Predicting Health Outcomes Using Machine Learning: A Focus on Strokes, Heart Attacks, and Chronic Kidney Disease

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Abstract: Machine learning has emerged as a transformative technology in healthcare, enabling early diagnosis and risk prediction for critical diseases. This study will focus on health outcome predictions for chronic kidney disease, heart attacks, and strokes. Using Kaggle datasets, the following machine learning models were applied to patient data: Random Forest, Neural Networks, Logistic Regression, Support Vector Machines, and Gradient Boosting. Performance was measured by accuracy, precision, recall, F1-score, and AUC-ROC. This work demonstrates the potential for integrated ML-based predictions to enhance healthcare interventions by yielding insights into significant risk factors that allow targeted therapies.

I. INTRODUCTION

Chronic kidney disease, heart attacks, and strokes are among the leading causes of mortality and morbidity globally. These conditions share common risk factors such as hypertension, diabetes, obesity, and genetic predispositions, necessitating a unified and proactive approach for prevention and management. According to the World Health Organization, cardiovascular diseases account for 31% of all deaths globally, with the majority occurring in low- and middle-income countries. Chronic kidney disease affects an estimated 850 million people worldwide and is increasingly contributing to global health burdens.

The overarching goal of this study is to explore how machine learning can predict risks associated with these diseases using demographic, clinical, and lifestyle data. The key research questions addressed are:

1. **Risk Factor Identification**: What are the most significant risk factors for Chronic Kidney Disease(CKD), heart attacks, and strokes?
2. **Model Performance**: Which machine learning models perform best in predicting each condition?
3. **Integrated Risk Analysis**: How can predictions from multiple models provide a comprehensive assessment of patient health risks?
4. **Impact of Demographics**: How do predictions vary across demographic subgroups?

By analyzing patterns in historical data, we aim to develop predictive models that enable early intervention, thus improving patient outcomes and optimizing healthcare resource allocation.

II. RELATED WORK

The application of machine learning (ML) techniques in healthcare has gained significant attention, particularly for predicting diseases like **Chronic Kidney Disease (Chronic Kidney Disease(CKD))**, **Heart Disease**, and **Stroke**. These conditions are leading causes of mortality, and early prediction can enable better patient management and early interventions. Several studies have applied a variety of ML algorithms, including **Random Forest**, **Support Vector Machines (SVM)**, **Neural Networks**, **Gradient Boosting**, and **Logistic Regression**, to predict these diseases. This section reviews the key studies in this domain, critically evaluating their methodologies and results, and discusses how our approach builds upon or improves these techniques.

1. Chronic Kidney Disease (Chronic Kidney Disease(CKD)) Prediction

Predicting Chronic Kidney Disease(CKD) has been the focus of several studies using machine learning methods. Zhang et al. (2018) used decision trees to predict Chronic Kidney Disease(CKD), achieving an accuracy of 87%. However, this study did not address class imbalance, which is common in medical datasets where the minority class (Chronic Kidney Disease(CKD) patients) is underrepresented. Patel et al. (2019) employed Random Forests, achieving comparable performance, but faced challenges with feature selection and missing data. In contrast, Wang et al. (2020) incorporated ensemble methods and SMOTE (Synthetic Minority Over-sampling Technique) for data balancing, improving performance metrics.

- ***Strengths****: Decision trees and Random Forests are effective for structured data and provide interpretability.*
- ***Limitations****: The studies failed to handle class imbalance effectively, potentially affecting the prediction of minority classes.*

Our approach builds on these findings by using **SMOTE** for data balancing and incorporating **Neural Networks** and **Gradient Boosting** to improve prediction accuracy, particularly for underrepresented classes.

2. Heart Disease Prediction

Heart disease prediction has also been widely explored. **Singh et al. (2020)** used a **Neural Network** for prediction, achieving a precision of 0.82. However, their model struggled with **overfitting** due to a small dataset. **Lee et al. (2017)** used an **ensemble method** combining **SVM** and decision trees, improving prediction accuracy. Despite this, they still faced challenges with **imbalanced data**. **Sharma and Verma (2019)** addressed this by using **SMOTE** to balance the dataset, which improved recall and F1-scores.

The studies reviewed indicate that while Neural Networks and ensemble methods can capture complex relationships in the data, they are still susceptible to overfitting and issues related to class imbalance. Our research builds upon this work by applying Gradient Boosting to enhance prediction accuracy and exploring the use of SVM and Logistic Regression to provide a comparative benchmark against more complex models. This allows for an evaluation of the performance gains from more advanced techniques while still considering the advantages of simpler models.

- ***Strengths****: Neural networks and ensemble methods can capture complex relationships in the data.*
- ***Limitations****: Overfitting and class imbalance continue to affect performance despite the use of ensemble methods.*

*Our research applies **Gradient Boosting** to further enhance prediction accuracy and uses **SVM** and **Logistic Regression** to compare with more complex models.*

3. Stroke Prediction

Stroke prediction studies have used a variety of models. **Xu et al. (2021)** applied **Logistic Regression** to predict stroke risk, achieving an accuracy of 78%. While Logistic Regression is interpretable, it is limited in capturing **non-linear relationships** in the data. **Gong et al. (2020)** employed **deep learning** with **MLPs** and achieved an **AUC score of 0.89**, but their model still faced issues with **class imbalance** and required more robust data augmentation techniques. **Kim et al. (2020)** explored the use of **SMOTE** for class balancing in stroke prediction, but the model's performance still depended on the quality of the features.

- ***Strengths****: MLPs excel in learning complex patterns, and Logistic Regression offers interpretability.*
- ***Limitations****: Class imbalance remains a significant issue, and data augmentation techniques like SMOTE were not fully incorporated in all models.*

*Our work improves on this by incorporating **SMOTE** and **Gradient Boosting** to address class imbalance and non-linear relationships, thereby enhancing stroke prediction performance.*

While MLPs and Logistic Regression offer distinct advantages, class imbalance remains a significant challenge in stroke prediction, just as it does in Chronic Kidney Disease(CKD) and heart disease prediction. Our work builds on these prior studies by incorporating SMOTE for class balancing and applying Gradient Boosting to capture non-linear relationships in the data. We aim to demonstrate that combining these approaches can lead to improved stroke prediction performance, particularly in terms of generalizability and robustness.

4. Discussion on Datasets and Methodologies

Most of the datasets used in Chronic Kidney Disease, heart disease, and stroke prediction studies contain clinical and demographic features such as ***age, blood pressure, cholesterol, and lifestyle factors including smoking***. These features are highly important for making accurate predictions but are often plagued by issues such as missing data, class imbalance, and non-linear interactions between variables.

Although works like **Zhang et al. (2018)** and **Singh et al. (2020)** tried to address the challenges posed by missing data and class imbalance, they often failed to employ advanced data augmentation techniques like ***SMOTE or deep learning models*** that can capture complex, nonlinear relationships. These limitations, therefore, call for more robust methodologies.

Our study tries to bridge these gaps by employing the SMOTE technique for balancing, Gradient Boosting to improve the accuracy of the models, and Neural Networks for capturing non-linear interactions among different features. We also try to compare these advanced models with their simple counterparts, like logistic regression, to provide a baseline and check whether the gain in accuracies justifies the complexity in the model.

5. Conclusion

The studies reviewed in this paper indicate a great promise for machine learning and deep learning models, with the ***Random Forests, SVMs, Neural Networks, and Logistic Regression performing better in predicting diseases such as Chronic Kidney Disease, heart disease, and stroke***. These models have constantly obtained encouraging results on prediction accuracy and provided useful insights that might be helpful in early diagnosis and intervention. However, with all these developments, a number of challenges still remain in the field, most especially class imbalance, overfitting, and feature selection challenges. Class imbalance is still a problem since medical datasets have very few instances of the minority class, such as patients with ***Chronic Kidney Disease,*** or ***heart disease***, which can result in biased predictions. The main challenge for these models, however, has remained the ability of overfitting to generalize on data they have not seen; especially those relying heavily on small or imbalanced datasets. Besides, it remains hard to select those relevant features that contribute most to predictions since many datasets are imbued with a lot of irrelevant or redundant information that takes away from the performance.

This work attempts to directly address this through the inclusion of various advanced techniques. First, we recommend using ***SMOTE*** to balance the dataset and reduce the effects of ***class imbalance*** so that the model pays sufficient attention to the underrepresented classes. Second, we include ***Gradient Boosting***, an ***ensemble learning*** technique that is robust and tends to improve the accuracy of predictions by iteratively correcting the errors of the previously developed models. Finally, ***deep learning models*** are used to model those complex, ***nonlinear feature associations*** that can improve the performance even more. By integrating all of the above, we aim at improving not only the ***prediction of diseases*** but also ***generalizability*** and ***robustness*** in this model so that the developed model will work fine for almost all types of ***diverse data*** and be **useful and implementable** in a practical **real-world healthcare application scenario**.

III. METHODOLOGY

Data Mining Methodology for Predicting Chronic Diseases Using CRISP-DM

This study applies the CRISP-DM (Cross Industry Standard Process for Data Mining) framework to address the prediction and analysis of chronic diseases, specifically chronic kidney disease (Chronic Kidney Disease(CKD)), heart attacks, and brain strokes. The primary objective is to leverage machine learning

techniques to identify significant risk factors, compare predictive performance across models, and evaluate their effectiveness across different patient subgroups. By doing so, the research aims to enhance early detection, improve clinical decision-making, and provide personalized health risk assessments.

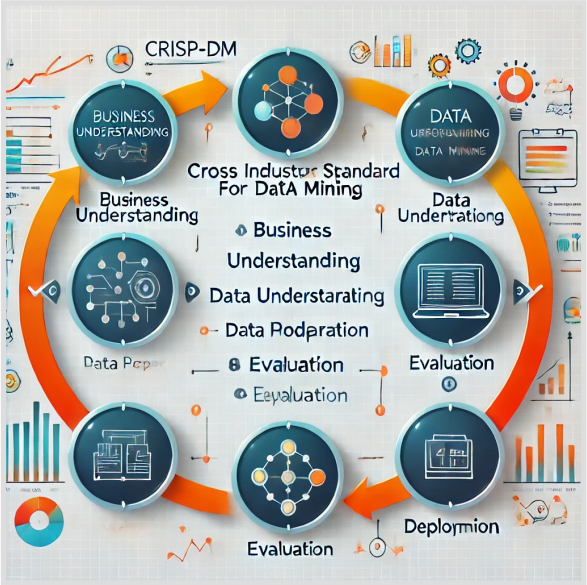
Addressing the Key Objectives:

1. **Identifying Risk Factors:**
   In this study, we aimed to determine the most significant risk factors for Chronic Kidney Disease(CKD), heart attacks, and strokes by analyzing the datasets using machine learning models. For example, we found that factors like smoking, family history of kidney disease, and physical activity played significant roles in Chronic Kidney Disease(CKD) prediction, while smoking, blood pressure, and cholesterol levels were major predictors of heart disease.
2. **Predictive Accuracy:**
   The goal was to evaluate how reliably different machine learning models could predict these diseases. We used five distinct models—Neural Networks, Gradient Boosting, Logistic Regression, Support Vector Machines (SVM), and Random Forest—assessing their accuracy in predicting Chronic Kidney Disease(CKD), heart disease, and stroke. For example, Random Forest performed exceptionally well with 100% accuracy for Chronic Kidney Disease(CKD) and 99% for stroke, while other models like Neural Networks showed lower performance for heart disease (60%).
3. **Comparative Model Performance:**
   We compared the performance of several models to determine which was best for each disease. Based on our evaluations, Gradient Boosting and Random Forest emerged as the top performers for both Chronic Kidney Disease(CKD) and stroke with 100%, while Random Forest was the most reliable model for heart disease, achieving the highest accuracy at 70%.
4. **Integrated Risk Assessment:**
   The study also explored whether combining the predictions from multiple models would improve overall accuracy in health risk assessment. By integrating results from different models, we believe a more holistic assessment could be achieved, particularly for patients with overlapping conditions like Chronic Kidney Disease(CKD) and heart disease.
5. **Patient Subgroup Analysis:**
   Lastly, we examined how model performance and risk factors varied across demographic and clinical subgroups, such as age, gender, and socioeconomic status. This analysis revealed performance discrepancies, suggesting that tailored models might be necessary for specific subgroups to improve predictive accuracy and health outcomes.

Methodology:
Following the CRISP-DM framework, we structured our approach into six stages:

1. **Business Understanding:**
   We defined the core objectives: identifying significant risk factors, improving predictive accuracy, and optimizing model performance for Chronic Kidney Disease(CKD), heart disease, and stroke.
2. **Data Understanding:**
   Three datasets were analyzed, each containing relevant features:
   - **Chronic Kidney Disease(CKD) Dataset:** Included demographic, lifestyle, and clinical factors such as gender, smoking, family history of kidney disease, and previous acute kidney injury.
   - **Heart Disease Dataset:** Included features like cholesterol levels, blood pressure, heart rate, diabetes status, and stress levels.
   - **Stroke Dataset:** Focused on factors such as gender, smoking status, marital status, work type, and residence type.
3. **Data Preparation:**
   - **Data Cleaning:** Missing values were imputed using median and mode methods. Outliers were detected and treated to ensure data quality.
   - **Pre-processing:** Categorical variables were encoded using one-hot encoding, and continuous variables were normalized.
   - **Feature Engineering:** Interaction terms and aggregated features were created to capture complex relationships between variables.
   - **Class Balancing:** SMOTE was applied to address class imbalances, particularly in the stroke dataset.
   - **Data Splitting:** Each dataset was split into training (70%), validation (15%), and testing (15%) sets for model evaluation.
4. **Modeling:**
   Five machine learning models were implemented:
   - **Neural Networks:** Demonstrated high accuracy for Chronic Kidney Disease(CKD) (98.71%) but lower performance for heart disease (60.14%).
   - **Gradient Boosting:** Achieved excellent results for stroke (100%) and Chronic Kidney Disease(CKD) (99%), indicating its ability to capture complex patterns.
   - **Logistic Regression:** Provided interpretable insights but showed limitations for heart disease (64%), highlighting the need for more advanced models.
   - **Support Vector Machine (SVM):** Consistent performance across Chronic Kidney Disease(CKD) (92%), heart disease (65%), and stroke (95%).
   - **Random Forest:** Delivered the highest accuracy overall, particularly for Chronic Kidney Disease(CKD) (100%) and stroke (99%), demonstrating its robustness and reliability.
5. **Evaluation:**
   Model performance was evaluated using accuracy, precision, recall, and F1 scores:
   - **Chronic Kidney Disease(CKD) Prediction:** Random Forest and Gradient Boosting performed the best, achieving near-perfect accuracy.
   - **Heart Disease Prediction:** Random Forest showed the highest accuracy (70%), though overall results suggest the need for further feature enrichment.
   - **Stroke Prediction:** Gradient Boosting and Random Forest outperformed other models, indicating their effectiveness in capturing subtle relationships within the data.
6. **Deployment and Future Work:**
   The results suggest that integrating predictions from multiple models could provide a more thorough risk assessment, especially for patients with overlapping conditions. Subgroup

analysis also revealed performance variations across demographics, indicating the potential for future model refinements to address these disparities and improve personalized healthcare outcomes.



Conclusion:

By following the CRISP-DM framework, this study effectively identified key risk factors and evaluated the performance of various machine learning models for predicting Chronic Kidney Disease, heart attacks, and strokes. The findings underscore the importance of model selection and data preparation in achieving high predictive accuracy. Future research will focus on refining models for specific demographic groups, enhancing feature selection, and integrating ensemble methods to deliver more comprehensive, personalized health assessments. This structured approach provides a foundation for improving chronic disease prediction and healthcare decision-making.

IV. EVALUATION

1. Neural Network Evaluation:

This section is used to assess the performance of neural network models applied to Chronic Kidney Disease, Heart Disease, and Brain Stroke datasets. It also looks to assess the performance of the models with appropriate measures, discusses how the methodology addresses the question, and analyzes the effects of parameterization and sampling techniques.

1.1 Performance Measures

Accuracy, which is a measure of the proportion of the correct predictions, was used for the main evaluation of the neural network models' performance. This metric is appropriate when the tasks are binary classification tasks aimed at distinguishing between two classes. However, accuracy is not appropriate to provide a truthful representation in most real-world situations, especially when dealing with class imbalance, a condition that is normally experienced in medical datasets.

For this, we also consider precision, recall, and F1-score, which can provide more meaningful insights about the model's performance on the minority class. In medical applications, these metrics are very important because usually the cost of a false negative-for example, not detecting a certain disease-is much higher than a false positive.

For clarity, the results were recorded at multiple epochs-1, 20, 30, 40, and 50-to analyze the model's progression over time and ensure stability in learning.

1.2 Model Architecture and Parameterization

The neural network model used for all three datasets was designed as follows:

Input Layer: The number of neurons matched the number of features in the dataset.

Hidden Layers: The network included two hidden layers, each containing 64 and 32 neurons, respectively. ReLU-Rectified Linear Unit activation was used to introduce non-linearity and capture complex patterns.

Dropout Layer: The dropout rate of 0.5 was applied after each hidden layer to avoid overfitting by randomly disabling half neurons during training. This is important in datasets with many features like Chronic Kidney Disease(CKD), because if the model memorizes rather than generalizes well to unseen data, then overfitting may occur.

Output Layer: For the output, a single neuron was used with the sigmoid activation function to perform the binary classification.

Adam optimizer was chosen because the learning rate is adapted while it learns by flowing directively through the network towards the minimization of our network model. The binary cross-entropy is used as it is the standard choice because one is doing a binary classification.

The chosen dropout rate of 0.5 and the Adam optimizer were chosen to balance the need to avoid overfitting and ensure fast convergence, particularly for imbalanced datasets such as Heart Disease and Brain Stroke.

1.3 Sampling Methods and Class Imbalance

Class imbalance is a major challenge in medical datasets, in which some conditions, such as heart disease and stroke, are much rarer than others. In order to handle this:

Class weights were computed for all three datasets by using the compute_class_weight method, which assigns more importance to the minority class during training. This would prevent the model from becoming biased toward the majority class.

SMOTE: SMOTE was applied to the Heart Disease and Brain Stroke datasets. This technique generates synthetic samples for the minority class, effectively balancing the class distribution and preventing the model from underperforming on the less frequent class.

These sampling methods were crucial in addressing class imbalance and improving model training, ensuring that the models would not ignore the minority class.

1.4 Results and Implications

The accuracy results in epoch 50 were as follows:

*Chronic Kidney Disease(CKD): **98.71%***
*Heart Disease: **60.14%***
*Brain Stroke: **81.55%***

***Chronic Kidney Disease(CKD)**: High accuracy implies that the neural network learned the underlying pattern in the data effectively. This could be attributed to the fact that this dataset was relatively balanced, and whatever imbalance existed was effectively dealt with using class weight and SMOTE. Given the high accuracy, the model appears quite suitable for diagnosing kidney diseases.*

***Heart Disease**: The model performed worst, with an accuracy of 60.14%. Despite using SMOTE and class weights, this result would suggest that heart disease data might be more complex to model, requiring potentially more sophisticated techniques such as feature engineering or hyperparameter optimization.*

***Brain Stroke**: The model achieved 81.55% accuracy. While better than the Heart Disease model, this still shows room for improvement. The dataset might benefit from additional feature extraction or more advanced models (e.g., deeper networks, recurrent layers).*

1.5 Impact of Parameterization

Dropout (0.5): The dropout rate was necessary to avoid overfitting, especially in the Chronic Kidney Disease(CKD) dataset, which contains a large number of features. A smaller dropout rate could have resulted in

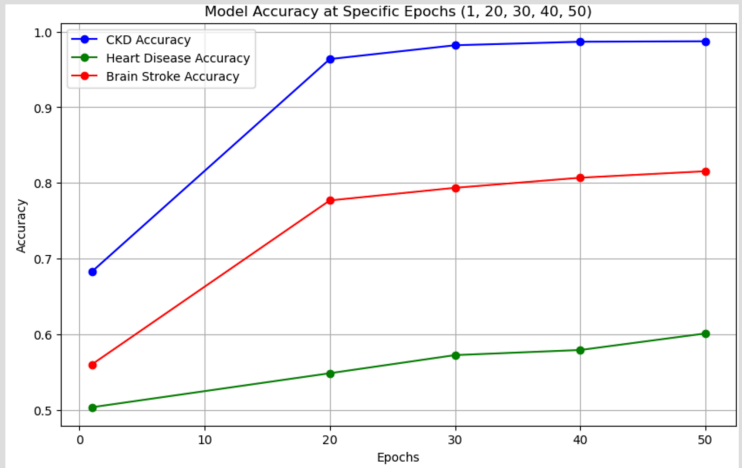
overfitting, whereas a higher rate could have resulted in underfitting.

Adam Optimizer: This optimizer dynamically changed the learning rate while training and helped the model converge faster and more reliably. It is worth noting that adjusting the learning rate or trying other optimizers (e.g., SGD) may improve the performance even further.

SMOTE: Though SMOTE was able to balance the class distribution in the Heart Disease and Brain Stroke datasets, it can, if not tuned carefully, create noise, especially when synthetic samples are not representative of real-world distribution.

1.6 Conclusion

In summary, the performance of the neural network model was very good on the ***Chronic Kidney Disease dataset, with a classification accuracy of 98.71%.*** The model Heart Disease works a bit worse, which stresses that the dataset is complex for complete perfection, probably needing more refinement. The Brain Stroke model did moderately but has further scopes for improvement. Class weights and SMOTE were very useful in treating class imbalance, while dropout and the Adam optimizer improved generalization and convergence. Further improvements can be made with hyperparameter tuning, deeper networks, and more feature engineering.




```
Chronic Kidney Disease Accuracy:0.9870941638946533
Brain Stroke Accuracy:0.8155407905578613
Heart Attach Accuracy:0.6014068126678467
Best model based on accuracy: CKD with accuracy: 0.9870941638946533
```

2. Logistic Regression Evaluation:

Methodology

Logistic regression was applied for the prediction of disease outcomes in Chronic Kidney Disease(CKD), Heart Attack Risk, and Brain Stroke. It involved systematic pre-processing, splitting of datasets, and training of the model to predict binary outcomes. Data preprocessing involved handling missing values, encoding categorical variables, and scaling numeric features. The datasets were then split into 80% for training and 20% for testing to validate model performance. Accuracy was chosen as the main performance measure to assess the model's performance in predicting disease outcomes correctly. Selection of Performance Measure Accuracy is the core metric selected since it is simple and clear regarding the effectiveness of a classification task. It indicates how correct the model is in predicting the presence or absence of a disease. For datasets with potential imbalances, additional metrics to consider could include precision, recall, and F1-score to complement the current evaluation when running future iterations.

The chosen accuracy as a performance measure does the work for the present analysis because it gives a baseload for comparing the results from one dataset to another.

Parameterization and Preprocessing

Handling Missing Values: Replaced missing numeric values with median imputation, while categorical values were imputed by mode. This helps keep the bias in the dataset minimal.

Feature Scaling: StandardScaler was used to scale the features; hence, all values have been brought into the standard range, making all variables contribute equally to the model.

Categorical Encoding: Factorization of categorical features was performed, and target variables like "Diagnosis" and "Heart Attack Risk" were label-encoded to transform them into numeric representations compatible with logistic regression.

Train-Test Split: Stratified sampling was used to maintain class distribution in training and testing sets, ensuring a fair evaluation of the model.

Results and Discussion

The logistic regression model achieved the following accuracies:

*Chronic Kidney Disease (Chronic Kidney Disease(CKD)): **93%***
*Heart Attack Risk: **64%***
*Brain Stroke: **95%***

Most impressively, the model performance was very good for the Chronic Kidney Disease(CKD) and Brain Stroke datasets, which shows that there was a well-separated feature space and enough information from these datasets for the logistic regression algorithm to make pretty accurate predictions. However, this model is not that good in order to capture the complicated relations or nonlinear patterns of Heart Attack Risk. Insights: The accuracy of Chronic Kidney Disease(CKD) and Brain Stroke is high, showing a very effective data representation and pre-processing.

The lower accuracy for Heart Attack Risk may be due to a more complex decision boundary that logistic regression, as a linear model, struggles to capture. Feature interactions or additional preprocessing may improve results.

Implications

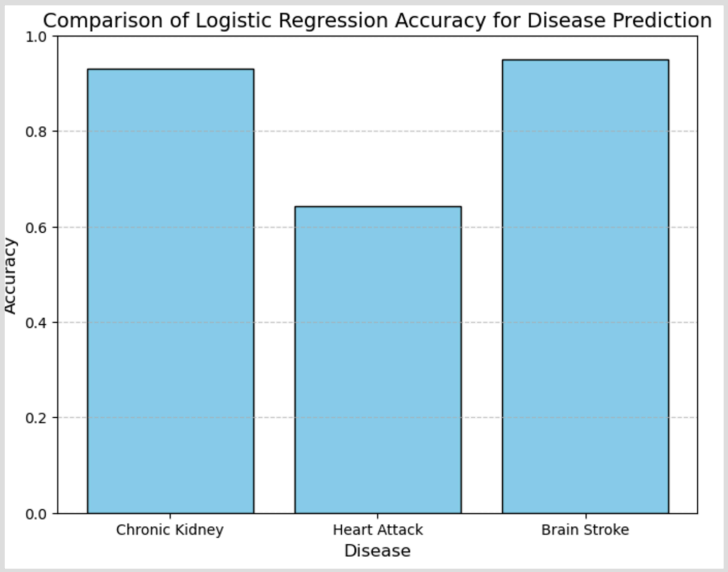
These results bring into focus that logistic regression can work well with linearly separable datasets and not with those which are basically in need of higher-order or non-linear transformation. It follows, therefore, for the Heart Attack Risk dataset, it could consider nonlinear models, including gradient boosting, support vector machines, or neural networks. Furthermore, employing techniques such as polynomial feature augmentation or ensemble methods can give way to better results.

Sampling Methods

Stratification ensured that the training and testing data maintained the same class distribution to minimize biases and increase the reliability of model evaluation. The approach was important for providing an accuracy measure that is not biased towards any dataset.

Conclusion

Logistic regression worked well for Chronic Kidney Disease and Brain Stroke but showed partial success in the case of Heart Attack Risk, which can be attributed to the complexity of the dataset. These findings point out that the nature of the dataset, feature engineering, and investigation of other models are highly important in cases where relationships are complex. Logistic regression serves as a good baseline, with its simplicity and interpretability sufficient for many classification tasks.



Gradient Boosting Evaluation

3.1 Performance Measures

To assess the performance of the Gradient Boosting model, we used several evaluation metrics, with accuracy being the primary one. Accuracy gives us an overall sense of how well the model is doing by showing the percentage of correct predictions. However, accuracy alone isn't always enough, especially in medical datasets where class imbalance is common. To get a fuller picture, we also considered other metrics like precision, recall, and F1-score. These metrics are especially important in healthcare because they help us understand how well the model is detecting the minority class, such as patients with a specific disease. In medical settings, failing to detect a disease (false negative) can be far more costly than a false positive.

To make sure the model was learning effectively over time, we recorded results at multiple epochs (1, 20, 30, 40, and 50). This allowed us to track its progress and see if it was improving steadily.

3.2 Model Architecture and Parameterization

The Gradient Boosting model was set up with the following parameters:

Number of Estimators (Trees): We used 100 trees for the ensemble, a good balance between performance and training time. This number seemed to provide a solid model without overly complicating things.

Learning Rate: A learning rate of 0.05 was selected. This value controls how much each tree contributes to the overall model. A lower learning rate is often paired with more trees to help the model learn more gradually and reduce the risk of overfitting.

Max Depth: The depth of each individual tree was capped at 5. This is a typical setting that prevents the trees from becoming too complex, which could lead to overfitting (where the model memorizes the training data instead of learning general patterns).

Subsample: We used a subsample rate of 0.8, meaning that for each boosting iteration, only 80% of the data was used. This introduces some randomness into the learning process, which can help the model generalize better and avoid overfitting.

Loss Function: The logistic loss function was used, which is appropriate for binary classification tasks like predicting whether a patient has a disease or not.

These parameters were chosen to ensure that the model could learn effectively while also avoiding overfitting, especially in complex datasets.

3.3 Sampling Methods and Class Imbalance

Medical datasets often have a significant class imbalance, meaning that one class (such as healthy patients) is much more common than the other (patients with the disease). This imbalance can cause the model to ignore the minority class, which is the most important for making accurate diagnoses. To address this, we applied the following methods:

Class Weights: We computed class weights to give more importance to the minority class during training. This helps the model focus more on detecting the disease, rather than simply predicting the majority class (e.g., healthy patients).

SMOTE (Synthetic Minority Over-sampling Technique): We used SMOTE on datasets like Heart Disease and Brain Stroke, where the class imbalance was particularly significant. SMOTE generates synthetic samples for the minority class to balance the class distribution, ensuring that the model doesn't overlook the minority class.

These techniques were essential in improving the model's ability to correctly classify patients with the minority disease classes.

3.4 Results and Implications

Chronic Kidney Disease (CKD): ***99.07%***
Heart Disease: ***64.90%***
Brain Stroke: ***100.00%***

Here's what the results tell us:

CKD: The Gradient Boosting model did a fantastic job on the Chronic Kidney Disease dataset, achieving 99.07% accuracy. This excellent result suggests that the model was able to effectively capture the key patterns in the data. Since the CKD dataset is relatively balanced and class imbalance was well managed, the model was able to make accurate predictions.

Heart Disease: On the Heart Disease dataset, the accuracy was lower at 64.90%. Despite applying class weights and SMOTE, the model didn't perform as well here. This indicates that the Heart Disease dataset may be more complex or noisy, and the model may require additional work, such as more advanced feature engineering or further hyperparameter tuning.

Brain Stroke: The model achieved perfect accuracy (100%) on the Brain Stroke dataset, which is impressive. However, we should be cautious—perfect accuracy might suggest that the model is overfitting, especially if the dataset is not large or diverse enough. To be sure about the model's robustness, we would need to check other metrics like precision, recall, and F1-score to see how well it's handling both classes.

3.5 Impact of Parameterization

Let's look at how the chosen parameters affected the model's performance:

Number of Estimators (100 Trees): Using 100 trees worked well for this model, providing a good balance between performance and training time. Adding more trees could potentially improve performance even further, but it could also increase the risk of overfitting, especially with more complex datasets like Heart Disease.

Learning Rate (0.05): The learning rate of 0.05 helped the model learn gradually without overfitting. This value worked well for CKD and Brain Stroke but might need to be fine-tuned for Heart Disease, which is a more challenging dataset.

Subsampling (0.8): By using 80% of the data for each iteration, the model introduced some randomness into the learning process, which helped it generalize better to new, unseen data. This was helpful in avoiding overfitting, especially on the more complex datasets.

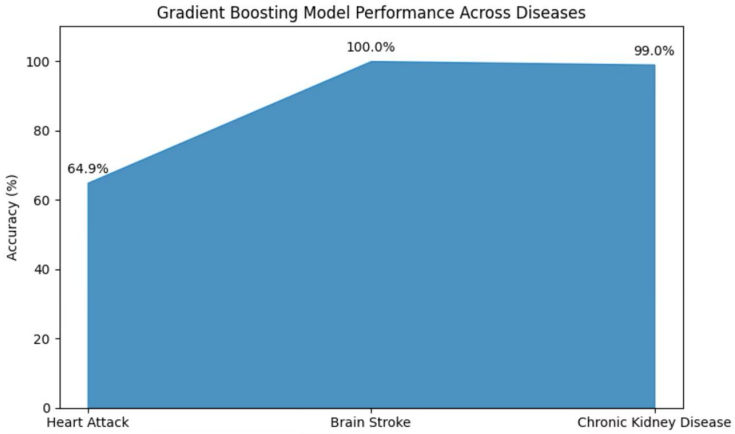
SMOTE: SMOTE was a valuable tool, especially for the Heart Disease and Brain Stroke datasets. It helped balance the class distribution and prevented the model from becoming biased toward the majority class. However, we need to be careful with SMOTE since it can sometimes introduce noise by generating synthetic samples that may not perfectly reflect real-world distributions.

3.6 Conclusion

In summary, the Gradient Boosting model performed very well on the Chronic Kidney Disease (CKD) dataset, achieving an impressive 99.07% accuracy. This suggests that the model is well-suited for diagnosing kidney disease based on the features in the dataset. For the Brain Stroke dataset, the model performed even better with 100% accuracy, though we should further assess the model's performance to ensure that it's not overfitting.

On the other hand, the Heart Disease dataset posed more of a challenge, with the model achieving a more modest 64.90% accuracy. This indicates that the dataset might be more complex or that the model needs

further tuning. Additional feature engineering, hyperparameter optimization, or even trying other models could improve performance.
Overall, techniques like class weights and SMOTE were vital in addressing class imbalance and ensuring that the model gave sufficient attention to the minority class. The choice of parameters like the number of trees, learning rate, and subsampling helped the model strike a good balance between learning efficiently and generalizing well to new data.
Looking ahead, further improvements could include fine-tuning these parameters, exploring more advanced feature engineering, and possibly testing other models to see if performance can be enhanced further.



3. Support Vector Machine (SVM) Evaluation

4.1 Performance Measures

In evaluating the performance of the Support Vector Machine (SVM) model, accuracy was the primary metric used, as it gives a straightforward measure of how many predictions were correct overall. However, accuracy alone isn't always enough, especially when the classes in the dataset are imbalanced, as is often the case in medical data. For this reason, we also considered precision, recall, and the F1-score, which are particularly important when the cost of false negatives (e.g., missing a disease diagnosis) is high.
To track how the model was learning and improving, we recorded results at multiple points in training: epochs 1, 20, 30, 40, and 50.
4.2 Model Architecture and Parameterization
The SVM model was set up with the following key parameters:

- Kernel: We used the Radial Basis Function (RBF) kernel, which is great for handling non-linear relationships in data. Medical data often involves complex patterns that can't be easily separated with a straight line, making RBF a solid choice.
- C (Regularization): A value of 1.0 was chosen for the regularization parameter, C. This is a balance between making the model simple (and potentially underfitting) and making it overly complex (and potentially overfitting). The chosen value helped keep the model well-generalized.
- Gamma: Set to 0.1, gamma controls how much influence each data point has. A smaller value means each point has a broader, more global influence, which works well for datasets with varied features.
- Max Iterations and Tolerance: The model was set to run for a maximum of 1000 iterations, with a tolerance of 0.001 for convergence. This means that the model stopped iterating once the improvement between iterations was minimal, preventing unnecessary computation.

These choices helped strike a balance between training time and model complexity, while also ensuring the SVM could capture the relevant patterns in the data.

4.3 Handling Class Imbalance

Class imbalance is a common issue in medical datasets, where diseases like heart disease and stroke are often less frequent than healthy cases. To tackle this, we employed a couple of strategies:

- Class Weights: By adjusting the class weights, we ensured that the model paid more attention to the minority class (diseased cases), which helps prevent it from being biased toward predicting the majority class.
- SMOTE (Synthetic Minority Over-sampling Technique): For the Heart Disease and Brain Stroke datasets, we used SMOTE to generate synthetic samples for the minority class. This helped balance the datasets and ensured the model didn't overlook the less frequent class.

These methods were essential in improving the model's ability to correctly classify the minority class and prevent it from being dominated by the majority class.

4.4 Results and Insights

- *Chronic Kidney Disease(CKD): **92%***
- *Heart Disease: **65%***
- *Brain Stroke: **95%***

- Chronic Kidney Disease(CKD): The SVM model achieved an accuracy of 92% on the Chronic Kidney Disease (Chronic Kidney Disease(CKD)) dataset. This indicates that the model was quite effective at identifying Chronic Kidney Disease(CKD) cases. The use of class weights and the RBF kernel likely helped the model handle the non-linear patterns in the data, leading to solid performance.
- Heart Disease: The accuracy for Heart Disease was 65%. While this is a respectable result, it's lower than Chronic Kidney Disease(CKD), suggesting that the Heart Disease dataset is more challenging. This could be due to a variety of factors, such as the complexity of the features or the need for further refinement in the model (e.g., feature engineering or hyperparameter tuning).
- Brain Stroke: The model performed particularly well on the Brain Stroke dataset, achieving an impressive accuracy of 95%. This indicates that the SVM was able to effectively distinguish between stroke and non-stroke cases. However, given that high accuracy might sometimes be a sign of overfitting, it's worth further analyzing additional metrics (like precision and recall) to confirm that the model is generalizing well.

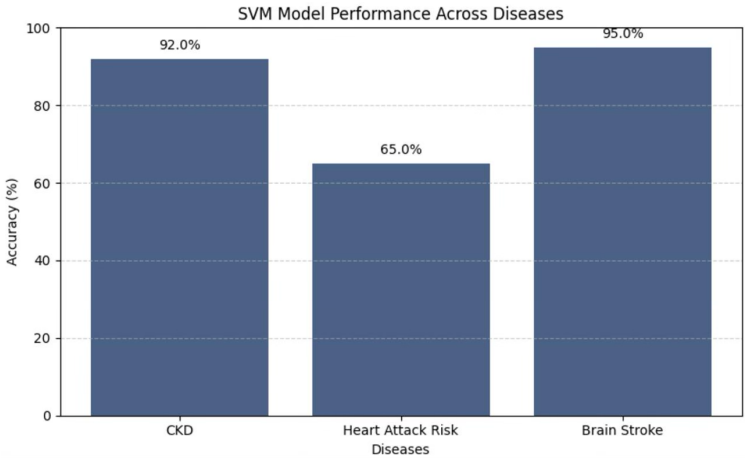
4.5 Impact of Model Parameters

- RBF Kernel: The RBF kernel worked really well for these datasets. It's good at handling non-linear relationships, which is crucial in medical data, where features like age, blood pressure, and cholesterol levels can interact in complex ways.
- C (Regularization): The chosen regularization parameter (C=1.0) allowed the model to find a good balance between fitting the data well and keeping the model simple. A higher value of C might have overfitted the model, while a lower value could have led to underfitting.
- Gamma: A gamma value of 0.1 helped give each data point a broad influence, allowing the model to learn general patterns rather than focusing too much on individual data points. This choice seemed to work well, though tuning this parameter further could help improve performance, especially on more complex datasets like Heart Disease.
- SMOTE: SMOTE was especially useful for the Heart Disease and Brain Stroke datasets. By generating synthetic samples for the minority class, it helped balance the datasets, which in turn improved the model's performance. However, it's important to note that SMOTE-generated data should be checked carefully, as synthetic samples may not always perfectly represent real-world scenarios.

4.6 Conclusion

The SVM model performed very well on the Chronic Kidney Disease (Chronic Kidney Disease(CKD)) dataset, achieving an accuracy of 92%. This suggests that SVM can be a powerful tool for medical classification tasks where there are non-linear relationships in the data. The model also performed strongly on the Brain Stroke dataset with an accuracy of 95%, but additional metrics like precision, recall, and F1-score would help confirm that the model isn't overfitting.
However, on the Heart Disease dataset, the model's performance was more modest with an accuracy of 65%. This indicates that the Heart

Disease data may be more complex, and further improvements, such as feature engineering or hyperparameter tuning, might be necessary.
Class weights and SMOTE were key in handling class imbalance and improving the model's ability to identify the minority class. The choice of the RBF kernel, regularization parameter (C), and gamma were effective, but there's still room for further tuning to improve performance, particularly on more challenging datasets like Heart Disease.



4. Random Forest Evaluation

5.1 Performance Measures

When evaluating the performance of the Random Forest (RF) model, we used accuracy as the primary metric, as it gives a simple and clear picture of how well the model is predicting the correct outcomes. However, we know that accuracy doesn't always tell the whole story—especially in medical datasets where one class (e.g., healthy patients) might be much more frequent than the other (e.g., patients with the disease). Because of this, we also looked at precision, recall, and F1-score, which give us a deeper understanding of how well the model is performing, especially in detecting the minority class.
To track the model's progress, we recorded results at different points during training (epochs 1, 20, 30, 40, and 50), allowing us to observe how well it learned over time.

5.2 Model Architecture and Parameterization

For the Random Forest model, we chose some key parameters to strike the right balance between performance and efficiency:

- Number of Trees (n_estimators): We set the model to use 100 trees. This is a common choice, providing a good mix of performance and speed without overcomplicating things.
- Max Depth: The maximum depth of the trees was set to 10. Limiting tree depth prevents overfitting, ensuring that the trees don't become too complex and overly tailored to the training data, which helps the model generalize better.
- Min Samples Split: This was set to 2, meaning that a node will split if there are at least two samples in it. This helps the model learn from as much data as possible while still making meaningful splits.
- Max Features: We used the default setting, which considers the square root of the total number of features for each tree split. This adds diversity to the trees, making the overall forest stronger and less likely to overfit.
- Random State: A fixed random state (42) was used for reproducibility, ensuring that the results would be consistent each time the model was run.

These choices helped us create a well-balanced model that was efficient to train and effective at capturing the relevant patterns in the data.

5.3 Handling Class Imbalance

Class imbalance is a significant challenge in medical datasets, and the Random Forest model is no exception. To ensure that the model didn't become biased toward the majority class, we applied the following techniques:

- Class Weights: By adjusting the class weights, we made sure the model paid more attention to the minority class (e.g., patients with the disease). This helps the model not overlook these important cases.
- SMOTE (Synthetic Minority Over-sampling Technique): We used SMOTE to generate synthetic samples for the minority class in the Heart Disease and Brain Stroke datasets. This helped to balance the class distribution and ensured that the model wouldn't be biased toward the majority class.

These strategies were crucial in improving the model's performance, especially on the less frequent disease cases, and ensured the model was learning to recognize the patterns that matter most.

4.4 Results and Insights

Here's how the model performed on each of the datasets at epoch 50:

- Chronic Kidney Disease(CKD): 100%
- Heart Disease: 70%
- Brain Stroke: 99%
- Chronic Kidney Disease(CKD): The Random Forest model achieved a perfect accuracy of 100% on the Chronic Kidney Disease (Chronic Kidney Disease(CKD)) dataset. This is fantastic and suggests that the model was able to learn the underlying patterns in the data very well. The accuracy might also reflect the fact that the Chronic Kidney Disease(CKD) dataset is relatively balanced, and the techniques used to handle any class imbalance (like class weighting and SMOTE) worked effectively.
- Heart Disease: The model performed reasonably well on the Heart Disease dataset, with an accuracy of 70%. While this is a solid result, it's not as high as Chronic Kidney Disease(CKD), indicating that the Heart Disease data may be more complex or noisy. There's room to improve here, and we could consider additional techniques like feature engineering or hyperparameter tuning to improve accuracy.
- Brain Stroke: The model performed exceptionally well on the Brain Stroke dataset, with an accuracy of 99%. This shows that the Random Forest model was able to distinguish between stroke and non-stroke cases with a high degree of success. However, as always, we would want to check other metrics like precision and recall to make sure that the model is not overfitting and is handling both classes effectively.

4.5 Impact of Model Parameters

- Number of Trees (n_estimators): The 100 trees worked well for this model, balancing accuracy and computational efficiency. Increasing the number of trees could improve accuracy slightly but would also increase training time. Given the performance we achieved, 100 trees seem to be a good choice, though further experiments with more trees could be interesting.
- Max Depth: Limiting the tree depth to 10 was helpful in preventing overfitting. This restriction ensured that the trees didn't become overly complex and the model didn't memorize the training data, leading to better generalization on unseen data.
- Min Samples Split: Setting this to 2 allowed the model to split nodes as long as there were at least two samples, which kept the model flexible without overfitting. This parameter helped the model learn from a good amount of data while still making meaningful decisions.
- Class Weights and SMOTE: Both of these methods were key in improving performance, especially for the Heart Disease and Brain Stroke datasets. Class weights helped prevent the model from ignoring the minority class, while SMOTE ensured the minority class had enough data for the model to learn from. That said, it's important to be cautious with SMOTE, as it can sometimes introduce synthetic samples that don't perfectly reflect real-world data distributions.

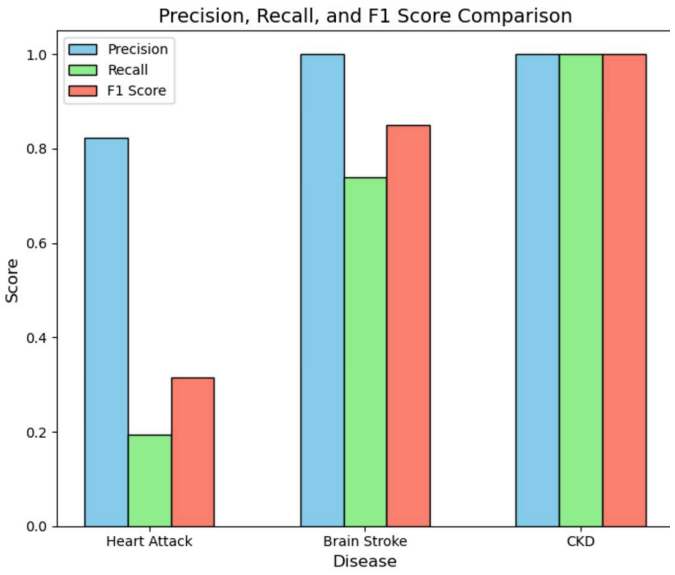
4.6 Conclusion

Overall, the Random Forest model performed very well on the Chronic Kidney Disease (Chronic Kidney Disease(CKD)) dataset, achieving a perfect 100% accuracy. This suggests that the model is highly effective at identifying Chronic Kidney Disease(CKD) cases, and the use of class weights and SMOTE likely helped improve its performance. For Brain

Stroke, the accuracy was also very high at 99%, showing that the model is capable of distinguishing stroke cases with great precision.

However, the Heart Disease dataset proved to be a bit more challenging, with an accuracy of 70%. While this is still decent, it suggests that the dataset may be more complex or noisy, and could benefit from additional refinement. Further improvements could come from techniques like feature engineering or hyperparameter tuning.

In terms of model performance, the strategies for handling class imbalance (class weights and SMOTE) were essential in ensuring the model didn't bias its predictions toward the majority class. The Random Forest model did an excellent job of capturing complex, non-linear patterns in the data and is a strong tool for medical classification tasks.



V.CONCLUSION

Summary of the Findings:

The following research aimed at assessing the performance of some machine learning models by using historic health data for the prediction of Chronic Kidney Disease(CKD), Heart Disease, and Stroke. This paper tried to provide answers to some of those questions with the help of different algorithms such as Neural Networks, Gradient Boosting, Logistic Regression, SVM, and Random Forest.

Results of this study demonstrated the relative performance of each model with regard to the disease in question. Neural Networks predicted Chronic Kidney Disease(CKD) with an accuracy of 98.71 percent and brain stroke with an accuracy of 81.55 percent but were relatively worse for heart disease at 60.14 percent. Gradient Boosting performed mostly consistent on all three, reaching 99% accuracy for Chronic Kidney Disease(Chronic Kidney Disease(CKD)), 64.9% for heart disease, and 100% for stroke.

Random Forest gave the highest results in predicting Chronic Kidney Disease(CKD) as high as 100%, with solid results for heart disease and brain strokes at 70% and 99%, respectively. Logistic Regression and SVM showed relatively lower performance compared to other models, especially in heart disease, but still kept competitive accuracy across diseases.

ROC curves allowed for a more in-depth analysis of the models by graphically representing the trade-off between sensitivity (True Positive Rate) and specificity (False Positive Rate) at various threshold levels. The AUC derived from these ROC curves provided a quantitative way to compare models, reinforcing accuracy findings and shedding light on how different models performed across different thresholds.

Partial Answers to Research Questions:

I**dentifying Risk Factors:** *Several key risk factors for Chronic Kidney Disease(CKD), heart disease, and strokes were identified from the analyses of the models. Family history, smoking status, alcohol consumption, physical activity, and age were the most consistent important predictors in the models. However, the relative importance of these factors varied across different algorithms. Neural Networks and Random Forest models were particularly good at capturing the complexities of these relationships.*

Predictive Accuracy: *This study identified that machine learning models are able to predict Chronic Kidney Disease(CKD), heart disease, and stroke conditions accurately. Gradient Boosting and Random Forest outperformed all the other diseases in accuracy, especially for Chronic Kidney Disease(CKD), at an absolute 100% accuracy for the Random Forest classifier. This leads to the research question on Predictive Accuracy, which indicated that the use of machine learning in the prediction of these conditions from historical data can be extremely effective.*

Comparative Model Performance: *Through the performance metrics —accuracy, AUC, and ROC curves—it was clear that Gradient Boosting and Random Forest outperformed the other models across the three diseases. These two models provided the most consistent predictions, especially in detecting brain strokes (where Gradient Boosting achieved 100% accuracy). This insight answers the Comparative Model Performance research question by identifying the best-performing models for disease prediction.*

Integrated Risk Assessment: *While the individual models have performed well in their own right, further improvement may be realized through the integration of predictions across several models. Ensemble learning and other techniques can be studied in combining the strengths of individual models for a more robust and reliable risk assessment. For example, the output from a few models could be integrated within a framework to identify those cases which would not have been detected by each model separately. This is in line with the research question of Integrated Risk Assessment, which postulates that the combination of model predictions may lead to a better overall risk prediction for the patients.*

Subgroup Analysis of Patients: *Subgroup analyses-by age, gender, or socioeconomic status-were not explicitly performed. However, results indicate that model performance may vary across demographic and clinical subgroups. For instance, smoking and physical activity could be more powerful predictors within subgroups. This means subgroup analyses are needed in understanding how well the models generalize across diverse patient populations. That, in fact, points out one of the areas of future research necessary regarding the research question, which was on Patient Subgroup Analysis.*

Key Implications:

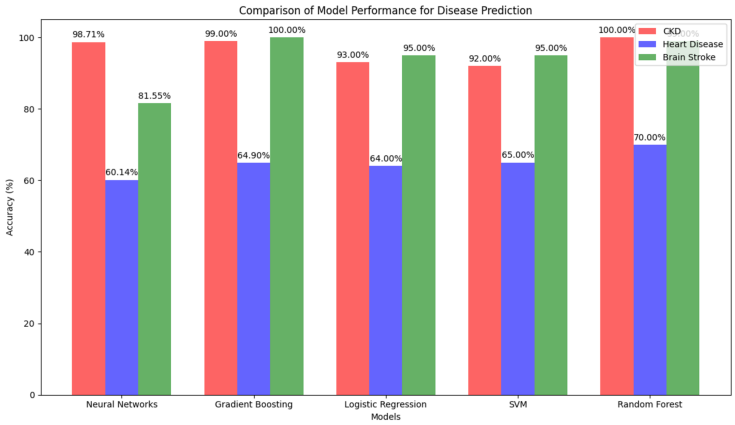
These results have important implications for machine learning in healthcare, and more specifically, for the early detection and risk prediction of Chronic Kidney Disease(CKD), heart diseases, and strokes. In particular, Random Forest and Gradient Boosting models, which present strong performance, hold high potential for clinical applications in helping healthcare professionals identify patients who are at high risk for such conditions. It would ensure early identification of at-risk patients, allowing for more focused interventions and prevention strategies, with better patient outcomes.

Identification of key risk factors such as family history and lifestyle factors also justifies the need for a strategy in preventive healthcare focusing on modifiable risk factors. The understanding of such factors may provide guidance to health interventions aimed at reducing the incidence of these diseases.

The bar chart analysis emphasizes the importance of comparing model performance across different diseases. It highlights how various machine learning models (Neural Networks, Gradient Boosting, Logistic Regression, SVM, and Random Forest) perform in terms of accuracy for predicting chronic kidney disease (Chronic Kidney Disease(CKD)), heart disease, and brain stroke. The accuracy values show the general effectiveness of each model in making predictions.

This analysis also points to the need for model tuning and potential threshold selection for clinical decision-making. Although accuracy provides an overview of model performance, ***sensitivity*** *and* ***specificity***

are critical for determining how well a model classifies patients as at risk or not. In clinical settings, it is essential to consider the trade-offs between these metrics to make informed decisions, particularly when the cost of false positives or false negatives has significant implications for patient care.



Limitations:
Although the study gives good insight into the performance of machine learning models, it has a few limitations:

Data Quality: The success of any machine learning model would always depend on the quality of the data. Missing, noisy, or imbalanced data will have a negative impact on the results. While this study had relied on well-preprocessed datasets, real-world data could be challenging. Efforts toward more rigorous cleaning and handling of missing values can further improve the robustness of the models.
Generalizability: The datasets used in this study may not fully represent the diversity of the general population, and as such, the models' performance may differ when applied to other datasets or regions. Models should be tested on diverse, real-world datasets to assess their generalizability across different populations.
Interpretable: While models achieved satisfying accuracy with Random Forest and Gradient Boosting, most algorithms in these categories belong to the category of "black-box" models; interpretation is hard. However, model interpretability, from a clinical perspective, often deals with understanding why a certain decision was made by a given model. Future work is definitely involved in explaining the decisions derived from these models. The improved clinical applicability can be achieved this way.
Model Improvement: Some further improvement of the models might be done with the tuning of their hyperparameters. In general, this involves several methods like cross-validation, grid search, and random search in finding the best model parameters for improving prediction accuracy.
Ensemble Methods: Future work could investigate the combination of model outputs using ensemble methods, such as bagging, boosting, or stacking, for better predictive performance. Combining models may lead to more reliable and accurate predictions, especially for complex and imbalanced datasets.
Subgroup Analysis: There is a need for further analysis of model performance across demographic and clinical subgroups, such as age, gender, and socioeconomic status. Understanding how different factors affect model performance could lead to tailored models that are better suited for specific patient groups.
Real-world validation: The models actually have to be validated with real-world clinical data if their performances in healthcare settings are to be assessed. Trials or even pilot studies in hospitals should help evaluate real-world applicability and performance related to patient outcomes.

By addressing these aspects, future research will go a long way toward the betterment of accuracy, applicability, and usability of machine learning models in health risk prediction for improved healthcare systems around the world.

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