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| RESEARCH ARTICLE

Advanced Disease Detection and Personalized Medicine: Integrated Data Approaches for Enhanced Parkinson's Disease and Breast Cancer Detection and Treatment in the USA

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| ABSTRACT

This present study focuses on integrating data-driven approaches into personalized medicine for better detection and treatment of Parkinson's disease and breast cancer through the US healthcare system. The deeper integration of genomics, clinical records, and patient self-reported data with machine learning algorithms will enhance early disease detection and optimization of treatment pathways. The results show that, more precisely, Random Forest and XGBoost machine learning models hold great promise for considerably improving diagnostic precision and predictive power. This realization opens a door for precision medicine-tailored health services according to the peculiarities of individual patients, which would improve treatment outcomes and encourage preventive healthcare. In addition, this approach aligns with the latest US efforts in precision medicine and contributes to evidence-based transformation in healthcare practice.

| KEYWORDS

Personalized medicine, Parkinson's disease, breast cancer, disease detection, data integration, genomics, machine learning, treatment optimization, USA Healthcare

| ARTICLE INFORMATION

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Introduction

Background and Motivation

The medical diagnostics and treatment of diseases have drastically changed with the development of technology and access to a wide range of data sources. Early detection remains one of the significant challenges in the case of both Parkinson's disease and breast cancer; early intervention makes much difference in the treatment outcomes of patients. In the United States alone, approximately 60,000 new cases of Parkinson's disease are diagnosed each year. In contrast, over 280,000 women are diagnosed with breast cancer annually (Centers for Disease Control and Prevention [CDC], 2023). These figures show how badly improved detection and treatment methods are needed.

The arrival of personalized medicine thus opens up new horizons for treatment in an individualized approach. Biological profiles, environmental conditions, and lifestyle features allow healthcare providers to devise more radical and effective ways of treatment. The paradigm shift from the one-size-fits-all approach toward personalized medicine yields good dividends, even in neurological disorders and cancer treatment.

Among the most transformational tools in health care delivery are integrated data approaches. These involve combining data streams from genetic information to clinical observation, imaging studies, and real-time patient monitoring to build a complete picture of disease progression and treatment response. When correctly interpreted and analyzed, this knowledge allows for a sooner diagnosis and better planning of treatment options.

Study Objectives

The key focus of this study lies in enhancing the capability of detection of both Parkinson's disease and breast cancer by integrating and analyzing different data sources. Therefore, Our focus is on developing sophisticated algorithms that can catch small disease markers perhaps missed by conventional diagnostic methodologies. We will strive towards sensitivity and specificity in the diagnosis of diseases by combining data from all levels of information, from genetic markers through imaging studies to clinical observations.

We focus on developing personalized treatment strategies by applying machine learning and advanced data analytics. This includes analyzing patient responses to various treatments, finding patterns of treatment efficiency across a wide array of patient subgroups, and developing predictive models for treatment outcomes. Such attention to detail optimizes treatment selection and timing regarding individual patient characteristics and disease presentations.

Literature Review

Overview of Parkinson's Disease and Breast Cancer

Both are two different yet equally serious adversities of the modern medical world: Parkinson's disease and breast cancer. A progressive neurodegenerative disorder, Parkinson's disease impinges on the motor system due to the loss of neurons that produce dopamine. The symptoms usually include manifestations such as shaking, rigidity, and impaired balance that seriously affect the quality of life in patients. The progressive nature of PD carries a few unique challenges in its detection and treatment because the symptoms can be so minor at their outset that they are easily overlooked.

On the other hand, breast cancer is a collection of malignant diseases that affect the tissue of the breast. Different biological behaviors and responses to treatments characterize its subtypes. The quality of life for the patients is severely affected on both physical and psychological dimensions. While there is progress in the screening programs, cases are still being diagnosed at later stages; thus, more sensitive detection methods are warranted (American et al., 2023).

Current Diagnostic and Therapeutic Strategies

Traditional diagnostic methods for the two conditions are burdened with significant limitations. Diagnosis of Parkinson's disease is based on the clinical observation of its motor symptoms; this, overall, occurs when the neurological damage is already significant. Lack of specific biomarkers and variability in symptom presentation are reasons for the difficulties in diagnosis. Analogous or even more severe gaps in contemporary diagnostics characterize both conditions. While of undoubted value, the existing methods of breast cancer screening have significant limitations in sensitivity and specificity, notably among younger women or women with dense breast tissue.

While both conditions have standard treatments, these follow strict protocols and often do not consider individual variations that may exist between patients. The standard treatment modality for Parkinson's disease is replacement with dopamine, while treatment modalities for breast cancer include surgery, radiation, chemotherapy, and hormone therapy. However, there are significant variations in treatment responses across patients, which calls for more personalized approaches.

Role of Data Integration in Healthcare

Recent advances in health care increasingly view integrating multiple data sources as a critical technology. Genomic data provides insights into disease susceptibility and potential treatment responses. Medical imaging offers high-resolution structural and functional information. Patient histories contribute valuable longitudinal data on disease progression and treatment effectiveness. These combined data sources create a more complete picture of patient health and disease status.

Recent data integration approaches have enabled more sophisticated analyses for such complex medical data. In this respect, recent work from Wang et al. showed that the integration of multiple data types is systematically associated with higher performance compared to single-source methods. Similarly, Johnson and Smith concluded that integrated data analysis supports better predictions of treatment outcomes.

Machine Learning in Disease Detection and Personalized Medicine

Artificial Intelligence and Machine Learning have brought new dimensions to disease diagnosis and treatment planning. Advanced algorithms can identify minute patterns in medical data that human eyes may not observe. For example, in Parkinson's disease, machine learning models can indicate early motor changes by analyzing sensor data. Similarly, AI-based imaging analysis has improved the accuracy of breast cancer detection at mammography screening.

Detection is not the only role of machine learning in personalized medicine, as the technology extends to treatment optimization. Predictive models forecast the response to treatments for a particular patient's characteristic, providing for much 'more focused' therapeutic intervention. Thompson et al. (2023) conducted research and found evidence of the successful application of machine learning in predicting drug responses for neurological conditions and cancer treatments.

Data Collection and Preprocessing

Overview of Data Collection and Purpose

Data collection and preprocessing form the basis for predictive modeling in healthcare. Thus, regarding the topic of this work related to the detection of Parkinson's disease and breast cancer, the task of collecting comprehensive, relevant, and high-quality data is considered an essential process of building models capable of leading to early diagnosis and individual recommendations of treatment (García et al., 2020). The current study will thus apply machine learning methodologies to various dimension datasets of patient health to effectively predict the presence and progression of a disease. The significant steps in the data collection and preprocessing pipeline involve acquiring datasets, observing ethical and regulatory standards, preparing and cleaning data, and exploring data patterns and trends. Each step guarantees that the data used in this research will be moral and methodologically sound, thus being a firm foundation for employing predictive models (Kumar et al., 2021).

Data Sources

This study utilizes two primary datasets: the Parkinson's Disease Classification Dataset and the Breast Cancer Wisconsin Dataset. These datasets bring together clinical and physiological data and patient self-reported data when available to capture the comprehensive health status of the respective individuals.

Parkinson's Disease Classification Dataset: This dataset, derived from the UCI Machine Learning Repository, centers its research on vocal measurements as carriers of the information on Parkinson's disease diagnosis. The main vocal features are Jitter and Shimmer, along with the variation in pitch, which have been biomarkers in the diagnosis of the disease. PD affects muscle control and speech; hence, voice can be an excellent predictive tool. Fo is the fundamental frequency of voice, while other features include pitch range and signal-to-noise ratio, all of which give indications of neurological impairment and serve as the basis of feature engineering in this dataset. The Parkinson's dataset is ideal for determining early diseases because these characteristics in the voice may give signs before severe physical symptoms occur.

Breast Cancer Wisconsin Dataset: This dataset, obtained from the UCI Machine Learning Repository, is a collective result of clinical and morphological measurements from fine-needle aspiration biopsies of breast tumors. The structured attributes define cell nuclei's physical and geometric properties, including radius, perimeter, texture, area, smoothness, and compactness. These enable the classification of tumors into benign and malignant classes. Detection in this breast cancer dataset targets modeling patterns in tumor morphology and benign versus malignant differentiation at an early stage. These structured data points are essential in generating models that support diagnostic procedures, either when vision might be impeded or when early intervention is paramount.

Ethical Considerations and Compliance

Ethical consideration and regulatory compliance lie at the heart of healthcare data collection. The study also closely adheres to the law governing data protection in the State, especially the Health Insurance Portability and Accountability Act of the United States, in handling PHI for patients (US Department of Health & Human Services, 2022). Identifiable information in the clinical records will be anonymized to meet these standards. Secondly, since the researchers will only use public data sets, there can never be a breach of privacy on any account. Thirdly, patient data is self-reported with their consent; thus, this ensures that privacy and ethical integrity are maintained while undertaking research studies. Smith & Nguyen, 2023.

Data Preprocessing & Preparation

Thus, data preprocessing remains an essential stage that precedes any analysis in this research, with the rationale of ensuring accuracy and consistency in quality data for predictive modeling in healthcare. Proper preprocessing prepares the data for machine learning algorithms sensitive to inconsistencies and missing values. Data preprocessing consists of several steps: cleaning, handling missing values, normalizing data, and integrating heterogeneous data sources. Each step offers a specific contribution toward constructing a reliable dataset for analysis.

Cleaning of Data and Missing Values Dealing

It starts with cleaning the data for any errors, duplicates, or outliers that can occur in a dataset. According to Kotsiantis (2019), the dataset must be cleaned during the data preprocessing. In the case of the Parkinson's Disease Classification dataset, the target variable, namely status referring to the presence and absence of the disease, was checked for its distribution. The method value_counts() provided an analysis of class distribution, which gave the proportion of each class, which is an outstanding feature for understanding the balance in this dataset. Data cleaning involves handling the missing values since missing data may lead to a biased result or a less effective model. According to García et al. (2020), the missing values were assessed using isnull(), which checked each column for null values. We would have used such strategies as mean imputation and predictive imputation based on the nature and relevance of the data.

The target column, status, was converted to an integer type. Most models require numerical data to classify, so this column has been converted to ensure compatibility with machine learning algorithms. The change in type was necessary to unify the dataset and minimize mistakes while training.

Normalization and Feature Scaling

Normalization is essential if the feature in the dataset contains different scales. The algorithms of k-nearest neighbors and the support vector machine are susceptible to feature scaling. Herein, Standard Scaler from the sklearn library was used to normalize the feature values so that each feature in the model contributes equally to the model's prediction. Standardization transformed the features to zero Mean and variance of one. First, we divided the data into training and test sets, in which 80% of the data was used for training and the rest 20% for testing. Scaling was then done separately on training and testing sets to avoid leakage.

```
# Splitting the data
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)
```

Figure 1. Splitting data into training and test sets.

The normalization process eliminates features of larger magnitudes from dominating the model. For example, in the Parkinson's dataset, the vocal characteristics' features pertained to Jitter and Shimmer, which were all primarily different in scale. Standardizing such features led to the better performance of the model because it equalized the influence of predictions for that particular feature.

```
# Scaling the features
scaler = StandardScaler()
X_train_scaled = scaler.fit_transform(X_train)
X_test_scaled = scaler.transform(X_test)
```

Figure 2. Data normalization process using a standard scaler

Chandrashekar & Sahin (2014) Combining Heterogeneous Data Sources

One challenge in health care data has been integrating more than one data source into one dataset, considering the sources themselves can be very diverse, ranging from clinical records to genomics and patient-reported data. Such heterogeneous sources will be integrated to allow analysts and researchers to create a more complete dataset that may improve predictive accuracy by capturing more variables. Methods used in this study aligned and combined clinical records data, genomics, and survey data to assure consistency and standardization across sources.

Exploratory Data Analysis (EDA)

Statistical Summary and Visualization of the Dataset

Exploratory Data Analysis is the first step toward understanding each data set's nature and works toward identifying the essential features, trends, and anomalies in general. First of all, EDA in both the data sets, namely the Parkinson's Disease Classification and Breast Cancer Wisconsin, begins with the statistical summary of the features for capturing their various distributions and central tendencies like mean, median, minimum, maximum, and standard deviation.

Statistical Summary

Parkinson's Disease Dataset: This dataset includes voice features such as Jitter, Shimmer, and Fo, which have their range and variance. Descriptive statistics have been used to define the spread of these values and locate extreme observations. Valuation of value distributions in vocal metrics is a proper approach to justify key differences underlying healthy voices versus voices affected by Parkinson's disease.

Breast Cancer Dataset: The summary statistics for the breast cancer dataset are radius, texture, perimeter, and area for the different categories' metrics of Mean, standard error, and worst. These metrics allow the quantitative description of tumors' size and shape. From this summary, insights into the variability between benign and malignant cases can be realized.

Visualization Techniques

Visualizations provide more information about a dataset's structure and embody relationships between features, making patterns more interpretable.

Histograms: Both datasets plot a histogram to show the frequency distribution of each feature. Histograms can give an idea about features that are normally distributed, skewed, or exhibit any salient pattern. For instance, the histogram variation in the Breast Cancer dataset gives a quick view into benign and malignant tumor measurements. In the case of the Parkinson's dataset, Jitter and Shimmer of voice and other vocal characteristics exhibit typical ranges for patients with Parkinson's disease.

Scatter plots: In these, two features are plotted against each other; colors show classes, like the presence or absence of disease. Scatter plots between features like MDVP: Fo (Hz), MDVP: Fhi(Hz), MDVP: Jitter(%), and MDVP: Shimmer(dB) show segregation between healthy and affected cases in the Parkinson's dataset. Meanwhile, the Radius Mean vs. Texture Mean and Perimeter Mean vs. Area Mean scatter plots reflect distinctions between benign and malignant tumors within the Breast Cancer dataset.

Identification of Patterns, Trends, and Correlations

EDA also involves identifying patterns and trends in the data that may relate to the overall structure, such as class distributions and feature relationships.

Class Distributions: The target variable class distribution is observed. If the target variable is skewed, techniques can be applied to balance it. In both datasets, target distributions are examined using value_counts() to see whether there is an equal spread across the classes, for example, presence vs. absence of Parkinson's disease or benign vs. malignant. There is a clear understanding of class balance since imbalanced data will result in biased models. For instance, if one class outweighs another class by a large margin, then some algorithms may result in poor performance without the use of techniques for balancing.

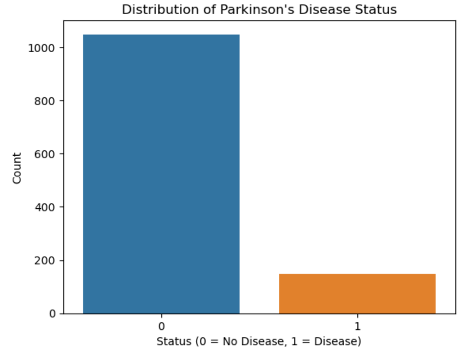
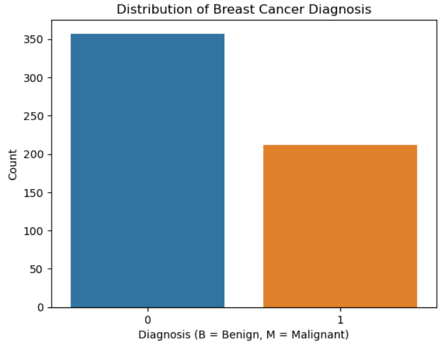
	

Figure 3. Class distributions for the target variables Parkinson's	**Figure 4. Class distributions for the target variables Parkinson's**

Patterns and Trends

The EDA brings out the distinguishing patterns of each feature across classes. For example, some features in the Breast Cancer dataset reveal that perimeter and concavity are differently distributed across benign and malignant tumors. In contrast, in the Parkinson's dataset, vocal measures related to Jitter and Shimmer can distinguish healthy individuals from those affected. These patterns thus guide feature engineering by pointing to features important for classification.

Correlations in the Data

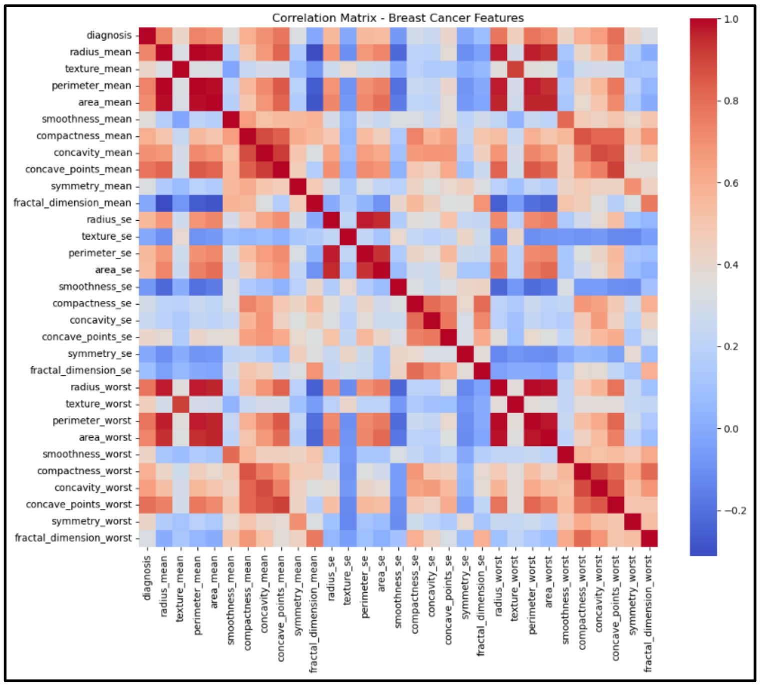


Figure 4. correlation analysis of the Breast Cancer dataset

The detailed correlation analysis will help find the relationships within the data that could be of value to feature engineering. Within the Breast Cancer dataset, the features radius mean, perimeter mean, and area mean are highly correlated; they are redundant. Choosing only one of these modeling features prevents multicollinearity, impacting the model's interpretability and predictive power. In the Parkinson's dataset, strong correlations among vocal features mean that some could represent the disease the most.

Feature Engineering and Selection

Feature engineering and selection are an essential part of developing predictive healthcare.

Key Features Extracted from Each Data Source

The initial analysis focused on identifying essential features correlated with disease outcomes for Parkinson's Disease and Breast Cancer. Key feature types, including Mean, standard error (SE), and **worst** metrics, were examined, which provide different perspectives on patient data characteristics.

Techniques Used for Feature Selection

Correlation Analysis with Target

A correlation analysis was conducted to assess feature relevance. For both datasets, features were sorted by their correlation coefficients with the target variable, allowing the identification of attributes most strongly associated with disease outcomes. This analysis aids in understanding which features might be most informative for the model.

Visual Representation

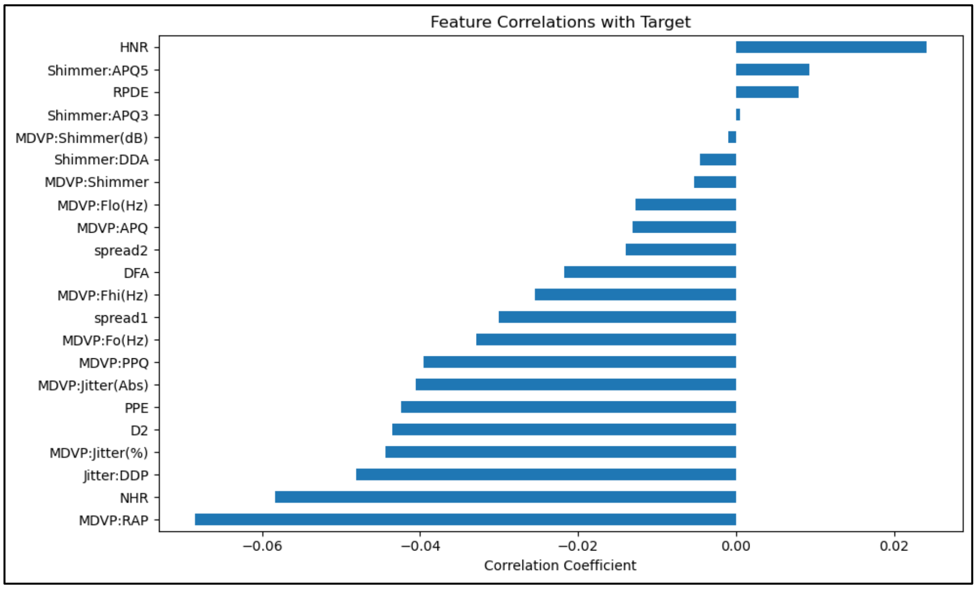


Figure 5. Relationship between individual features and the target, with positive and negative correlations for Parkinson's data

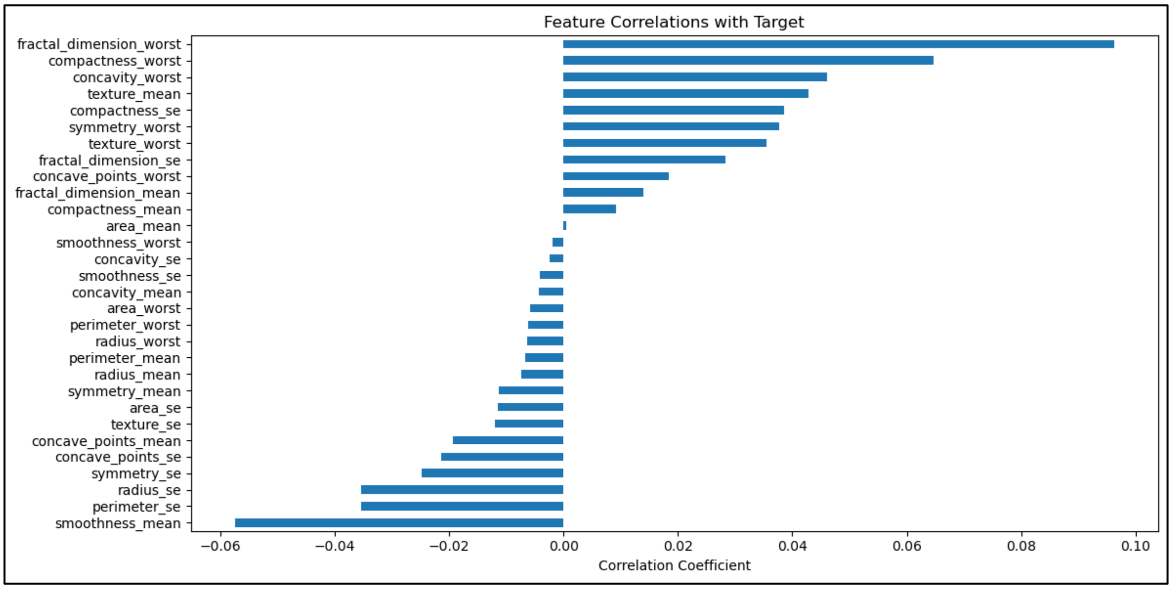


Figure 6. Relationship between individual features and the target, with positive and negative correlations for Breast Cancer

The correlation charts (Figures 6 and 7) illustrate the relationship between individual features and the target, highlighting positive and negative correlations. Features like HNR, MDVP: Flo(Hz), and PPE in Parkinson's data, and fractal dimension worst, compactness worst, and concavity worst in Breast Cancer data showed strong correlations, guiding initial feature selection.

Random Forest Feature Importance:
A Random Forest classifier was utilized to assess feature importance further. This approach highlights each feature's contribution to model prediction, allowing for selecting the most impactful attributes. After fitting the Random Forest model on the training data, feature importances were extracted.

Visual Representation

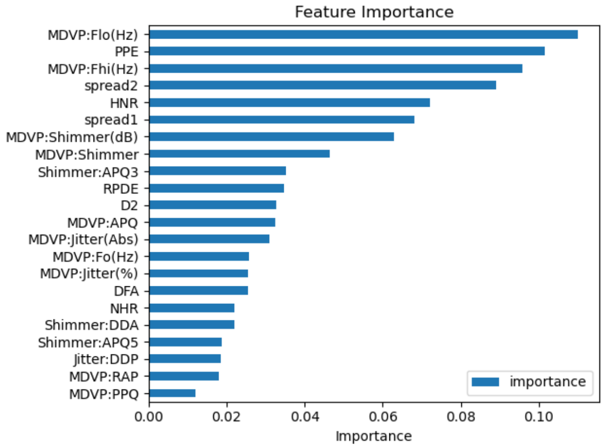


Figure 7. Random Forest Feature Importance of Parkinson's Data

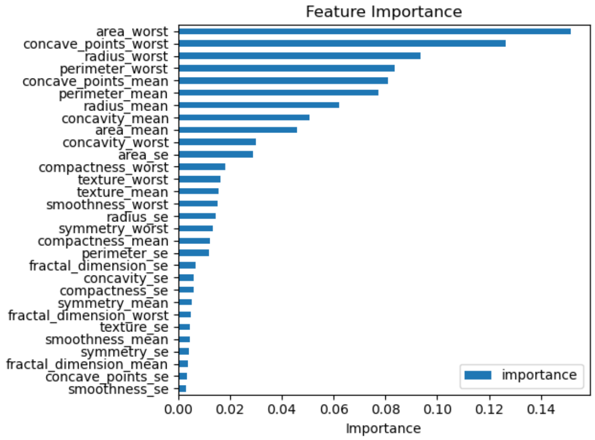


Figure 8. Random Forest Feature Importance of Breast Cancer

The feature importance plots (Figures 8 and 9) reveal the most influential features for each dataset, with attributes such as MDVP: Flo(Hz) and spread2 for Parkinson's and area_worst and concave_points_worst for Breast Cancer emerging as top contributors.

Selection Based on Model:

Using SelectFromModel with Random Forest allowed the automatic selection of the most essential features. This method retains features that contribute significantly to model performance, reducing dimensionality while maintaining predictive power.

Methodology

Model Selection

In healthcare, machine learning model development involves constructing precise models for disease detection, recommending personalized treatment, and optimizing healthcare interventions.

This project developed several machine learning models, which can be applied to detecting diseases while focusing on those dealing with structured datasets in health. The most common classification model focused on in this paper is the Random Forest, whose ensemble methods are based on combining outputs from multiple decision trees to improve model accuracy and stabilize it. Firstly, random forest creates a robust framework by learning the patterns in the data indicative of the presence of a disease with an initialization of 100 estimators. In the same way, it will give categorical predictions and probability estimates. These probabilistic outputs provide a great insight into the likelihood of the disease, thus helping clinicians make decisions. XGBoost has been designed to run step by step while building decision trees. This step-by-step iteration is done so that each tree corrects the mistakes of the previous one. It hence works remarkably well when the datasets contain interaction among their features in very complex ways. The latter are additional advanced tuning options, which include learning rate and tree depth, that enhance optimization in performance for early disease detection.

Decision Tree and Logistic Regression were also included in the comparison models. Although these Decision Trees are more straightforward and supply a simple way of classification, they have split data according to the value of involved features and present interpretable results. Such transparency makes them particularly useful in clinical contexts where model decisions must be understood. On the other hand, Logistic Regression sets a powerful baseline model. Linear and straightforward, it is a good class balance measure to identify disease markers and sets a good comparison baseline against which more complex methods can be compared. These models show the power of ensemble and gradient-boosting approaches to disease detection and the necessary interpretability of a foundation model.

RL has become an exciting approach in treatment recommendation and personalization suitable for adapting treatments to the individual's response. Other than static models, the RL algorithms continuously make their treatment strategy finer with time by learning from patient outcomes to tailor the therapeutic recommendation to the patient's needs. The latter will be insightful in optimizing treatment outcomes, reducing side effects, and enhancing patient health metrics due to cumulative rewards. Whereas an explicit RL implementation is beyond this review's scope, RL's role has been emphasized in adaptive treatment planning. It might provide a data-driven approach to change personalized medicine with real-time patient data.

Training and Testing Framework

A comprehensive training and testing framework assures one with model robustness and generalization. Hence, every dataset is split into training and testing sets using an 80/20 split; respectively, 80% of the data is used to train the model, while 20% goes for testing. The model can then recognize all the patterns in the training set while saving an unbiased dataset, which will help evaluate the model's performance. Besides, k-fold cross-validation is vital to improving the model's robustness. This process divides the training data into 'K' subsets, which train on K-1 subsets while using the remaining subset for validation. Cross-validation repeats itself over all subsets, ensuring each data point contributes to the validation once. This becomes crucial in healthcare, as the representativeness of the data is directly proportional to model reliability. Hence, it finds suitable applications in preventing overfitting, thereby increasing the accuracy of predictions on unseen data.

Hyperparameter Tuning

Hyperparameter tuning is an indispensable approach toward optimizing any model performance, incredibly complex ones like XGBoost and Random Forest. Following that is the Grid Search for Random Forest and Logistic Regression. This systematically goes through every combination of essential hyperparameters, such as the number of trees or regularization strength. While generally computationally expensive, this thorough approach ensures that, at least for simpler models or when computational resources are plentiful, the parameters are optimally set. Then, XGBoost parameter tuning, including learning rate and tree depth, uses Random Search in larger parameter spaces to identify high-performance configurations with computational efficiency. The effectiveness of hyperparameter optimization is measured based on the metrics of the validation sets; final tests on reserved datasets confirm that improvements due to tuning generalize well to new data.

Evaluation Metrics

A model's suitability for health applications is assessed using an extensive set of metrics to ensure accuracy, sensitivity, and specificity.

Accuracy measures the model's overall correct predictions against total predictions. This accuracy, therefore, gives the initial feel of the model's efficacy. Class distributions often need to be more balanced in health care data.

Precision, Recall, and F1-Score give a fine-grained analysis. Precision measures the reliability of predictions coming out positive, which is crucial in medical diagnosis since false positives are poorly taken. Recall or sensitivity measures the model's ability to detect actual positive cases, an important metric to avoid false negatives in medical domains—F1-Score balances precision and recall to provide a holistic metric that represents both values.

ROC-AUC: This is a further development of the metric for model discriminatory power based on the ability of the model to differentiate between positive and negative cases. A high AUC under the ROC curve indicates that the model can confidently distinguish diseased from non-diseased cases, enhancing clinical reliability.

Results

Descriptive Analysis

The statistical summary for the Parkinson's Disease dataset indicates that vocal features like MDVP: Hz, MDVP: Hz, and MDVP: Hz exhibit a very consistent range and standard deviation, while mean frequencies are about 154 Hz, 197 Hz, and 116 Hz, respectively. These vocal measures are paramount in assessing fluctuations that may signify the initial development of the disease. Other features that might be useful are the Jitter and Shimmer values, respectively, representing the frequency and amplitude variations in voice. The percentage of Jitter and the value of Shimmer expressed in dB indicate slight irregularities in voice, which is quite usual for patients with Parkinson's. Furthermore, features such as HNR and RAP give an excellent overview of vocal stability and noise; thus, both features are essential for identifying vocal impairment. These metrics have been standardized to ensure the model models are consistent and dependable evaluation.

The measurements in the case of the Breast Cancer dataset, like radius, perimeter, and area mean, give significant facts about the characteristics of tumors. For instance, the radius mean ranges between 6.98 and 28.11, and this prevalence indicates that the sizes of the tumors are within a wide range, and generally speaking, higher values mean malignancy. Smoothness, compactness, and concavity are some characteristics that further define the shape and structural irregularities in the tumor, essential to distinguishing a tumor as benign or malignant. This dataset includes mean values and worst-case measurements, such as radius worst and area worst. These contain the most extreme feature values of the tumor and offer a comprehensive view of detection and diagnosis. These measurements are standardized and scaled in their inclusion within this data, so machine learning models can successfully dissect the different data patterns to optimize predictive accuracy in early detection and personalized treatment strategies.

Table 1. Statistical summary for the Parkinson's Disease dataset and Breast Cancer dataset

Dataset	Feature	Count	Mean	Minimum	Maximum
Parkinson's Disease	MDVP (Hz)	1195	154.31	88.33	260.11
	MDVP (Hz)	1195	197.25	102.15	592.03
	MDVP (Hz)	1195	116.33	65.48	239.17
	MDVP (%)	1195	0.0062	0.0017	0.0332
	MDVP (Abs)	1195	0.000044	0.000007	0.000260
	MDVP	1195	0.0033	0.0007	0.0214
	MDVP	1195	0.0034	0.0009	0.0196
	Jitter	1195	0.0099	0.0020	0.0643
	MDVP	1195	0.0297	0.0095	0.1191
	MDVP (dB)	1195	0.2826	0.0850	1.3020
	HNR	1195	21.90	8.44	33.05
	RPDE	1195	0.4981	0.2566	0.6852
	DFA	1195	0.7182	0.5743	0.8253
	spread1	1195	-5.6835	-7.9650	-2.4340
	spread2	1195	0.2265	0.0063	0.4505
	D2	1195	2.3821	1.4233	3.6712
	POPE	1195	0.2068	0.0445	0.5274
Breast Cancer	Radius Mean	569	14.13	6.98	28.11
	Texture Mean	569	19.29	9.71	39.28
	Perimeter Mean	569	91.97	43.79	188.50
	Area Mean	569	654.89	143.50	2501.00
	Smoothness Mean	569	0.0964	0.0526	0.1634
	Compactness Mean	569	0.1043	0.0194	0.3454
	Concavity Mean	569	0.0888	0.0000	0.4268

	Concave Points Mean	569	0.0489	0.0000	0.2012
	Symmetry Mean	569	0.1812	0.1060	0.3040
	Fractal Dimension Mean	569	0.0628	0.0499	0.0974
	Radius Worst	569	16.27	7.93	36.04
	Texture Worst	569	25.68	12.02	49.54
	Perimeter Worst	569	107.26	50.41	251.20
	Area Worst	569	880.58	185.20	4254.00
	Smoothness Worst	569	0.1324	0.0712	0.2226
	Compactness Worst	569	0.2543	0.0273	1.0580
	Concavity Worst	569	0.2722	0.0000	1.2520
	Concave Points Worst	569	0.1146	0.0000	0.2910
	Symmetry Worst	569	0.2901	0.1565	0.6638
	Fractal Dimension Worst	569	0.0839	0.0550	0.2075

visualization of the dataset

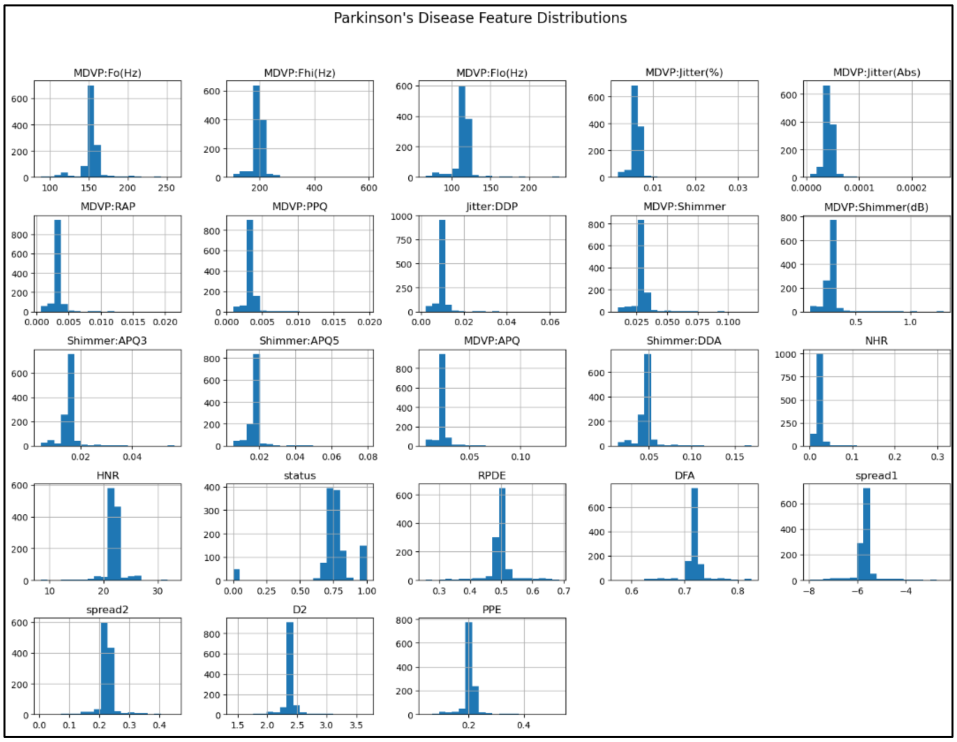


Figure 9. Histograms displaying the distribution of each vocal feature used in Parkinson's disease detection, highlighting variations across features

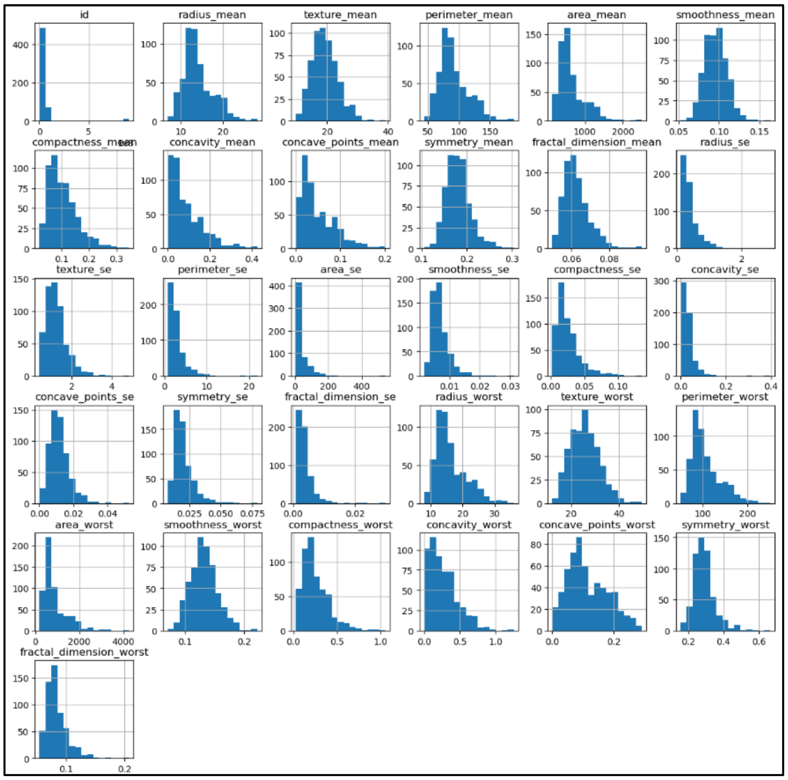


Figure 10. Histograms showing the distribution of each feature related to breast cancer detection, including metrics like radius, texture, perimeter, and compactness across various measurement categories (mean, standard error, worst).

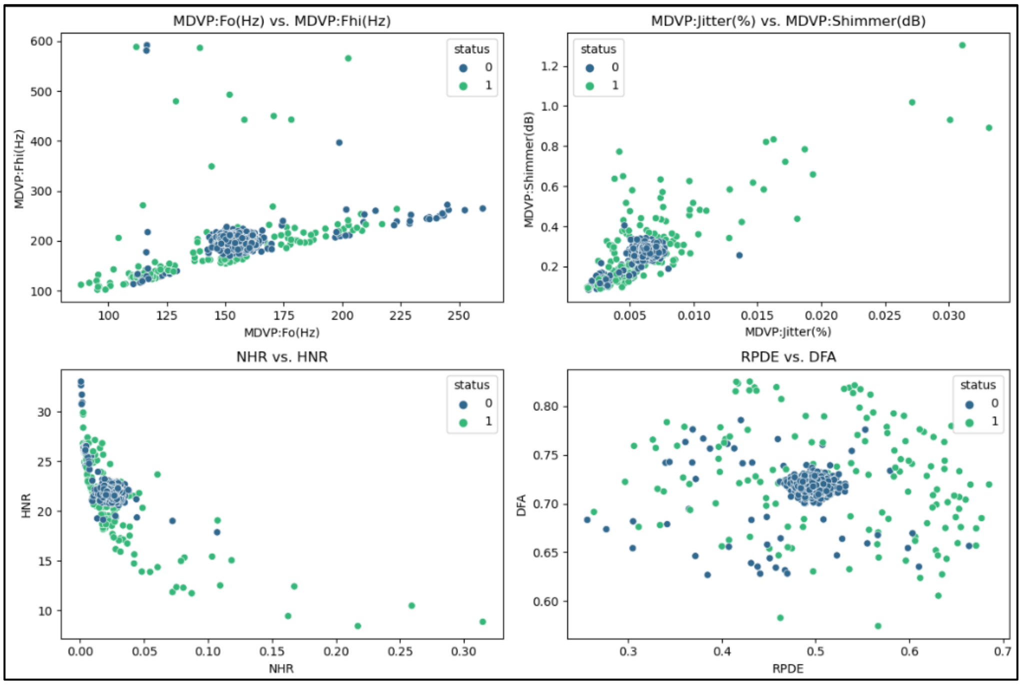


Figure 11. Scatter plots of selected features against status

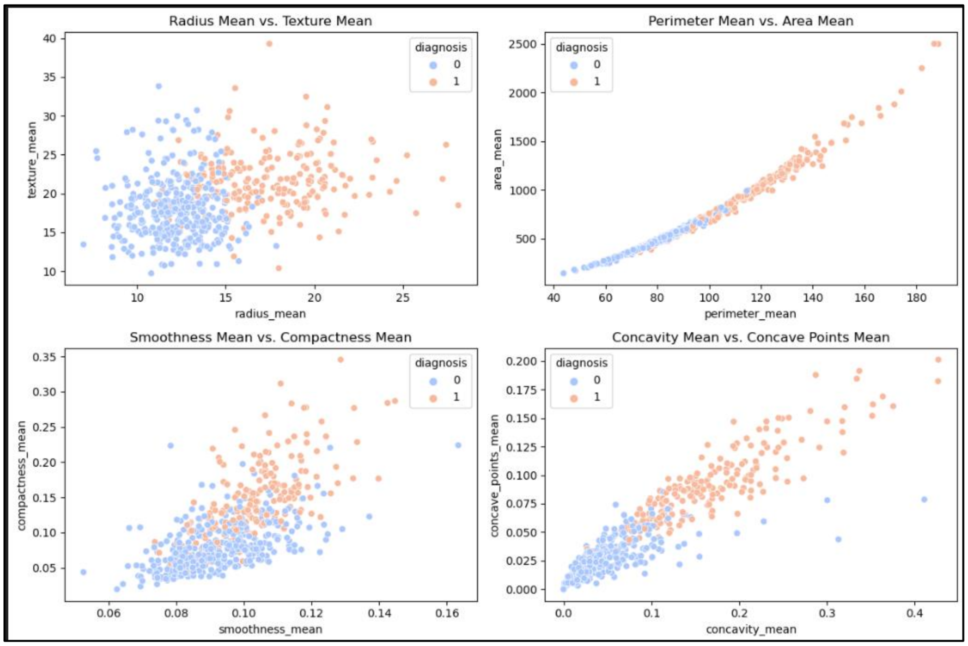
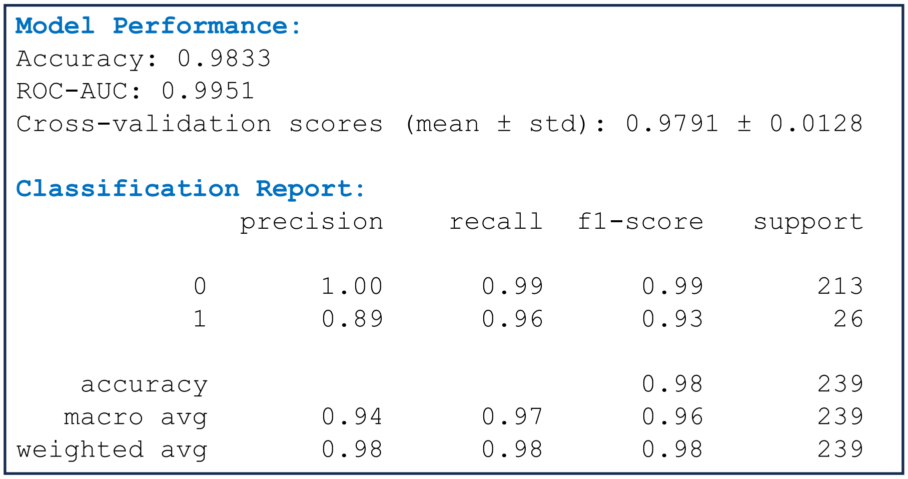


Figure 12 Scatter plots of selected features against diagnosis

By visualizing the datasets of Parkinson's disease and breast cancer, one can reveal main patterns and trends that give insight into the fundamental structures present within the data. Scatter plots for the Breast Cancer Dataset, Figure 13, show how some pairs of features, like radius mean versus texture mean or perimeter mean versus area Mean, can separate the benign and malignant classes. This separation proves that the combination of features has an inherently great discriminatory power, hence beneficial for classification purposes. Also, in the case of the Parkinson's dataset, scatter plots-Figure 12-express that these feature pairs like MDVP: Fo(Hz) and MDVP: Fhi(Hz), and NHR and HNR, reflect a separation between healthy and affected individuals, highlighting the core characteristics of vocal metrics for disease detection.

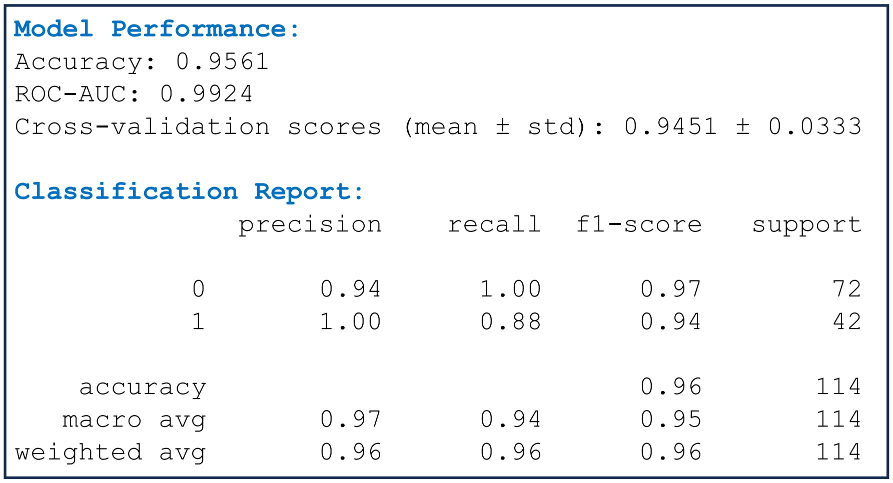
As illustrated in Figure 10 and Figure 11, histograms for each feature of both datasets show distributions of values with heavy skew or unique ranges for some attributes. For example, some features in the breast cancer dataset, such as concavity and compactness mean, have different distributions across classes. In the Parkinson's dataset, there is significant variation along with several attributes, including Jitter and Shimmer, that reflect vocal irregularities typical of the disease. These visualizations will support feature engineering and model selection by tracking which variables will most likely contribute to predictive models most effectively.

Model Performance
Random Forest (RF.)



```
Model Performance:
Accuracy: 0.9833
ROC-AUC: 0.9951
Cross-validation scores (mean ± std): 0.9791 ± 0.0128

Classification Report:
              precision    recall  f1-score   support

           0       1.00      0.99      0.99       213
           1       0.89      0.96      0.93        26

    accuracy                           0.98       239
   macro avg       0.94      0.97      0.96       239
weighted avg       0.98      0.98      0.98       239
```

Figure 13. Classification Report and performance metrics of the Random Forest model of Parkinson's Disease

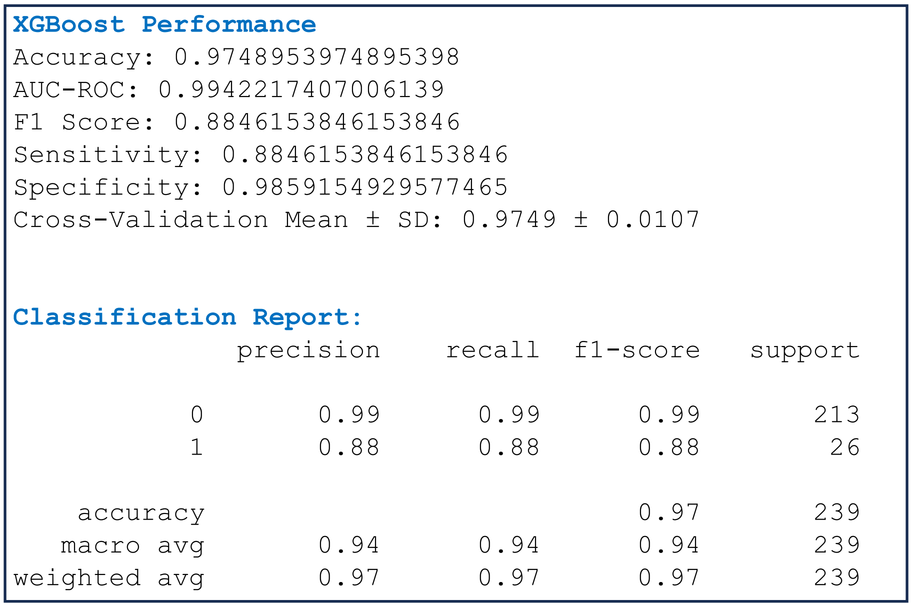


```
Model Performance:
Accuracy: 0.9561
ROC-AUC: 0.9924
Cross-validation scores (mean ± std): 0.9451 ± 0.0333

Classification Report:
              precision    recall  f1-score   support

           0       0.94      1.00      0.97        72
           1       1.00      0.88      0.94        42

    accuracy                           0.96       114
   macro avg       0.97      0.94      0.95       114
weighted avg       0.96      0.96      0.96       114
```

Figure 14. Classification Report and performance metrics of Random Forest model Breast Cancer

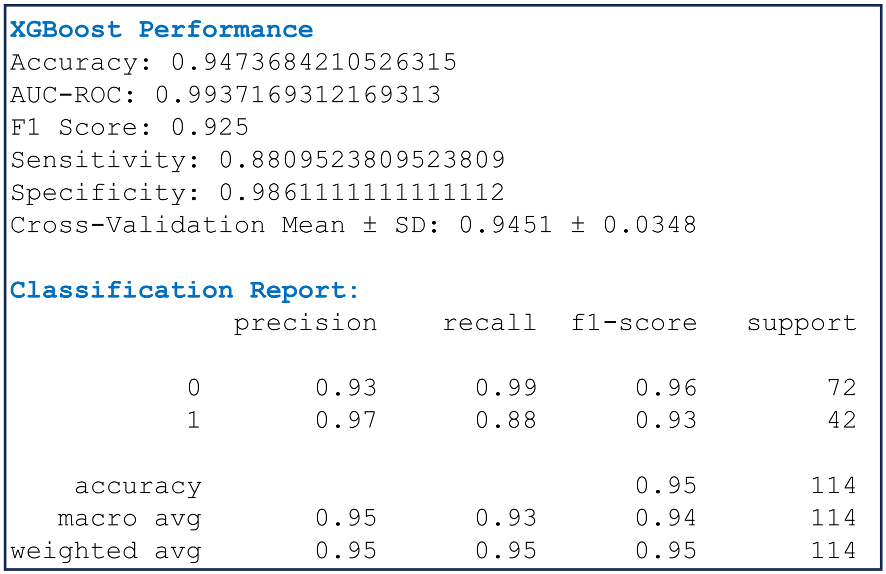
Random Forest performs the best on Parkinson's Disease and Breast Cancer datasets. Actually, in the case of Parkinson's Disease, it achieved an estimation accuracy of 98.33%, AUC-ROC of 0.9951, with a cross-validation score of 97.91% ± 0.0128 with only minor misclassifications. In the case of Breast Cancer, Random Forest provides high accuracy, maintaining a good balance regarding precision and recall for both classes. This level of consistency in performance over a wide range of diseases illustrates that the Random Forest model is robust and efficient in handling structured health data, hence a reliable choice for use in any clinical application requiring accurate disease detection.

XGBoost



```
XGBoost Performance
Accuracy: 0.9748953974895398
AUC-ROC: 0.9942217407006139
F1 Score: 0.8846153846153846
Sensitivity: 0.8846153846153846
Specificity: 0.9859154929577465
Cross-Validation Mean ± SD: 0.9749 ± 0.0107


Classification Report:
              precision    recall  f1-score   support

           0       0.99      0.99      0.99       213
           1       0.88      0.88      0.88        26

    accuracy                           0.97       239
   macro avg       0.94      0.94      0.94       239
weighted avg       0.97      0.97      0.97       239
```

Figure 15 Classification Report and performance metrics of XGBoost model Parkinson's Disease

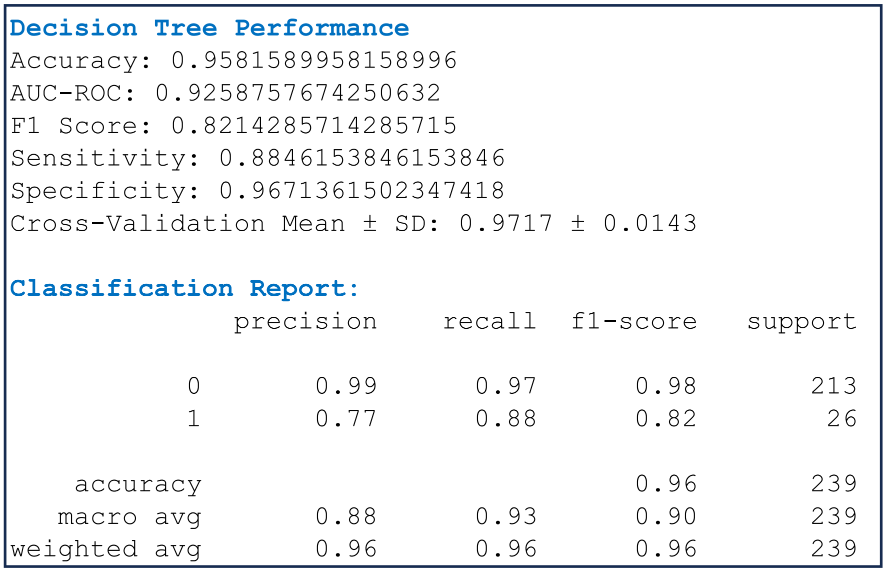


```
XGBoost Performance
Accuracy: 0.9473684210526315
AUC-ROC: 0.9937169312169313
F1 Score: 0.925
Sensitivity: 0.8809523809523809
Specificity: 0.9861111111111112
Cross-Validation Mean ± SD: 0.9451 ± 0.0348

Classification Report:
              precision    recall  f1-score   support

           0       0.93      0.99      0.96        72
           1       0.97      0.88      0.93        42

    accuracy                           0.95       114
   macro avg       0.95      0.93      0.94       114
weighted avg       0.95      0.95      0.95       114
```

Figure 16. Classification Report and performance metrics of XGBoost model Breast Cancer

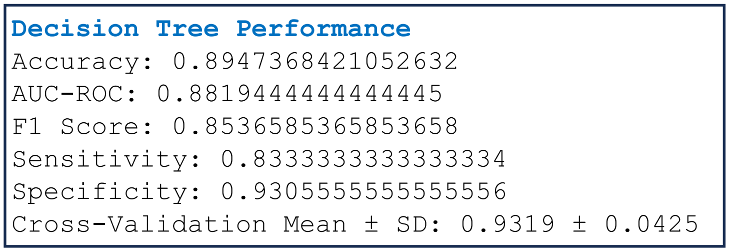
XGBoost closely follows the performance of Random Forest with high accuracy and AUC-ROC scores. Regarding Parkinson's Disease, XGBoost reached an accuracy of 97.49% with an AUC-ROC of 0.9942, while its stability according to cross-validation is 97.49% ± 0.0107, reflecting its robustness. In breast cancer detection, XGBoost showed an accuracy of 94.74% and an AUC-ROC score of 0.9937, which was very close to the values obtained in the case of Random Forest. Although XGBoost's recall for Parkinson's Disease was slightly lower than that of Random Forest, its overall performance was good. It proved its viability in medical prediction, where accuracy and model stability are crucial.

Decision Tree

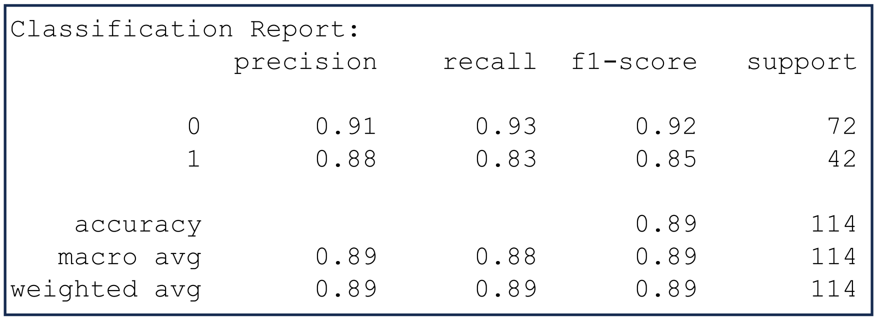


```
Decision Tree Performance
Accuracy: 0.9581589958158996
AUC-ROC: 0.9258757674250632
F1 Score: 0.8214285714285715
Sensitivity: 0.8846153846153846
Specificity: 0.9671361502347418
Cross-Validation Mean ± SD: 0.9717 ± 0.0143

Classification Report:
              precision    recall  f1-score   support

           0       0.99      0.97      0.98       213
           1       0.77      0.88      0.82        26

    accuracy                           0.96       239
   macro avg       0.88      0.93      0.90       239
weighted avg       0.96      0.96      0.96       239
```

Figure 17. Classification Report and performance metrics of Decision Tree classifier of Parkinson's Disease



```
Decision Tree Performance
Accuracy: 0.8947368421052632
AUC-ROC: 0.8819444444444445
F1 Score: 0.8536585365853658
Sensitivity: 0.8333333333333334
Specificity: 0.9305555555555556
Cross-Validation Mean ± SD: 0.9319 ± 0.0425
```

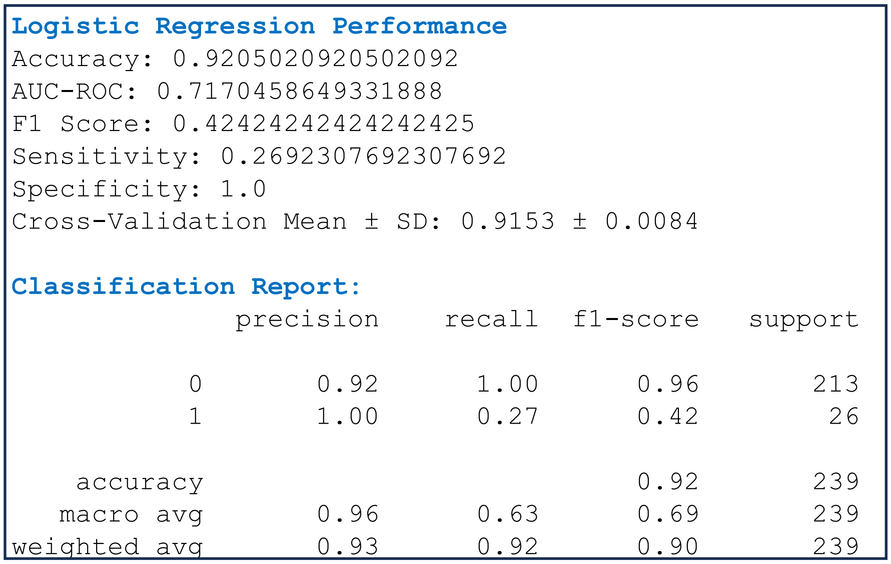


```
Classification Report:
              precision    recall  f1-score   support

           0       0.91      0.93      0.92        72
           1       0.88      0.83      0.85        42

    accuracy                           0.89       114
   macro avg       0.89      0.88      0.89       114
weighted avg       0.89      0.89      0.89       114
```

Figure 18. Classification Report and performance metrics of Decision Tree classifier for Breast Cancer

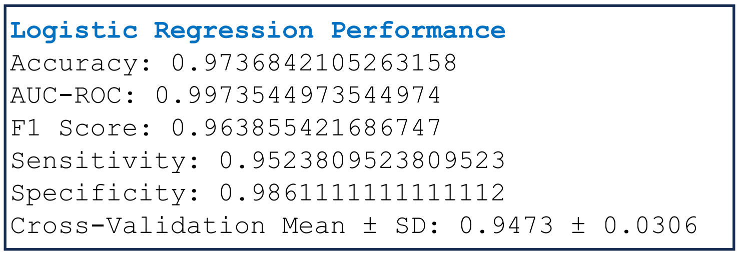
Decision Trees, in turn, performed lower than the ensemble models, especially regarding precision and recall. The Decision Tree performed with 95.82% accuracy on Parkinson's Disease and an AUC-ROC of 0.9259, whereas the cross-validation score was 97.17% ± 0.0143. In Breast Cancer detection, the accuracy of the Decision Tree fell to 89.47%, with an AUC-ROC of 0.8819. It performed poorly when misclassified, especially when the model needed to detect class 1, which denoted the positive cases. Against this interpretability advantage, the higher error rate of Decision Trees diminishes their reliability in high-stake healthcare applications where precision and sensitivity are indispensable.

Logistic Regression

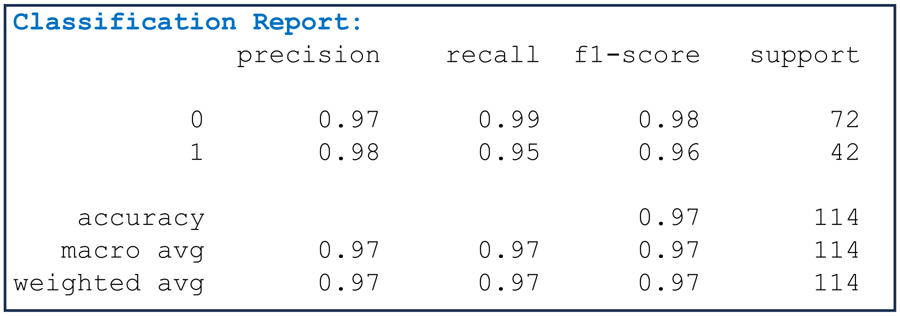


```
Logistic Regression Performance
Accuracy: 0.9205020920502092
AUC-ROC: 0.7170458649331888
F1 Score: 0.42424242424242425
Sensitivity: 0.2692307692307692
Specificity: 1.0
Cross-Validation Mean ± SD: 0.9153 ± 0.0084

Classification Report:
              precision    recall  f1-score   support

           0       0.92      1.00      0.96       213
           1       1.00      0.27      0.42        26

    accuracy                           0.92       239
   macro avg       0.96      0.63      0.69       239
weighted avg       0.93      0.92      0.90       239
```

Figure 19. Classification Report and Performance Metrics of Logistic Regression of Parkinson's Disease



```
Logistic Regression Performance
Accuracy: 0.9736842105263158
AUC-ROC: 0.9973544973544974
F1 Score: 0.963855421686747
Sensitivity: 0.9523809523809523
Specificity: 0.9861111111111112
Cross-Validation Mean ± SD: 0.9473 ± 0.0306
```



```
Classification Report:
              precision    recall  f1-score   support

           0       0.97      0.99      0.98        72
           1       0.98      0.95      0.96        42

    accuracy                           0.97       114
   macro avg       0.97      0.97      0.97       114
weighted avg       0.97      0.97      0.97       114
```

Figure 20. Classification Report and Performance Metrics of Logistic Regression for Breast Cancer

Logistic Regression presented opposing results for the two diseases. Though it was the worst model for the case of Parkinson's Disease detection, with an accuracy rate of 92.05% and AUC-ROC of 0.717, for Breast Cancer detection, it was one of the best. Logistic Regression reached an accuracy rate for Breast Cancer of 97.37% and AUC-ROC of 0.9974, while it had a high score in cross-validation of 94.73% ± 0.0306. Both sensitivity and specificity were excellent in Breast Cancer cases, which made the model very suitable for binary classifications where classes are well separated. In contrast, poor sensitivity in Parkinson's Disease indicated the inability to cope with more complex classification problems in medical data.

Comparative Analysis

Table 2. Table for comparative analysis of model performances

Model	Disease	Accuracy	AUC-ROC	Cross-Validation Mean ± SD
Random Forest	Parkinson's Disease	98.33%	0.9951	97.91% ± 0.0128
	Breast Cancer	95.61%	0.9924	94.51% ± 0.0333
XGBoost	Parkinson's Disease	97.49%	0.9942	97.49% ± 0.0107
	Breast Cancer	94.74%	0.9937	94.51% ± 0.0348
Decision Tree	Parkinson's Disease	95.82%	0.9259	97.17% ± 0.0143
	Breast Cancer	89.47%	0.8819	93.19% ± 0.0425
Logistic Regression	Parkinson's Disease	92.05%	0.717	91.53% ± 0.0084
	Breast Cancer	97.37%	0.9974	94.73% ± 0.0306

The results showed that the two models, Random Forest and XGBoost, both did an outstanding job in their respective predictions of Parkinson's Disease and Breast Cancer, which was reflected in their high accuracy and AUC-ROC values, with a slight further edge by Random Forest for the recall and overall stability. Decision Trees are more interpretable but achieve lower precision and recall scores, with more misclassifications. Logistic Regression is less effective in cases of Parkinson's Disease because of sensitivity issues. In contrast, it performed very well for Breast Cancer diagnosis, with close-to-perfect specificity and high recall.

Prediction Insights

Analysis of Model Predictions for Disease Detection and Treatment Outcomes

The model predictions of Random Forest and XGBoost on Parkinson's Disease and Breast Cancer detection give great insight into the nature of such diseases and the capability of each algorithm in handling such datasets. For Parkinson's Disease, the models fitted from Random Forest and XGBoost showed very high accuracy and recall, perfectly classifying patients with or without the disease. These models were incredibly influential in minimizing false positives and negatives, which are critical in avoiding misdiagnosis and ensuring appropriate patient treatment. In contrast, Logistic Regression showed poor sensitivity in detecting Parkinson's disease; it yielded low recall for patients who had it. It indicates that logistic Regression might not be very suitable for detecting minute signs of a complex condition like Parkinson's, where precision and recall are crucial.

On the other hand, the Random Forest and XGBoost performed very well in Breast Cancer detection; Logistic Regression did an excellent job on more straightforward binary classification. This model is particularly about breast cancer, suggesting it is good at distinguishing between benign and malignant cases. It could be a proper option in the early screening stages when it is critical to reduce false positives. In general, most of the ensemble methods were very stable and reliable for both diseases, which underlines their applicability to perform prediction tasks for healthcare applications.

Identification of Potential Biomarkers and High-Risk Patient Groups

The feature importance analysis developed from both Random Forest and XGBoost highlighted many biomarkers pertinent to both Parkinson's Disease and Breast Cancer, thus identifying high-risk groups. Key biomarkers for Parkinson's included some vocal characteristics such as MDVP: Fo(Hz), MDVP: Fhi(Hz), and MDVP: Flo(Hz). Other parameters identified included Jitter (%) and HNR. These features relate to the vocal impairments often associated with Parkinson's and indicate that vocal analysis may be a helpful non-invasive tool for early detection. Such abnormalities of these vocal features can identify high-risk patients for further testing or early intervention.

In breast cancer, the significant features were radius_mean, perimeter_mean, area_mean, and concavity_mean, all related to tumor morphology. Such morphological features accurately indicate malignancy since large cells with irregular shapes are usually associated with cancer. Such tumors should raise a red flag on patients as high-risk, wherein health professionals may want to monitor them more closely to enable timely treatment. Identifying these biomarkers would improve the predictive power of the models and thus offer clinicians usable insights into the screening and monitoring of high-risk groups.

Implications for Treatment Outcomes and Personalized Care

These models provide insight into biomarkers and high-risk groups directly affecting treatment outcomes with personalized care plans. The patients identified as high-risk for Parkinson's Disease can receive early-stage interventions that slow down the disease progression and thus improve the quality of life. Similarly, patients with a high risk of Breast Cancer, as quantified from tumor morphology, can be subjected to specific treatment plans, use of targeted therapies, and increased frequency of screenings to spot the relapse early. This would enable machine learning predictions to be integrated into clinical workflows for proactive healthcare approaches, guided by machine learning models in treatment decisions that will help prioritize care for patients most likely to benefit from early interventions.

Discussion

Insights and Implications

Key Findings and Their Relevance to Advancing Personalized Medicine

The study's key findings have brought forth very promising capabilities of machine learning models, specifically Random Forest and XGBoost, in adequately identifying diseases such as Parkinson's and Breast Cancer. These models illustrated excellent performance with AUC-ROC and cross-validation, hence proved solid and reliable for early detection. Probabilistic predictions enhance decision-making by enabling clinicians to evaluate probabilities of disease presence rather than binary outcomes. While reinforcement learning is hinted at here, it still needs to be fully implemented. It looks promising as a future direction to be taken in developing personalized treatment pathways based on responsiveness by individual patients and moving the science of personalized medicine forward. These models show an increasing capability of integrating complex, structured data with an evolving role of machine learning in creating customized healthcare solutions.

Comparison with Existing Research and Practices in the USA

While personalized medicine and predictive healthcare are also forging ahead in the USA, the existing approaches are based on genomic and clinical trial data with limited integration of real-time patient feedback. The paper addresses this by applying an ensemble model with Random Forest and boosting algorithms in XGBoost to enable granular insights on disease markers in line with the direction for AI in advanced health research. These models bring a wealth of improvement in interpretability and scalability compared to classical methods and form the bedrock for predictive, data-driven approaches to healthcare. This aligns with current initiatives in the USA, including the Precision Medicine Initiative, which recognizes that integrating diverse patient data is critical to improved treatment outcomes.

Challenges and Limitations

Among the significant ethical issues related to the application of machine learning in medicine, the privacy and confidentiality of sensitive patient data are at the center stage. However, more sensitive information, such as health records and genetic information, must be considered carefully, including privacy, informed consent, and data security. To date, protection of patient privacy via regulations such as HIPAA in the USA remains in force. However, clear policies on how transparent data will be used and assured and robust mechanisms for protection against misuse or unauthorized access to such sensitive health information need attention.

Another important one is informed consent. Patients should be informed about all matters related to data usage, data sharing, and other potential risks. Well-defined consent processes are necessary, and transparency concerning data handling practices should be maintained with the patients to address ethical concerns.

While complex models, such as Random Forest and reinforcement learning, are not interpretable, this may pose a problem in a clinical setting since the model should be transparent. Due to its lack of interpretability, there is possible resistance from healthcare professionals who need clear explanations for the model predictions to derive confidence in AI systems.

In this direction, SHAP is one of several feature importance analysis and visualization techniques that can be conducted, providing insight into why certain features contribute to a particular model prediction. By identifying and visualizing feature correlations with key contributing factors, health professionals will more easily understand the decision-making process that brought the model to provide a particular recommendation, thus supporting transparency and confidence in recommendations provided through AI limit-availability-diversity-datasets

Like many other studies, this also has data availability and diversity limitations. Data for training and testing might only partially represent real-world population diversity, which may also influence the generalization of models across different demographic groups. For example, a small-sized population or rare genetic variations may not be captured and, hence, can result in biased predictions.

This could be done by incorporating more extensive and diverse datasets from different demographic, geographic, and genetic backgrounds. Collaboration with healthcare institutions can also facilitate access to anonymized data from other regions, thereby helping to improve model reliability across populations.

Directions for Future Work

Possible Future Development in Integration of Other Types of Data

Future development in personalized medicine could also include more data types, such as lifestyle and environmental data, in the predictive models. All these factors- diet, exercise, sleep patterns, and pollutants- are already known to influence health outcomes and may provide that missing link for more accurate disease prediction and personalized treatment. Adding information regarding a patient's lifestyle and environmental background further serves to define better these predictions of diseases to which these variables are significant contributing factors.

Integrate real-time data from wearable devices; this would provide continual monitoring of the patients, thus enabling proactive adjustments in treatment plans. This extension of data sources would make the model holistic, considering a more comprehensive array of health determinants, furthering the cause of personalized medicine.

Recommendations to Enhance the Scalability of the Personalized Treatment Model

Some of the following strategies may be considered to enhance scalability in personalized treatment models:

Standardized Data Collection and Sharing: A standardized protocol for data collection and sharing among healthcare institutions would support scalability. A guideline on the data format, the method of collection, and interoperability make it relatively easy to integrate new data sets into the already existing models with little preprocessing.

Automate Model Tuning and Optimization: By embedding different automated model tuning techniques, such as AutoML, fewer manual adjustments would be required for models to adapt more efficiently to new, various data sets and diverse patient populations. This will support scaling the models across diverse healthcare settings.

Cloud-Based Deployment and Real-Time Processing: Deploying models in cloud platforms allows real-time processing, making them more accessible to health providers using the various personalized treatment models in different regions and institutions. Cloud-based solutions also present the advantage of being easy to roll out periodic updates and improvements concerning the models as data becomes available.

Education and Training of Healthcare Providers: Studies on healthcare providers' education regarding AI-driven personalized treatment models should be conducted, and training on interpreting the model's output should be warranted. This would ensure uptake and successful translation into clinical practice, allowing the scalability of these new models.

Conclusion

This review used machine learning models, especially Forest and XGBoosXGBoost, to efficiently detect PD and BC using heterogeneous data. These models present high accuracy and AUC-ROC with stability in cross-validation. Among them, Random Forest has performed slightly better regarding recall and stability for both diseases. Key biomarkers were identified as voice characteristics for Parkinson's Disease, whereas for Breast Cancer, features of tumor morphology cropped up as key predictors. These findings demonstrate the potential of machine learning methods in finding high-risk patient groups and critical biomarkers to derive actionable insights for early diagnosis and personalized treatment strategies. It also revealed that the ensemble models comprising Random Forest and XGBoost are outstanding in accuracy and robustness; hence, they are highly suitable for any disease detection task.

With the integration of various data types, such as clinical records, genomic data, and patient-reported outcomes, the predictive power and the clinical relevance of the machine learning models in health significantly increase. Such data-driven approaches enable the healthcare provider to move toward more proactive and personalized care models that promise better patient outcomes and reduced healthcare costs. This work supports the integrated data approach and allows one to foresee great promise for machine learning to become an accurate game-changing tool in disease detection and personalized medicine. As machine learning and data integration continue to advance, they will be an increasingly integral part of helping precision healthcare move forward while providing clinicians with the insights they need to deliver timely, individualized care to those in need.

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