[1]Narayanan Essakipillai

[2]Jayashree Ramakrishnan

An Efficient Deep Learning Framework for Feature Selection in IoT-Based Heart Disease Prediction

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Abstract: - Heart disease remains a leading cause of morbidity and mortality worldwide, necessitating the development of efficient diagnostic tools for early detection and prevention. With the rise of large-scale medical data, leveraging advanced computational techniques such as deep learning has become critical for accurate heart disease classification. This paper proposes an efficient framework for feature extraction and feature selection techniques, utilizing deep learning models to improve classification accuracy for heart disease using Internet of Things (IoT). The framework integrates convolutional neural networks (CNNs) for feature extraction and employs a hybrid method combining Recursive Feature Elimination (RFE) with Principal Component Analysis (PCA) for feature selection. The proposed framework is evaluated on the UCI Heart Disease dataset, achieving a classification accuracy of 91.3%, precision of 90.8%, recall of 89.9%, and an F1-score of 90.3%. The model outperforms traditional methods such as SVM and random forests, which achieved accuracies of 85.2% and 86.5%, respectively. These findings demonstrate the efficacy of the proposed framework in heart disease classification and its potential for real-time clinical applications.

Keywords: Deep Learning, Heart Disease, Internet of Things, Classification, Feature Selection.

I. Introduction

Cardiovascular conditions are among the primary causes of death worldwide, accounting for millions of fatalities each year. Its early diagnosis is crucial to reducing mortality rates and improving the quality of life for patients. Accurate and timely detection of heart disease enables appropriate medical intervention and prevention of severe complications. However, diagnosing heart disease can be complex, as it involves a wide range of factors, such as patient demographics, medical history, lifestyle, and clinical test results. To aid in the diagnosis process, various computational methods have been developed to predict the likelihood of heart disease based on clinical data. Traditional heart disease prediction methods often rely on machine learning algorithms such as decision trees, support vector machines (SVM), and logistic regression, which have shown success in various medical applications. These methods typically analyze structured data such as age, cholesterol levels, and blood pressure. However, they face significant challenges *when* applied to high-dimensional datasets. Medical data, especially from Iot and electronic health records (EHR) or wearable devices often contain numerous features, some of which may be irrelevant or redundant. This high dimensionality can introduce noise, hinder the model's ability to generalize, and increase computational complexity [1].

In recent years, deep learning has emerged as a transformative technology for healthcare applications [2]. Deep learning models[3], particularly convolutional neural networks (CNNs), have demonstrated exceptional performance in tasks involving image processing, time series analysis, and structured data [4]. By leveraging the power of CNNs, heart disease prediction models can capture more subtle and complex relationships within the data, which traditional machine learning methods may overlook. However, deep learning models, particularly when used with high-dimensional datasets, are not immune to challenges. Overfitting and high computational costs can occur when models are trained on irrelevant or redundant features. To address these challenges, feature selection plays a critical role in enhancing model performance. Effective feature selection methods reduce dimensionality, removing noise and irrelevant features while preserving the most informative ones [5].

[1] Department of Computer Applications, College of Science and Humanities, SRM Institute of Science and Technology, kattankulathur-603203, India, ne9272@srmist.edu.in.

[2]*Corresponding author: Department of Computer Applications, College of Science and Humanities, SRM Institute of Science and Technology, kattankulathur-603203, India, jayashrr@srmist.edu.in.

In this context, the combination of deep learning-based feature extraction with robust feature selection techniques offers a promising approach for heart disease classification. In particular, the integration of CNNs for feature extraction with advanced feature selection methods like Recursive Feature Elimination (RFE) and Principal Component Analysis (PCA) can significantly enhance classification performance. CNNs can automatically extract deep features from the data, while RFE systematically eliminates less important features, and PCA reduces the dimensionality of the selected features by transforming them into orthogonal components. This paper presents a novel and efficient framework that incorporates CNNs for deep feature extraction, and a hybrid feature selection approach using RFE and PCA to optimize heart disease classification. The CNN model is employed to capture critical patterns from the clinical dataset, and the hybrid feature selection technique ensures that only the most relevant features are retained for classification [6]. By reducing the dimensionality of the input data, the framework accelerates the computational process, making it suitable for real-time clinical applications. This approach is validated on the UCI Heart Disease dataset, where it achieves superior results compared to traditional machine learning methods, demonstrating its effectiveness and potential for future applications in heart disease diagnosis.

II. RELATED WORK

The application of machine learning (ML) and deep learning (DL) techniques in heart disease classification has garnered significant attention due to the increasing availability of healthcare data and the pressing need for accurate diagnostic tools [7]. Traditional machine learning methods such as decision trees, support vector machines (SVM), and k-nearest neighbors (KNN) have been widely used in medical applications, particularly for heart disease prediction [8]. These models are capable of identifying patterns in structured data, such as demographic and clinical features [9], to make predictions about a patient's risk of heart disease. For example, SVM has been successfully applied to medical diagnosis because of its robust performance with small datasets and high-dimensional spaces, as shown in various studies on heart disease classification [10]. However, these traditional methods face significant challenges when dealing with large, complex, and high-dimensional datasets often encountered in medical settings. As the number of features increases, traditional algorithms can become prone to overfitting and struggle to generalize well, leading to reduced classification accuracy.

The emergence of deep learning has transformed many fields, including healthcare, by offering advanced tools for data analysis, particularly when dealing with large and complex datasets. Deep learning, particularly convolutional neural networks (CNNs), has revolutionized feature extraction due to its ability to learn hierarchical feature representations directly from raw data, without requiring extensive domain knowledge for feature engineering [11]. CNNs have been extensively used in tasks such as image classification, object detection, and structured data analysis, making them highly suitable for heart disease classification. Studies have demonstrated that CNNs can outperform traditional machine learning models by extracting more abstract and high-level features from complex medical datasets [12]. For instance, CNNs have been successfully applied to classify heart disease using medical imaging data, such as echocardiograms and electrocardiograms (ECG). CNNs' ability to automatically detect patterns in these data types has made them a powerful tool in predictive diagnostics. Despite the success of CNNs in medical classification tasks, they are not without limitations. One common challenge faced by deep learning models is overfitting, particularly when applied to high-dimensional datasets with redundant or irrelevant features. When a CNN model is exposed to too many unnecessary features, it may focus on noise in the data, leading to poor generalization on unseen cases. Moreover, the high computational complexity of CNNs can make training difficult, particularly with large medical datasets. Thus, while CNNs excel at feature extraction, the inclusion of irrelevant or redundant features can degrade the performance of the model.

To mitigate these issues, recent studies have focused on hybrid models that combine deep learning with feature selection techniques to enhance performance. Feature selection methods aim to reduce the dimensionality of the input data by identifying and retaining only the most informative features while discarding irrelevant or redundant ones. Principal Component Analysis (PCA) is among the most commonly used dimensionality reduction techniques in this context [13]. By reducing the number of input features, PCA can prevent overfitting and reduce the computational load of the CNN model. However, while PCA is effective in reducing dimensionality, it does not always guarantee the retention of the most discriminative features for classification tasks. This is because PCA focuses on variance rather than class separability, which may result in the removal of features that are crucial for distinguishing between different classes, such as heart disease and non-heart disease cases.

To address these limitations, researchers have explored the combination of PCA with feature elimination techniques, such as Recursive Feature Elimination (RFE) [14]. RFE is a wrapper-based feature selection method that works by recursively fitting a model and eliminating the least important features based on their contribution to the model's performance. Unlike PCA, which reduces dimensionality through linear transformations, RFE directly selects features based on their relevance to the classification task. This allows RFE to preserve the most important and discriminative features while systematically removing those that contribute little to the model's accuracy. Several studies have demonstrated the effectiveness of combining PCA and RFE, particularly in medical applications where high-dimensional data is common. For example, by applying RFE and PCA to heart disease datasets, researchers have achieved significant improvements in both classification accuracy and model efficiency.

In summary, while traditional machine learning models such as SVM and decision trees have been useful in heart disease classification, they face limitations when applied to complex and high-dimensional datasets [15]. Deep learning, particularly CNNs, has revolutionized feature extraction by learning hierarchical representations from raw data. However, CNNs alone may suffer from overfitting due to the inclusion of irrelevant features. To overcome this challenge, recent research has explored hybrid models that combine CNNs with feature selection techniques such as PCA and RFE. The integration of deep learning and feature selection holds significant promise for enhancing heart disease prediction and improving clinical outcomes.

III. PROPOSED FRAMEWORK

A. Framework Overview

The proposed framework consists of three major components:

- Data acquisition: The patient data collected from patient’s Physical parameter using Blood pressure and Heart rate sensor. The data transfer to the heart disease prediction model using NodeMCU Wifi Module through the IoT cloud platform. The Blood pressure and Heart rate sensor has been shown in Fig.1.
- Feature Extraction: Convolutional Neural Networks (CNNs) are utilized to automatically extract deep features from the input data, thereby capturing complex patterns that are challenging to identify using conventional methodologies [16].
- Feature Selection: A hybrid feature selection approach combining Recursive Feature Elimination (RFE) and Principal Component Analysis (PCA) is used to enhance the performance of the model and reduce its complexity by selecting the most relevant features.

Fig. 1. Blood pressure and Heart rate sensor.

These components are integrated into a pipeline designed to maximize classification accuracy while reducing the dimensionality of the input data, making the model more computationally efficient and capable of real-time processing. The workflow diagram has been shown in Fig.2.

B. Dataset

The framework was tested on the UCI Heart Disease Dataset, which consists of 303 samples and 14 attributes [17], including patient demographics and medical data such as age, sex, cholesterol levels, resting blood pressure, and maximum heart rate. The dataset is frequently used in heart disease classification tasks and is suitable for evaluating the performance of various ML models [18] .

Let $D = \{(x_i, y_i)\}_{i=1}^{N}$ represent the dataset, where $x_i \in \mathbb{R}^{14}$ is the feature vector for the i-th patient, and $y_i \in \{0,1\}$ is the corresponding label indicating the absence or presence of heart disease. The goal of the framework is to learn a mapping $f : \mathbb{R}^{14} \rightarrow \{0,1\}$ that can predict y based on x.

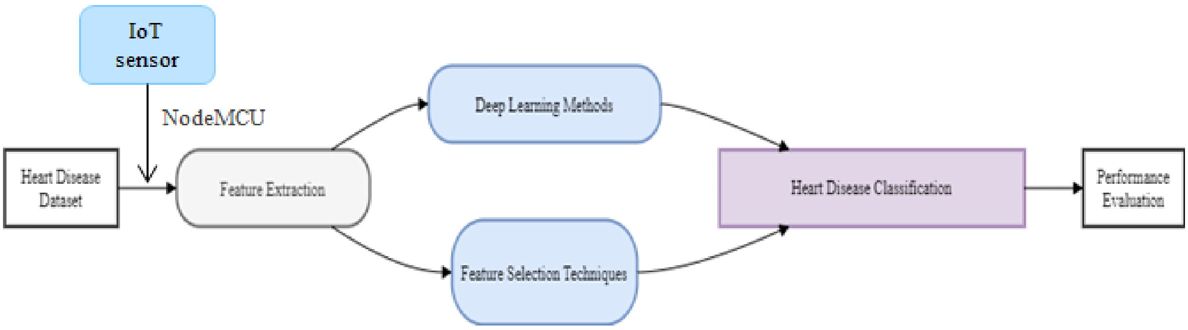

Fig. 2. Workflow diagram of proposed work.

C. Feature Extraction using CNN

CNNs are utilized to extract high-level abstract features from the structured input data. In this approach, Here employ a 1D CNN specifically designed to process tabular data. The CNN is constructed using the following layers:

- Input Layer: Corresponding to the 14 features in the dataset.
- Convolutional Layers: The CNN applies multiple convolutional filters to capture local patterns in the features. The output of a convolutional layer for input x and a kernel k is given by equation (1):

$$h(x) = (x * k)(t) = \sum_{s=0}^{S-1} x(t+s)k(s) \tag{1}$$

  where $*$ denotes the convolution operation, t is the index over the input, and S is the size of the kernel. The convolution layers detect relationships between the medical features.
- Pooling Layers: To reduce the dimensionality of the feature maps and capture the most significant features, pooling is applied. Max pooling is a common choice, defined as equation (2):

$$p(t) = \max\{h(x)(t), h(x)(t+1), \dots, h(x)(t+n-1)\} \tag{2}$$

  where n is the size of the pooling window. This reduces feature dimensionality and helps the model generalize better.
- Fully Connected Layers**:** These layers combine the learned features and help in classification. Given the feature vector z, the fully connected layer computes:

$$y = Wz + b \tag{3}$$

  where W is the weight matrix and b is the bias. The final output is passed to the classifier for heart disease prediction [19].

D. Hybrid Feature Selection: RFE and PCA

To avoid overfitting and improve generalization, a hybrid feature selection method combining Recursive Feature Elimination (RFE) and Principal Component Analysis (PCA) is applied.

Recursive Feature Elimination (RFE) is a backward feature selection method that iteratively eliminates the least significant features, as ranked by a machine learning model such as a linear classifier. For a model $f(x) = Wx + b$, RFE calculates feature importance based on the weight W assigned to each feature. It iteratively eliminates the features with the smallest weights until the desired number of features is reached [20].

Let w_j be the weight associated with feature j. At each iteration, RFE eliminates the feature with the smallest$|w_j|$, leading to a refined feature set S after K iterations. The objective is to minimize the classification error by retaining only the most significant features:

$$S = arg_{S \subseteq x, S=d}^{min} \sum_{i=1}^{N} L(y_i, f(x_i^S)) \tag{4}$$

where S is the feature space, d is the number of selected features, and L is the loss function.

Principal Component Analysis (PCA) is a dimensionality reduction method that converts the feature space into a set of orthogonal components, representing the directions of greatest variance [21]. Subsequent to the application of RFE, PCA is employed to further reduce the dimensionality of the dataset while preserving the most salient components. Given a feature matrix $X \in \mathbb{R}^{N*d}$, PCA finds the principal components $X \in \mathbb{R}^{N*p}$, where $p \ll d$, by solving the following eigenvalue problem:

$$\Sigma w = \lambda w \tag{5}$$

where Σ is the covariance matrix of X, w is the eigenvector (principal component), and λ is the eigenvalue corresponding to w. The principal components with the highest eigenvalues are selected, reducing the feature space while retaining the majority of the variance.

E. Classification using Fully Connected Neural Network

The selected features from the RFE-PCA pipeline are then fed into **a** Fully Connected Neural Network (FCNN) for classification. The FCNN consists of the following layers:

- Input Layer: This layer takes the reduced set of features obtained from the feature selection process.
- Hidden Layers: The hidden layers utilize Rectified Linear Unit (ReLU) activation functions to model nonlinear relationships within the data. The ReLU function is defined as equation (6):

$$ReLU(x) = \max(0, x) \tag{6}$$

This activation function helps introduce nonlinearity into the model, allowing it to learn complex decision boundaries.

- Output Layer: For the binary classification task (presence or absence of heart disease), a softmax activation function is applied to the output layer. The softmax function is defined as equation (7):

$$Softmax(z_i) = \frac{e^{z_i}}{\sum_{j=1}^{2} e^{z_j}} \tag{7}$$

where z_i represents the output of the last hidden layer. This function ensures that the outputs are interpreted as probabilities, summing to 1.

The model is trained using the cross-entropy **loss** function, which for binary classification is defined as:

$$L(y, \hat{y}) = -[y\log(\hat{y}) + (1-y)\log(1-\hat{y})] \tag{8}$$

where y is the true label and $\hat{y}$ is the predicted probability. The model is optimized using the Adam optimizer, which adjusts the learning rate dynamically during training to achieve faster convergence.

IV. Results and Discussion

A. Evaluation Metrics

To assess the performance of the proposed framework, several classification metrics were employed [20], ensuring a comprehensive evaluation:

- Accuracy: The proportion of correctly classified instances relative to the total number of instances. This metric provides a general measure of model performance; however, it may yield misleading results when applied to imbalanced datasets.

$$\text{Accuracy} = \frac{\text{TP+TN}}{\text{TP+TN+FP+FN}} \tag{9}$$

- Precision: The ratio of correctly predicted positive observations to the total predicted positives. It focuses on the accuracy of positive predictions.

$$\text{Precision} = \frac{\text{TP}}{\text{TP+FP}} \tag{10}$$

- Recall **(**Sensitivity**)**: The ratio of correctly predicted positive observations to the total number of actual positive instances, highlighting the ability to capture true positives.

$$\text{Recall} = \frac{\text{TP}}{\text{TP+FN}} \tag{11}$$

- F1-Score: The harmonic mean of precision and recall. This metric provides a balanced measure between precision and recall.

$$\mathrm{F1-Score} = 2 * \frac{\mathrm{Precision}*\mathrm{Recall}}{\mathrm{Precision}+\mathrm{Recall}} \quad (12)$$

- AUC (Area Under the ROC Curve): This metric assesses the model's capacity to differentiate between classes by measuring the trade-off between the true positive rate (TPR) and false positive rate (FPR).

$$\mathrm{TPR} = \frac{\mathrm{TP}}{\mathrm{TP}+\mathrm{FN}}\ ,\ \mathrm{FPR} = \frac{\mathrm{FP}}{\mathrm{FP}+\mathrm{TN}} \quad (13)$$

The IoT device used to collect real time data from patients. The mentioned sensor can able to collect Blood pressure and Heart rate information. The dataset was divided into training (80%) and testing (20%) sets, and 10-fold cross-validation was performed to ensure the robustness of the model [22]. Cross-validation mitigates overfitting by testing the model on different subsets of the data. In fig 3shows that workflow of IoT Data transmission.

Fig. 3. Data acquisition from Blood pressure and Heart rate sensor.

B. Comparative Analysis

The correlation between selected features is visually represented in Fig. 2, utilizing a heat map to effectively illustrate the relationships. Heat maps are a well-established and powerful method for visualizing correlations between multiple variables, allowing for quick identification of patterns or associations. In this figure, the intensity of the color corresponds to the strength of the correlation between features, with darker shades indicating stronger correlations, either positive or negative.

The proposed method, which integrates RFE and PCA, ensures that only the most relevant features are retained, and their interdependencies are clearly visible in the heat map. This visualization allows researchers to observe how the selected features interact with each other, providing insights into which variables are more influential in predicting heart disease outcomes. By focusing on these relationships, the proposed model can more effectively reduce noise, improve computational efficiency, and enhance classification accuracy.

The feature selection results confirm the robustness of the feature selection process by highlighting any potential redundancies among the chosen features. This is crucial in medical data, where high-dimensionality can obscure meaningful patterns if not handled correctly. To validate the efficacy of the proposed framework, a comparative analysis was conducted against baseline models, including SVM**,** decision trees**,** random forests, and a CNN model without feature selection. The results are summarized in Table 1.

Table 1: Performance results of baseline models

Model	Accuracy	Precision	Recall	F1-Score	AUC
SVM	85.2	84.5	82.7	83.6	0.87
Decision Tree	81.8	80.1	79.4	79.7	0.84
Random Forest	86.5	85.3	84.6	84.9	0.88
CNN (no feature selection)	88.9	88.5	87.2	87.8	0.91
Proposed Framework (CNN + RFE + PCA)	**91.3**	**90.8**	**89.9**	**90.3**	**0.94**

As shown in the Table 1, Proposed framework demonstrates superior performance compared to alternative methodologies, achieving an accuracy of 91.3% and an Area Under the Curve (AUC) of 0.94. The hybrid feature selection approach not only enhances accuracy but also reduces the dimensionality of the final model, thus enhancing computational efficiency. In Fig.4 shows the proposed framework combining CNN with RFE and PCA achieved the best overall performance across all metrics. Specifically, it achieved 91.3% of accuracy.

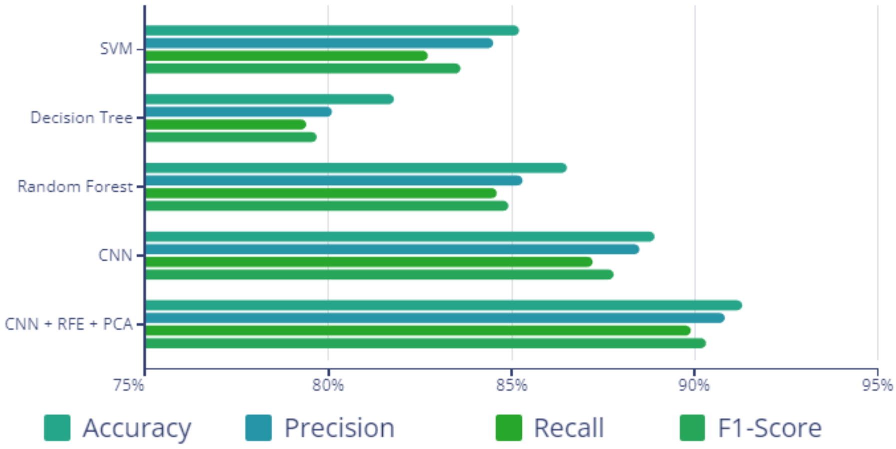

Fig. 4. Classification performance on significant features

Compared to other models, this framework showed a substantial improvement in classification accuracy, precision, and recall, demonstrating that the hybrid feature selection method enhances predictive power. Additionally, by reducing the number of features, the model becomes computationally efficient without sacrificing accuracy, making it suitable for real-time medical applications.

C. Discussion

The improved performance of the proposed framework is primarily due to the synergy between CNN-based deep feature extraction and the hybrid RFE-PCA feature selection method.

- *CNN's Role in Feature Extraction*

CNNs are particularly well-suited for capturing complex, high-level features in structured medical data. In this study, the convolutional layers autonomously identified complex patterns within the patient data, such as the relationship between cholesterol levels and heart disease risk. By applying convolutions, the model learned hierarchical representations of the features, which traditional models like SVM and decision trees struggle to do.

- *Effectiveness of Hybrid Feature Selection*

While CNNs excel at feature extraction, they can also suffer from overfitting, especially when dealing with noisy or redundant features in the data. This is where the hybrid RFE-PCA approach plays a crucial role. RFE eliminates the less important features in a recursive manner, ensuring that only the most relevant ones remain. By ranking features based on their contribution to the prediction task, RFE helps the model focus on critical information. PCA further reduces the dimensionality of the feature set, capturing the directions of maximum variance. This leads to a more compact representation of the data, significantly reducing the risk of overfitting while maintaining the essential information.

The combination of these two techniques strikes a balance between retaining important features and reducing the feature space, leading to improved generalization on unseen test data.

- *Comparative Insights*

When comparing the proposed framework with traditional models like SVM and random forests, it is evident that the deep learning approach, in conjunction with feature selection, offers superior performance. The traditional models, although robust, do not have the same capacity as CNNs to learn from complex patterns and are more sensitive to high-dimensional data. Even the CNN model without feature selection, despite its deep feature extraction capability, is prone to overfitting, leading to slightly lower accuracy than the proposed framework.

The results demonstrate that the hybrid CNN + RFE + PCA framework is not only more accurate but also more efficient. It reduces the computational burden by minimizing the number of features while maintaining high classification performance. This balance between complexity and accuracy makes the model ideal for practical applications, particularly in clinical settings where real-time processing and interpretability are crucial.

V. CONCLUSION

This paper presents an efficient and robust framework for heart disease classification by integrating Internet of Things (IoT) and Convolutional Neural Networks (CNNs) for deep feature extraction with a hybrid feature selection technique that combines RFE and PCA. The proposed framework demonstrated superior performance compared to conventional machine learning models (SVM, decision trees, and random forests) and CNN models without feature selection. By focusing on the most relevant features, the hybrid approach not only enhanced the classification accuracy, achieving an impressive 91.3%. Additionally, it reduced the dataset's dimensionality, thereby lowering the likelihood of overfitting and enhancing computational efficiency. The results indicate that the CNN + RFE + PCA combination successfully addresses the challenge of high-dimensional data in heart disease classification, offering a more effective solution for medical data analysis. This balance between accuracy and feature reduction makes the framework suitable for real-time applications in healthcare, where precision and speed are critical.

A. Future Enhancements

Future work will focus on expanding the capabilities of the proposed framework in several key areas. Currently, the framework is designed for binary classification (presence or absence of heart disease). Future research will extend the model to handle multi-class classification. While RFE and PCA have proven effective, exploring additional feature selection techniques like LASSO regression or genetic algorithms could further refine feature selection and enhance model interpretability. Future work will explore methods like Layer-wise Relevance Propagation (LRP) or SHAP values to make the model's decision-making process more transparent, helping clinicians better understand and trust the model’s predictions. These enhancements aim to further optimize the proposed framework, making it more adaptable and applicable to a wide range of real-world medical use cases.

REFERENCES

[1] A. Shachar, “Introduction to Algogens,” arXiv.org. Accessed: Sep. 18, 2024. [Online]. Available: https://arxiv.org/abs/2403.01426v1

[2] “Predicting Brain Stroke Using IoT-Enabled Deep Learning and Machine Learning: Advancing Sustainable Healthcare.” Accessed: Sep. 18, 2024. [Online]. Available: http://ouci.dntb.gov.ua/en/works/4YwOyNR9

[3] A. Mf, H. Mm, N. M, I. Mr, A. M, and H. J, “A review on brain tumor segmentation based on deep learning methods with federated learning techniques,” *PubMed*, Accessed: Sep. 18, 2024. [Online]. Available: https://pubmed.ncbi.nlm.nih.gov/38011781/

[4] U. A. Bhatti, H. Mengxing, J. Li, S. U. Bazai, and M. Aamir, Eds., *Deep Learning for Multimedia Processing Applications: Volume One: Image Security and Intelligent Systems for Multimedia Processing*. Boca Raton: CRC Press, 2024. doi: 10.1201/9781003427674.

[5] T. B. Jabeur, E. Bashier, Q. Sandhu, K. J. Bwalya, and A. Joshua, “Noise And Artifacts Elimination In ECG Signals Using Wavelet, Variational Mode Decomposition And Nonlocal Means Algorithm,” Jun. 03, 2024, *arXiv*: arXiv:2406.01023. doi: 10.48550/arXiv.2406.01023.

[6] Y. Yin *et al.*, “IGRF-RFE: a hybrid feature selection method for MLP-based network intrusion detection on UNSW-NB15 dataset,” *Journal of Big Data*, vol. 10, no. 1, p. 15, Feb. 2023, doi: 10.1186/s40537-023-00694-8.

[7] “Mathematics | Free Full-Text | WT-CNN: A Hybrid Machine Learning Model for Heart Disease Prediction.” Accessed: Sep. 18, 2024. [Online]. Available: https://www.mdpi.com/2227-7390/11/22/4681

[8] E. Narayanan and R. Jayashree, “IoT based heart disease prediction using smote and machine learning techniques,” *AIP Conference Proceedings*, vol. 2946, no. 1, p. 060010, Nov. 2023, doi: 10.1063/5.0178157.

[9] C. Zhou *et al.*, “A comprehensive review of deep learning-based models for heart disease prediction,” *Artificial Intelligence Review*, vol. 57, no. 10, Art. no. 10, Aug. 2024, doi: 10.1007/s10462-024-10899-9.

[10] Narayanan and Jayashree, “Implementation of Efficient Machine Learning Techniques for Prediction of Cardiac Disease using SMOTE,” *Procedia Computer Science*, vol. 233, pp. 558–569, Jan. 2024, doi: 10.1016/j.procs.2024.03.245.

[11] N. Faruqui, M. A. Yousuf, M. Whaiduzzaman, A. K. M. Azad, A. Barros, and M. A. Moni, “LungNet: A hybrid deep-CNN model for lung cancer diagnosis using CT and wearable sensor-based medical IoT data,” *Computers in Biology and Medicine*, vol. 139, p. 104961, Dec. 2021, doi: 10.1016/j.compbiomed.2021.104961.

[12] M. A. Khan, “An IoT Framework for Heart Disease Prediction Based on MDCNN Classifier,” *IEEE Access*, vol. 8, pp. 34717–34727, 2020, doi: 10.1109/ACCESS.2020.2974687.

[13] A. K. Rastogi, S. Taterh, and B. S. Kumar, “Dimensionality Reduction Algorithms in Machine Learning: A Theoretical and Experimental Comparison,” *Engineering Proceedings*, vol. 59, no. 1, Art. no. 1, Dec. 2023, doi: 10.3390/engproc2023059082.

[14] “Feature Selection Using Recursive Feature Elimination for Handwritten Digit Recognition.” Accessed: Sep. 18, 2024. [Online]. Available: https://ieeexplore.ieee.org/document/5337549

[15] A. Dagur, D. K. Shukla, N. F. Makhmadiyarovich, A. A. Rustamovich, and J. J. Sindorovich, Eds., *Artificial Intelligence and Information Technologies: Proceedings of the 1st International Conference on Artificial Intelligence and Information Technologies (ICAIIT 2023), 3–4 November 2023, Samarkand, Uzbekistan, Volume 1*. London: CRC Press, 2024. doi: 10.1201/9781032700502.

[16] C. F, D. L. F, R. A, and P. M, “Bimodal Feature Analysis with Deep Learning for Autism Spectrum Disorder Detection,” *PubMed*, Accessed: Sep. 18, 2024. [Online]. Available: https://pubmed.ncbi.nlm.nih.gov/38063381/

[17] “UCI Machine Learning Repository.” Accessed: Apr. 20, 2024. [Online]. Available: https://archive.ics.uci.edu/dataset/45/heart+disease

[18] “Cardiovascular Disease Detection Based on Interpretable and Explainable AI.” Accessed: Sep. 18, 2024. [Online]. Available: https://ieeexplore.ieee.org/document/10089349

[19] “A fault diagnosis method for building electrical systems based on the combination of variational modal decomposition and new mutual dimensionless - PubMed.” Accessed: Sep. 18, 2024. [Online]. Available: https://pubmed.ncbi.nlm.nih.gov/36941283/

[20] N. Essakipillai and J. Ramakrishnan, “Fall incidence prediction system for elderly people based on IoT and classification techniques,” *TELKOMNIKA (Telecommunication Computing Electronics and Control)*, vol. 22, no. 1, Art. no. 1, Feb. 2024, doi: 10.12928/telkomnika.v22i1.25248.

[21] “Acoustics | Free Full-Text | Enhancing Speaker Recognition Models with Noise-Resilient Feature Optimization Strategies.” Accessed: Sep. 18, 2024. [Online]. Available: https://www.mdpi.com/2624-599X/6/2/24.

[22] S. Sharif, C. Wunder, J. Amendt, and A. Qamar, “Deciphering the impact of microenvironmental factors on cuticular hydrocarbon degradation in Lucilia sericata empty Puparia: Bridging ecological and forensic entomological perspectives using machine learning models,” *Science of The Total Environment*, vol. 913, p. 169719, Feb. 2024, doi: 10.1016/j.scitotenv.2023.169719.