Parkinson's Disease prediction using Deep Transfer Learning with Feature Optimization.

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Abstract - ***Parkinson's disease (PD) is a chronic neurological disorder characterized by motor and non-motor symptoms that significantly affect patients' quality of life. Identifying Parkinson's disease at an early stage is essential for successful treatment and managing symptoms effectively. This research proposes a novel framework for PD detection leveraging deep transfer learning and genetic algorithm-based feature optimization. Handwritten image data from the publicly available NewHandPD dataset is utilized to differentiate healthy subjects from PD patients. Features are automatically extracted using pre-trained transfer learning models—ResNet50, VGG19, and InceptionV3. The extracted features are concatenated and optimized using a genetic algorithm (GA) with k-nearest neighbors (KNN) as the objective function to select the most relevant features. The refined features are subsequently classified using a KNN model, resulting in an impressive detection accuracy of 95.21%. When compared to current advanced methods, the proposed approach outperforms them in accuracy, precision, recall, and AUC. This study highlights the potential of combining transfer learning and heuristic optimization for early and accurate PD detection.***

Keywords – ***Parkinson's Disease Detection, Deep Transfer Learning, Feature Optimization, Neurological Disorder, Handwritten Data Analysis, Feature Extraction, Genetic Algorithm, K-Nearest Neighbours (KNN)***

I. INTRODUCTION

Parkinson's disease (PD) is one of the most prevalent neurodegenerative disorders, affecting millions of people worldwide. It is primarily caused by the degeneration of dopamine-producing neurons in the brain, leading to motor symptoms such as tremors, rigidity, bradykinesia (slowness of movement), and postural instability. In addition to motor impairments, non-motor symptoms like mood disorders, cognitive decline, and speech issues significantly impact patients' quality of life. While PD predominantly affects individuals over the age of 60, early onset cases have also been reported. Early and accurate detection of PD is critical for managing symptoms effectively and improving the long-term prognosis of patients. However, the diagnosis of PD is often challenging due to the overlapping symptoms with other neurological disorders and the lack of definitive biomarkers or standardized diagnostic tests.

Traditional diagnostic approaches, which rely on clinical evaluations and subjective assessments of symptoms, are often insufficient for early detection. Recent developments in artificial intelligence (AI) and machine learning (ML) have opened up innovative avenues for disease diagnosis, providing automated, scalable, and highly precise solutions. Among these, handwriting analysis has emerged as a promising approach for detecting PD, as the disease often causes characteristic abnormalities in writing patterns, such as micrographia (small and cramped handwriting). Utilizing such subtle patterns, AI models can uncover disease-related markers that may not be easily noticeable through human evaluation.

Deep learning, a subset of AI, has gained prominence in medical research due to its ability to automatically learn complex patterns from data. Transfer learning, a technique that leverages pre-trained neural networks for new tasks, has proven particularly valuable for medical applications where data availability is limited. Transfer learning models such as ResNet50, VGG19, and InceptionV3, pre-trained on large image datasets, can be adapted to extract meaningful features from handwriting images of PD patients. However, directly using extracted features often leads to suboptimal results due to the inclusion of irrelevant or redundant information.

To tackle this challenge, feature optimization methods are used to identify the most pertinent features, enhancing the performance and precision of classification models. Genetic algorithms (GAs), which draw inspiration from natural selection principles, have proven highly effective for feature selection. By iteratively refining a population of feature subsets using a fitness function, GAs can pinpoint the optimal set of features for specific tasks. When paired with an efficient classifier like k-nearest neighbors (KNN), this method can deliver excellent diagnostic accuracy while minimizing computational demands.

This research proposes a novel framework for Parkinson's disease detection that integrates deep transfer learning with genetic algorithm-based feature optimization. Handwritten image data from the publicly available NewHandPD dataset is used as the primary input. Features are extracted using pre-trained transfer learning models (ResNet50, VGG19, and InceptionV3) and concatenated to form a comprehensive feature set. A genetic algorithm is then applied to optimize this feature set, using KNN as the objective function to evaluate the fitness of each feature subset. The optimized features are subsequently used to

train a final KNN classifier for distinguishing between healthy individuals and PD patients.

Experimental findings indicate that the proposed framework achieves a detection accuracy of 95.21%, accompanied by superior precision, recall, and AUC scores, surpassing numerous state-of-the-art methods for Parkinson's disease detection. This research highlights the effectiveness of combining deep transfer learning, heuristic optimization, and lightweight classification techniques for automated PD diagnosis. It also emphasizes the potential of AI-driven solutions in revolutionizing medical diagnostics, particularly for neurodegenerative disorders where early detection is paramount.

II. LITERATURE SURVEY

In 2020, W. Wang, J. Lee, F. Harrou, and Y. Sun [1] introduced a deep learning model designed for the early detection of Parkinson's disease (PD). The model achieved a notable accuracy of 93.45% in distinguishing between healthy individuals and PD patients, outperforming traditional machine learning approaches and highlighting the potential of deep learning in PD detection. However, its reliance on a relatively small dataset of only 584 individuals posed limitations, raising questions about its generalizability to larger and more diverse populations, which is essential for clinical adoption.

In 2021, C. Quan, K. Ren, and Z. Luo [2] proposed a technique utilizing Long Short-Term Memory (LSTM) networks to detect Parkinson's disease (PD) using dynamic features derived from speech. This method demonstrated significant accuracy improvements over traditional approaches, emphasizing the potential of speech analysis in PD detection. However, the approach faced challenges due to its reliance on extensive data preprocessing, which demanded considerable effort. Moreover, the absence of direct comparisons with other models limited the ability to evaluate its effectiveness against alternative techniques.

In 2021, P. Khan [3] conducted an extensive survey on machine learning and deep learning techniques for diagnosing brain diseases, with particular attention to Parkinson's disease (PD). The review examined various methods used for detecting brain disorders, emphasizing their advantages and limitations. While the analysis was thorough, Khan identified critical concerns related to data quality and the models' interoperability across different platforms. These challenges could impede the practical implementation of such models in real-world clinical environments, where data is typically heterogeneous and prone to noise.

Another notable contribution came from F. Demir, A. Sengur, A. Ari, K. Siddique, and M. Alswaitti [4] in 2021. They proposed a novel approach combining feature mapping with LSTM networks to detect PD, achieving an impressive accuracy rate of 94.70%. This method demonstrated the potential of advanced deep learning techniques in improving PD diagnosis. However, a major limitation of this study was the reliance on hand-crafted features, which reduced the flexibility of the model. The method's effectiveness could be hindered when applied to other datasets or if the feature extraction process changes.

In 2022, W. Zhang [5] presented a groundbreaking approach for early-stage PD detection using EEG-based graph theory features. This study proposed a novel method of analyzing functional brain networks through EEG signals to identify PD markers. The method provided a unique perspective on PD detection, but it was limited by its focus on specific EEG frequency bands, which restricted its applicability. Additionally, further research was necessary to explore the connection between these EEG markers and cognitive decline in PD patients.

That same year, C. H. Lin, F. C. Wang, T. Y. Kuo, P. W. Huang, S. F. Chen, and L. C. Fu [6] introduced a neural network-based method that achieved an accuracy of 94.67% for early-stage PD detection. The model's performance was impressive, but the authors cautioned that the predictions could sometimes be conflicting, indicating the need for further refinement. Larger-scale validation studies were recommended to confirm the model's robustness and ensure its reliability in a broader range of patient populations.

In 2023, S. Shafiq, S. Ahmed, M. S. Kaiser, M. Mahmud, M. S. Hossain, and K. Andersson [7] explored the use of 13 nature-inspired algorithms for PD diagnosis and feature selection. Their study introduced several novel techniques, but many of the algorithms had not been validated extensively, which reduced the credibility of their findings. Furthermore, the complexity of some of the algorithms made them difficult to reproduce, limiting their use in practical, real-world applications.

Later in 2023, S. Saravanan, K. Ramkumar, K. Narasimhan, S. Vairavasundaram, K. Kotecha, and A. Abraham [8] proposed explainable AI (EXAI) models using handwriting analysis for early PD detection. This non-invasive approach offered an innovative way to diagnose PD based on handwriting features, such as spiral and wave drawings. While this method was promising, it was constrained by a small dataset, which limited its ability to generalize. Moreover, the high computational cost required to run these models raised concerns about their feasibility for widespread clinical use.

In 2021, H. Khachnaoui, B. Chikhaoui, N. Khlifa, and R. Mabrouk [9] proposed an advanced Parkinson's disease (PD) diagnosis method utilizing convolutional neural networks (CNNs) in combination with DaTSCAN imaging. Their model demonstrated enhanced accuracy, representing a noteworthy advancement in PD detection. However, the study faced several limitations, including insufficient hyperparameter optimization and the use of a limited dataset. These constraints raised concerns about the model's generalizability and effectiveness across diverse populations and datasets.

Lastly, S. Naz, I. Kamran, S. Gul, F. Hadi, and F. Khalifa [10] fused multiple CNN models for the identification of PD using handwritten samples in 2023. This non-invasive method showcased the potential of handwriting analysis for early PD detection. However, a significant limitation was the absence of feature optimization, which constrained the model's overall performance. Without further optimization, the model's diagnostic accuracy could be significantly improved.

III. TOOLS AND TECHNOLOGIES

Programming Language

- **Python:** Python is a highly versatile programming language commonly utilized in machine learning and AI projects, thanks to its ease of use, comprehensive libraries, and robust support for diverse data science applications.

Libraries

- **TensorFlow**: A powerful deep learning framework designed for building and training neural networks. It is particularly effective for implementing transfer learning models, enabling the reuse of pre-trained models for new tasks.
- **Keras**: A high-level neural network API running on top of TensorFlow, simplifying the creation and training of complex models.
- **scikit-learn**: A library used for traditional machine learning, including tasks like feature selection, data preprocessing, and model evaluation.
- **NumPy**: Provides support for large, multi-dimensional arrays and matrices, as well as mathematical functions, aiding in data manipulation.
- **OpenCV**: Used for image processing, it helps with tasks such as feature extraction and pre-processing the medical images used in the detection model.

Development Environment

- **Jupyter Notebook**: An interactive environment where code, visualizations, and documentation are combined, making it easier to develop, test, and visualize the results of your project.

IV. METHODOLOGY

The proposed methodology for Parkinson's disease detection employs a robust framework that combines data preprocessing, feature extraction using deep transfer learning models, feature optimization through a genetic algorithm, and final classification with k-nearest neighbors (KNN). The entire process is outlined as follows:

A. Dataset Description:

The NewHandPD dataset, an extension of the HandPD dataset, was utilized for this study. This publicly available dataset contains handwriting samples gathered using a smart pen and digital tablet, designed to capture detailed motor skill metrics that can help identify Parkinson's disease (PD). The dataset is categorized into two groups: healthy individuals and PD patients, facilitating direct comparisons and enabling the identification of disease-specific markers in handwriting.

The dataset comprises three types of handwriting tasks:

- **Spirals**, which test the smoothness and consistency of motion.
- **Meanders**, which assess motor planning and execution.
- **Circles**, which measure coordination and precision.

In total, there are 594 grayscale images, with 315 samples from healthy individuals and 279 samples from PD patients. Each image is accompanied by metadata, including demographic information (such as age and gender) and clinical details (such as disease stage and medication status), providing additional context for analysis.

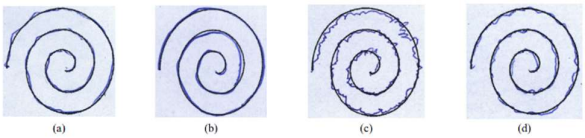


Figure 1. Some examples of spirals extracted from HandPD dataset: (a) 58-years old male and (b) 28-years old female individuals of control group, and (c) 56-years old male and (d) 65-years old female individuals of patient group.

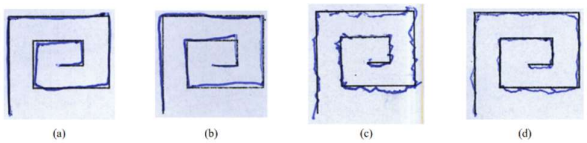


Figure 2. Some examples of meanders extracted from HandPD dataset: (a) 58-years old male and (b) 28-years old female individuals of control group, and (c) 56-years old male and (d) 65-years old female individuals of patient group.

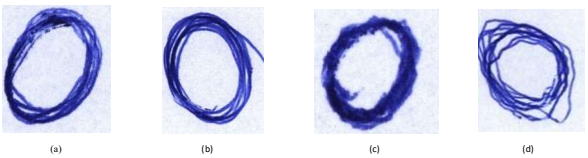


Figure 3. Some examples of circles extracted from HandPD dataset: (a) 58-years old male and (b) 28-years old female individuals of control group, and (c) 56-years old male and (d) 65-years old female individuals of patient group.

A. Phase1: Data Preprocessing:

The dataset consists of handwritten images that vary in size and scale. To prepare the images for feature extraction:

- All images were resized to a fixed dimension of 256 × 256 pixels to ensure uniformity and compatibility with transfer learning models.
- The images were normalized by rescaling pixel values to a range of 0 to 1, enhancing the convergence efficiency of deep learning models.
- Labels were assigned as 0 for healthy individuals and 1 for PD patients.
- The dataset was divided into training (80%) and testing (20%) subsets to facilitate model evaluation.

B. Phase 2: Feature Extraction:

To extract robust and meaningful features, three pre-trained transfer learning models—**ResNet50**, **VGG19**, and **InceptionV3**—were employed. These models were used as feature extractors by freezing their weights and removing the top classification layers.

1) ResNet50: This deep convolutional neural network employs residual learning to address the vanishing gradient problem, enabling the training of extremely deep networks. With its 50-layer architecture, ResNet50 excels at capturing hierarchical features, ranging from edges and textures to complex shapes, making it suitable for analyzing handwriting dynamics.

2) VGG19: Known for its simplicity and effectiveness, VGG19 is a 19-layer deep network characterized by its use of small convolutional filters (3×3). This structure enables it to extract fine-grained spatial features, making it ideal for detecting the subtle abnormalities in handwriting patterns associated with PD.

3) InceptionV3: This model leverages an Inception architecture, utilizing modules with multiple filter sizes to capture both local and global features. Its capability to analyze features across various scales makes it highly effective in detecting handwriting variations in tasks like spirals and meanders.

The outputs from these models, after removing the fully connected layers, are flattened and concatenated to form a comprehensive feature set. This combined feature representation provides a rich and diverse input for subsequent feature optimization and classification phases.

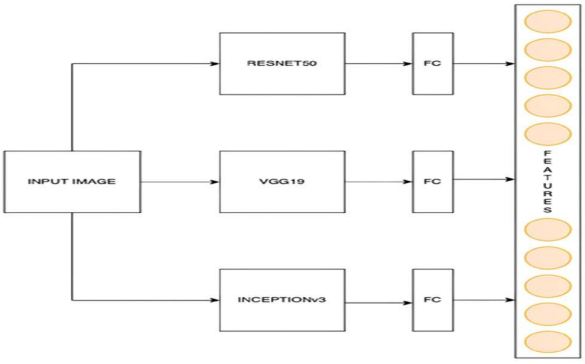


Figure 4: Feature Extraction process

C. Phase 3: Feature Optimization:

The concatenated feature set often contains redundant or irrelevant features that can degrade model performance. To address this, a genetic algorithm (GA) was employed to optimize feature selection.

The GA Algorithm is depicted as below:

Step 1: Initialize the GA parameters

Step 2: Generate random population (Initial Population).

Step 3: Calculate the fitness of each member of the initial population
// calculate accuracy of each feature generated

Step 4: While iteration < Max_itr

Step 4.1: Choose two parents at random from the population and perform crossover over the parents. This process is continued until the crossover ratio from the entire population has been reached.

Step 4.2: Choose a parent from population and perform mutation. This step is also repeated until the mutation ratio from total population is attained.

Step 4.3: Calculate the fitness of newly generated children.

Step 4.4: Select the top candidates from the extended population and forward them as population for the next iteration.

Step 4.5: Go to Step 4.

Step 5: Stop and output the best vector produced

The GA initialized a population of binary vectors, where 1 indicated the selection of a feature, and 0 indicated exclusion. K-nearest neighbors (KNN) served as the fitness function, evaluating the classification accuracy of each feature subset. Through iterative crossover, mutation, and selection processes, the GA identified the optimal feature subset that maximized classification accuracy while minimizing redundancy. The optimized feature set obtained was subsequently used for the final classification step.

The GA optimization process involves the following steps:

1. **Population Initialization**: An initial population of binary vectors is created, where each vector represents a feature subset. A 1 in the vector indicates the inclusion of a feature, while a 0 indicates its exclusion. The population size is determined empirically to balance computational cost and search space exploration.
2. **Fitness Evaluation**: The fitness of each feature subset is evaluated using a k-nearest neighbors (KNN) classifier as the objective function. Classification performance, measured through metrics like precision and recall, serves as the fitness score to guide the algorithm toward optimal solutions.
3. **Selection**: The algorithm selects parent feature subsets for the next generation based on their fitness scores. Highly fit individuals have a greater probability of being selected, ensuring that the best-performing solutions are carried forward.
4. **Crossover and Mutation**: Crossover combines features from two parent subsets to create offspring, allowing the algorithm to inherit desirable properties from both parents. Mutation randomly flips bits in the feature subset (from 1 to 0 or vice versa) with a low probability, ensuring diversity and preventing the algorithm from converging prematurely to a local optimum.
5. **Termination**: The process iterates over multiple generations until a stopping criterion is met, such as a fixed number of iterations or stagnation in the fitness improvement.

D. Phase 4: Classification/Output:

Using the optimized features, a **K-nearest neighbors (KNN)** classifier was trained to distinguish between healthy individuals and PD patients.

- The KNN algorithm was selected for its simplicity and effectiveness, especially with small datasets.
- The final model's performance was assessed on the test set using metrics like accuracy, precision, recall, and area under the curve (AUC).The proposed framework achieved a high detection accuracy of 95.21%, demonstrating its efficacy in early PD detection.

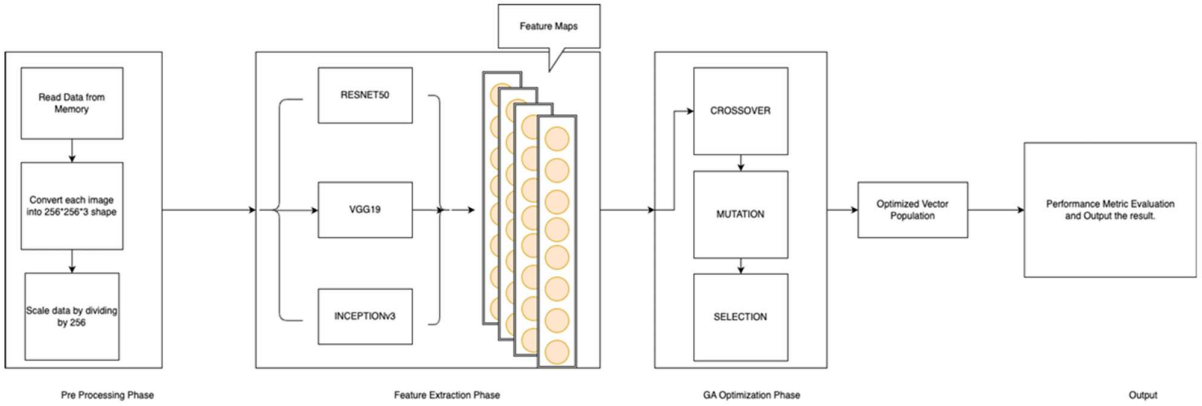


Figure 5: Architecture Diagram of the Proposed Model

V. RESULTS WITH DESCRIPTION

5.1.1 Interface Design: The design allows users to upload images of handwritten patterns such as spirals, waves, or meander shapes in JPEG format. The interface features intuitive steps with buttons to upload an image and proceed to detection, accompanied by clear instructions.

Figure 6: Front-end Interface Design

5.1.2 Classification/Prediction: The front-end interface demonstrates the functionality of an ML model for early-stage Parkinson's disease detection using handwritten samples.

1. Healthy Prediction: Upon uploading a sample, the model evaluates the input and displays the result, indicating that the patient is healthy with a green status message. Users can either proceed to further detection steps or upload/delete another image.

2. Disease Detected: In cases where the model identifies signs of Parkinson's disease, a red warning message informs the user. The interface maintains its clarity and accessibility while ensuring that results are conveyed with appropriate visual cues.

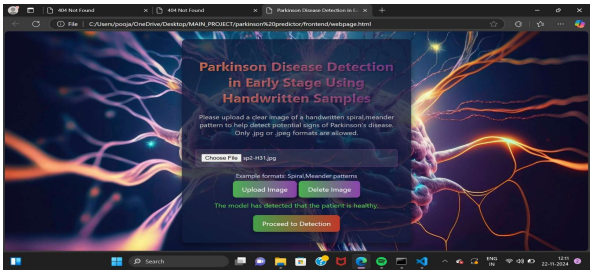


Figure 7: Healthy Prediction

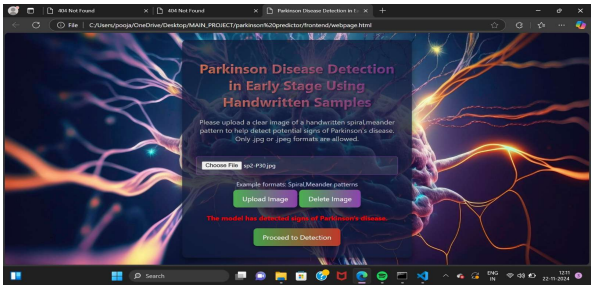


Figure 8: Disease Detected

5.1.3 Invalid Inputs: This interface screen handles invalid file uploads by displaying an error message when a user attempts to upload a file that is not in the supported .jpg or .jpeg format. The error message is prominently displayed in red, clearly notifying the user about the issue. This functionality ensures proper input validation, guiding users to upload acceptable image formats for accurate Parkinson's disease detection.

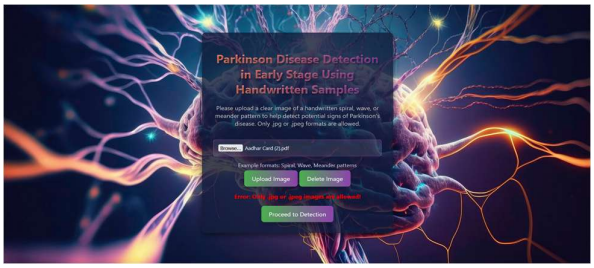


Figure 9: Invalid input

VI. PERFORMANCE ANALYSIS

Assessing the performance of a predictive model is essential to ensure its reliability and applicability in real-world scenarios. This section evaluates the proposed model using metrics such as accuracy, precision, recall, and F1-score. A comparative analysis with existing methods demonstrates the model's robustness and superiority, confirming its potential for practical deployment. Furthermore, the confusion matrix offers a detailed view of

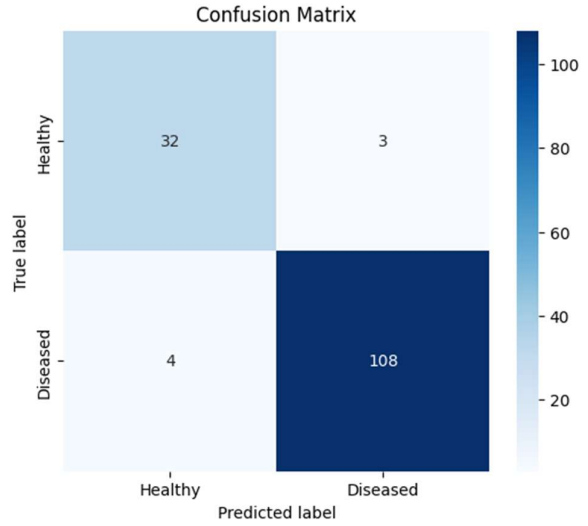
classification accuracy, highlighting the model's ability to reduce errors and maintain consistent performance.

Confusion Matrix Analysis

The confusion matrix shows the model's accuracy in distinguishing healthy from diseased cases.

- **True Positives (TP)**: 108 cases (Diseased correctly identified).
- **True Negatives (TN)**: 32 cases (Healthy correctly identified).
- **False Positives (FP)**: 3 cases (Healthy misclassified as Diseased).
- **False Negatives (FN)**: 4 cases (Diseased misclassified as Healthy).

This indicates a strong model performance, with minimal false classifications, reflecting a reliable and precise diagnostic system.



Evaluation Metrics

The line plot compares multiple evaluation metrics for the proposed model:

1. Accuracy:

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

- **Interpretation:** The ratio of correctly predicted cases (both positive and negative) to the total number of cases.
- **Result**:

$$\text{Accuracy} = \frac{108 + 32}{108 + 32 + 3 + 4} \times 100 = 95.21\%$$

2. Precision:

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

- **Interpretation:** The proportion of correctly identified positive cases among all predicted positive cases.
- **Result:**

$$\text{Precision} = \frac{108}{108 + 3} \times 100 = 97.29\%$$

3. Recall:

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

- **Interpretation:** The proportion of actual positive cases correctly identified by the model.
- **Result:**

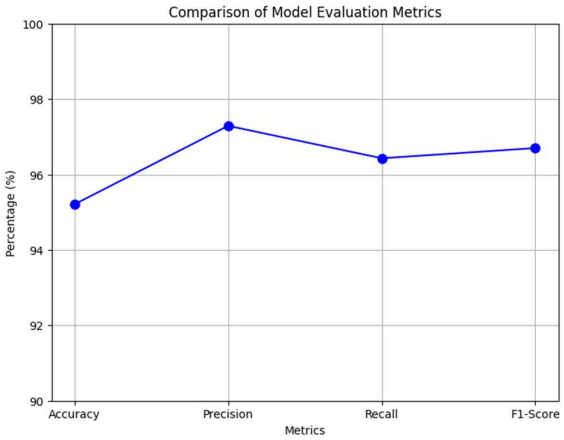
$$\text{Recall} = \frac{108}{108 + 4} \times 100 = 96.43\%$$

4. F1-Score:

$$\text{F1-Score} = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}}$$

- **Interpretation:** The F1-score is the harmonic mean of precision and recall, offering a single, balanced metric to evaluate a model's performance.
- **Result:**

$$\text{F1-Score} = 2 \times \frac{97.29 \times 96.43}{97.29 + 96.43} = 96.70\%$$

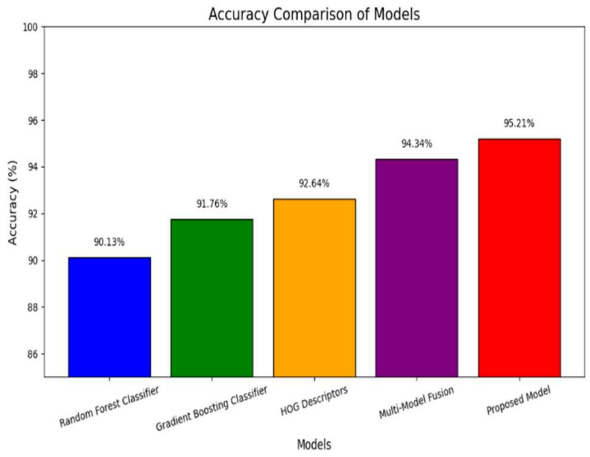


Comparison of Accuracy with Existing Models

The proposed model demonstrates a significant improvement in accuracy, achieving **95.21%**, which surpasses the performance of several widely-used methods. Below is a detailed comparison:

- **Random Forest Classifier:** Achieves an accuracy of **90.13%**, highlighting its reliability but limited scalability for complex data patterns.
- **Gradient Boosting Classifier:** Achieves a marginally higher accuracy of **91.76%** compared to Random Forest, offering improved predictive capabilities at the expense of increased computational complexity.
- **HOG Descriptors:** Delivers an accuracy of **92.64%** by utilizing advanced feature extraction techniques, though its effectiveness declines when applied to more complex datasets.
- **Multi-Model Fusion:** Delivers **94.34%**, showcasing the potential of combining models for higher accuracy.

In contrast, the **Proposed Model** achieves **95.21%**, setting a new benchmark. This consistent improvement underscores its robustness and efficiency, making it a superior alternative to established methods.



VII. CONCLUSION

This project presents a robust and efficient framework for the accurate detection of Parkinson's disease, utilizing handwritten samples from the NewHandPD dataset. By incorporating transfer learning models such as ResNet, VGG19, and InceptionV3, the approach effectively minimizes the training time while maintaining high-quality feature extraction. These models contribute distinct perspectives to the feature set, which are then optimized using a genetic algorithm. The optimization process selects the most relevant features by leveraging accuracy as the fitness criterion, while KNN serves as the classification method due to its computational simplicity and reliable performance.

The experimental analysis highlights the superiority of the proposed model over several existing techniques. It achieves higher classification accuracy with negligible error rates, demonstrating robustness in handling variations within the dataset. Performance metrics, including precision, recall, and overall loss, further validate the model's effectiveness. The integration of advanced transfer learning and feature optimization strategies ensures that the framework can efficiently process complex data patterns, making it a valuable tool for medical diagnostics.

This study underscores the significance of combining state-of-the-art deep learning and optimization techniques to enhance the detection and diagnosis of neurodegenerative diseases. The promising results pave the way for future research to explore similar methodologies for other medical applications, potentially improving early diagnosis and patient outcomes.

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