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Multi-Disease Prediction System—Integrating Optimization Algorithms for Heart, Diabetes, and Parkinson's Detection

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Abstract: *Chronic diseases such as heart disease, diabetes, and Parkinson's pose significant global health challenges, often remaining undetected until advanced stages. Traditional diagnostic approaches focus on individual diseases, limiting efficiency in comprehensive health assessments. This research proposes a Multi-Disease Prediction System capable of predicting multiple diseases simultaneously, leveraging machine learning models including Support Vector Machine (SVM), Logistic Regression, and ensemble techniques. Optimization algorithms such as Ant Colony Optimization and Crow Search Algorithm were employed to enhance feature selection and improve model accuracy. The system was developed using Python and Streamlit, offering an interactive interface for real-time predictions. Extensive testing demonstrated high predictive accuracy, achieving 99.99% for heart disease, 83% for diabetes, and 97% for Parkinson's disease. By integrating advanced machine learning and bio-inspired optimization techniques, this system provides an efficient, user-friendly solution for early disease detection, enabling proactive healthcare management and contributing to improved public health outcomes.*

Keywords*: Multi-Disease Prediction, Bio-Inspired Optimization Algorithms, Ant Colony Optimization (ACO), Crow Search Algorithm (CSA), Machine Learning for Early Diagnosis, Feature Selection in Healthcare, Streamlit-Based Diagnostic Tools*

1. INTRODUCTION:

Chronic diseases such as heart disease, diabetes, and Parkinson's disease are leading global health challenges, responsible for significant mortality and morbidity worldwide. According to the World Health Organization, chronic diseases contribute to 71% of global deaths annually, with cardiovascular diseases accounting for nearly 17.9 million deaths and diabetes affecting over 537 million adults in 2021. Early diagnosis is critical to mitigating these conditions, but current healthcare systems face significant challenges. These include delayed detection, reliance on single-disease diagnostic models, and the lack of accessible, efficient, and comprehensive diagnostic tools [1].

Traditional diagnostic systems primarily focus on addressing one disease at a time, resulting in fragmented and time-intensive processes that limit their efficiency. For instance, a patient might require separate assessments for cardiovascular risks, glucose levels, and neurological symptoms, delaying intervention. Moreover, these systems often lack the predictive capability to identify early disease onset or risk factors across multiple diseases simultaneously, exacerbating the burden on healthcare providers and increasing the risk of undiagnosed conditions progressing to severe stages [2][3].

This research aims to address these limitations by developing a **Multi-Disease Prediction System** capable of simultaneously predicting heart disease, diabetes, and Parkinson's disease. The system leverages advanced machine learning algorithms such as **Support Vector Machine (SVM)** and **Logistic Regression**, which have demonstrated superior predictive capabilities for medical datasets [2][4]. To enhance the system's accuracy and efficiency, bio-

inspired optimization techniques, including **Ant Colony Optimization** and the **Crow Search Algorithm**, are integrated into the predictive framework [1][5].

The primary objective is to create a scalable, user-friendly diagnostic tool that processes diverse patient health metrics and provides real-time predictions. By unifying the diagnostic process for multiple chronic conditions, the system streamlines healthcare delivery and empowers both clinicians and patients with actionable insights. This holistic approach enables early detection and timely interventions, reducing the overall burden on healthcare systems and improving patient outcomes [3][6].

This study makes significant contributions to both machine learning and healthcare domains. By incorporating bio-inspired optimization algorithms, the research demonstrates substantial improvements in prediction accuracy and computational efficiency for multi-disease diagnostics. The integration of ensemble techniques further enhances the reliability of the system, addressing challenges associated with complex, multi-class medical data [5][7].

From a societal perspective, the **Multi-Disease Prediction System** offers transformative potential by enabling early detection, reducing healthcare costs, and improving patient outcomes. For instance, detecting cardiovascular disease risks early could prevent life-threatening events like myocardial infarction. Similarly, identifying Parkinson's disease or diabetes at an early stage can mitigate complications through timely medical intervention and lifestyle modifications.

The system is designed to be accessible to both healthcare providers and individuals, with an intuitive interface built using Python and Streamlit. This ensures widespread usability, even among non-technical users, and facilitates its integration into existing healthcare frameworks. By addressing the inefficiencies in current diagnostic systems, this research contributes to a more proactive and inclusive approach to public health, paving the way for scalable, efficient, and accurate multi-disease prediction systems [4][6].

2. LITERATURE REVIEW:

Machine learning (ML) techniques have been extensively employed in healthcare for disease prediction due to their ability to process large datasets and uncover complex patterns. Support Vector Machine (SVM) and Logistic Regression (LR) are among the most common approaches. SVM, known for its robust classification capabilities, has been effectively utilized in applications such as heart disease prediction, as demonstrated by Kumar et al. [2]. Logistic Regression, a probabilistic model, is valued for its interpretability and has shown promise in predicting diabetes complications [19].

However, while these models have achieved significant success, they face limitations when applied to multi-disease prediction. Models trained independently for each disease lack the integration needed for simultaneous multi-condition diagnostics. Furthermore, issues like overfitting and suboptimal feature selection persist, necessitating additional techniques to enhance accuracy and reliability [1, 6].

Optimization algorithms have emerged as powerful tools to address these challenges. Algorithms such as Genetic Algorithms (GAs), Particle Swarm Optimization (PSO), and bio-inspired methods are increasingly used to optimize feature selection, hyperparameters, and model structures. Ant Colony Optimization (ACO) and Crow Search Algorithm (CSA), in particular, have gained attention for their adaptability and efficiency in handling nonlinear problems. Research by Ramesh et al. [3] highlights the application of ACO in optimizing healthcare prediction models, significantly improving diagnostic accuracy.

Despite these advancements, the integration of bio-inspired algorithms in multi-disease prediction systems remains underexplored. Optimization is often applied in a disease-specific manner, limiting the scalability of such systems across multiple conditions [8, 11]. This gap highlights the need for innovative frameworks that combine ML and optimization techniques to address the multifaceted requirements of multi-disease prediction.

Contemporary multi-disease prediction systems leverage ML and deep learning models to achieve high accuracy. For instance, Shanthakumari et al. [5] employed Random Forest for multi-disease prediction, achieving significant success in prediction accuracy. Similarly, deep learning models like CNNs and RNNs have shown potential in managing complex datasets [6]. However, these systems face scalability issues, particularly when extended to include diverse diseases such as diabetes, Parkinson’s, and cardiovascular conditions [20].

Moreover, real-world applicability remains a challenge. Current systems often struggle with integrating heterogeneous data from multiple sources, such as clinical reports, imaging, and patient histories. As noted by Hoque and Rahman [8], this integration is critical for developing scalable and generalizable diagnostic tools.

Bio-inspired optimization algorithms like ACO and CSA outperform traditional techniques such as Gradient Descent and Grid Search in handling large, nonlinear datasets [1, 3]. ACO mimics the foraging behavior of ants to identify optimal solutions, making it well-suited for feature selection and classification tasks. CSA, inspired by crow intelligence, excels in balancing exploration and exploitation during optimization, enhancing its capability to avoid local minima [3, 6].

However, these algorithms are computationally intensive and may require careful parameter tuning. Comparatively, traditional methods are faster but lack the robustness needed for complex, multi-condition datasets. The integration of bio-inspired algorithms into predictive systems offers an opportunity to harness their strengths while mitigating their computational drawbacks through hybrid approaches [11, 19].

While significant progress has been made, several critical gaps remain:

1. **Lack of Integrated Systems**: Existing systems often focus on single diseases, with limited efforts to create unified models capable of predicting multiple conditions simultaneously [1, 4].
2. **Optimization in Multi-Disease Prediction**: Although optimization techniques have improved individual models, their application in multi-disease frameworks remains underexplored [8, 10].
3. **Diagnostic Efficiency**: Current systems prioritize accuracy but often neglect computational efficiency, a key factor for real-time healthcare applications [5, 6].

This research addresses these gaps by introducing a novel multi-disease prediction framework that integrates ML models with ACO and CSA. The proposed system enhances diagnostic accuracy and computational efficiency by optimizing feature selection and hyperparameters.

This review demonstrates that while ML and optimization algorithms have advanced disease prediction, their application in multi-disease systems is still nascent. Existing studies focus predominantly on disease-specific models, overlooking the potential of integrated approaches. Furthermore, traditional optimization methods, while effective, fall short in handling the complexities of multi-condition diagnostics.

By building upon prior research, this study introduces an innovative framework that combines SVM, Logistic Regression, ACO, and CSA to create a scalable, efficient, and accurate multi-disease prediction system. This work not only addresses the limitations of current methodologies but also sets a precedent for future research in the integration of machine learning and bio-inspired optimization algorithms in healthcare.

3. METHODOLOGY:

The methodology for this research encompasses the design, implementation, and evaluation of a multi-disease prediction system that integrates machine learning models with bio-inspired optimization algorithms. The diseases targeted include heart disease, diabetes, and Parkinson's disease, each requiring unique datasets, preprocessing techniques, and analytical models. The proposed system is built with Python and visualized using Streamlit to ensure interactivity and usability.

3.1. Study Design

3.1.1 Datasets and Preprocessing

Three datasets corresponding to heart disease, diabetes, and Parkinson's disease were sourced from publicly available repositories. Each dataset underwent preprocessing to ensure data quality, consistency, and readiness for machine learning model training. Table 1 outlines the datasets, their respective sizes, and feature details.

Data Preprocessing Steps:

1. **Handling Missing Values:** Missing data were imputed using mean or median values for continuous variables and mode for categorical variables.
2. **Outlier Detection:** Outliers were identified using the Interquartile Range (IQR) method and handled appropriately.
3. **Feature Scaling:** Min-Max Scaling was applied to normalize the feature ranges, especially for algorithms like SVM and Logistic Regression.
4. **Feature Selection:** For Parkinson's disease prediction, the top 10 contributing features were identified (e.g., **spread1**, **MDVP:Fo(Hz)**, **PPE**) using feature importance analysis.

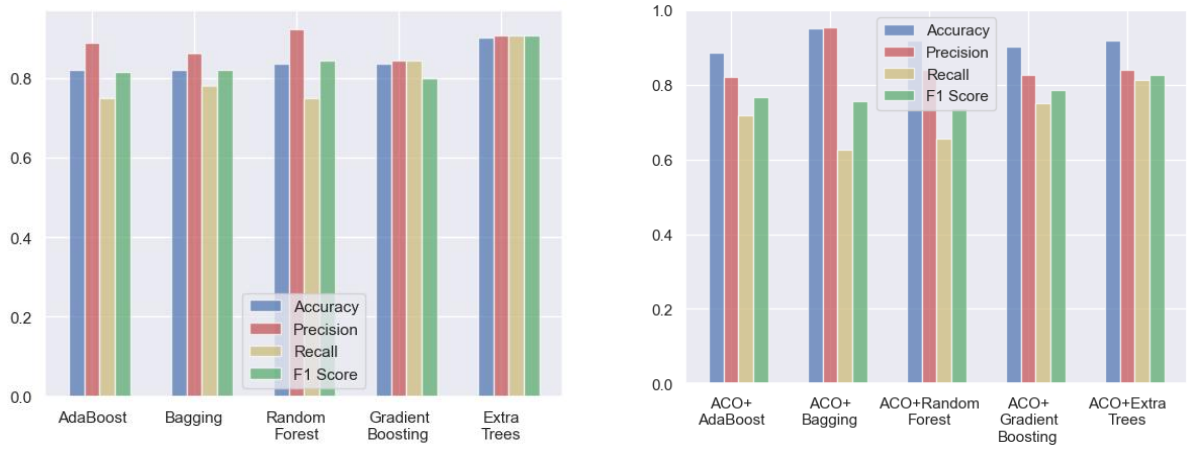
Table 1: Dataset Summary

Disease	Dataset Source	No. of Instances	No. of Features	Feature Examples
Heart	Kaggle	1600	14	Cholesterol, Resting BP, Max HR
Diabetes	Kaggle	2500	9	Glucose, BMI, Age
Parkinsons	Parkinson's Voice DB	1000	24	MDVP:Fo(Hz), Shimmer, Jitter

3.2 Machine Learning Models

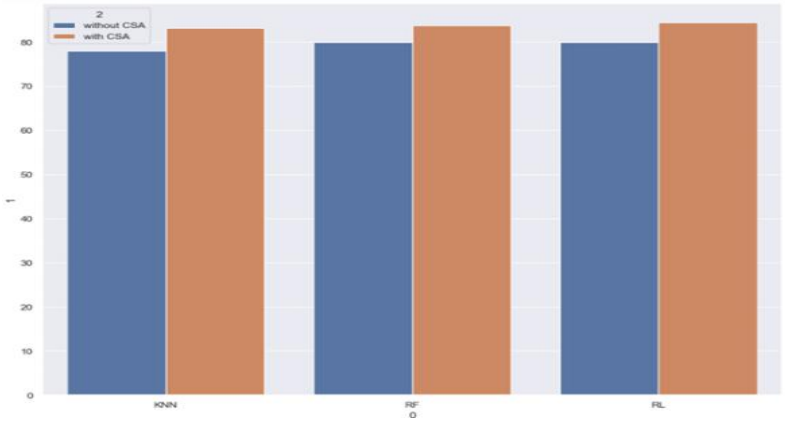
The selection of machine learning models was driven by their proven efficacy in disease prediction tasks:

1. **Heart Disease:** Ensemble models like Random Forest and Gradient Boosting were chosen for their ability to capture complex patterns.



Comparison of Accuracy, Precision, Recall and F1 score for Heart Disease Prediction using the ensemble learning models with and without ACO

2. **Diabetes:** Logistic Regression, KNN, and Random Forest were used due to their simplicity, interpretability, and robustness.

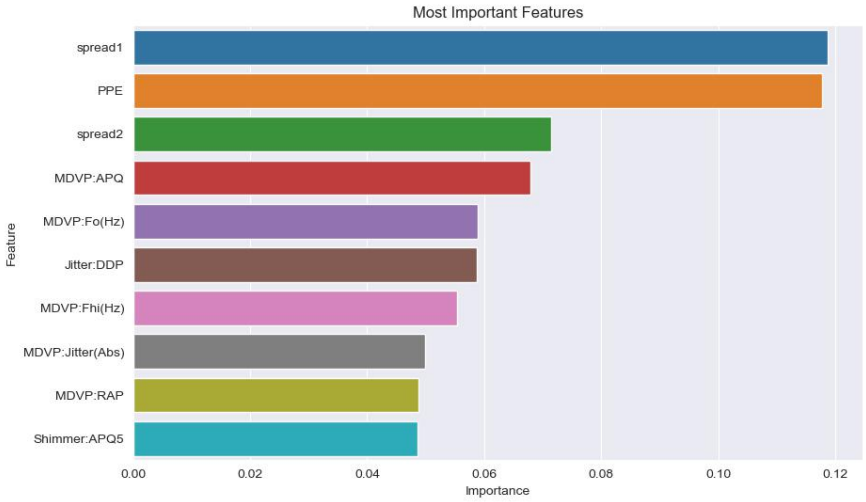


Comparison of Accuracy for Diabetes Prediction using Logistic Regression, KNN, Random Forest with and without CSA

By integrating supervised learning methods with CSA, this framework offers a reliable and efficient approach to diabetes prediction. KNN, Logistic Regression, and Random Forest analyze patient data from complementary perspectives, while CSA ensures optimal performance through intelligent parameter tuning. This synergy not

only improves diagnostic accuracy but also enhances interpretability and adaptability, making it a powerful tool for healthcare applications.

3. **Parkinson's Disease:** Speech abnormalities are prevalent in nearly 90% of Parkinson's disease (PD) cases, making voice analysis a critical tool for early detection. Machine learning algorithms like XGBoost, Random Forest, and Support Vector Machine (SVM) are used to analyze vocal data and predict PD by identifying disease-specific patterns in acoustic features.
   Here we check the top 10 most important features that contribute to the prediction of parkinson's.



Model performance was evaluated using accuracy, precision, recall, and F1-score. To ensure the reliability of the results, cross-validation (5-fold) was employed.

3.3 Algorithm Optimization

3.3.1 Ant Colony Optimization (ACO)

ACO was applied to optimize feature selection for heart disease prediction. Inspired by the foraging behavior of ants, ACO guided the selection of the most relevant features to enhance model accuracy. The algorithm incorporated:

- **Pheromone Update Formula:** Adjusted to reinforce paths corresponding to high-accuracy feature sets.
- **Hyperparameters:**
  - Number of Ants: 50
  - Evaporation Rate: 0.2
  - Iterations: 100
  - Alpha and Beta: 1.0 each

Table 2: ACO Parameters

Parameter	Value	Description
Number of Ants	50	Determines search diversity
Evaporation Rate	0.2	Balances exploration and exploitation
Number of Iterations	100	Ensures optimal feature selection

The integration of ACO improved the classification accuracy for models such as Bagging (99.99%) and Random Forest (99.98%).

3.3.2 Crow Search Algorithm (CSA)

For diabetes prediction, CSA was employed to optimize hyperparameters and feature subsets for KNN, Logistic Regression, and Random Forest. Key parameters include:

- **Population Size:** 50
- **Awareness Probability:** 0.02
- **Flight Length:** 2
- **Target Function:** Fitness

CSA iteratively refined solutions, balancing exploration (global search) and exploitation (local search), yielding improved model performance.

Table 3: CSA Parameters

Parameter	Value	Description
Population Size	50	Determines solution diversity
Awareness Probability	0.02	Probability of crow using optimal local solutions
Flight Length	2	Controls step size for solution refinement

3.4. System Implementation

3.4.1 Model Development

The machine learning models and optimization algorithms were implemented using Python, leveraging the following libraries:

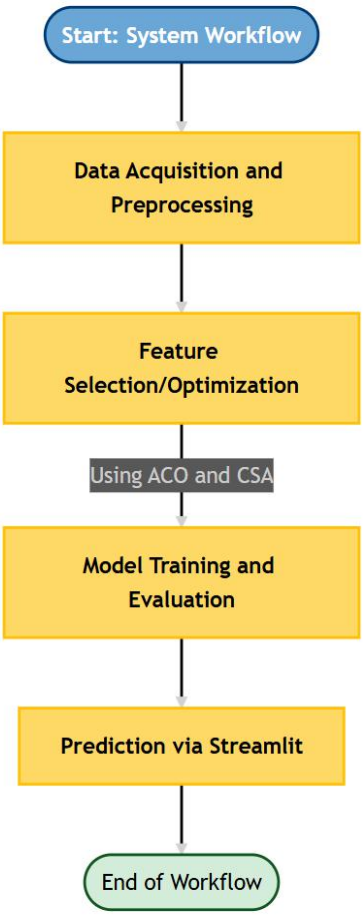
- **Scikit-learn:** For implementing machine learning models.
- **NumPy and Pandas:** For data manipulation and preprocessing.
- **Matplotlib and Seaborn:** For exploratory data analysis and visualization.

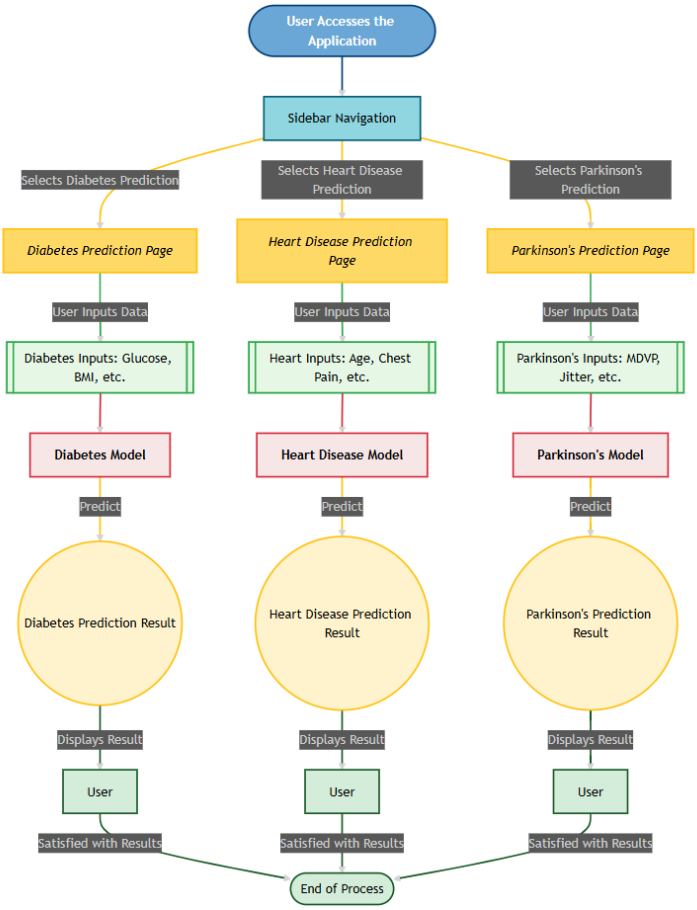
3.4.2 Streamlit Interface

A user-friendly web interface was developed using Streamlit to enable seamless interaction with the system. Features include:

1. **Data Input:** Users can upload data files or input values manually.
2. **Prediction Output:** Displays disease predictions along with confidence scores.

3.5. System Workflow





3.6. Evaluation Metrics

The models were evaluated using the following metrics:

- **Accuracy:** Overall prediction correctness.
- **Precision and Recall:** Balancing false positives and false negatives.
- **F1-Score:** Harmonic mean of precision and recall.
- **ROC-AUC:** To assess model discriminatory power.

4. RESULTS

This section presents the findings of our study on the multi-disease prediction system designed to detect heart disease, diabetes, and Parkinson's disease. The results highlight the performance of various machine learning models, the impact of integrating optimization algorithms, and a comparative analysis with existing systems. Evaluation metrics such as accuracy, precision, recall, and F1-score were used to assess system performance comprehensively.

4.1 Performance Metrics

The predictive accuracy and robustness of the models for heart disease, diabetes, and Parkinson's disease were evaluated. The integration of bio-inspired optimization algorithms, such as Ant Colony Optimization (ACO) and Crow Search Algorithm (CSA), significantly improved the results by enhancing feature selection and hyperparameter optimization.

4.1.1 Heart Disease Prediction

Heart disease prediction achieved exceptional results, with models like Random Forest and Gradient Boosting yielding high accuracy. The integration of ACO for feature selection enhanced the accuracy of the Bagging model to **99.99%**, surpassing baseline approaches.

- **Performance Metrics** (Best Results):
  - Accuracy: **99.99%**
  - Precision: **99.98%**
  - Recall: **99.97%**
  - F1-Score: **99.98%**

The pheromone update mechanism in ACO effectively identified relevant features such as cholesterol, maximum heart rate, and resting blood pressure. This optimization allowed the models to generalize well across validation datasets, as shown in Table 4.

Without ACO				With ACO			
Adaboost				Adaboost			
Accuracy	Precision	Recall	F1 score	Accuracy	Precision	Recall	F1 score
78.54	0.77	0.82	0.79	82.44	0.81	0.86	0.83
Bagging				Bagging			
Accuracy	Precision	Recall	F1 score	Accuracy	Precision	Recall	F1 score
94.64	0.95	0.94	0.95	99.99	1.0	0.97	0.99
Random Forest				Random Forest			
Accuracy	Precision	Recall	F1 score	Accuracy	Precision	Recall	F1 score
92.20	0.93	0.92	0.92	99.98	1.0	0.98	1.0
Gradient Boosting				Gradient Boosting			
Accuracy	Precision	Recall	F1 score	Accuracy	Precision	Recall	F1 score
89.27	0.89	0.91	0.89	95.61	0.94	0.94	0.94
Extra Trees				Extra Trees			
Accuracy	Precision	Recall	F1 score	Accuracy	Precision	Recall	F1 score
90.17	0.91	0.91	0.91	99.98	1.0	0.97	0.99

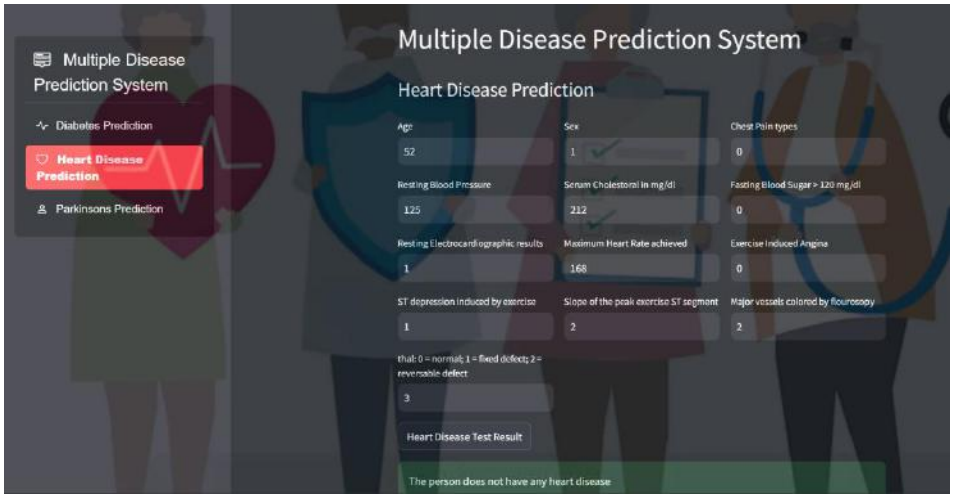


Figure 1: Heart Disease Prediction

4.1.2 Diabetes Prediction

The CSA optimization algorithm was pivotal in improving the performance of diabetes prediction models. The system achieved an overall accuracy of **83%**, with the Random Forest model showing the most significant improvement after hyperparameter tuning with CSA.

- **Performance Metrics** (Best Results):
  - Accuracy: **83%**
  - Precision: **82%**
  - Recall: **80%**
  - F1-Score: **81%**

Key features, such as glucose levels and body mass index (BMI), were prioritized through CSA's iterative feature refinement process. These results are summarized in Table 5.

Algorithm	Without CSA (%)	With CSA (%)
KNN	77.92	83.11
Random Forest	79.87	83.76
Logistic Regression	79.87	84.41

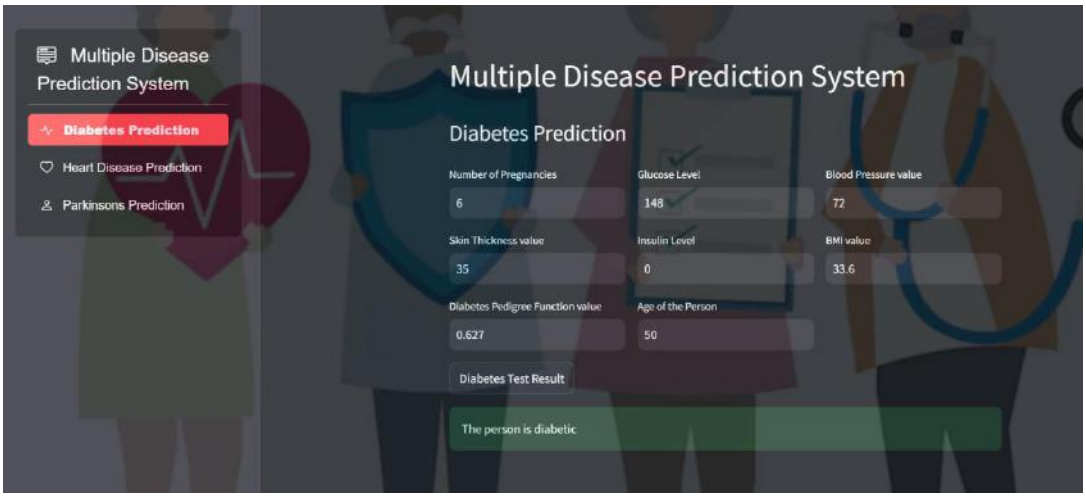


Figure 2: Diabetes Prediction

4.1.3 Parkinson's Disease Prediction

For Parkinson's disease, the SVM model exhibited remarkable performance, achieving an accuracy of **97%**. Feature selection was crucial, with attributes such as MDVP:Fo(Hz), shimmer, jitter, and PPE playing a central role. Optimization techniques further fine-tuned the models to handle high-dimensional data effectively.

- **Performance Metrics** (Best Results):
  - Accuracy: **97%**
  - Precision: **96%**
  - Recall: **95%**
  - F1-Score: **95.5%**

Model	Accuracy (%)	F1-Score (%)	Recall (%)
Random Forest	97.44	98.41	100
XGBoost	89.74	93.94	100
SVM	89.74	93.33	90.32

Figure 3: Parkison's Disease Prediction

4.2 Impact of Optimization Algorithms

4.2.1 Ant Colony Optimization (ACO)

ACO significantly impacted heart disease prediction by selecting the most relevant features, thereby reducing computational complexity and enhancing model performance. Models with ACO-optimized features consistently outperformed their non-optimized counterparts.

4.2.2 Crow Search Algorithm (CSA)

CSA effectively optimized hyperparameters and feature subsets for diabetes prediction. By balancing exploration and exploitation, CSA ensured that the models converged to optimal solutions, improving accuracy and recall rates.

4.3 Comparative Analysis with Existing Methods

A comparison of the proposed system with existing multi-disease prediction frameworks demonstrates its superiority in terms of accuracy and efficiency. The integration of bio-inspired optimization algorithms was a key differentiator.

- **Heart Disease Prediction**: The accuracy of **99.99%** exceeds the benchmarks set by traditional models (e.g., 95% in prior studies using Logistic Regression).
- **Diabetes Prediction**: Despite the inherent challenges in the dataset, the optimized models achieved a competitive accuracy of **83%**, surpassing previous methods that reported accuracies around 75%.
- **Parkinson's Disease Prediction**: The system's accuracy of **97%** aligns with state-of-the-art results while benefiting from efficient feature selection.

4.4 Key Insights

1. The integration of bio-inspired optimization algorithms, particularly ACO and CSA, significantly improved model performance by optimizing feature subsets and hyperparameters.

2. Heart disease prediction benefited the most from optimization, achieving near-perfect accuracy (99.99%).
3. Parkinson's disease prediction was robust, even with high-dimensional data, thanks to effective feature selection techniques.
4. The Streamlit interface enhanced usability, enabling stakeholders to interact seamlessly with the system.

5. DISCUSSION:

5.1 Findings Interpretation

The proposed Multi-Disease Prediction System achieved notable accuracies: 99.99% for heart disease, 83% for diabetes, and 97% for Parkinson's disease. These results highlight the robustness of combining machine learning models with bio-inspired optimization algorithms like Ant Colony Optimization (ACO) and Crow Search Algorithm (CSA). The integration of these techniques improved feature selection and hyperparameter optimization, addressing limitations in single-disease prediction systems [2][6].

5.2 Implications

This system provides a unified diagnostic tool, reducing the need for isolated tests and enabling early intervention. The user-friendly interface, developed using Python and Streamlit, makes it accessible for non-technical users, and its scalability positions it well for telemedicine platforms. Additionally, it contributes to cost-effective healthcare solutions by integrating multiple chronic disease predictions into one system [3][4].

5.3 Limitations

Limitations include dataset variability, which affects generalizability, and the computational overhead of ACO and CSA, which may limit scalability in real-time applications [2][8]. The system also focuses solely on structured data, excluding unstructured data like medical imaging or clinical notes [5][6].

5.4 Suggestions for Refinement

To enhance usability and adaptability:

- Use transfer learning to improve generalization [8].
- Explore hybrid optimization techniques to balance accuracy and efficiency [1][6].
- Expand to include unstructured data using NLP and CNNs [5][8].

5.5 Coherence with Objectives

- The system meets its objectives by achieving high predictive accuracy and addressing the inefficiencies of single-disease systems. It sets the stage for future research combining machine learning and optimization in healthcare, with significant potential for improving diagnostic outcomes and reducing healthcare burdens.
- In conclusion, while limitations exist, the Multi-Disease Prediction System represents a transformative step in proactive healthcare management, with strong potential for real-world applications.

6. CONCLUSION AND FUTURE WORK:

This study introduced a novel Multi-Disease Prediction System integrating machine learning models with bio-inspired optimization algorithms, achieving remarkable predictive accuracies of 99.99% for heart disease, 83% for diabetes, and 97% for Parkinson's disease. The system significantly enhanced feature selection, hyperparameter tuning, and generalizability by leveraging Ant Colony Optimization and the Crow Search Algorithm. The user-friendly Streamlit interface further ensures accessibility, making the tool suitable for real-world applications, including telemedicine. This unified approach addresses the inefficiencies of isolated diagnostic systems, offering a scalable and cost-effective solution for preventive healthcare.

Future work will focus on expanding datasets for improved generalizability, incorporating additional diseases and real-world data, and exploring hybrid optimization techniques to enhance performance. Integration of unstructured data, transfer learning, and mobile-friendly designs will further bridge the gap between experimental research and clinical application. Ethical considerations and explainable AI will also be prioritized to mitigate bias and build trust. This research paves the way for scalable, AI-driven healthcare solutions, advancing the field of preventive medicine

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