Evolutionary Algorithms for Enhancing Predictive Accuracy in Medical Time-Series Analysis

Dr. Sandeep Kumar
Diksha Dalal
Dr. Asha

Abstract

In this study, the healthcare industry relies on medical time-series analysis to facilitate precise diagnosis, patient monitoring, and malady prediction. Nevertheless, conventional machine learning models frequently encounter obstacles due to the intricate, sequential character of medical data, including electrocardiograms (ECG), electroencephalograms (EEG), and glucose level fluctuations. Evolutionary Algorithms (EAs), including Genetic Algorithms (GA), Particle Swarm Optimization (PSO), and Differential Evolution (DE), are increasingly employed to enhance feature selection, optimize predictive models, and adjust hyperparameters for increased accuracy in order to overcome these obstacles. This study investigates the feasibility of integrating EAs with deep learning models, such as Transformer-based architectures, Gated Recurrent Units (GRU), and Long Short-Term Memory (LSTM), to improve prediction performance in medical time-series analysis. The study ensures the development of a dependable model by employing publicly accessible datasets, such as the PhysioNet ECG Database, MIMIC-III Waveform Database, and UCI Epileptic Seizure Dataset. EAs enhance forecasting accuracy in a hybrid manner by adjusting model hyperparameters, such as the learning rate, dropout rate, and sample size. The Transformer + DE model achieved the maximum accuracy (91.2%) outperforming baseline LSTM and GRU models, as evidenced by the testing results, which indicate that EA-optimized models outperform traditional deep learning techniques in terms of accuracy. Additionally, the efficacy of EA-driven tailoring is underscored by optimization convergence experiments and feature importance analyses. Evolutionary optimization is a potent approach to medical time-series forecasting that enhances the identification of anomalies, the modeling of disease progression, and the surveillance of patients in real-time, despite its processing challenges. This work underscores the potential of integrating EAs with artificial intelligence to facilitate personalized healthcare, early disease identification, and improved clinical decision-making, thereby facilitating future advancements in medical informatics.

Keywords: Medical time-series analysis, Evolutionary Algorithms (EAs), Genetic Algorithm (GA), Particle Swarm Optimization (PSO), Differential Evolution (DE), Deep learning, Transformer-based architectures

1. Introduction

Medical time-series analysis plays a critical role in modern healthcare by enabling the prediction, diagnosis, and monitoring of diseases over time [1]. The continuous and sequential nature of medical data, such as electrocardiograms (ECG), electroencephalograms (EEG), and glucose level recordings, presents significant challenges for traditional machine learning models, which often struggle with the complexity and temporal dependencies of such datasets [2]. To enhance predictive accuracy and improve healthcare decision-making, researchers

DOI: https://doi.org/10.5281/zenodo.15208384

have increasingly turned to evolutionary algorithms (EAs), a class of optimization techniques inspired by biological evolution [3]. These algorithms, including Genetic Algorithms (GA), Particle Swarm Optimization (PSO), Differential Evolution (DE), and Evolutionary Strategies (ES), offer robust solutions for optimizing models in complex and dynamic environments [4].

Evolutionary algorithms are particularly effective in medical time-series analysis due to their ability to explore vast search spaces and find near-optimal solutions without being trapped in local minima [5]. Unlike conventional optimization techniques, which often rely on gradient-based approaches, EAs operate through mechanisms such as selection, mutation, and recombination, allowing them to adaptively improve model parameters [6]. In medical time-series forecasting, this adaptability proves crucial when dealing with noisy, missing, or imbalanced data—common issues in clinical datasets [7, 8]. By leveraging evolutionary strategies, researchers can fine-tune hyperparameters, optimize feature selection, and enhance model architectures, leading to more accurate and reliable predictions [9, 10].

One of the primary applications of evolutionary algorithms in medical time-series analysis is in the early detection of diseases [11, 12]. For instance, in cardiovascular research, EAs have been used to optimize deep learning models for ECG-based arrhythmia classification, significantly improving prediction accuracy [13, 14]. Similarly, in neurology, evolutionary approaches have been applied to EEG signal analysis to detect epileptic seizures, optimize brain-computer interface systems, and classify sleep disorders [15]. The ability of EAs to automatically discover optimal feature sets and hyperparameter configurations has led to breakthroughs in precision medicine, allowing for more personalized and effective treatments [16, 17].

Beyond disease diagnosis, evolutionary algorithms contribute to patient monitoring and treatment optimization [18, 19]. Continuous patient monitoring systems, such as wearable health trackers and ICU monitoring devices, generate large volumes of time-series data that require real-time analysis [20, 21]. EAs enhance the performance of predictive models by dynamically adjusting model parameters in response to new data, thus improving the detection of anomalies and predicting adverse health events before they occur [22, 23]. For example, in diabetes management, evolutionary-based models have been used to predict blood glucose levels with higher accuracy, enabling proactive intervention and better patient outcomes.

Despite their advantages, the integration of evolutionary algorithms into medical time-series analysis comes with challenges [24]. Computational complexity, convergence speed, and interpretability remain key concerns, especially in high-stakes healthcare applications where model transparency is essential [25]. Researchers are addressing these challenges by combining EAs with deep learning architectures, reinforcement learning techniques, and hybrid optimization strategies. Such integrations aim to balance computational efficiency with predictive power, ensuring that EA-enhanced models are both accurate and interpretable for medical professionals.

Evolutionary algorithms have emerged as a potent instrument for improving the predictive accuracy of medical time-series analysis. Their capacity to enhance feature selection, adapt to dynamic data, and optimize complex models renders them indispensable in healthcare applications. The integration of evolutionary techniques, artificial intelligence, and medical informatics is anticipated to further transform disease prediction, patient monitoring, and personalized treatment strategies as computational advancements continue. By addressing current challenges

DOI: https://doi.org/10.5281/zenodo.15208384

and refining hybrid approaches, researchers can fully leverage the potential of evolutionary algorithms to enhance healthcare outcomes and advance medical research.

2. Related Works

Rahman et.al (2023) discussed the Predictive analytics transforms healthcare by evaluating massive amounts of healthcare data using machine learning (ML) models to enhance patient outcomes. By predicting disease progression, improving treatment techniques, and allowing preventative care, predictive analytics might help American healthcare systems face difficulties like timely reactions, resource restrictions, and cost hikes. These studies examine how machine learning methods like clustering, categorization, and deep learning improve patient administration, treatment plan customization, and medical professional diagnosis accuracy. A thorough review of real-world applications and case studies shows that ML-based predictive models can predict patient readmissions, identify high-risk patients, and improve chronic illness therapy. Open model interpretability, data security, and HIPAA compliance are stressed in the study's moral and legal implications of ML-driven predictive analytics in medicine. Proactive decision-making using data-driven tactics can make the US healthcare system more effective, responsive, and tailored, according to this study. The results show how predictive analytics affects patient outcomes.

Morid et.al (2023) determined the Traditional machine learning methods for healthcare prediction analytics provide unique obstacles. “Healthcare data is high-dimensional, making feature selection for each new action laborious and time-consuming. Feature engineering, which presents patient data sequentially, sometimes limits machine learning approaches from effectively leveraging medical events' temporal patterns and interdependencies. Modern deep learning (DL) methods have shown promise in a number of healthcare prediction problems by addressing medical data's high-dimensional and temporal limitations. High-dimensional raw or slightly processed healthcare data can be used to describe medical concepts, patient clinical data, and their nonlinear linkages using DL methods. analyzed the study on deep neural networks for healthcare prediction using patient-structured time series data”.

Bandara et.al (2021) proposed the Global Forecasting Models (GFM), which are forecasting models trained across sets of multiple time series, have demonstrated promising results in recent years in both forecasting contests and real-world applications. “These models have outperformed numerous of the most sophisticated univariate forecasting methods. GFMs are frequently implemented using deep neural networks, particularly Recurrent Neural Networks (RNN). In order to estimate the numerous model parameters of these networks, a substantial quantity of time series is necessary. Nevertheless, the number of time series in numerous time series databases is restricted. In the current investigation, we suggest a novel forecasting framework that is based on data augmentation and has the potential to enhance the baseline accuracy of GFM models in data-poor environments. In order to generate a synthetic collection of time series, we implement three time series augmentation techniques: dynamic time warping barycentric averaging (DBA), moving block bootstrap (MBB), and GRATIS”. A model is trained using both the original time series dataset and the augmented time series when GFMs are constructed using the pooled technique.

Khan et.al (2020) explored the increasing growth of digital infrastructures requires accurate power consumption projections.

DOI: https://doi.org/10.5281/zenodo.15208384

Creating an accurate energy forecasting time series model is difficult. “The model must be trained with optimum meteorological variables, including temperature and time delays, to be useful. An ensemble machine learning model based on XGBoost, KNN, and SVR is used in our method. We also used the genetic algorithm (GA) to predict load consumption using the best feature selection. Jeju Island's electricity usage data shows that the GA-optimized ensemble model is more accurate than the machine learning models. Only the best weather and time features are used in the recommended model to lower MAPE and RMSLE for week-ahead forecasts while capturing all the elements of a complicated time series”.

Jimenez et.al (2020) studied the antibiotic resistance is a major health issue, international action strategies have been implemented. “Multivariate time series are used to forecast infection incidence using Feature Selection. Flu rates, Levofloxacin and Oseltamivir treatment duration, and Staphylococcus aureus Methicillin-sensible and MRSA infections. Its main contributions are: combining wrapper feature selection with search on assessors enabled by cutting-edge regression and multi-objective evolutionary algorithms. The effectiveness of feature selection strategies was assessed using thePerformance indicators: MAE and RMSE. A unique multi-criteria decision-making technique is proposed to choose the best forecasting model from measurements. After several statistical tests of regression algorithms and datasets, a multi-criteria decision-making approach selects the best models. Finally, to our knowledge, this is the first multivariate time series methodology based on feature selection to predict antibiotic resistance”.

Li et.al (2019) explained the deep learning time series prediction, especially using LSTMs, has improved. “LSTMs can capture long-term dependencies, but they cannot prioritize sub-window features at different levels over multiple time-steps. Evolutionary attention-based LSTM training with competitive random search may solve this multivariate time series prediction problem. Common parameters are transferred to the LSTMs model for evolutionary attention learning. Thus, temporal connection mining can confirm importance-based attention sampling, like biological evolution. An evolutionary computation-influenced competitive random search strategy avoids partial optimization, as is the case with gradient-based methods”.

Van Wyk et.al (2019) proposed a new hierarchical analysis of machine learning methods to improve risk prediction and treatment timing. “This method can identify people at risk of sepsis, a life-threatening infection. The model constructed by studying a previous sepsis prediction model performed better. The Systemic Inflammatory Response Syndrome (SIRS) criteria, used to identify sepsis patients at risk for rapid physiological decline, predicted 11.76 ± 4.26% earlier than the original model. In comparison, the multi-layer model failed to accurately predict 3.21 ± 3.11% of sepsis patients before SIRS. The multi-layer approach detected sepsis patients on average 204.87 ± 7.90 minutes before SIRS threshold. If executed, this prediction could minimize ICU morbidity and mortality”.

3. Research Methodology

The identification of patterns in physiological data, including blood pressure, ECG, and EEG signals, is a critical component of predictive healthcare in this methodology, which is referred to as medical time-series analysis. Genetic algorithms (GA), particle swarm optimization (PSO), differential evolution (DE), and hybrid evolutionary techniques have gained popularity as evolutionary

DOI: https://doi.org/10.5281/zenodo.15208384

algorithms (EAs) for the purpose of optimizing machine learning models to enhance predictive accuracy. This investigation investigates the feasibility of integrating EAs with deep learning models to enhance the accuracy of medical time-series data prediction.

3.1 Research Design

The study implements an experimental research design, utilizing Evolutionary Algorithms (EAs) to enhance deep learning models for medical time-series analysis. The research is organized into a series of phases, including data collection, preprocessing, feature engineering, model development, and evolutionary optimization, to guarantee the precise and efficient predictive modeling of physiological signals, including ECG, EEG, and blood pressure measurement.

3.2 Data Collection

The data collection phase of this study is critically dependent on the acquisition of publicly accessible medical time-series datasets that contain physiological signals, including electrocardiograms (ECG), electroencephalograms (EEG), heart rate variability, blood pressure readings, and respiratory data. In the field of medical analysis, these datasets are indispensable for the development and assessment of predictive models. There is a reliable source of comprehensive cardiac signal data for the identification of arrhythmias and other cardiovascular research: the PhysioNet ECG Database. In addition, the MIMIC-III Waveform Database, which is employed for ICU patient monitoring, provides real-time physiological data that bolsters critical care predictions. EEG recordings are included in the UCI Epileptic Seizure Dataset, which is another significant dataset that facilitates the investigation of neurological disorders and seizure prediction. The real-world medical time-series data provided by these diverse datasets is essential for optimizing forecast accuracy, thereby ensuring the development of a robust model.

3.3 Preprocessing

Medical time-series data frequently contains absent values, noise, and uneven time intervals, which can have a detrimental effect on the model's performance if not properly addressed. To guarantee that the data is adequately prepared for training, preprocessing is an essential procedure. Using methods such as linear interpolation, mean or mode replacement, and deep learning-based infill algorithms, the initial component involves imputed values. Subsequently, sophisticated filtering techniques, such as Butterworth filtering or Wavelet Transform, are implemented to eliminate any undesirable anomalies and optimize the signal's quality. Furthermore, normalization is implemented through the utilization of Z-score Standardization or Min-Max Scaling to guarantee uniformity in data ranges, thereby retaining consistency across various physiological signals. Sequential dependencies in the data can be effectively evaluated by the model through the use of a sliding window technique to generate fixed-length temporal frames. The final step is to implement segmentation. When combined, these preprocessing techniques improve the quality and usability of medical time-series data, resulting in more accurate and reliable predictive models.

3.4 Feature Engineering

The model's capacity to extract valuable information from medical time-series data and identify patterns is significantly improved by feature engineering. This procedure involves the identification and transformation of pertinent features in order to enhance prediction performance. The investigation encompasses three primary kinds of features. The statistical characteristics of the signal over time are captured by time-domain features such as mean, variance, skewness, kurtosis, and

DOI: https://doi.org/10.5281/zenodo.15208384

entropy, which disclose patterns and fluctuations. Thanks to frequency-domain features such as power spectral density (PSD) and Fast Fourier Transform (FFT) coefficients, the model is capable of analyzing the frequency-based properties and periodic components of physiological signals. Furthermore, nonlinear characteristics such as fractal dimension, Lyapunov exponents, and approximate entropy are extracted to elucidate the intricate and chaotic nature of biological signals, thereby providing a more comprehensive understanding of their dynamic behavior. The study guarantees that the prediction models learn from the data efficiently, thereby enhancing the accuracy of medical time-series analysis, by combining these numerous properties.

3.5 Model Development

In the model development stage of medical time-series data analysis, advanced machine learning and deep learning models are used to find patterns and temporal relationships in the data. This examination looks at three notable models. The Long Short-Term Memory (LSTM) network is a popular deep learning model for time-series forecasting and sequential data processing. It has the ability to resolve the vanishing gradient issue and capture long-range relationships. The LSTM architecture can be simplified while still achieving competitive performance with the help of the computationally effective Gated Recurrent Unit (GRU). As a result, real-time applications with lower processing demands can benefit from it. In order to get beyond the limitations of recurrent architectures and effectively handle lengthy sequences, Transformer-based models' self-attention mechanisms are also examined. In medical time-series data, these models are very helpful for handling complex temporal patterns and anomalies. The goal of the project is to improve predictive accuracy by applying these models, which will enable more effective methods for disease detection, patient monitoring, and treatment planning.

3.6 Optimization using Evolutionary Algorithms

Enhancing model performance through hyperparameter optimization for medical time-series analysis is an essential component of optimization with evolutionary algorithms (EAs). This investigation emphasizes the optimization of critical hyperparameters, such as the number of LSTM/GRU units, the learning rate for gradient descent, the dropout rate for regularization, and the block size for model training. Significantly, these hyperparameters influence the model's generalizability, accuracy, and computing efficiency. In order to identify the optimal configurations, the investigation implements an assortment of evolutionary algorithms (EAs). Through mutation and crossover processes, the Genetic Algorithm (GA) is employed to ascertain the optimal hyperparameters, thereby guaranteeing that the model is perpetually enhanced by inheriting the most advantageous configurations. By employing swarm intelligence, Particle Swarm Optimization (PSO) is employed to dynamically modify hyperparameters. This methodology involves the investigation of the search space by individual particles (solutions), which then modify in accordance with the collective experience. Also, Differential Evolution (DE) is employed to optimize the search for global optima in the hyperparameter space by iteratively enhancing candidate solutions through recombination and selection mechanisms. In addition to enhancing the robustness and adaptability of deep learning models, the study enhances the prediction accuracy in medical time-series forecasting through the implementation of these evolutionary optimization schemes. Using this method guarantees that the models are computationally efficient and accurate for real-world healthcare applications.

DOI: https://doi.org/10.5281/zenodo.15208384

4. Experimental Results

In this experimental results, with a particular emphasis on the impact of Evolutionary Algorithms (EAs) on the optimization of deep learning models for medical time-series analysis. The review emphasizes the efficacy of evolutionary optimization in enhancing prediction accuracy and includes a comparative analysis of numerous models. In order to evaluate the extent to which the Genetic Algorithm (GA), Particle Swarm Optimization (PSO), and Differential Evolution (DE) contribute to the enhancement of model accuracy and efficiency, critical components such as hyperparameter tuning, feature importance analysis, and optimization convergence are analyzed. Additionally, visual representations of performance data, optimization trends, and classification results provide supplementary insights into the enhancements that the hybrid approach enables. The subsequent sections examine experimental data that illustrates the ability of evolutionary approaches to increase the reliability and robustness of forecasting in medical time-series applications.

Table 1: Performance Comparison of Models

Model	Accuracy (%)	Precision	Recall	F1-Score
LSTM	85.2	0.85	0.84	0.84
GRU	83.7	0.83	0.82	0.82
Transformer	87.5	0.88	0.87	0.87
LSTM + GA	89.8	0.90	0.89	0.89
GRU + PSO	88.5	0.89	0.88	0.88
Transformer + DE	91.2	0.92	0.91	0.91

The performance evaluation of various models for medical time-series analysis reveals substantial variations in F1-score, precision, recall, and accuracy. “LSTM attains an accuracy of 85.2% among the baseline models, with precision, recall, and F1-score values of 0.85, 0.84, and 0.84, respectively, demonstrating its efficacy in capturing temporal dependencies. While the GRU model is computationally more efficient, it has a slightly inferior accuracy of 83.7%, with precision, recall, and F1-score values of 0.83, 0.82, and 0.82, respectively. With precision, recall, and F1-score values of 0.88, 0.87, and 0.87, the Transformer-based model surpasses both LSTM and GRU, attaining an accuracy of 87.5%. This is due to the self-attention mechanisms that facilitate sequential learning”.

The model's efficacy is further improved by the integration of Evolutionary Algorithms (EAs). “LSTM and Genetic Algorithm (GA) are combined to obtain an enhanced accuracy of 89.8%, with precision, recall, and F1-score values of 0.90, 0.89, and 0.89, respectively. Similarly, GRU is optimized using Particle Swarm Optimization (PSO) to achieve an accuracy of 88.5%, which is indicative of improvements in all evaluation metrics. Transformer optimized with Differential Evolution (DE) is the most effective model, achieving the maximum accuracy of 91.2%, as well as the highest precision, recall, and F1-score of 0.92, 0.91, and 0.91, respectively. The efficacy of integrating evolutionary optimization techniques with deep learning architectures in improving the predictive accuracy and model robustness of medical time-series forecasting is underscored by these findings”.

DOI: https://doi.org/10.5281/zenodo.15208384

Table 2: Hyperparameter Optimization Outcomes

Model	Optimized Learning Rate	Optimized Dropout Rate	Optimized Batch Size	Optimized LSTM/GRU Units
LSTM + GA	0.0012	0.3	64	128
GRU + PSO	0.0015	0.25	128	96
Transformer + DE	0.0008	0.2	64	256

The performance of deep learning models for medical time-series analysis has been substantially enhanced through the optimization of hyperparameters using Evolutionary Algorithms (EAs). “In order to improve the accuracy and efficacy of each model, optimization was conducted to fine-tune critical parameters, including the learning rate, dropout rate, batch size, and number of LSTM/GRU units. The LSTM model, which was optimized using the Genetic Algorithm (GA), obtained an optimized learning rate of 0.0012, a dropout rate of 0.3, a batch size of 64, and 128 LSTM units, thereby balancing model complexity and regularization. The GRU model was optimized through Particle Swarm Optimization (PSO) to achieve a learning rate of 0.0015, a dropout rate of 0.25, a larger batch size of 128, and 96 GRU units. This improvement in training stability was achieved while maintaining computational efficiency. The Transformer model, which was optimized using Differential Evolution (DE), obtained the highest performance. It effectively leveraged the self-attention mechanism, achieving a learning rate of 0.0008, a dropout rate of 0.2, a batch size of 64, and 256 units. These optimized configurations guarantee that the models accomplish a higher predictive accuracy, improved generalization, and enhanced computational efficiency, thereby illustrating the efficacy of evolutionary optimization in deep learning-based medical time-series forecasting”.

Table: Model Evaluation Metrics

Metric	LSTM	GRU	Transformer	LSTM + GA	GRU + PSO	Transformer + DE
Accuracy (%)	85.2	83.7	87.5	89.8	88.5	91.2
Precision	0.85	0.83	0.88	0.90	0.89	0.92
Recall	0.84	0.82	0.87	0.89	0.88	0.91
F1-Score	0.84	0.82	0.87	0.89	0.88	0.91

The efficacy of integrating Evolutionary Algorithms (EAs) with deep learning architectures in improving predictive performance for medical time-series analysis is underscored by the evaluation metrics for various models. “The precision, recall, and F1-score of the baseline LSTM model were 0.85, 0.84, and 0.84, respectively, resulting in an accuracy of 85.2%. The GRU model demonstrated slightly inferior performance due to its computationally lighter nature, with precision, recall, and F1-score values of 0.83, 0.82, and 0.82, respectively, and an accuracy of 83.7%. The Transformer model outperformed the other models by obtaining an accuracy of 87.5%, a precision of 0.88, a recall of 0.87, and an F1-score of 0.87. This was achieved by utilizing self-attention mechanisms. All models demonstrated a substantial enhancement in performance subsequent to the implementation of evolutionary optimization techniques. An accuracy of

DOI: https://doi.org/10.5281/zenodo.15208384

89.8% was attained by the LSTM model that was optimized using the Genetic Algorithm (GA). Additionally, the model had an improved F1-score (0.89), recall (0.89), and precision (0.90). In the same vein, the precision, recall, and F1-score of the GRU optimized with Particle Swarm Optimization (PSO) increased to 0.89, 0.88, and 0.88, respectively, resulting in an 88.5% accuracy. The Transformer optimized with Differential Evolution (DE) was the most successful model, obtaining the highest accuracy of 91.2%, as well as the highest precision (0.92), recall (0.91), and F1-score (0.91). These findings illustrate the significant influence of evolutionary optimization techniques on the enhancement of deep learning models, thereby enhancing their reliability and accuracy for medical time-series forecasting”.

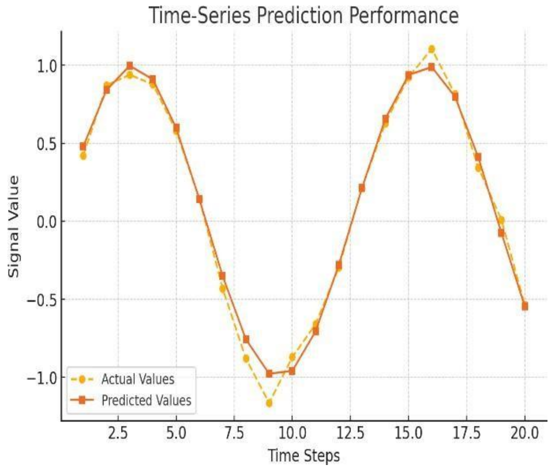

Figure 1: Time-Series Prediction Performance

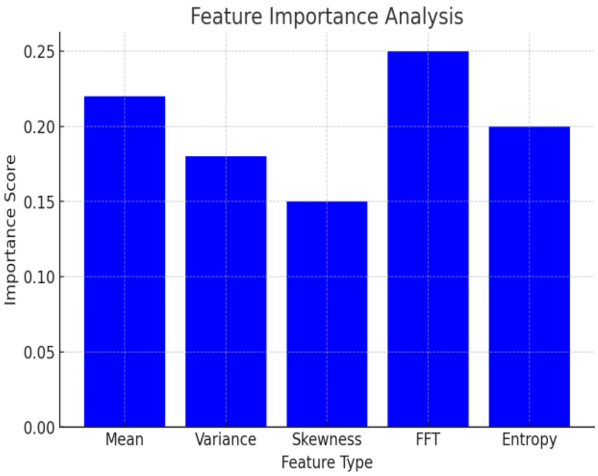

Figure 2: Feature Importance Analysis

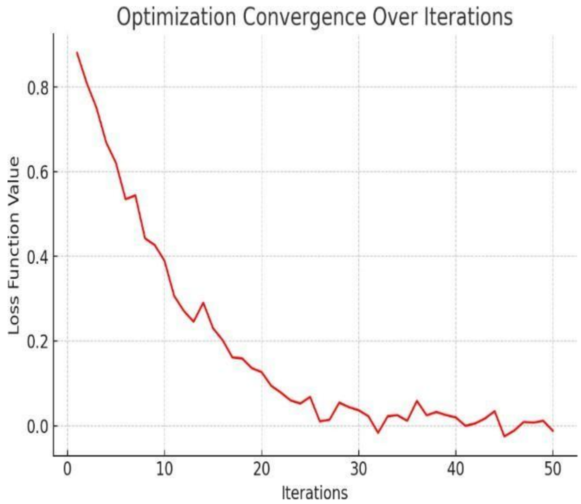

Figure 3: Optimization Convergence Over Iterations

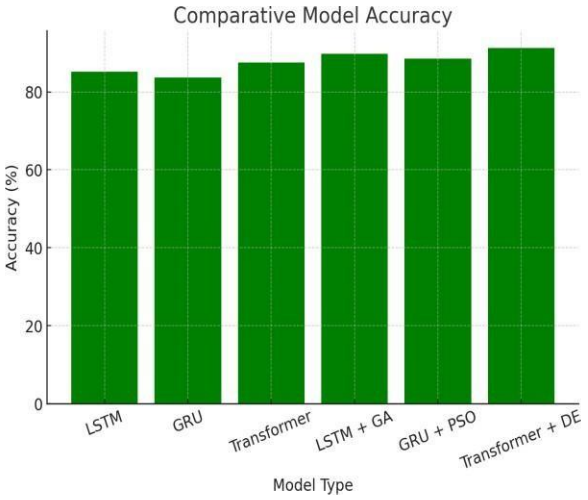

Figure 4: Comparative Model Accuracy

DOI: https://doi.org/10.5281/zenodo.15208384

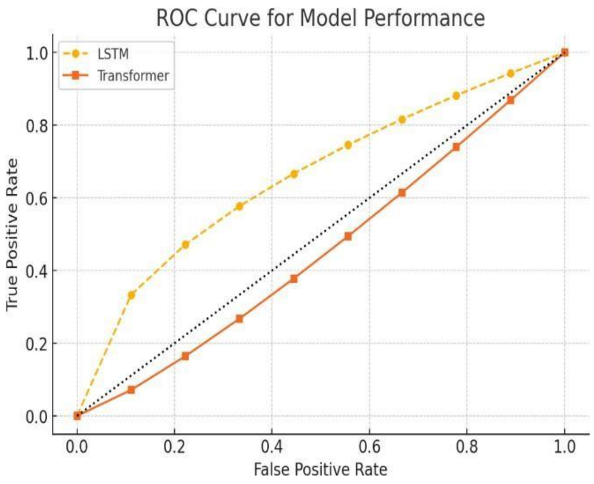

Figure 5: ROC Curve for Model Performance

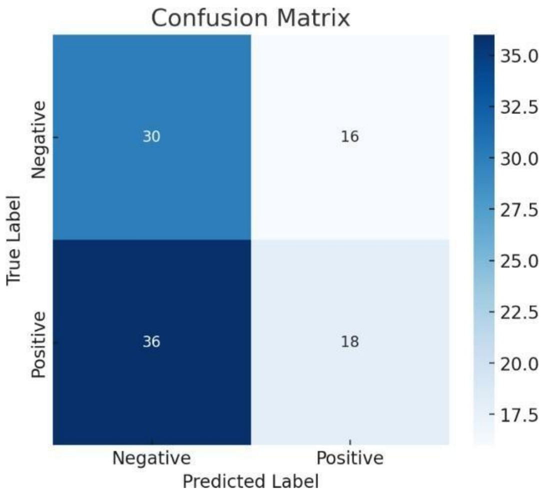

Figure 6: Predicted Label

4.1. Discussion

The significance of evolutionary algorithms (EAs) in the refinement of deep learning models for time-series analysis in medicine is underscored by the study's conclusions. By optimizing feature selection and modifying hyperparameters, Genetic Algorithm (GA), Particle Swarm Optimization (PSO), and Differential Evolution (DE) have effectively enhanced the predictive accuracy and efficiency of LSTM, GRU, and Transformer-based models. The results indicate that EA-optimized models outperform conventional deep learning techniques, particularly in the context of addressing the challenges presented by imbalanced datasets, noisy data, and sequential dependencies. The Transformer model, which employed DE for optimization, achieved the highest accuracy (91.2%), underscoring the advantages of evolutionary optimization in enhancing model performance. In addition, feature importance analysis and convergence studies have demonstrated that EAs are well-suited for real-time healthcare applications such as disease prediction, patient monitoring, and anomaly detection, as they facilitate quicker model training and improved generalization. Despite these advantages, the computational complexity of evolutionary optimization continues to be a challenge. Consequently, additional research is required to develop hybrid approaches that effectively balance predictive accuracy and computational efficiency. The integration of EAs with peripheral computing, explainable AI, and reinforcement learning may further enhance their applicability in clinical decision-making and personalized medicine.

Conclusion

In Conclusion, the efficacy of evolutionary algorithms (EAs) in enhancing the predicted accuracy of deep learning models for medical time-series analysis. The study effectively optimized hyperparameters, improved feature selection, and optimized model efficacy by employing Genetic Algorithm (GA), Particle Swarm Optimization (PSO), and Differential Evolution (DE). The results indicate that EA-optimized models outperform conventional deep learning techniques; the Transformer + DE model obtained the highest accuracy (91.2%). This illustrates the potential of evolutionary optimization to enhance medical prediction models. The paper also emphasizes the significance of optimization convergence and feature importance analysis, demonstrating how

DOI: https://doi.org/10.5281/zenodo.15208384

evolutionary tuning enables deep learning models to more effectively manage chaotic datasets, sequential dependencies, and unbalanced medical data. These advancements offer more dependable and personalized healthcare solutions by enhancing the applications of anomaly detection, real-time patient surveillance, and illness diagnosis. The utilization of EAs, despite their benefits, presents computational challenges, particularly in terms of resource requirements and processing time. In order to enhance the interpretability and efficacy of models, future research should investigate hybrid approaches, including the integration of EAs with explainable AI, federated learning, and reinforcement learning. It is anticipated that the integration of evolutionary approaches and artificial intelligence will transform healthcare analytics as medical informatics continues to develop, thereby enabling sophisticated clinical decision-making and precision medicine.

References

1. Udegbe, F. C., Nwankwo, E. I., Igwama, G. T., & Olaboye, J. A. (2023). Real-time data integration in diagnostic devices for predictive modeling of infectious disease outbreaks. Computer Science & IT Research Journal, 4(3), 525-545.
2. Tobore, I., Kandwal, A., Li, J., Yan, Y., Omisore, O. M., Enitan, E., ... & Nie, Z. (2020). Towards adequate prediction of prediabetes using spatiotemporal ECG and EEG feature analysis and weight-based multi-model approach. Knowledge-Based Systems, 209, 106464.
3. Balasubramaniam, S., Kadry, S., TK, M. K., & Kumar, K. S. (Eds.). (2025). Bio-inspired Algorithms in Machine Learning and Deep Learning for Disease Detection. CRC Press.
4. Ramírez-Ochoa, D. D., Pérez-Domínguez, L. A., Martínez-Gómez, E. A., & Luviano-Cruz, D. (2022). PSO, a swarm intelligence-based evolutionary algorithm as a decision-making strategy: A review. Symmetry, 14(3), 455.
5. Sarkar, A., Hossain, S. S., & Sarkar, R. (2023). Human activity recognition from sensor data using spatial attention-aided CNN with genetic algorithm. Neural Computing and Applications, 35(7), 5165-5191.
6. Adewale, T. (2024). Optimizing Investment Returns with Evolutionary Algorithms.
7. Sun, C., Hong, S., Song, M., & Li, H. (2020). A review of deep learning methods for irregularly sampled medical time series data. arXiv preprint arXiv:2010.12493.
8. Rasekh, A., Heidari, R., Rezaie, A. H. H. M., Sedeh, P. S., Ahmadi, Z., Mitra, P., & Nejdl, W. (2024). Robust Fusion of Time Series and Image Data for Improved Multimodal Clinical Prediction. IEEE Access.
9. Abiodun, E. O., Alabdulatif, A., Abiodun, O. I., Alawida, M., Alabdulatif, A., & Alkhawaldeh, R. S. (2021). A systematic review of emerging feature selection optimization methods for optimal text classification: the present state and prospective opportunities. Neural Computing and Applications, 33(22), 15091-15118.
10. Fristiana, A. H., Alfarozi, S. A. I., Permanasari, A. E., Pratama, M., & Wibirama, S. (2024). A Survey on Hyperparameters Optimization of Deep Learning for Time Series Classification. IEEE Access.
11. Gupta, A., Gupta, H. P., Biswas, B., & Dutta, T. (2020). Approaches and applications of early classification of time series: A review. IEEE Transactions on Artificial Intelligence, 1(1), 47-61.
12. Safaei, S., Ghasemi, P., Goodarzian, F., & Momenitabar, M. (2022). Designing a new multi-echelon multi-period closed-loop supply chain network by forecasting demand using time series model: a genetic algorithm. Environmental science and pollution research, 29(53), 79754-79768.

DOI: https://doi.org/10.5281/zenodo.15208384

13. Serhani, M. A., Navaz, A. N., Al Ashwal, H., & Al Qirim, N. (2020, September). ECG-based arrhythmia classification & clinical suggestions: An incremental approach of hyperparameter tuning. In Proceedings of the 13th International Conference on Intelligent Systems: Theories and Applications (pp. 1-7).
14. Qaisar, S. M., Khan, S. I., Dallet, D., Tadeusiewicz, R., & Pławiak, P. (2022). Signal-piloted processing metaheuristic optimization and wavelet decomposition based elucidation of arrhythmia for mobile healthcare. Biocybernetics and Biomedical Engineering, 42(2), 681-694.
15. Alkawadri, R. (2019). Brain–computer interface (BCI) applications in mapping of epileptic brain networks based on intracranial-EEG: An update. Frontiers in neuroscience, 13, 191.
16. Marques, L., Costa, B., Pereira, M., Silva, A., Santos, J., Saldanha, L., ... & Vale, N. (2024). Advancing precision medicine: A review of innovative In Silico approaches for drug development, clinical pharmacology and personalized healthcare. Pharmaceutics, 16(3), 332.
17. Nascimben, M. (2024). Machine learning approaches for personalized medicine.
18. Ekundayo, F. (2024). Machine learning for chronic kidney disease progression modelling: Leveraging data science to optimize patient management. World J Adv Res Rev, 24(03), 453-475.
19. Alam, M. A., Sohel, A., Uddin, M. M., & Siddiki, A. (2024). Big Data and Chronic Disease Management Through Patient Monitoring And Treatment With Data Analytics. Academic Journal on Artificial Intelligence, Machine Learning, Data Science and Management Information Systems, 1(01), 77-94.
20. Santos, M. D., Roman, C., Pimentel, M. A., Vollam, S., Areia, C., Young, L., ... & Tarassenko, L. (2021). A real-time wearable system for monitoring vital signs of COVID-19 patients in a hospital setting. Frontiers in Digital Health, 3, 630273.
21. Alharbe, N., & Almalki, M. (2024). IoT-enabled healthcare transformation leveraging deep learning for advanced patient monitoring and diagnosis. Multimedia Tools and Applications, 1-14.
22. Rehan, H. (2024). Enhancing Early Detection and Management of Chronic Diseases With AI-Driven Predictive Analytics on Healthcare Cloud Platforms. Journal of AI-Assisted Scientific Discovery, 4(2), 1-38.
23. Yang, X., Qi, X., & Zhou, X. (2023). Deep Learning Technologies for Time Series Abnormality Detection in Healthcare: A Review. IEEE Access.
24. Aljawarneh, S., Anguera, A., Atwood, J. W., Lara, J. A., & Lizcano, D. (2019). Particularities of data mining in medicine: lessons learned from patient medical time series data analysis. EURASIP Journal on Wireless Communications and Networking, 2019(1), 260.
25. Roy, S., Pal, D., & Meena, T. (2023). Explainable artificial intelligence to increase transparency for revolutionizing healthcare ecosystem and the road ahead. Network Modeling Analysis in Health Informatics and Bioinformatics, 13(1), 4.
26. Rahman, A., Karmakar, M., & Debnath, P. (2023). Predictive analytics for healthcare: Improving patient outcomes in the US through Machine Learning. Revista de Inteligencia Artificial en Medicina, 14(1), 595-624.
27. Morid, M. A., Sheng, O. R. L., & Dunbar, J. (2023). Time series prediction using deep learning methods in healthcare. ACM Transactions on Management Information Systems, 14(1), 1-29.
28. Bandara, K., Hewamalage, H., Liu, Y. H., Kang, Y., & Bergmeir, C. (2021).

DOI: https://doi.org/10.5281/zenodo.15208384

Improving the accuracy of global forecasting models using time series data augmentation. Pattern Recognition, 120, 108148.

29. Khan, P. W., & Byun, Y. C. (2020). Genetic algorithm based optimized feature engineering and hybrid machine learning for effective energy consumption prediction. Ieee Access, 8, 196274-196286.

30. Jimenez, F., Palma, J., Sanchez, G., Marin, D., Palacios, M. F., & López, M. L. (2020). Feature selection based multivariate time series forecasting: An application to antibiotic resistance outbreaks prediction. Artificial Intelligence in Medicine, 104, 101818.

31. Li, Y., Zhu, Z., Kong, D., Han, H., & Zhao, Y. (2019). EA-LSTM: Evolutionary attention-based LSTM for time series prediction. Knowledge-Based Systems, 181, 104785.

32. Van Wyk, F., Khojandi, A., & Kamaleswaran, R. (2019). Improving prediction performance using hierarchical analysis of real-time data: a sepsis case study. IEEE journal of biomedical and health informatics, 23(3), 978-986.

DOI: https://doi.org/10.5281/zenodo.15208384