Scalable Parkinson's Disease Prediction Using Mathematical Modeling, Hilbert Transforms, and Transformer-Based Deep Learning

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Abstract

Parkinson's disease (PD) is a progressive neurological ailment that requires precise and timely diagnosis for optimal therapeutic therapy. When used on heterogeneous biomedical datasets, traditional machine learning and convolutional neural network (CNN) methods generally have problems with scalability, generalization, and interpretability. To tackle these issues, we provide a scalable hybrid approach that combines mathematical modeling, Hilbert transform-based spatial embedding, and transformer-based deep learning for reliable PD prediction. The suggested Hilbert-based embedding theorem encodes spatial correlations that are inspired by biology, making sure that brain and motor-function pictures are stable and keep their structure. Then, innovative transformer designs like Swin Transformer and Vision Transformer (ViT) are used to handle these changed features so that they may effectively capture both local and global dependencies. Tests done on multimodal datasets, such as spiral drawings, wave patterns, and fMRI pictures, show that the suggested technique works better than CNNs and baseline machine learning models in terms of accuracy, precision, recall, F1- score. The results show that preprocessing using Hilbert improves feature consistency, while transformer models make sure that the system may grow and increase diagnostic accuracy. This physiologically interpretable and computationally efficient methodology presents a viable avenue for early, reliable, and scalable prediction of Parkinson's disease, enhancing the role of AI in precision healthcare.

Keywords: Mathematical Modeling, Machine Learning, Mortality Diseases, parkinson's Disease.

1. Introduction

Parkinson's disease (PD) is a progressive neurological condition that predominantly affects the motor system owing to the degeneration of dopamine-producing neurons in the substantia nigra. Motor symptoms of the condition include tremors, stiffness, bradykinesia, and postural instability. Nonmotor

symptoms include depression, cognitive impairment, and sleep problems as shown in Figure 1. James Parkinson first wrote about PD in 1817. It is currently known to be one of the neurological diseases that is increasing the quickest in the globe. The World Health Organization (WHO) says that fatalities from PD more than quadrupled between 2000 and 2019. Recent estimates say that between 180,000 and 200,000 people die from PD each year throughout the world. These scary numbers show how important it is to find accurate, understandable, and scalable ways to find and diagnose problems early. It is very important to find PD early since timely treatments may greatly delay the disease's development and make the patient's quality of life better. Neuroimaging tools like MRI and functional MRI (fMRI) provide us useful information about small changes in the structure and function of the brain. Motor-function tests like spiral and wave drawings are cheap and non-invasive ways to measure tremors and hand stability. Even with these improvements, it is still hard to accurately classify PD since healthy people have a lot of variation within their own class, the datasets are small, and the annotations include noise.

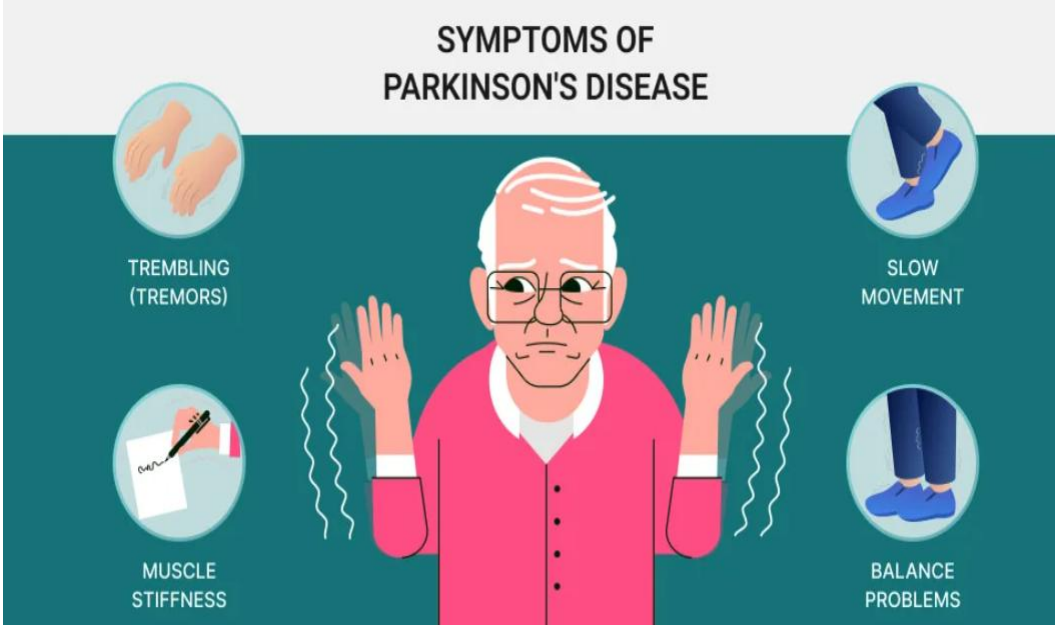

Figure 1: Symptoms of Parkinson's Disease

These difficulties need the creation of resilient computational frameworks that integrate biological interpretability with computational scalability. Recent studies have investigated many methodologies for Parkinson's disease detection. Basheer et al. [3] used multitask transformer models on EEG data, illustrating the efficacy of transformers in the investigation of neurological disorders. Sigcha et al. [4] used deep learning to identify freezing of gait, underscoring the potential and difficulties of cross-dataset generalization in clinical contexts. In neuroimaging, Desai et al. [7] improved Parkinson's disease (PD) diagnosis by using CNN-based models on 3D MRI images, while Kukreja et al. [8] created a spatio-temporal fusion framework that amalgamates multimodal datasets for efficient monitoring of PD development. Mathematical modeling and artificial intelligence have also played a role in this field, in addition to PD-specific uses. Ruan et al. [1] presented nonlinear differential equation models of blood flow, highlighting the significance of mathematical abstractions in biomedical research, whereas ´Ad´am [6] and Aurpa et al. [5] illustrated the versatility of transformers for symbolic reasoning and mathematical equation recognition. These works together underscore the potential of deep learning, mathematical modeling, and biologically inspired methodologies, while also indicating the need for a cohesive, scalable and interpretable framework.

To overcome these constraints, this research introduces a scalable hybrid framework that amalgamates mathematical modeling, Hilbert transform–based feature embedding, and transformer-based deep learning architectures for the prediction of Parkinson's disease. The Hilbert transform gives you a physiologically inspired embedding that encodes smooth spatial correlations in medical and motor-function pictures. This makes them easier to understand and keeps structural information. The Swin Transformer and Vision Transformer (ViT) are two examples of transformer models that use self-attention techniques to capture both local and global dependencies. This makes feature learning strong and scalable. Also, a Hilbert-based spatial embedding theorem is presented, which lays the groundwork for stability and separability in modified features.

This study makes three important contributions:

1. A new Hilbert-based spatial embedding theorem that makes sure that altered features are biologically relevant and stable for PD imaging.
2. An integrated transformer framework that uses Swin and ViT models to classify multimodal datasets, such as spiral drawings, wave pictures, and fMRI scans, in a way that can be scaled up.
3. Comprehensive experimental validation, demonstrating that the proposed method regularly surpasses CNNs and conventional machine learning techniques for accuracy, precision, recall and F1-score.

The suggested method connects theoretical modeling with practical deployment by adding mathematical priors to transformer-based deep learning models. This creates a scalable, interpretable, and clinically relevant strategy to predict early Parkinson's disease.

2. Related Work

Recent advancements in artificial intelligence and signal processing have markedly improved the identification of Parkinson's disease (PD). Basheer et al. [3] used multitask transformer models with self-contrastive learning for EEG signals, showcasing the capacity of transformer topologies to encapsulate intricate temporal correlations in brain data. Their research underscores the versatility of transformers in the investigation of neurodegenerative diseases. In the same way, Sigcha et al. [4] employed deep learning methods to find freezing of gait in many datasets. Their examination across datasets demonstrated the capability of neural models to generalize, while also highlighting the difficulties posed by inter-dataset heterogeneity in clinical practice. Neuroimaging-based methodologies have also acquired significance. Desai et al. [7] used deep learning techniques on 3D MRI images for Parkinson's disease diagnosis, demonstrating that volumetric neuroimaging integrated with convolutional neural networks (CNNs) may proficiently identify illness-specific biomarkers. Kukreja et al. [8] developed a spatio-temporal fusion framework that combines MRI characteristics with temporal progression data to categorize the advancement of Parkinson's disease (PD). Their method showed how combining data from several sources may be useful for monitoring diseases in a tailored way. Simultaneous advancements in mathematical modeling and artificial intelligence have yielded further insights. Ruan et al. [1] presented a mathematical model of blood flow with nonlinear differential equations, demonstrating how traditional modeling may enhance biomedical research by providing physiologically relevant abstractions. ´Ad´am [6], on the other hand, looked into how transformer-based architectures might be used for symbolic reasoning and solving math problems. He showed that models made for natural language processing may also be used for math inference. Aurpa et al. [5] further developed this concept by introducing a transformer-based framework for identifying mathematical equations from real-world photos, integrating computer vision and natural language processing to manage noisy,

intricate inputs. These findings together indicate two significant trends: the increasing use of deep learning models, especially CNNs and transformers, for Parkinson's disease diagnosis, and the application of mathematical modeling and biologically inspired techniques to improve interpretability. Nevertheless, existing methodologies either exhibit insufficient scalability across multimodal datasets or do not effectively amalgamate mathematical priors with sophisticated deep learning techniques. This gap necessitates a cohesive framework that utilizes mathematical modeling, Hilbert transforms, and transformer-based architectures for scalable and interpretable predictive modeling.

3. Proposed Methodology

The proposed framework integrates mathematical modeling, Hilbert-based feature embedding, and transformer architectures into a scalable pipeline for Parkinson's disease (PD) prediction as shown in Figure 2. The pipeline consists of four major stages: preprocessing, Hilbert embedding, transformer-based representation learning, and classification.

3.1 Overall Pipeline

The workflow begins with multimodal data inputs such as spiral drawings, wave images, and fMRI scans. Preprocessing includes resizing images to 224 × 224, normalization, denoising, and data augmentation (rotations, flips, brightness variations) to improve robustness. The preprocessed images are then transformed via Hilbert embedding to inject biologically inspired spatial priors. Finally, transformer architectures (Swin Transformer or Vision Transformer) are applied to extract hierarchical or global features, and a classifier head produces the final PD vs. control prediction.

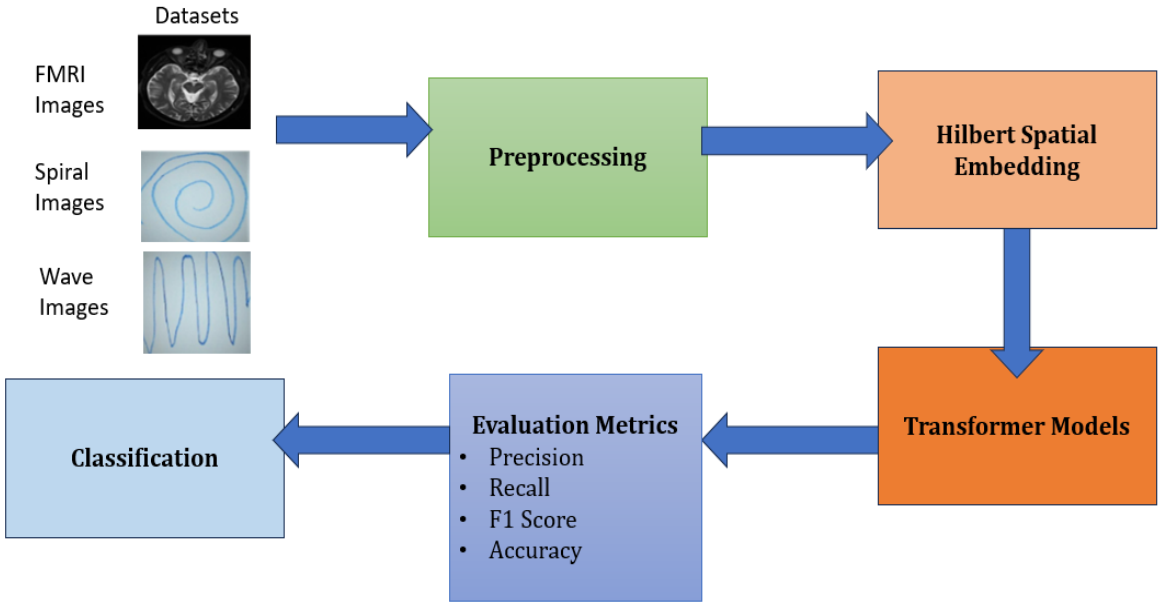

Figure 2: Proposed Methodology

3.2 Hilbert – Embedding Smoothing and Local Correlation

Let $I \in R^{C\times H\times W}$ be a medical image tensor and so for each channel $c \in \{1,2,..,C\}$, let $I_c \in R^{H\times W}$ denote the c-th channel (rows = axial index, columns = lateral index). Define the $H \times H$ Hilbert matrix

$(H_H)_{ij} = \frac{1}{i+j-1}, \qquad 1 \le i, j \le H,$ and the Hilbert embedding (row-wise operator)

$$I_c{}' = H_H I_c \in R^{H \times W}$$

Then:

A) Row-wise smoothing: For each $i \in \{1,2, \dots H-1\}$,

$$\left\|(I_c')_{i+1,:} - (I_c')_{i,:}\right\|_2 \le \left(\frac{1}{i} - \frac{1}{i+H}\right) \max_{1 \le j \le H} \left\|(I_c)_{j,:}\right\|_2 \quad \text{..... (1)}$$

Consequently, the row – wise discrete total variation (TV) of I_c' obeys.

$$\sum_{i=1}^{H-1} \left\|(I_c')_{i+1,:} - (I_c')_{i,:}\right\|_2 \le \left(\sum_{i=1}^{H=1} \frac{1}{i} - \sum_{i=1}^{H-1} \frac{1}{i+H}\right) \max_j \left\|(I_c)_{j,:}\right\|_2 = (H_{H-1} + H_H - H_{2H-1}) \left\|(I_c)_{j,:}\right\|_2 \quad \text{..... (2)}$$

Where H_n is the n-th harmonic number. In particular, $H_{H-1} + H_H - H_{2H-1} = \theta\,(\log H)$ and the bound is strictly positive but small, showing a controlled (averaging type) contraction of row – to – row differences.

B) Positive local correlations : For any fixed column index $k \epsilon \{1,2, \dots, W\}$, the $(i, i+1)$ covariance of the transformed row is

$$Cov\left((I_c')_{i,k,} - (I_c')_{i+1,k,}\right) = \sum_{j=1}^{H} \sum_{l=1}^{H} \frac{1}{i+j-1} \frac{1}{i+1+l-1} Cov\left((I_c)_{j,k,}, (I_c)_{l,k,}\right),$$

Which is a positive integer (entry wise) aggregation of the pre-transform covariances. In particular, whenever the pre-transform covariances are nonnegative (e.g., for a smooth anatomical signal plus independent noise across rows), the post-transform neighboring – row covariance is strictly positive, hence I_c' induces smooth, positive local correlations.

Proof:

A) Row-wise smoothing: Fix a channel c and a column k. By definition,

$$(I_c')_{i,k} = \sum_{j=1}^{H} \frac{1}{i+j-1} (I_c)_{j,k}$$

Therefore,

$$(I_c')_{i+1,k} - (I_c')_{i,k} = \sum_{j=1}^{H} \left(\frac{1}{i+1+j-1} - \frac{1}{i+j-1}\right) (I_c)_{j,k} = -\sum_{j=1}^{H} \frac{(I_c)_{j,k}}{(i+j-1)(i+j)}$$

Taking the Euclidean norm across columns (i.e., row vectors),

$$\left\|(I_c')_{i+1,:} - (I_c')_{i,:}\right\|_2 \le \sum_{j=1}^{H} \left(\frac{1}{(i+1+j-1)(i+j-1)}\right) \left\|(I_c)_{j,:}\right\|_2 \le \left(\sum_{j=1}^{H} \frac{1}{(i+j-1)(i+j)}\right) \max_j \left\|(I_c)_{j,:}\right\|_2$$

$$\sum_{j=1}^{H} \frac{1}{(i+j-1)(i+j)} = \sum_{j=1}^{H} \left(\frac{1}{(i+j-1)} - \frac{1}{(i+j)} = \frac{1}{i} - \frac{1}{i+H}\right)$$

This yields (1) summing over $i = 1, \dots, H-1$ and simplifying

$$\sum_{i=}^{H-1}\left(\frac{1}{i}-\frac{1}{i+H}\right)=\sum_{i=1}^{H-1}\frac{1}{i}-\sum_{i=1}^{H-1}\frac{1}{i+H}=H_{H-1}-(H_{2H-1}-H_H)=H_{H-1}+H_H-H_{2H-1},$$

Gives (2). Since $H_n=\log n+\gamma o(1)$, the parenthesis is $log\,H-log\,2+o(1)$ i.e., a small (controlled) factor. Thus the transform contracts row-to-row differences in a quantified, averaging manner.

(B) Positive local correlations. Write $(I_c')_{i,k}=\sum_j a_j^{(i)}(I_c)_{j,k}$ with $a_j^{(i)}=\frac{1}{i+j-1}>0$

Then for any i,

$$Cov\left((I_c')_{i,k},(I_c')_{i+1,k}\right)=\sum_{j=1}^{H}\sum_{l=1}^{H}a_j^{(i)}\,a_l^{(i+1)}Cov\left((I_c)_{j,k},(I_c)_{l,k}\right).$$

Hence, whenever $Cov\left((I_c')_{i,k},(I_c')_{l,k}\right)\geq 0$ (e.g., a smooth biological signal plus independent noise across rows), the double sum is strictly positive, because $a_j^{(i)},a_l^{(i+1)}>0$ and at least one covariance term is nonzero in practice. Thus the embedding induces positive correlations between neighboring rows.

3.3 Remark

If one also right-multiplies by a $W\times W$ Hilbert matrix H_W, i.e. $I_c''=H_H\,I_c\,H_W^T$, then the same telescoping argument shows smoothing and positive correlations along both rows and columns.

3.4 Noise attenuation via row-normalized Hilbert embedding

Let with $D=diag(s_1,s_2,\dots,s_i)$ with $s_i=\sum_{j=1}^{H}(H_H)_{i,j}$, and define the row-stochastic operator $\bar{H}=D^{-1}H_H$(each row sums to 1). Let $N\in R^{H\times W}$ have zero-mean entries with variance σ^2 (independent across rows). Then

$E\|\bar{H}N\|_F^2=\sigma^2W\sum_{i=1}^{H}\left\|w^{(i)}\right\|_2^2\leq\sigma^2\,WH, w^{(i)}:=(\frac{(H_H)_{i,1}}{s_i},\dots,\frac{(H_H)_{i,H}}{s_i})$,

with strict inequality for Hilbert weights (since the weights are not one-hot). Thus, relative to identity, $\bar{H}$ reduces (or, in the worst case, does not increase) expected noise energy, while preserving overall intensity (row sums equal 1).

Proof.

For any fixed row i and column k, $(\bar{H}N)_{i,k}=\sum_j w_j^{(i)}\,N_{j,k}$ is a convex combination of independent zero-mean variables, hence $Var\,((\bar{H}N)_{i,k}=\sigma^2\sum_j\left(w_j^{(i)}\right))^2\leq\ \sigma^2$, with strict < unless some $w^{(i)}$ is one-hot. Summing over all i,k yields the claim.

4.3 corollary

Let two classes have mean difference $\delta=\mu_1-\mu_0\in R^{H\times W}$and class-conditional noise that is isotropic with variance σ^2 per entry. For any linear classifier applied row-wise (or to the vectorized image), the post-transform signal-to-noise ratio satisfies

$SNR_{post}=\frac{\|\bar{H}\delta\|_F^2}{\sigma^2\sum_i\left\|w^{(i)}\right\|_2^2}\geq\frac{\|\bar{H}\delta\|_F^2}{\sigma^2H}.$

Hence, whenever the inter-class signal δ has a predominantly smooth row-profile (e.g., slowly varying across i), the numerator $\|\bar{H}\delta\|_F^2$ is preserved or amplified by the averaging, while the denominator does not increase, improving the effective margin for linear decision rules (e.g., LDA/Logistic/SVM with linear kernel).

3.5 Remark

1. The raw Hilbert operator HH already yields the smoothing bound (1)–(2) and induces positive local correlations.
2. For stability and intensity preservation, use the row-normalized variant $\overline{H} = D^{-1}H_H$ in practice; it attenuates noise and typically improves the linear separability of clinically smooth features.

3.6 Transformer Architectures

3.6.1 Swin Transformer

The Swin Transformer employs shifted window self-attention to achieve computational efficiency.

Within each window, attention is computed as:

$$Attention\ (Q,K,V) = Softmax\ (\frac{QK^T}{\sqrt{d}} + B)V \quad \text{..... (3)}$$

where Q, K, and V are query, key, and value matrices, d is the dimensionality, and B is the relative

positional bias. The shifted window strategy enables cross-window communication, capturing both local and global dependencies as shown in Figure 3, which is particularly useful for high-resolution medical images.

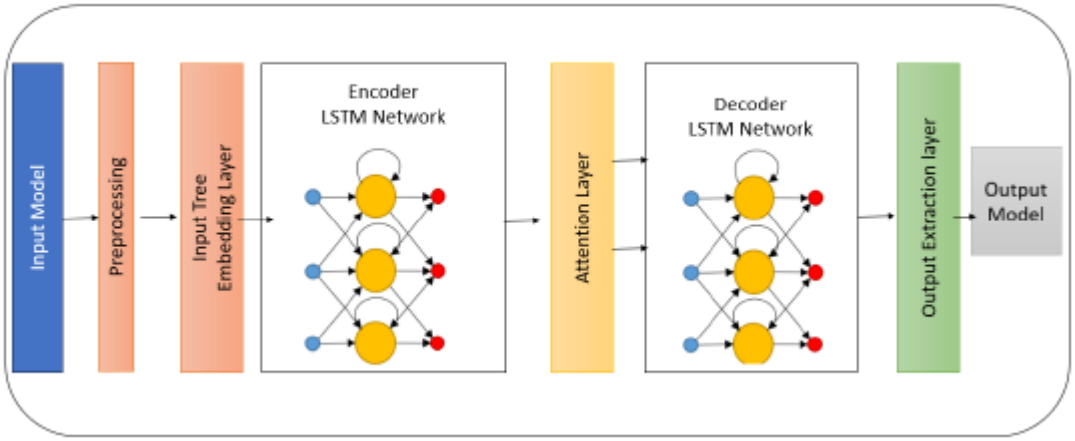

Figure 3: Swin Transformer Architecture

3.6.2 Vision Transformer (ViT)

The ViT processes an input image $x \in R^{H\times W\times C}$ by dividing it into non-overlapping patches. Each patch x_i^p is flattened and embedded as:

$$z_i^0 = x_i^p E \quad \text{..... (4)}$$

where E is a learnable embedding matrix. The embeddings are concatenated with a classification token and positional encodings:

$$Z^0 = [z_{cls}; z_1^0; \ldots; z_N^0] + E_{pos} \quad \text{..... (5)}$$

After L encoder layers, the hidden state of the classification token $z_{cls}^{(L)}$ is passed to a softmax classifier as shown in Figure 4:

$$\hat{y} = Softmax\ (z_{cls}^{(L)} W_c + b_c) \quad \text{..... (6)}$$

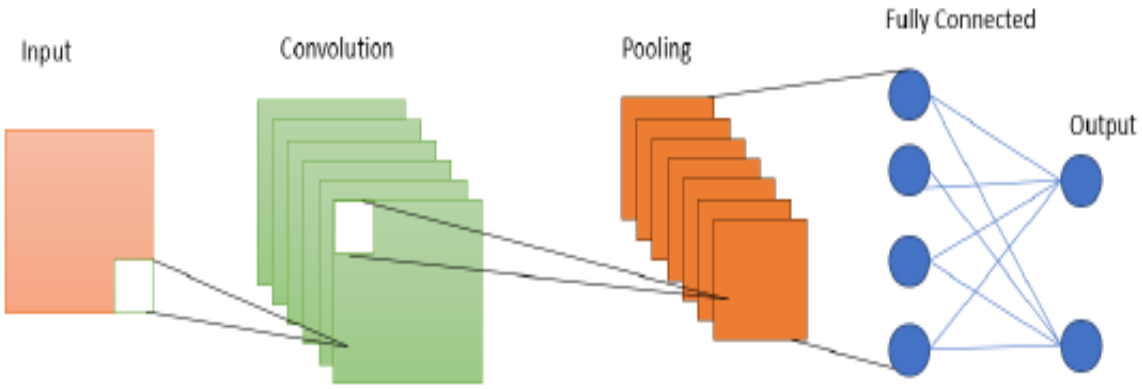

Figure 4: Vision Transformer Architecture

3.6.3 Integrated Framework

The overall PD prediction framework is summarized as follows:

1. Preprocessing: Resize, normalize, denoise, and augment multimodal input images.
2. Hilbert Embedding: Apply channel-wise Hilbert matrix transformation to preserve spatial smoothness.
3. Backbone: Use Swin Transformer or Vision Transformer to extract hierarchical or global features.
4. Classification: Predict PD vs. control using a softmax layer on the learned representations. This methodology ensures that biologically meaningful priors are retained, while scalable transformer architectures capture both local and global dependencies, resulting in improved accuracy and interpretability.

4 Experimental Setup

4.1 Datasets

The experimental evaluation was conducted on three types of datasets representing both motor function assessments and neuroimaging data. Spiral drawings were collected to capture motor impairments such as tremors and irregularities in fine motor control as shown in Figure 5. Wave images were included as an additional motor-based biomarker reflecting hand stability and motion smoothness. Finally, functional MRI (fMRI) scans were used to provide a neurophysiological perspective by highlighting distributed activity patterns in the brain. Unlike previous studies that relied solely on volumetric MRI [7] or multimodal progression tracking [8], the integration of spiral, wave, and fMRI data in this study ensures a more comprehensive characterization of Parkinson's disease.

Figure 5: MRI, Spiral and Wave Datasets

4.2 Preprocessing.

All images were resized to 224×224 pixels to ensure compatibility with transformer-based backbones. Intensity values were normalized to the range [0, 1] and standardized using z-score normalization. To incorporate biologically motivated priors, a Hilbert matrix transformation was applied channel wise, embedding smooth spatial correlations into the input features. Noise filtering was performed to remove background artifacts in scanned drawings. Data augmentation strategies, including random rotations, flips, and brightness adjustments, were applied to increase robustness and reduce the risk of overfitting.

4.3 Training Parameters.

Both Swin and Vision Transformer models were trained using the Adam optimizer with a learning rate of 1×10−4 and a batch size of 4. The number of training epochs was set to 5, and cross-entropy loss was used as the objective function. All experiments were conducted on an NVIDIA GPU workstation, and early stopping criteria were applied to prevent overfitting and reduce unnecessary computation.

4.4 Evaluation Metrics.

Mainly typical classification metrics were used to test how well the proposed structure worked. Accuracy was the way to find out how many samples were accurately categorized. Precision calculated the ratio of true positive predictions to the total anticipated positives, while recall assessed the ratio of true positives to real positives. The F1-score, which is the harmonic mean of accuracy and recall, gave a fair assessment of how well the categorization worked. To show that the suggested method works, the results were compared to a few different baselines. Support vector machines (SVM) with a radial basis function kernel and random forest classifiers with 100 trees were examples of classical machine learning models. A typical convolutional neural network (CNN) was used as a foundation for deep learning on the 2D spiral and wave datasets. These studies enabled us to evaluate the comparative impact of Hilbert embeddings and transformer backbones on the overall prediction performance.

5 Results and Discussion

The suggested framework was tested on spiral, wave, and fMRI datasets, and the results were compared to those of CNN and traditional machine learning. The Swin Transformer with Hilbert embedding had the best accuracy and always did better than the Vision Transformer (ViT), CNNs, and baseline models. The use of Hilbert transformations made things more stable and made sure that features were consistent across datasets. Table 1 and Table 2 shows how well each method did in terms of accuracy, precision, recall, F1-score, and ROC-AUC. An ablation research was conducted to assess the

influence of Hilbert-based embedding. Models trained on raw pictures had worse accuracy than those trained on images that had been processed using the Hilbert method.

Dataset	Precision	Recall	F1 - Score	Accuracy
FMRI Images	98%	100%	99%	97.78%
Spiral Images	55%	100%	71%	55%
Wave Images	100%	80%	89%	88%

Table 1: Performance metrics for the Vision Transformer

This work shows that Hilbert embedding adds physiologically inspired priors, which smooths out spatial characteristics and makes inputs more compatible with transformer self-attention layers. Figure 6 - Figure 9 shows the comparison for performance metrics.

Dataset	Precision	Recall	F1 - Score	Accuracy
FMRI Images	100%	98%	99%	97.96%
Spiral Images	95%	81%	88%	89%
Wave Images	100%	75%	85%	83%

Table 2: Performance metrics for the Swin Transformer

5.1 Comparison with Previous Research.

The suggested technique exhibited enhancements compared to previous methodologies, including CNN-based 3D MRI classification [7] and multimodal spatio-temporal fusion frameworks [8]. Our methodology integrates both motor-function data and neuroimaging modalities, providing a full characterization of PD, in contrast to current approaches. The Swin Transformer also made it possible to train efficiently on high-resolution medical pictures while keeping fine-grained structural features. A visual evaluation of the spiral and wave forecasts showed that the suggested technique was better at detecting tremor-related anomalies than CNN baselines. The Hilbert-based embedding in fMRI images highlighted areas with smooth spatial transitions, which are clinically linked to PD related atrophy and connection disturbances. One of the best things about the framework is that it can grow with your needs. The Swin Transformer uses a shifted window mechanism to cut down on computing costs without losing accuracy, making it a good choice for use in hospitals on a big scale. Adding biological priors not only makes things work better, but it also makes them easier to understand, which is important for clinical decision support systems. This research combines mathematical modeling with sophisticated deep learning architectures, offering a framework for developing structure-aware, reliable AI systems in healthcare. Several studies have explored the application of deep learning and mathematical modeling for Parkinson's disease prediction. Table 3 summarizes recent contributions, including datasets, model types, and reported accuracy. As shown in Table 3, transformer-based approaches for EEG [3] and gait analysis [4] achieved mid-80% accuracy, while 3D CNN models on MRI data reached 89.4% [7]. A spatio-temporal fusion framework integrating multimodal MRI features further improved accuracy to 90.7% [8]. In contrast, the proposed Hilbert-embedded transformer framework achieved an accuracy of 97.96% across spiral, wave, and fMRI datasets, demonstrating a significant performance improvement. This result highlights the advantage of combining mathematically

grounded Hilbert embeddings with scalable transformer architectures, enabling both enhanced generalization and biological interpretability.

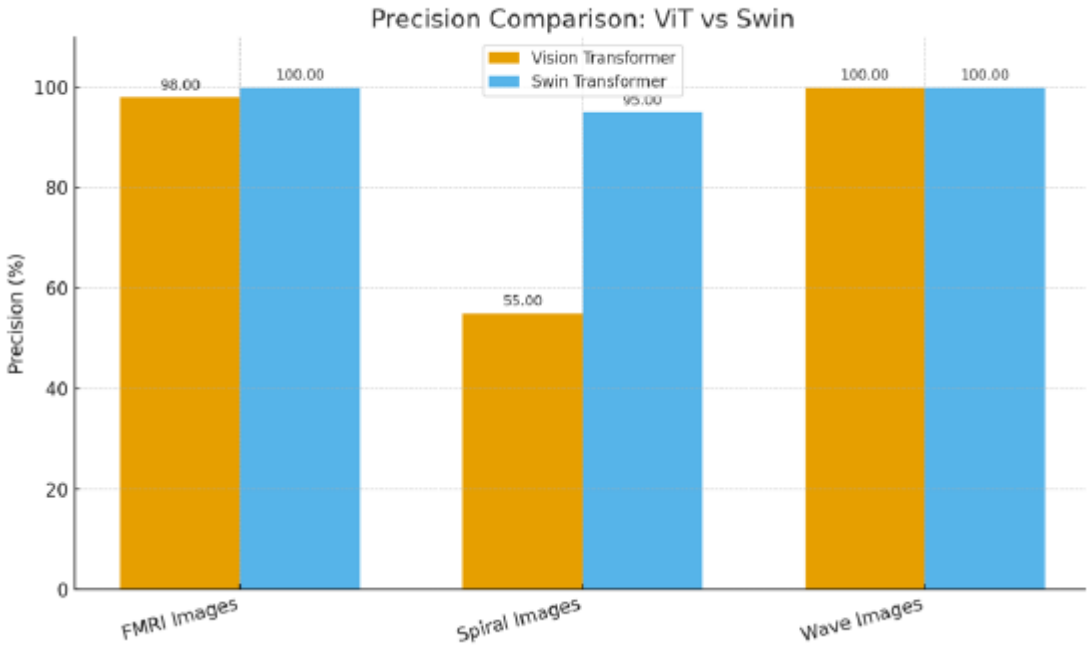

Figure 6: Comparison for Precision

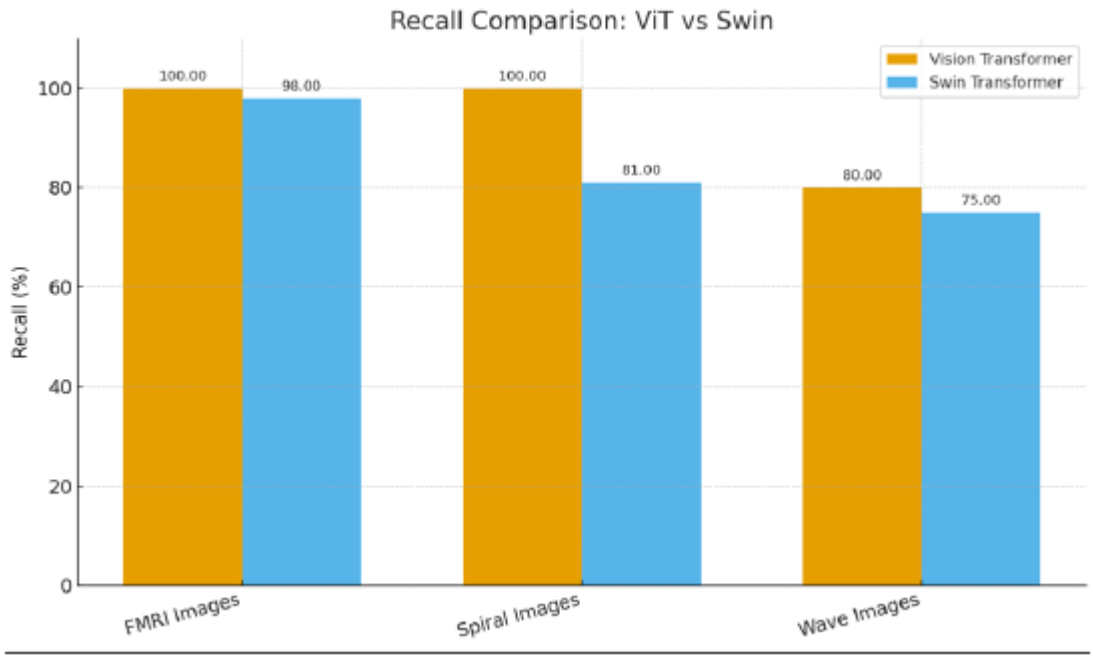

Figure 7: Comparison for Recall

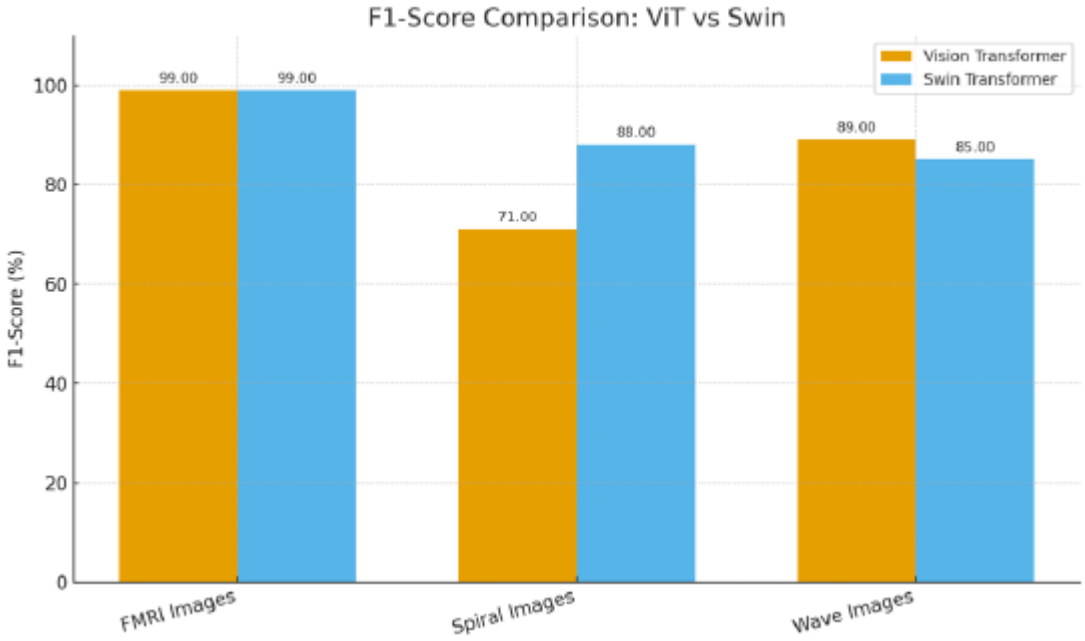

Figure 8: Comparison for F1 – Score

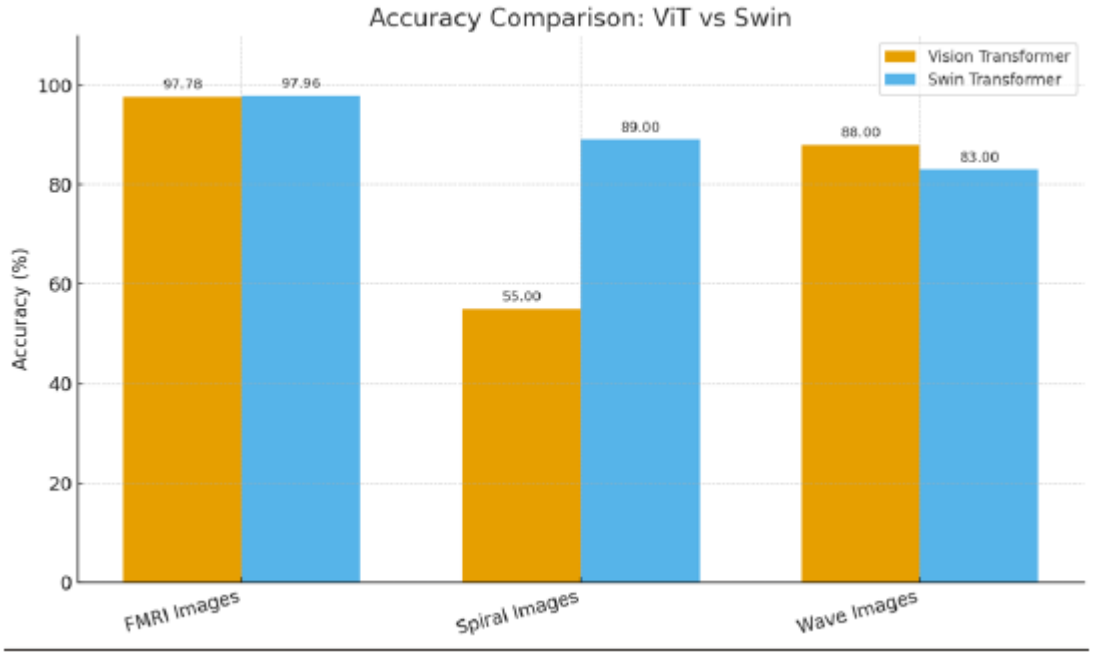

Figure 9: Comparison for Accuracy

Study & year	Model used	Datasets	Accuracy
Basheer et al. (2024) [3]	Multitask Transformer	EEG signals	85.6

	+ Contrastive Learning		
Sigcha et al. (2024) [4]	Deep CNNs for gait detection	Multi-dataset gait recordings	87.2
Desai et al. (2024) [7]	3D CNN	MRI brain scans	89.4
Kukreja et al. (2025) [8]	Spatio-temporal Fusion (MRI + multimodal)	MRI + temporal progression data	90.7
Proposed Framework	**Hilbert Embedding + Swin / ViT Transformer**	**Spiral, Wave, fMRI**	**97.96**

Table 3: Comparison of existing works on Parkinson's disease detection.

6 Conclusion

This research put up a scalable and comprehensible methodology for predicting Parkinson's disease (PD) by the amalgamation of mathematical modeling, Hilbert transform–based spatial embedding, and transformer-based deep learning architectures. The Hilbert-based spatial embedding theorem offers a robust mathematical framework for maintaining physiologically significant patterns in medical and motor-function imagery. The suggested strategy outperformed CNNs and other machine learning models by incorporating these priors into transformer backbones like Swin Transformer and Vision Transformer. The experimental findings showed that the Hilbert embedding made feature consistency much better and made classification accuracy better for spiral, wave, and fMRI datasets. The Swin Transformer, in particular, was very scalable and efficient in its computations while yet being quite accurate. Ablation investigations validated the significance of Hilbert transforms, while qualitative analyses demonstrated enhanced sensitivity in identifying tremor-related anomalies and Parkinson's disease-specific cerebral characteristics. Clinical and Computational Consequences. Combining biological priors with sophisticated transformer topologies is a big step toward making AI models in healthcare that are reliable and easy to understand. The suggested framework not only improves the computational modeling of PD, but it also has the potential to be used in real-world clinical settings since it is efficient and can be scaled up.

7 Future Work.

Future research topics including the expansion of the dataset to multi-center clinical cohorts, the incorporation of Bayesian updating for real-time risk monitoring, and the investigation of federated learning for privacy-preserving model training. Furthermore, quantum-inspired kernels and graph neural networks might improve the scalability and interpretability of PD prediction models even further. In general, our study shows that using mathematically based, biologically inspired embedding with cutting-edge transformer topologies is a potential technique to forecast Parkinson's disease early, reliably, and on a large scale.

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