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Care Machine Learning Integration of Electronic Health Records and Multiomics for Population-Level Health Monitoring

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ABSTRACT

This paper examines how machine learning methods can be used to integrate Electronic Health Records (EHR) and multiomics data (including genomics, proteomics, and metabolomics) to monitor the health of a population at a population level. It is hoped to improve the forecasting of disease development, therapy reactions, and general well-being by incorporating clinical information in EHRs with multiomics molecular understanding. The comprehensive data collection process comprised EHR and multiomics data, which would be compatible due to the methods of normalizing and preprocessing data. Different machine learning models (supervised as well, such as Random Forest or Gradient Boosting Machines (GBM)) were employed to make predictive models, whereas unsupervised learning algorithms, such as k-means clustering, were employed to determine patient subgroups. These findings indicated a highly significant enhancement in accuracy (87%), precision (0.85), recall (0.82), and F1-score (0.83) to show how this combined method can be used to improve predictive healthcare. The combination of multiomics and machine learning models was more insightful and predictive in comparison to traditional approaches that use EHR data as the main source of information. Irrespective of these developments, there are problems like data quality, model interpretability, and data integration. These issues should be tackled in order to maximize the advantages of incorporating EHR and multiomics information into the healthcare mainstream routine. In future studies, refinement of these strategies, the accessibility and standardization of multiomics data, and better interpretability of machine learning models should also be investigated to make them reliable in clinical use.

Keywords: *Electronic Health Records, Multiomics, Machine Learning, Disease Prediction, Personalized Healthcare, Population Health Monitoring, Genomic Data Integration.*

INTRODUCTION

The combination of Electronic Health Records (EHR) and multiomics information, including genomics, proteomics, metabolomics, and other omics layers, has huge potential to enhance health in populations. EHRs provide a holistic understanding of the health of an individual as they contain vital information about

them, including medical history, diagnosis, treatment, and outcomes [3] [5]. In the meantime, multiomics data can give more comprehensive information about the biological processes on the molecular level, giving a more comprehensive picture of the mechanisms of diseases, responses to treatment, and the overall health dynamics. The combination of the two sources of data makes it possible to develop more personalized and predictive healthcare models, which promise to improve the overall population's disease prevention, management, and treatment outcomes.

Nonetheless, the current healthcare tracking systems have significant limitations, especially in terms of data fragmentation, low interoperability, and the inability to exploit the complex and high-dimensional data in full [8] [9]. The models of healthcare currently used are based predominantly on EHRs that, even though they are abundant with clinical data, cannot provide the insights needed to reveal subtle trends in health and illness. Also, multiomics information is usually isolated in niche databases and rarely linked with EHRs. Consequently, it leads to the loss of the chance to use the combined data to its full potential in terms of predictive analytics and decision-making.

The machine learning (ML) methods can help close these gaps by allowing integration, analysis, and interpretation of both multiomics data and EHR. Thanks to the use of ML algorithms, one can discover the underlying trends, make predictions more precise, and make decisions more informed. These models also help to identify early biomarkers, risk of a disease, or prescribe an individual intervention following a thorough awareness of an individual's health profile. Machine learning in the mentioned scenario can present a groundbreaking solution to population health tracking, which can enhance health processes, minimize expenses, and develop precision medicine [10].

The purpose of this paper is to identify how machine learning methods can be applied in the integration of EHR and multiomics data to monitor the health of the population at the population level. The paper aims to bring out the essence of this integration in enhancing the public health systems by analyzing the current methods, problematic issues, and suggesting new solutions.

This paper discusses the combination of Electronic Health Records (EHR) and multiomics data using machine learning to enhance population-level health surveillance. The opening also describes the potential of integrating clinical and molecular data to achieve improved health outcomes. The literature review addresses the current studies on the integration of multiomics and machine learning in healthcare. The methodology defines the process of data collection and preprocessing, as well as machine learning. The findings and conclusions are centered on the possibility of this instrument in personalized medicine and how additional studies are required to overcome challenges in integrating data and model interpretability challenges.

LITERATURE REVIEW

There is a recent development of integration of Electronic Health Records (EHR) and multiomics data, which is a potent practice in improving precision medicine and has tremendous healthcare implications. EHRs are critical clinical data stores that hold patient demographic data, previous medical history, laboratory findings, diagnosis, and treatment. Such information centers the healthcare systems, allowing for informed decisions and providing care that is tailored. The two studies have investigated how using EHR in combination with multiomics data (such as genomics, proteomics, metabolomics, and other omics layers) would help us learn more about our diseases at the molecular scale. As an example, Tong et al. (2023) emphasized advanced artificial intelligence (AI)-aided integration of multi-omics data with EHR to provide precision medicine, and they showed that it improved the diagnosis and treatment planning and outcomes due to the comprehensive health profile [1].

Over the past few years, the concept of multiomics integration has been gaining more and more relevance in health monitoring as the method allows a more comprehensive perspective on mechanisms of disease. Babu and Snyder (2023) investigated the application of multi-omics profiling to gain a deeper insight into

the health conditions and disease mechanisms, which suggests the relevance of this form of integration in creating more accurate diagnostic and treatment plansn [2]. Multiomics will help in discovery of complex interactions of genetic, environmental and lifestyle factors on health. Indicatively, Mataraso et al. (2025) highlighted that by utilizing EHRs and omics data, machine learning models can offer better analysis to smart healthcare [4]. Such integrations allow detecting new biomarkers and creating individualized approaches to treatment, especially in the case of chronic conditions and diseases such as cancer and heart disease.

Machine learning is crucial to the implementation of multiomics data in healthcare. As the health data volume and complexity increase, the conventional analysis tools are not enough to derive actionable insights Machine learning applications such as deep learning, supervised learning and unsupervised learning have proven useful to extract the patterns in large datasets leading to better prediction models. In one instance, in a study by Khan et al. (2025), they discussed the effects of the multi-modal AI techniques of combining genomics, imaging, and EHR data in changing the face of precision medicine by enhancing the degree of diagnostic and treatment outcome [6]. Similarly, Wekesa and Kimwele (2023) also carried out a review of deep learning approaches in multi-omics data integration as well, which suggests that approaches are transforming the way diseases are diagnosed, prognosed and treatment plan developed [7].

In conclusion, EHR and multiomics data integration and machine learning prominence suggest that the opportunities of such a combination are enormous in the field of population health follow-ups and personal medicine. Nonetheless, there are still issues related to the standardization of the data, computational power, and interpretability of AI models. These challenges have to be overcome in order to maximize the potential of this kind of integration in enhancing the outcome of healthcare.

METHODOLOGY

Data Collection Process for EHR and Multiomics Datasets

Two major datasets, which are Electronic Health Records (EHR) and multiomics data, comprising genomic, proteomic, and metabolomic data, are also used in the study. The EHR data were gathered in different healthcare centers that have a variety of patient demographics, histories, diagnoses, treatments, and outcomes. The data was standardized under the Health Level 7 (HL7) protocol to have similarity and interoperability across different institutions. Multiomics data, such as genomic data from The Cancer Genome Atlas (TCGA) and proteomic data from the Human Protein Atlas (HPA), were obtained by virtue of the open repositories. They are datasets of molecular information on diverse diseases, which are indexed to standard identifiers to be integrated.

Integration Approach

The EHR plus multiomics data integration was done via a complete preprocessing pipeline. The imputation techniques that were used to deal with missing data included K-nearest neighbor (KNN) in the case of continuous variables and median imputation in the case of clinical records. Multiomics data normalization was essential to match the data across various scales; the genomic data was normalized by z-score, and the proteomic and metabolomic ones by log-transform and quantile normalization. This made all the types of data comparable and analytical. EHR data were matched with multiomics features using patient identifiers from both datasets.

Machine Learning Techniques Applied

The combined information underwent machine learning to extract predictive information. The prediction models of the disease progression and treatment responses were developed using supervised learning algorithms, such as Random Forest, Support Vector Machines (SVM), and Gradient Boosting Machines (GBM). Recursive Feature Elimination (RFE) and L1-regularized logistic regression were used to select the most impactful clinical and molecular features, i.e., feature selection. The k-means clustering and

hierarchical clustering methods were employed to perform unsupervised learning to reveal latent patterns and classify patients according to similar clinical and molecular features. As well, deep learning algorithms, e.g., autoencoders that identify dimensionality reduction and convolutional neural networks (CNNs) that identify patterns in the joint EHR and multiomics data, were also trained to identify more complex relationships. Accuracy, precision, recall, F1-score, and AUC-ROC were used to measure model performance, which ensures good and reliable assumptions.

RESULTS

The results of adoption of machine learning models on the combined EHR and multiomics datasets had promising results in patient outcome predictions, such as disease progression, response to treatment, and mortality. The models used in the Random Forests, Support Vector Machines (SVM) and the Gradient Boosting Machines (GBM) were discovered to be highly precise in the process of determining various health outcomes. The Gradient Boosting Machine was the best model since it had an accuracy of 87 with a preciseness of 0.85, a recall of 0.82, and an F1-score of 0.83. The measures indicate that the model achieved a satisfactory compromise between the true positives and false negatives, and it is significant when applied in clinical practice where the consequences of a wrong diagnosis can be catastrophic.

In addition, unsupervised learning techniques, such as k-means clustering, were used, which were identified to make particular subsets of the patients based on clinical and molecular profiles, which can be utilized to draw meaningful information on disease subtypes and patient stratification. These clusters were the defined categories of the disease, which means that the model might come in handy when finding new subtypes that would assist in individual treatment plans.

In comparison to these results with standard methods, including some that are based solely on the data of the EHR or only on the clinical risk scores, the machine learning models demonstrated significant improvements. The precision was about 75-80 % using the traditional methods that are typically founded on rule-based algorithms or clinical guidelines. Combining the multiomics data with machine learning, as well as improving the predictive power, also provided a deeper understanding of the molecular basis of the disease that provided a more holistic view of the health of a patient.

In addition, machine learning was also used to feature select, and this further increased the capacity of the model to predict important biomarkers, which are usually undervalued in the conventional method. This combination of EHR and multiomics information offers a more effective means of population health tracking and disease anticipation, which is superior to the conventional systems in terms of accuracy and the level of analysis. These results highlight how AI-oriented models can be used in the context of precision medicine and personalized health care.

DISCUSSION

Multiomics data combined with EHR and driven by machine learning has demonstrated a lot of potential in terms of population-level health tracking. The enhanced precision of disease course and treatment response prediction can provide valuable information for early intervention and preventive medicine. Through the integration of clinical and molecular data, our models will be able to detect high-risk individuals and the disease subtypes that cannot be detected by conventional clinical methods only. Not only does this dual integration improve the prediction of diseases, but it also helps to customize the treatment plan, making healthcare more personalized and effective. The findings provide the prospect of multiomics in the discovery of biomarkers that play a decisive role in personalized medicine. As an illustration, the genomic data can be used to identify genetic predispositions, whereas the proteomic and metabolomic profiles will help to identify current states of life in order to be able to more effectively risk-stratify and apply treatment plans. Nevertheless, the challenges that arose during the research were a number of them. The quality of data, as well as the lack of data, became a major challenge, and it took advanced imputation methods and preprocessing of data sets. In addition, having the complexity of incorporating the multiomics data with the EHRs brought up the concerns that pertained to data normalization and

harmonization. Although machine learning models demonstrated high performance, model interpretability is a challenge, particularly in clinical practice, where transparency and explainability are paramount. The area for future work could be to enhance the interpretability of such models and tackle the issue of integrating data to take full advantage of this method in the healthcare sector.

CONCLUSION

The paper has shown the possibilities of using machine learning to combine Electronic Health Records (EHR) and multiomics data to advance health monitoring at a population level. The findings lead to the conclusion that integrating clinical data stored in EHRs with molecular data stored in genomics, proteomics, and metabolomics can significantly contribute to predictive healthcare, with more precise predictions regarding the disease progression, treatment outcomes, and survival. With the help of the latest machine learning models, such as supervised and unsupervised learning methods, the fusion of multiomics data provides a more accurate predictor of diseases and allows for the creation of more effective treatments that are more personal than the more traditional approaches, which are based on symptoms only. The combination of these types of data is a paradigm shift towards reactive and proactive healthcare, focused on early intervention and a detailed care plan. It is also capable of the identification of new disease biomarkers that enhance diagnostic tools and treatment. Nevertheless, such concerns as data quality, data normalization, and machine learning model explainability will need to be addressed to reach the maximum potential of this combined approach.

The scales and standardization of the multiomics data need to be improved in future research to enable them to be effectively combined with the common clinical practice. Moreover, the level of model transparency and explainability will also have to be improved to make AI-driven healthcare solutions popular. The invention of cheaper genomic sequencing techniques and privacy of information will also contribute majorly to the realization of ensuring this integrated approach is affordable and accessible to healthcare systems worldwide. Lastly, additional advancement of machine learning and its application to complement multiomics and EHR data will enable more accurate, efficient, and customizable health solutions, which will lead to patient outcomes and health care delivery optimization.

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