

Learning Robust Spatiotemporal Features from RS-fMRI for Parkinson's Disease Classification Using CanICA, Dictionary Learning, and LSTM

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ABSTRACT:

Parkinson's disease (PD) is a progressive neurodegenerative disorder where early and accurate diagnosis remains a critical challenge. Machine learning applied to functional MRI (fMRI) data offers promising avenues for automated classification by extracting meaningful spatiotemporal features. In this preliminary study, we evaluate two data-driven feature extraction methods—Canonical Independent Component Analysis (CanICA) and Dictionary Learning (DL)—in combination with Long Short-Term Memory (LSTM) networks. Comparative experiments were conducted using different hidden unit configurations and region definition strategies. Results indicate that CanICA features, when paired with compact LSTM architectures, achieved peak accuracy of 85.17% with a loss of 0.54, outperforming DL in terms of discriminability. Conversely, DL features provided more stable performance across configurations, particularly with connected components, yielding consistent accuracy around 71.43% and lower variance in loss values. These findings highlight the complementary strengths of CanICA and DL: CanICA excels in compact models with high accuracy, while DL ensures robustness and generalization.

Keywords: RS-FMRI, LSTM

1 Introduction

Healthcare systems worldwide are designed to preserve and improve human health through prevention, diagnosis, treatment, and rehabilitation. Over the past decades, advances in biomedical research, digital health, and artificial intelligence (AI) have transformed many aspects of healthcare delivery. Yet, despite these developments, neurodegenerative disorders remain a formidable challenge due to their chronic nature, complex management, and profound impact on patients' quality of

life.

Parkinson's disease (PD) is one of the most prevalent neurodegenerative disorders, affecting millions globally. It is characterized by the progressive loss of dopaminergic neurons in the *substantia nigra pars compacta*, leading to motor symptoms such as tremors, rigidity, bradykinesia, and postural instability, as well as non-motor symptoms including depression, sleep disturbances, and cognitive decline [3]. The disease typically manifests after the age of 60, though early-onset cases have also been

reported. Its progression is gradual but relentless, making long-term care and monitoring essential.

Globally, PD represents a growing public health challenge. The World Health Organization has highlighted that disability and death due to PD are rapidly increasing, with prevalence projected to double in the next 30 years [3]. A recent modeling study further estimated that the number of people living with PD will continue to rise sharply through 2050, driven by aging populations and environmental risk factors.

From a healthcare perspective, PD presents unique challenges:

- **Diagnosis:** Clinical diagnosis relies heavily on neurological examination, as no definitive biomarker exists. This often results in delayed or misdiagnosis [15].
- **Treatment:** While medications such as levodopa alleviate symptoms, they do not halt disease progression. Advanced therapies like deep brain stimulation are effective but costly and not universally accessible [21].
- **Healthcare burden:** The Global Burden of Disease Study (2021) reported a substantial increase in PD prevalence between 1990 and 2021, underscoring its growing impact on healthcare systems worldwide [3].

Recent studies have explored machine learning (ML) and deep learning (DL) approaches to improve PD diagnosis and classification. [18] demonstrated that ML classifiers applied to speech and handwriting data achieved promising accuracy in early PD detection. [21] applied convolutional neural networks (CNNs) to MRI scans, showing improved sensitivity in distinguishing PD patients from healthy controls.

[15] reviewed DL applications in PD, highlighting the role of LSTM and CNN

architectures in analyzing temporal and spatial features of neuroimaging data. [22] emphasized the integration of multimodal data—speech, handwriting, and fMRI—for robust PD classification.

These studies illustrate the potential of AI-driven healthcare solutions to address diagnostic challenges, particularly when applied to complex datasets such as functional MRI (fMRI). By leveraging neural network architectures, researchers aim to reduce diagnostic uncertainty, enable earlier intervention, and guide personalized treatment strategies.

2 Dataset

Functional Magnetic Resonance Imaging (fMRI) is a non-invasive neuroimaging technique that measures brain activity by detecting changes associated with blood oxygenation levels. Specifically, fMRI relies on the blood-oxygen-level-dependent (BOLD) signal, which reflects neuronal activity through hemodynamic responses. This makes fMRI a powerful tool for studying both structural and functional aspects of the brain in neurodegenerative disorders such as Parkinson's disease (PD).

In the context of PD, fMRI has been widely used to investigate alterations in brain connectivity and activity patterns. Resting-state fMRI (rs-fMRI) allows researchers to examine intrinsic brain networks without requiring task performance, which is particularly useful for patients with motor impairments [4]. Studies have shown that patients with PD exhibit altered connectivity in motor and cognitive networks, including the basal ganglia, thalamus, and cortical regions [21].

2.1 fMRI Signal Representation

The observed fMRI signal at voxel v and time t is modeled as:

$$x_v(t) = s_v(t) + n_v(t) \quad (1)$$

where $s_v(t)$ represents the neural signal and $n_v(t)$ denotes noise components such as

motion artifacts and physiological fluctuations.

The full data matrix for each subject is represented as:

$$X = [x_1, x_2, \dots, x_V] \in \mathbb{R}^{T \times V} \quad (2)$$

where each column corresponds to a voxel time-series.

Recent advances in machine learning and deep learning have enabled the use of fMRI data for automated classification of PD patients. For example, [11] automated classification of PD patients using fMRI data to classify PD using 4D fMRI data, where preprocessing involved independent component analysis (ICA) and dual regression methods [11]. Similarly, [21] demonstrated that CNNs applied to magnetic resonance and fMRI scans improved sensitivity to distinguish PD patients from healthy controls [21]. These approaches highlight the potential of combining neuroimaging with computational models to enhance diagnostic accuracy.

Integration of fMRI data with Long Short-Term Memory (LSTM) networks has also been explored, given the temporal nature of fMRI signals. LSTMs can capture sequential

dependencies in brain activity, making them suitable for analyzing dynamic connectivity patterns in PD patients [15]. Such methods aim to reduce diagnostic uncertainty and provide insight into disease progression.

In general, fMRI data provide a rich source of information to understand PD pathology. When combined with advanced neural network architectures, it offers promising avenues for early diagnosis, patient classification, and personalized treatment strategies.

Resting-state fMRI data is considered for the study, which is freely available in the Parkinson Progression Markers Initiative (PPMI) repository, containing MRI, SPECT, PET, and fMRI scans from various research groups, including PD, normal controls, SWEED, etc., across various age groups from 30 years and above. CT, PET, and fMRI—acquired from diverse research cohorts such as individuals diagnosed with Parkinson's disease (PD), healthy controls, and participants from the SWEED study. The dataset is systematically organized by age groups, beginning from 30 years and above. The acquisition parameters for the resting-state fMRI data are summarized in Table 1. The raw fMRI scan for PD patient is shown in 1

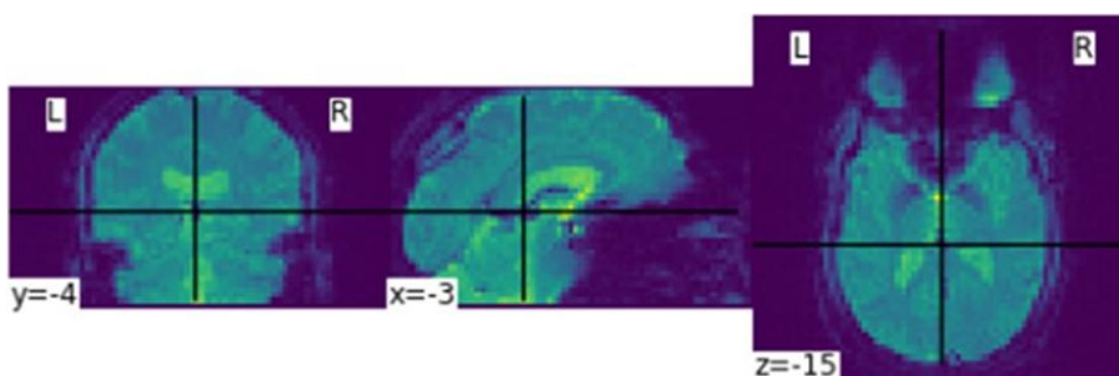


Figure 1: The raw fMRI scan for PD patient depicting the coronal, sagittal and axial functional regions of brain

Table 1: Functional MRI Acquisition Protocol

Parameter	Value
Field Strength	3.0 Tesla
Flip Angle	80°
Manufacturer	SIEMENS
Matrix Size	476 × 462 pixels
Pixel Spacing	3.3 mm (X), 3.3 mm (Y)
Pulse Sequence	Echo Planar Imaging (EP)
Number of Slices	210
Slice Thickness	3.3 mm
Echo Time (TE)	25 ms
Echo Rate (TR)	2400 ms

2.2 Data Preprocessing

For the present analysis, scans from 18 PD patients and 18 healthy controls were utilized, each comprising 211 volumetric images per subject. The original images were provided in DICOM format and subsequently converted into NIfTI format for preprocessing and further analysis using SPM tool in MATLAB [10].

The 3D fMRI volume acquired at each repetition time (TR) inherently contains both neural signals and various sources of physiological and technical fluctuations, such as head motion, random drifts, respiration, and cardiac activity, which are treated as noise. To

ensure data quality, certain artifacts are mitigated through statistical model fitting, while others are addressed during preprocessing steps, including motion correction, temporal filtering, and physiological noise regression.

Preprocessing steps such as realignment, normalization, and smoothing were performed using SPM12 [10], with additional validation through fMRIPrep [8]. These procedures follow established guidelines for preparing fMRI data for statistical analysis [17].

- Realignment, comprising the processes of estimation and reslicing, is performed to correct for head motion and ensure that all volumes are oriented consistently across the time series. This step involves within-subject registration of the image sequence, where the estimation procedure realigns the series of images acquired from the same subject using a least-squares approach and a six-parameter rigid body spatial transformation. Following estimation, reslicing is applied to the registered images so that each volume matches the first image voxel-for-voxel, thereby minimizing motion-related artifacts and improving the accuracy of subsequent analyses. The realigned scans for PD patients are shown in 2

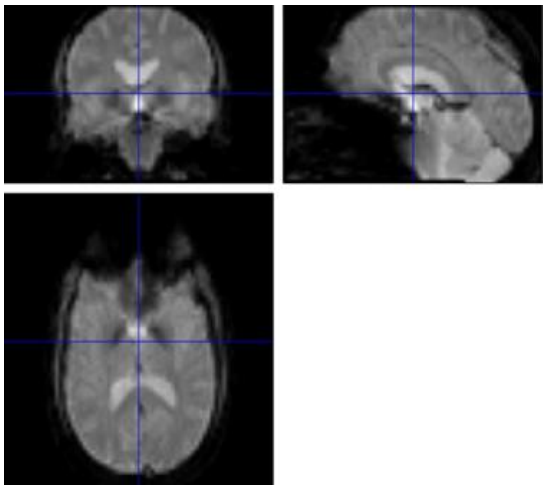


Figure 2: The realigned fMRI scans illustrating the aligned slices along the coronal, sagittal and axial axis of brain [6]

- Slice time correction as shown in 3 is applied to adjust for temporal differences in image acquisition across slices within each fMRI volume. This procedure compensates for the sequential nature of slice acquisition, ensuring that all slices are temporally aligned and thereby improving the accuracy of subsequent analyses.

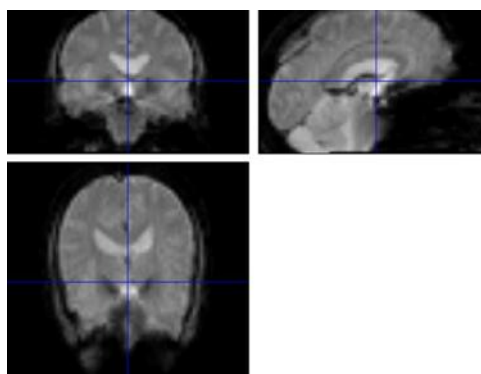


Figure 3: The slice timing corrected fMRI scan of PD patient [6]

- Co-registration that is Within-subject registration is performed using a rigid-body model to correct for motion across the time series. In three-dimensional space, a rigid-body transformation can be parameterized by six degrees of freedom, consisting of three translational shifts along the Cartesian axes and three rotational adjustments about those axes. The co-registered scan for PD patient is shown in 4

3 Neural Network Classification

Neural networks have been applied across diverse modalities to classify Parkinson's disease (PD), each exploiting unique pathological signatures. In the domain of speech analysis, early work introduced the public PD voice dataset, demonstrating that dysphonia measures such as jitter, shimmer, and harmonic-to-noise ratio could be used for telemonitoring of PD patients through machine learning models [14]. Building on this, Tsanas et al. employed advanced feature engineering and neural architectures to achieve accurate progression monitoring from sustained phonation and

connected speech [24]. Handwriting and spiral drawing tasks have also been investigated as diagnostic modalities. Drotár et al. analyzed digitized handwriting and spiral signals, showing that convolutional neural networks (CNNs) applied to rasterized spirals and temporal models such as LSTMs on pen kinematics could effectively discriminate PD patients from healthy controls [5].

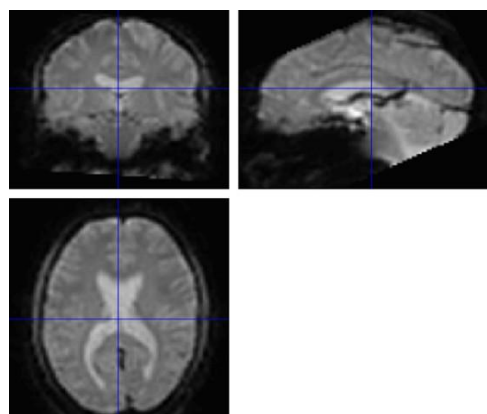


Figure 4: The Parkinson's patient scan after performing co-registration [6]

Wearable sensor data, particularly gait signals captured by inertial measurement units (IMUs), has been another promising modality. Eskofier et al. demonstrated that machine learning applied to gait analysis could classify PD patients by identifying stride variability and tremor-related activity [7]. Subsequent deep learning approaches have employed one-dimensional CNNs and hybrid CNN-LSTM architectures to learn temporal patterns from multi-axis accelerometer and gyroscope signals, enabling both classification and symptom quantification. Neuroimaging has provided yet another rich source of data for PD classification. Beyond structural MRI, functional modalities such as resting-state fMRI and PET/SPECT imaging have been used to capture alterations in brain connectivity and metabolism. Neural models including 3D CNNs on volumetric maps, graph neural networks (GNNs) on connectivity matrices, and autoencoders for representation learning have been employed to extract latent biomarkers from these high-dimensional datasets. These imaging-based

approaches typically involve rigorous preprocessing steps such as motion correction, physiological noise regression, and spatial normalization, ensuring that the learned features reflect disease-related patterns rather than acquisition artifacts. Together, these works illustrate the breadth of modalities—speech, handwriting, wearable sensors, and neuroimaging—through which neural networks have been applied to Parkinson's disease classification. Each modality offers complementary insights, and multimodal integration remains a promising direction for enhancing diagnostic accuracy and robustness.

In this work the fMRI modality data is applied on the following neural network architectures using various features extraction techniques.

3.1 Long Short Term Memory (LSTM)

Long Short-Term Memory (LSTM) networks are a type of recurrent neural network (RNN) designed to learn patterns in sequential data by retaining relevant information over time. Unlike traditional RNNs, LSTMs use gated mechanisms—namely the forget gate, input gate, and output gate—to control the flow

of information, allowing them to capture long-term dependencies effectively. This makes LSTM particularly suitable for analyzing time-based signals such as speech, movement, and neuroimaging data, which are often used in Parkinson's disease (PD) classification. Several recent studies have demonstrated the utility of LSTM-based models in PD detection. For instance, a hybrid CNN-LSTM architecture was applied to voice and movement data, achieving improved classification accuracy [13]. Another study employed recurrent convolutional transformers on sensor-based movement data to enhance early PD detection [20]. Additionally, a hybrid LSTM-GRU deep learning model was evaluated on speech and wearable sensor data, showing high performance across multiple metrics [2]. These works highlight the effectiveness of LSTM networks in capturing temporal dynamics associated with PD symptoms and support their integration into multimodal diagnostic pipelines.

3.1.1 Long Short-Term Memory (LSTM) Architecture

The core components of an LSTM cell include the forget gate, input gate, output gate, cell state, and hidden state as shown in figure 5.

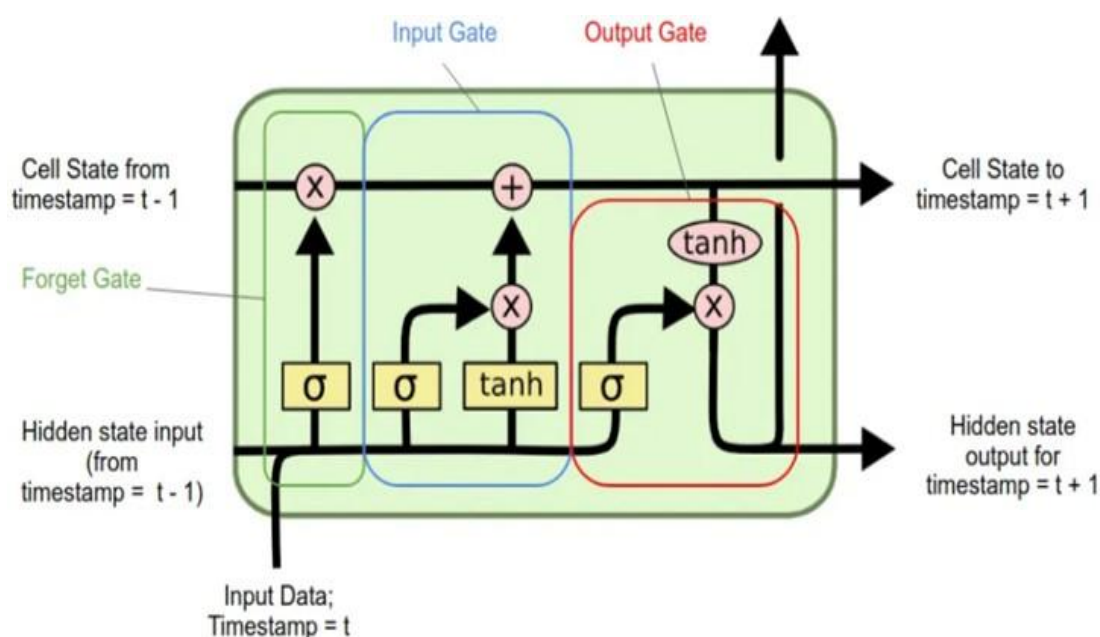


Figure 5: The single LSTM cell depicting different gates and components [12]

3.1.2 Output Layer and Classification

The following equations describe the operations within an LSTM unit at time step t :

Where:

$$f_t = \sigma(W_f x_t + U_f h_{t-1} + b_f) \quad (\text{Forget gate})$$

$$i_t = \sigma(W_i x_t + U_i h_{t-1} + b_i) \quad (\text{Input gate})$$

$$\tilde{c}_t = \tanh(W_c x_t + U_c h_{t-1} + b_c) \quad (\text{Candidate cell state})$$

$$c_t = f_t \cdot c_{t-1} + i_t \cdot \tilde{c}_t \quad (\text{Updated cell state})$$

$$o_t = \sigma(W_o x_t + U_o h_{t-1} + b_o) \quad (\text{Output gate})$$

$$h_t = o_t \cdot \tanh(c_t) \quad (\text{Updated hidden state})$$

- x_t is the input vector at time t
- h_{t-1} is the hidden state from the previous time step
- c_{t-1} is the previous cell state
- W_* and U_* are weight matrices for input and hidden state respectively
- b_* are bias vectors
- σ denotes the sigmoid activation function
- $\tanh$ denotes the hyperbolic tangent activation function
- f_t, i_t, o_t are the forget, input, and output gate activations
- $\tilde{c}_t$ is the candidate cell state
- c_t is the updated cell state
- h_t is the updated hidden state

The final LSTM output is passed through a softmax classifier:

$$y^{\wedge} = \text{softmax}(W_b h_t + b_b) \quad (9)$$

where: - W_b and b_b are learnable parameters, - $y^{\wedge}$ represents predicted class probabilities.

3.1.3 Loss Function

The network is trained using binary cross-entropy loss:

$$L = -\frac{1}{N} \sum_{i=1}^N [y_i \log(y_i^{\wedge}) + (1 - y_i) \log(1 - y_i^{\wedge})] \quad (10)$$

3.1.4 Optimization

The model parameters θ are optimized using Adam optimizer:

$$\vartheta_{t+1} = \vartheta_t - \eta \cdot \sqrt{\frac{\hat{m}_t}{v_t^{\wedge} + \epsilon}} \quad (11)$$

where $\hat{m}_t$ and $v_t^{\wedge}$ are bias-corrected first and second moments

These mechanisms allow LSTM networks to selectively retain or discard information, making them highly effective for modeling temporal dependencies in data such as speech, movement, and neuroimaging signals [9].

4 Methodology

In this study, the preprocessed fMRI data is not directly fed into the LSTM network. Instead, three-dimensional functional signals or time-series representations are first extracted from the scans using feature extraction methods. The work then compares the performance of features derived through Canonical Independent Component Analysis (CanICA) and Dictionary Learning (DL), evaluating the classification metrics obtained when these features are subsequently introduced into the LSTM network.

4.1 Problem Formulation

Let $D = \{(X_i, y_i)\}_{i=1}^N$ denote the dataset, where $X_i \in \mathbb{R}^{T \times V}$ represents the preprocessed rs-fMRI time-

series for subject i , with T time points and V voxels, and $y_i \in \{0, 1\}$ denotes the class label (0: control, 1: Parkinson's disease).

The objective is to learn a mapping function:

$$f_{\theta} : \mathbb{R}^{T \times V} \rightarrow \{0, 1\} \quad (12)$$

parameterized by θ , that minimizes classification error.

Instead of directly learning from X_i , a feature extraction function $\phi(\cdot)$ is applied:

$$Z_i = \phi(X_i),$$

$$Z_i \in \mathbb{R}^{T \times K} \quad (13)$$

where $K \ll V$ represents reduced feature dimensionality. The extracted features Z_i are then used as input to an LSTM-based classifier.

4.2 Canonical Independent Component Analysis (CanICA)

Canonical Independent Component Analysis (CanICA) is a data-driven technique used to extract functional components from fMRI scans by decomposing the data into statistically independent sources. Unlike traditional ICA, CanICA incorporates canonical correlation analysis to improve reproducibility and robustness across subjects, making it particularly suitable for group-level studies. In the context of Parkinson's disease (PD) classification, CanICA enables the identification of spatially independent brain networks whose temporal signals can be introduced into neural models such as LSTM for learning disease-related dynamics. This approach reduces the dimensionality of high-resolution fMRI data while preserving meaningful functional connectivity patterns. Studies have demonstrated that CanICA provides stable and interpretable components across populations, facilitating comparisons between patient and control groups [25, 1].

CanICA decomposes the fMRI signal into statistically independent spatial components:

$$X = AS \quad (14)$$

where: - $X \in \mathbb{R}^{T \times V}$ is the observed data matrix, - $A \in \mathbb{R}^{T \times K}$ is the mixing matrix, - $S \in \mathbb{R}^{K \times V}$

contains independent components.

The objective is to estimate S such that:

$$\max_{k=1}^K \mathbf{I}(s_k)$$

where $\mathbf{I}(s_k)$ measures non-Gaussianity (e.g., negentropy).

In CanICA, this is extended with group-level consistency by maximizing correlation across subjects:

$$\max_{i,j} \sum \text{corr}(S_i, S_j) \quad (16)$$

4.3 Dictionary Learning (DL)

Dictionary Learning (DL) is a sparse coding technique that decomposes fMRI data into a set of basis functions (the dictionary) and corresponding sparse coefficients. Unlike Independent Component Analysis (ICA), which enforces statistical independence, DL emphasizes sparsity, ensuring that only a small number of dictionary elements are active at a given time. This property makes DL particularly effective for extracting localized and interpretable brain networks from high-dimensional fMRI data. In the context of Parkinson's disease (PD) classification, DL enables the reduction of complex 4D fMRI signals into meaningful temporal features that can be introduced into sequential models such as LSTM [1, 25].

Dictionary Learning represents the fMRI data using a sparse linear combination of basis functions:

$$X \approx DZ \quad (17)$$

where: - $D \in \mathbb{R}^{T \times K}$ is the dictionary, - $Z \in \mathbb{R}^{K \times V}$ are sparse

coefficients. The optimization problem is:

$$\min_{D,Z} \|X - DZ\|_F^2 + \lambda \|Z\|_1 \quad (18)$$

where: - $\|\cdot\|_F$ is Frobenius norm, - $\|Z\|_1$ enforces sparsity, - λ controls sparsity penalty.

To define regions of interest (ROIs) from the extracted fMRI features, two complementary strategies are adopted. The first approach, termed *Local Regions*, selects each component based on its maximum peak value, which is used to establish a seed marker. These seed markers are subsequently processed using the random walker

segmentation algorithm to achieve accurate region separation. The second approach, referred to as *Connected Components*, automatically identifies and extracts regions by labeling each component according to the presence of distinct features within its spatial domain. Together, these methods provide robust and interpretable ROI delineation, thereby facilitating effective feature extraction for subsequent classification tasks. In this work, the 15th component is considered for defining ROIs in the Local Regions approach, while the 50th component is utilized for the Connected Components approach, for both CanICA and DL [6].

4.4 Feature Selection

To eliminate redundant features, correlation between feature vectors is computed:

$$\rho_{ij} = \frac{\text{Cov}(z_i, z_j)}{\sigma_{z_i} \sigma_{z_j}} \quad (19)$$

Highly correlated features are removed based on a threshold τ :

$$\rho_{ij} > \tau \Rightarrow \text{remove redundant feature} \quad (20)$$

To remove the redundant features correlation is calculated among the features. The redundant features are removed and less redundant features are introduced into LSTM network. The flow chart of the methodology is shown in figure 6.

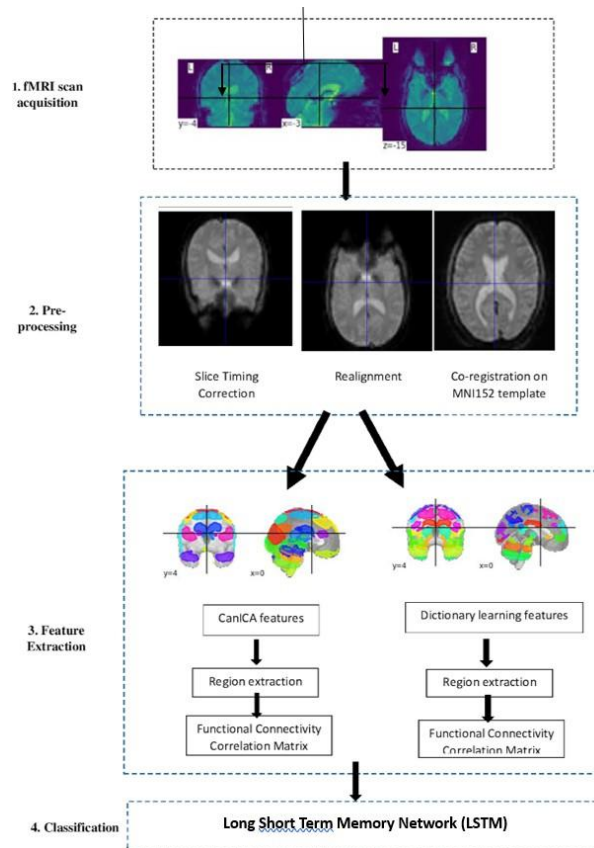


Figure 6: The flow chart depicting the methodology of the study

4.5 Overall Pipeline

The complete pipeline can be expressed as:

$$\hat{y} = f_{\text{LSTM}}(\phi(X)) \quad (21)$$

where: - $\phi(X)$ represents feature

extraction (CanICA or DL), - f_{LSTM} denotes the classification model.

5 Results and Discussions

The LSTM is trained for 100 epochs to balance convergence stability with the risk of

overfitting, allowing the network sufficient passes over the data to refine temporal feature representations while monitoring validation trends for early stopping if needed. The output layer uses softmax to yield normalized class probabilities, supporting probabilistic interpretation and calibrated decision thresholds, while hidden layers employ tanh to stabilize recurrent dynamics by bounding activations and preserving gradient flow across time steps. Binary cross-entropy was selected to optimize separability for a two-class decision boundary; when paired with softmax, this corresponds to either a single-logit formulation with sigmoid or a two-logit formulation with softmax, both minimizing the negative log-likelihood of correct labels. The Adam optimizer with a learning rate of 0.01 accelerates convergence via adaptive moment estimation, enabling efficient navigation of the non-convex loss landscape; the

selected rate was empirically tuned to avoid plateaus while preventing divergence in recurrent training. The comparative evaluation of LSTM classifiers as shown in Table 2 using features extracted through Canonical Independent Component Analysis (CanICA) and Dictionary Learning (DL) reveals distinct performance trends across varying hidden unit configurations and region definition strategies. When employing CanICA with local regions (15 components), the classifier achieved its highest accuracy of 85.17% with a relatively low loss of 0.54 at smaller unit sizes (18, 15, 12, 10, 5, 2). This indicates that compact LSTM architectures are well-suited to CanICA-derived features, which capture discriminative temporal dynamics while minimizing redundancy. However, as the number of units increased (25–50 range), accuracy declined sharply (down

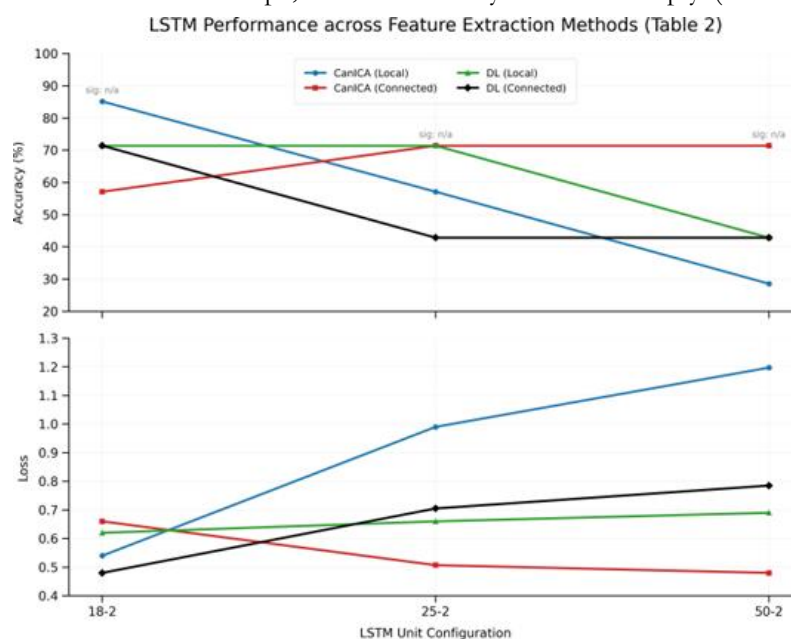


Figure 7: Accuracy and loss comparison across LSTM unit configurations using CanICA and Dictionary Learning feature extraction (values from Table 2). Statistical significance markers require repeated runs or per-fold results; hence not computed from Table 2 alone.

to 28.57% with loss 1.197), suggesting that larger networks may overfit or destabilize when processing CanICA features.

In contrast, DL demonstrated more consistent performance, particularly with connected components (50 components).

Across multiple unit configurations, accuracy remained stable at approximately 71.43%, with losses ranging between 0.48–0.66, highlighting the robustness of sparsity-driven DL features. DL with local regions achieved moderate accuracy (71.43%) at smaller unit sizes but dropped to 42.86% at higher unit

counts, reflecting sensitivity to overparameterization similar to CanICA. Notably, the lowest loss (0.48) was observed for DL connected components at larger unit sizes, reinforcing the advantage of DL in producing compact, interpretable features that generalize well across architectures. Taken together, these findings suggest a trade-off between discriminability and stability. CanICA excels in compact LSTM configurations, achieving peak accuracy but showing vulnerability to increased network complexity. DL, particularly with connected

components, provides more stable and generalizable performance across architectures, albeit with slightly lower peak accuracy. This complementary behavior underscores the importance of aligning LSTM unit selection with the chosen feature extraction method. For clinical applications such as Parkinson’s disease classification, CanICA may be preferable when maximizing accuracy in smaller models, while DL offers robustness and interpretability for broader deployment scenarios.

Table 2: Comparison of LSTM classifier performance using CanICA and Dictionary Learning features across different LSTM unit configurations.

LSTM Units	CanICA Local Regions (15 comps)		CanICA Connected Components (50 comps)		DL Local Regions (15 comps)		DL Connected Components (50 comps)	
	Accuracy (%)	Loss	Accuracy (%)	Loss	Accuracy (%)	Loss	Accuracy (%)	Loss
18, 15, 12, 10, 5, 2	85.17	0.54	57.14 .66 ⁰		71.43	0.62	71.43	0.48
25, 20, 15, 10, 5, 2	57.14	0.99	71.43 .507 ⁰		71.43	0.66	42.86	0.705
50, 40, 30, 20, 10, 2	28.57	1.197	71.43 .48 ⁰		42.86	0.69	42.86	0.785

Comparative Analysis with Existing Studies To assess the proposed LSTM architecture’s performance, a comparison is conducted between its performance and that of existing models in the field of Parkinson’s disease classification. El-Sayed et al. [19] proposed a hybrid CNN-LSTM model using clinical and histogram-oriented features, achieving an accuracy of 78.3%. Although their model incorporated convolutional layers for spatial encoding, it lacked neuroimaging integration and showed limited generalization across datasets. Mir et al. [16] developed an LSTM-based classifier using vertical ground reaction force (VGRF) gait signals from the PhysioNet database, reporting a peak

accuracy of 78% for freezing of gait detection. While effective for biomechanical signals, their approach did not leverage fMRI-derived spatial features. Singh et al. [23] employed Independent Component Analysis (ICA) for feature extraction from fMRI data and used a shallow neural network for classification, achieving 72.5% accuracy. In contrast, our model—particularly the configuration using CanICA with compact LSTM units (18, 15, 12, 10, 5, 2)—achieved an accuracy of 85.17% with a loss of 0.54, outperforming these benchmarks while maintaining architectural simplicity and interpretability as shown in Table 3. This highlights the advantage of combining spatially-

informed neuroimaging features with robust Parkinson’s disease classification.
temporally-aware recurrent architectures for

Table 3: Comparison of Parkinson’s disease classification performance between our proposed LSTM model and existing studies.

Study	Feature Type	Classifier	Accuracy (%)
Proposed Model CanICA,LSTM	CanICA (15 comps)	LSTM (units: 18–2)	85.17
El-Sayed et al. (2023)[19]	Clinical / histogram features	CNN-LSTM hybrid	78.3
Mir et al. (2024)[16]	Gait signals (VGRF)	LSTM	78.0
Singh et al. (2021)[23]	ICA (fMRI)	Shallow NN	72.5

6 Future Work

This study represents a preliminary investigation into the use of CanICA and Dictionary Learning features for Parkinson’s disease classification. While the current results demonstrate the discriminative power and stability of these individual feature extraction methods, future work will focus on integrating the complementary strengths of both approaches. By combining CanICA’s ability to capture reproducible group-level spatial components with Dictionary Learning’s capacity for sparse, localized representations, we aim to generate richer and more informative feature sets. These combined features will then be introduced into advanced neural network architectures such as Multi-Scale Deep Convolutional Neural Networks (M2DCNN) and Convolutional 3D LSTM models. The objective of this extension is to enhance classification accuracy, improve temporal modeling of neuroimaging signals, and achieve greater robustness across diverse patient populations. Ultimately, this line of research seeks to establish a unified framework that leverages both spatial and temporal dynamics for more reliable early detection of Parkinson’s disease.

7 Acknowledgment

The database that is used in the conduction of the described research is obtained from the Parkinson’s Progression Markers Initiative (PPMI) database (www.ppmi-info.org/access-data-specimens/download-data). PPMI – a public-private partnership – is funded by the Michael J. Fox Foundation for Parkinson’s Research and funding partners

Conflicts of Interest

There are no conflicts of interest regarding the publication of this work. The data supporting the findings of this study are freely available online, and the corresponding link has been provided in the Acknowledgement section.

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