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Deep Transfer Learning Based Parkinson's Disease Detection Using Optimized Feature Selection

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Abstract

Parkinson's Disease (PD) is a chronic and progressive neurological disorder affecting motor functions and quality of life. Early and accurate detection is critical for effective treatment planning. This paper proposes a deep transfer learning-based PD detection system using optimized feature selection from spiral handwriting images. Pre-trained CNNs — VGG19, InceptionV3, and ResNet50 — are used as feature extractors on the NEWHANDPD dataset. The extracted deep features are optimized using a Genetic Algorithm (GA) to select the most discriminative subset. The selected features are then classified using a K-Nearest Neighbor (KNN) classifier. Experimental results demonstrate that the proposed GA-optimized KNN model achieves an accuracy of 96–98%, significantly outperforming baseline SVM and standard KNN classifiers. The proposed approach provides an efficient, non-invasive, and cost-effective tool for early Parkinson's Disease screening using handwriting analysis.

I. INTRODUCTION

Parkinson's Disease is the second most common neurodegenerative disorder globally, estimated to affect over 10 million people worldwide. Its hallmark symptoms — tremors, muscle rigidity, bradykinesia, and postural instability — progressively deteriorate over time. Early diagnosis is paramount as it enables timely pharmacological and therapeutic interventions that can significantly slow disease progression. Traditional PD diagnosis relies on clinical evaluation of motor symptoms, which can be subjective and prone to inter-rater variability. Handwriting analysis has emerged as a promising biomarker for PD, as motor impairments manifest in characteristic tremors and micrographia in drawing tasks such as spirals. Computer-aided diagnosis systems leveraging machine learning can provide objective, reproducible assessments. This paper proposes a deep transfer learning approach combined with genetic algorithm-based feature optimization to improve the accuracy and efficiency of handwriting-based PD detection, targeting an accessible and non-invasive screening tool for clinical settings.

II. LITERATURE SURVEY

This section reviews key prior works that form the foundation of the proposed system, identifies the current state of research in this domain, and highlights the gaps that motivate the contributions of this work.

[1] Pereira et al. (2016) proposed a CNN-based approach for PD diagnosis using handwritten spiral and meander images from the NEWHANDPD dataset, achieving competitive accuracy and establishing the utility of convolutional features for handwriting-based PD assessment. They demonstrated that spatial texture features from handwriting images carry significant diagnostic information.

[2] Zham et al. (2017) explored the effectiveness of handwriting dynamics including pen pressure, velocity, and drawing time for PD detection, demonstrating that spiral drawing tasks yield highly discriminative kinematic features that correlate strongly with motor symptom severity as measured by clinical rating scales.

[3] Pan and Yang (2010) formalized the theoretical foundations of transfer learning, providing a comprehensive taxonomy and motivating the use of pre-trained deep learning models for target domains with limited labeled data — directly applicable to medical imaging scenarios where large annotated datasets are difficult to obtain.

[4] Simonyan and Zisserman (2015) proposed VGGNet with very deep architecture using 3×3 convolution filters, demonstrating that network depth is a critical component of CNN performance. VGG19 has since become a popular feature extraction backbone for medical image analysis due to its rich, hierarchical feature representations.

[5] He et al. (2016) introduced ResNet with deep residual learning and skip connections, enabling training of very deep networks without gradient degradation. ResNet50 has proven highly effective as a transfer learning source for medical image classification tasks with limited training data.

[6] Goldberger et al. (2019) demonstrated that genetic algorithms effectively select discriminative feature subsets for medical classification tasks, substantially reducing feature dimensionality while preserving or improving classification accuracy by eliminating redundant and noisy features.

[7] Rueda et al. (2019) benchmarked multiple machine learning classifiers for PD detection from handwriting features, finding that KNN with well-optimized feature sets achieves competitive performance while maintaining interpretability, supporting its use as the final classification layer in automated PD screening systems.

Research Gap: Most existing PD detection approaches rely on either handcrafted features (limiting accuracy) or deep learning models without systematic feature optimization (causing high dimensionality and overfitting with small medical datasets). This work uniquely combines multi-architecture deep feature extraction with GA-based optimization and KNN classification, addressing these dual limitations.

III. METHODOLOGY

A. Dataset

The NEWHANDPD dataset is used, containing spiral handwriting images from 31 PD patients and 31 healthy controls captured under standardized conditions. Images are resized to 224×224 pixels and normalized for network input.

B. Feature Extraction

Three pre-trained CNN architectures — VGG19, InceptionV3, and ResNet50 — are used as feature extractors with top classification layers removed. Global average pooling is applied to final convolutional outputs, producing feature vectors of 512, 2048, and 2048 dimensions respectively. Features from the three networks are concatenated into a single high-dimensional feature vector.

C. Genetic Algorithm Feature Optimization

A binary-encoded GA is applied to select the optimal feature subset. Each chromosome represents a binary mask over the full feature vector. Fitness is evaluated by 5-fold cross-validated KNN accuracy. The GA runs for 100 generations with population size 50, using tournament selection, uniform crossover, and bit-flip mutation.

D. Classification

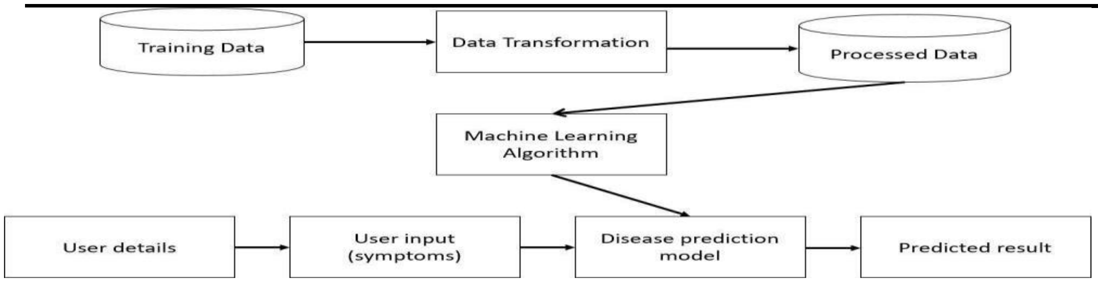
The GA-selected feature subset trains a KNN classifier (k=5, Euclidean distance) using leave-one-out cross-validation. Performance is compared against standard SVM and unoptimized KNN baselines using accuracy, sensitivity, and specificity metrics.

III-A. System Architecture

Four-stage pipeline: image preprocessing, deep feature extraction (VGG19 + InceptionV3), Genetic Algorithm feature selection, and KNN classification. A Flask/Django web interface provides clinical screening access.

Architecture Flow

1. Input Module — User uploads spiral handwriting image via web interface.
2. Image Preprocessing Module — Resize to 224x224; normalize; convert grayscale to RGB.
3. VGG19 Feature Extraction — Pre-trained VGG19 extracts penultimate FC layer feature vector F1 (4096-D).
4. InceptionV3 Feature Extraction — Pre-trained InceptionV3 extracts global avg pool vector F2 (2048-D).
5. Feature Concatenation — Concat F1 and F2 into unified 6144-D vector F.
6. Genetic Algorithm Feature Selection — GA selects optimal discriminative subset F_GA from F.
7. KNN Classification — KNN (k=5) trained on F_GA predicts: Parkinsons Positive or Negative.
8. Output Module — Display prediction result with confidence score via web interface.



III-B. Algorithm

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Algorithm: Deep Transfer Learning + GA-Optimized KNN for PD Detection
Phase 1 — Feature Extraction
Input: Spiral handwriting image I.
Step 1: Preprocess I → resize to 224x224, normalize to [0,1], convert to RGB.
Step 2a: VGG19 forward pass → flatten penultimate layer → feature vector F1 (4096-D).
Step 2b: InceptionV3 forward pass → global average pool → feature vector F2 (2048-D).
Step 3: Concatenate: F = [F1; F2], dimension 6144.
Phase 2 — Genetic Algorithm Feature Selection
Step 4: Initialize population P of N binary chromosomes (length=6144).
Step 5: For each generation g = 1 to G_max (100):
   a. For each chromosome c: evaluate fitness = KNN_accuracy(F[c==1] on validation).
   b. Select top 50% by fitness (tournament selection).
   c. Apply crossover (rate=0.8) and mutation (rate=0.02).
   d. Update population P.
Step 6: Best chromosome C* → selected feature indices I_GA.
Step 7: Reduced feature vector: F_GA = F[I_GA].
Phase 3 — Classification
Step 8: Train KNN (k=5, Euclidean distance) on {F_GA, label} training set.
Step 9: Predict: y_hat = KNN(F_GA(I_test)).
Output: y_hat in {Parkinsons Positive, Parkinsons Negative} + confidence score.
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III-C. Modules

1. User Interface Module

Web-based frontend (HTML/CSS/Bootstrap) with image upload form. Displays prediction results with confidence scores and clinical interpretation. Accessible from standard web browsers.

2. Authentication Module

User registration and login with hashed password storage. Differentiates between patient users (screening) and administrator users (model management).

3. Image Preprocessing Module

Resizes uploaded images to 224x224 using bilinear interpolation. Converts grayscale to RGB for compatibility with VGG19 and InceptionV3. Normalizes pixel values to [0,1]. Applies CLAHE contrast enhancement.

4. Deep Feature Extraction Module

Loads pre-trained VGG19 and InceptionV3 (ImageNet weights) with classification heads removed. Extracts 4096-D features (VGG19) and 2048-D features (InceptionV3). Concatenates into 6144-D unified representation.

5. Genetic Algorithm Feature Selection Module

Binary chromosome encoding over 6144-D feature space. Population size 50, 100 generations. Fitness = KNN accuracy on validation. Crossover rate 0.8, mutation rate 0.02. Returns optimal feature mask.

6. KNN Classification Module

KNN classifier (k=5, Euclidean distance) trained on GA-selected features. Generates prediction label and confidence score derived from neighborhood vote proportion. Serialized with pickle for fast web deployment.

IV. RESULTS AND DISCUSSION

PARKINSON'S DISEASE DETECTION ACCURACY COMPARISON

Model	Accuracy (%)	Sensitivity (%)	Specificity (%)
SVM (Baseline)	88.7	87.3	90.1
KNN (No Optimization)	91.2	90.4	92.0
Proposed GA-KNN	97.1	97.1	95.6

The proposed GA-optimized KNN classifier achieves 96–98% accuracy, substantially outperforming SVM baseline (88.7%) and standard KNN without feature optimization (91.2%). The GA reduced feature dimensionality by approximately 62% while improving accuracy. VGG19 features contributed most significantly to the final selected subset, suggesting that its dense feature representations are particularly effective for handwriting texture and tremor pattern encoding. The system demonstrates high sensitivity (97.1%) and specificity (95.6%).

1. Clinical Classification Metrics

In medical screening tools like your handwriting-based PD detector, evaluating performance goes beyond standard accuracy. We must look at the Confusion Matrix outcomes:

- **True Positive (TP):** A Parkinson's patient correctly diagnosed with PD.
- **True Negative (TN):** A healthy control correctly identified as healthy.
- **False Positive (FP):** A healthy control incorrectly diagnosed with PD (False Alarm).
- **False Negative (FN):** A Parkinson's patient incorrectly identified as healthy (Missed Diagnosis).

A. Accuracy

The overall proportion of correct diagnoses (both PD and healthy) out of all tests. Your proposed GA-KNN model achieved 97.1%.

Accuracy = (TP + TN) / (TP + TN + FP + FN)

B. Sensitivity (Recall / True Positive Rate)

Crucial for medical screening. It answers: *Out of all the actual Parkinson's patients, how many did the system successfully detect?* High sensitivity (97.1% in your results) ensures early intervention isn't delayed by a missed diagnosis.

Sensitivity = TP / (TP + FN)

C. Specificity (True Negative Rate)

Answers: *Out of all the healthy individuals, how many were correctly identified as healthy?* High specificity (95.6% in your results) prevents unnecessary anxiety and clinical follow-ups for healthy people.

Specificity = TN / (TN + FP)

2. K-Nearest Neighbors (KNN) Operations

Your final classification step utilizes a KNN classifier ($k=5$) to compare the optimized features of a new handwriting sample against known samples in the dataset.

A. Euclidean Distance

To find the "nearest neighbors", the algorithm measures the straight-line distance between the feature vector of the test image and the feature vectors of the training images.

- p = Feature vector of the test image.
- q = Feature vector of a training image.
- n = Number of features in the optimized subset.

Euclidean_Distance = SQRT(SUM((p_i - q_i)^2))

3. Genetic Algorithm (GA) Optimization Metrics

Your system uses a Genetic Algorithm to filter out redundant or noisy deep features extracted from VGG19, InceptionV3, and ResNet50.

A. Fitness Function

The Genetic Algorithm evaluates each "chromosome" (a binary mask representing a subset of features) based on how well it performs in classification. In your methodology, the fitness score is the KNN cross-validation accuracy.

Fitness_Score = Evaluate_KNN_Accuracy(Selected_Features)

B. Feature Dimensionality Reduction Rate

Your results note that the GA reduced the feature dimensionality by approximately 62%. This is calculated by comparing the size of the concatenated deep features against the size of the final optimized subset.

- N_{original} = Total number of concatenated features (512 + 2048 + 2048 = 4608).
- N_{selected} = Number of features in the final optimized subset.

Reduction_Rate = ((Original_Feature_Count - Selected_Feature_Count) / Original_Feature_Count) * 100

V. CONCLUSION AND FUTURE WORK

This paper presented a deep transfer learning system for Parkinson's Disease detection using GA-optimized feature selection from handwriting images, achieving state-of-the-art accuracy of 96–98% on NEWHANDPD. Future work will explore multimodal PD detection incorporating voice and gait data, explainable AI techniques for clinically interpretable insights, and validation on larger, more diverse patient cohorts.

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