept at identifying patterns and correlations within vast datasets that are beyond the reach of traditional statistical methods [8, 9]. The deployment of AI models in predictive analytics has demonstrated improved accuracy and has facilitated personalized medicine approaches [15].

However, the black-box nature of some AI models poses challenges in clinical settings, where interpretability is crucial for gaining clinician trust and ensuring transparency [10]. Recent efforts in developing explainable AI (XAI) frameworks aim to bridge this gap by providing insights into model decision-making processes [11].

5.4. Ethical Considerations and Model Deployment

The deployment of disease prediction models necessitates careful consideration of ethical issues, particularly concerning data privacy, bias, and equity [6]. The risk of perpetuating existing healthcare disparities through biased models underscores the need for fairness and

inclusivity in model development [3]. Ensuring that models are trained on diverse and representative datasets is paramount to avoiding discrimination and ensuring equitable healthcare access [9].

Moreover, the balance between data utility and privacy protection remains a significant concern. Techniques such as differential privacy and federated learning are being explored to mitigate privacy risks while maintaining model performance [15]. As predictive models increasingly inform clinical decisions, it is imperative to address these ethical considerations to foster trust and ensure the responsible use of technology in healthcare.

In conclusion, enhancing the accuracy of disease prediction models involves a multifaceted approach that integrates methodological advancements, diverse data integration, AI innovations, and ethical considerations. The ongoing evolution of these models promises to revolutionize predictive healthcare, ultimately leading to improved patient outcomes and more efficient healthcare systems.

6. Conclusion

In this paper, we have explored the multifaceted approaches to enhancing the accuracy of disease prediction models. The complexity inherent in predicting disease outcomes requires sophisticated and multifactorial methods, which we have dissected and analyzed comprehensively. By integrating advanced machine learning techniques with robust statistical methodologies, our study contributes to the existing literature on medical informatics and predictive analytics, offering new insights and strategies for improving predictive performance in clinical settings.

The growing body of research underscores the critical need for precise and reliable disease prediction models, particularly as healthcare systems become increasingly data-driven. Our research aligns with recent studies that emphasize the integration of heterogeneous data sources and the application of novel algorithms to tackle the inherent challenges in disease prediction [4, 5, 17]. The key contributions and implications of our findings are further elucidated in the following subsections.

6.1. Summary of Findings

Our study highlights the effectiveness of hybrid models that combine machine learning techniques with conventional statistical methods. Specifically, we demonstrated that ensemble learning methods, such as Random Forests and Gradient Boosting, significantly outperform traditional linear models in terms of predictive accuracy [1, 22]. The incorporation of feature selection algorithms also plays a pivotal role in enhancing model performance by

reducing dimensionality and improving interpretability [14, 21].

Additionally, our analysis reveals that leveraging deep learning architectures, such as Convolutional Neural Networks (CNNs) and Recurrent Neural Networks (RNNs), can capture complex patterns in clinical data that are often missed by simpler models [12, 20]. The application of these methods to time-series data, in particular, has shown promise in predicting disease progression with higher accuracy [2, 7].

6.2. Implications for Practice

The implications of our findings extend beyond theoretical advancements to practical applications in healthcare. The deployment of more accurate and reliable prediction models can significantly enhance clinical decision-making, leading to improved patient outcomes and optimized resource allocation [16, 18]. By integrating these models into electronic health record systems, healthcare providers can benefit from real-time predictions and early interventions, ultimately reducing the burden of disease [8, 13].

Moreover, our study underscores the importance of interdisciplinary collaboration in the development and implementation of disease prediction models. Engaging with experts in machine learning, clinical practice, and

health informatics is crucial for translating theoretical models into actionable insights [9, 15].

6.3. Future Directions

While our research presents significant advancements, it also opens the door to further investigation. Future studies should focus on the development of interpretable models that not only predict outcomes with high accuracy but also provide insights into the underlying mechanisms of disease [10, 19]. Additionally, the integration of genomic and proteomic data into prediction models represents a promising avenue for personalized medicine [3, 11].

Continued efforts to refine and validate these models in diverse clinical settings will be critical to their widespread adoption and success. Additionally, addressing ethical concerns related to data privacy and algorithmic bias remains a paramount consideration in the ongoing development of predictive models [6].

In conclusion, the advancements detailed in this paper reflect a meaningful step towards the realization of precision medicine. By leveraging state-of-the-art methodologies and fostering collaborative efforts across disciplines, we can continue to improve the accuracy and applicability of disease prediction models, ultimately transforming the landscape of healthcare delivery.

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