**Aims and objectives**

This research aims to develop a Parkinson’s disease progression model based on dendritic cell metrics to improve diagnosis and patient’s quality of life.

The specific objectives of the research are to:

1. develop a comprehensive dataset combining clinical features, dendritic cell data, and neuroimaging results from patients with Parkinson’s disease and vascular parkinsonism.
2. design and implement machine learning algorithms to analyze the relationship between dendritic cell functionality and the progression of Parkinson’s disease, focusing on quantifying vascular lesions such as white matter hyperintensities.
3. validate the machine learning models by comparing their predictions on disease progression and motor symptom severity

**Methodology**

1. Extensive consultation of relevant documents, and the literature related to methods/analysis of dendritic cell for classification of Parkinson’s disease using the DC metrics to classify the data into Parkinson’s and non-parkinson’s disease.
2. Acquisition of dendritic cell data with all the metrics will be taken from the github-mughanibu/dendritic spine-analysis dataset, the database will be of high quality from patients with genetically defined Parkinson’s gene traits and healthy controls.
3. Munging of the acquired dataset is to be prepared in a form useful for the machine and deep learning process. The data munging process will include normalization, discretization, labelling and selection of relevant features from the acquired parkinson’s and non-parkinson’s disease.

**Methodology**

1. Extensive consultation of relevant documents, and the literature related to methods/analysis of dendritic cell for classification of Parkinson’s disease using the DC metrics to classify the data into Parkinson’s and non-parkinson’s disease.
2. Acquisition of dendritic cell data with all the metrics will be taken from the github-mughanibu/dendritic spine-analysis dataset, the database will be of high quality from patients with genetically defined Parkinson’s gene traits and healthy controls.
3. Munging of the acquired dataset is to be prepared in a form useful for the machine and deep learning process. The data munging process will include normalization, discretization, labelling and selection of relevant features from the acquired parkinson’s and non-parkinson’s disease.
4. Ensemble deep learning algorithms will be developed in the Python programming language, deployed on a Spark cluster and engaged for the training of the labelled data to generate the classification model. While the Boosting ML methods will be employed to create predictive models for identification classification of dendritic dataset.
5. Also, a reinforcement learning will be applied to the dendritic cell data to learn to recognize patterns in DC data that is associated with Parkinson’s disease.
6. A new immune system dataset without known features parkinson’s and non-parkinson’s (test data) will be acquired from the NCBI repository and will be given as input into the classification model to predict the parkinson’s and non-parkinson’s disease
7. Standard performance metrics for evaluating the efficiency of deep learning algorithms and ML methods would be engaged to determine the effectiveness of the proposed ensemble deep learning algorithm, and the boosting ML methods for identification classification of dendritic cell dataset for parkinson’s disease.
8. A new immune system dataset without known features parkinson’s and non-parkinson’s (test data) will be acquired from the NCBI repository and will be given as input into the classification model to predict the parkinson’s and non-parkinson’s disease

Standard performance metrics for evaluating the efficiency of deep learning algorithms and ML methods would be engaged to determine the effectiveness of the proposed ensemble deep learning algorithm, and the boosting ML methods for identification classification of dendritic cell dataset for parkinson’s disease.