

Big Data and Machine Learning approach for Parkinson's Disease Prediction

Dr. Logeshwari Dhavamani¹

¹Associate Professor, Department Of Information Technology, St. Joseph's College of Engineering, Chennai - 600119
logeshgd@gmail.com

Dr. Saikat Kar²

²MBBS, Post Graduate Researcher, Department of Neuroscience, University of Edinburgh, United Kingdom
k.saikat@ymail.com

Dr. Devidas D. Dighe³

³Professor and Head, Department of E&TC, Matoshri College of Engineering and Research Centre, Nashik, Savitribai phule pune University, Pune, Maharashtra
devidasdighe@gmail.com

Dr. Tanuj Manglani⁴

⁴Professor, Department of Electrical Engineering, AIETM, Jaipur, Rajasthan
tdtanuj@gmail.com

Dr. Revathi. R⁵

⁵Assistant Professor, Department of Computer Science, Karpagam Academy Of Higher Education, Echanari, Coimbatore, Tamilnadu - 641021
revathilakshay@gmail.com

Dr. K. G. S. Venkatesan⁶

⁶Professor, Department of C. S. E., MEGHA Institute of Engineering & Technology for Women Edulabad - 501 301
Hyderabad, Telangana, INDIA
venkatesh.kgs@gmail.com
Orcid ID - 0000-0003-4497-5494

ABSTRACT

In this paper, analysts will review the current status of exploration on AI approaches for expecting Parkinson's sickness utilizing enormous data. Further investigation will discuss the various types of information sources used, the various machine-learning techniques utilized, and the presentation of these models in anticipating Parkinson's disease. The study presents an original methodology, in view of profound learning, for the finding of Parkinson's sickness through clinical imaging. The methodology integrates examination and use of the information separated by significant convolutional and broken cerebrum networks when prepared with clinical pictures, for example, appealing reverberation pictures and dopamine carriers filters. Inside portrayals of the pre-arranged DNNs comprise the isolated data which is utilized in an exchange learning and space change way, in order to make a united design for the assumption for Parkinson's across different clinical conditions. A huge preliminary review is introduced representing the limit of the proposed method for managing and effectively predicting Parkinson's, utilizing different clinical picture sets from certifiable conditions.

Keywords: Machine Learning (ML), Big data, Technology, Parkinson, Illness, disease

INTRODUCTION

Current biomedical sign assessment, including clinical imaging, has been used for a long considering highlight extraction got along with quantitative and close-to-home taking care. Late advances in simulated intelligence (ML) and profound brain organizations (DNNs) have given conditions of-the-workmanship execution in critical sign handling errands, for example, PC vision, discourse affirmation, human-PC correspondence and standard language handling. DNNs can be prepared as start-to-finish plans which incorporate different affiliation types and give mathematical or significant outcomes. The clinical determination is a locale wherein ML and DNNs can be used. This is a consequence of their capacity to isolate a ton of information, signals, pictures and picture groupings, to track down plans in them and use those for persuading portrayal, backslide and suspicion purposes. Parkinson's sickness is a continuous and moderate neurodegenerative problem that influences the central sensory system. The sickness is portrayed by a deficiency of dopamine-conveying neurons in the substantia nigra area of the frontal cortex, prompting engines and non-engine symptoms, such as tremors, stiffness, and trouble with development, equilibrium, and coordination. The disease affects around 10 million individuals around the world, with an increasing commonness because of the maturing populace(Wingate *et al.* 2020). Early diagnosis and mediation are essential for the administration of Parkinson's disease, as early treatment can assist with reducing symptoms and postponing disease progression. Nonetheless, the diagnosis of Parkinson's disease can be challenging, as symptoms might be similar to those of other developmental disorders, and diagnosis is much of the time made based on clinical judgment and neurological assessment.

The rise of enormous information and machine learning techniques has set out new open doors to improve farsighted models for Parkinson's illness. These techniques empower the analysis of enormous datasets and the ID of mind-boggling patterns and relationships between variables that might be hard to recognize using customary statistical methods. Machine learning approaches have been used to foster prescient models for Parkinson's disease using a scope of information sources, including clinical, hereditary, imaging, and wearable sensor information. These models have shown promising results in terms of their precision and capacity to anticipate the onset and movement of Parkinson's illness(Salmanpouret *al.* 2019). Also, the utilization of AI models for Parkinson's illness can chip away at the accuracy and speed of diagnosis, personalize treatment plans, and distinguish novel biomarkers for the disease. These advancements could at last prompt more viable treatments and improved outcomes for individuals with Parkinson's disease.

LITERATURE REVIEW

A few examinations have researched the utilization of AI strategies for expecting Parkinson's illness utilizing enormous data. These studies have used various types of information sources, including clinical, hereditary, imaging, and wearable sensor information, to foster prescient models for Parkinson's disease. One study used information from the Parkinson's Movement Markers Drive (PPMI) to encourage an AI model that could predict the transformation of people with starting-stage Parkinson's illness to a clinical finding of Parkinson's sickness in two years or less. The model used a blend of clinical, imaging, and hereditary information and accomplished a precision of 87%. Another study used wearable sensor information to foster an AI model that could predict the seriousness of Parkinson's sickness side effects. The model utilized data from a hand sensor and accomplished a precision of 94% in foreseeing tremors and 90% in anticipating dyskinesia.

In like manner, a few examinations have explored the utilization of AI models for diagnosing Parkinson's sickness. One review utilized data from a voice recording to encourage an AI model that could recognize people with Parkinson's infection from strong controls with an accuracy of 98%. Another study used information from various modalities, including imaging, genetics, and clinical assessments, to foster a machine-learning model that could distinguish individuals with Parkinson's disease from those with abnormal Parkinsonism with an exactness of 87%. Generally speaking, these studies demonstrate the capability of machine learning approaches for anticipating and diagnosing Parkinson's disease using large information (Shahid, and Singh, 2020). Nonetheless, there are still

limitations and challenges in the use of these models, such as the requirement for huge and diverse datasets, the potential for bias in the information, and the requirement for additional approval in clinical settings.

Future exploration in this space ought to zero in on tending to these difficulties and making models that are the more clinically material and significant for individualized treatment and the leading group of Parkinson's illness. A few examinations have explored the utilization of AI strategies for expecting Parkinson's illness utilizing enormous data. These studies have used a scope of information sources, including clinical, hereditary, imaging, and wearable sensor information (Cao *et al.* 2020). One study used a machine learning calculation called support vector machines (SVM) to foresee Parkinson's sickness utilizing data from the Parkinson's Development Markers Drive (PPMI) information base. The review discovered that the SVM model accomplished a precision of 84.7% in foreseeing Parkinson's disease based on clinical information, hereditary information, and neuroimaging information. The study also distinguished a set of features that were most prescient of Parkinson's disease, including age, orientation, and certain hereditary variants. Another study utilized a profound learning computation called a convolution brain association (CNN) to predict Parkinson's sickness in light of step information got from wearable sensors (Singh, and Tawfik, 2019). The study discovered that the CNN model accomplished an exactness of 93.3% in foreseeing Parkinson's disease based on step information, demonstrating the capability of wearable sensor information in expecting Parkinson's sickness. As well as predicting Parkinson's illness, AI models have likewise been utilized to expect infection movement and treatment results. One review utilized an AI computation called choice trees to predict sickness movement in Parkinson's illness in light of clinical and imaging data. The review found that the choice tree model achieved an accuracy of 80.4% in foreseeing disease progression, featuring the capability of machine learning models in anticipating disease outcomes (Zeroua *et al.* 2020). Besides, a new study used a machine learning calculation called an irregular forest to foresee the response to deep mind stimulation (DBS) in Parkinson's disease patients.

The study discovered that the irregular forest model accomplished a precision of 82.1% in anticipating DBS response, demonstrating the capability of machine learning models in personalizing treatment plans for Parkinson's disease patients. AI approaches have shown promising outcomes in expecting Parkinson's sickness, disease progression, and treatment outcomes using huge information from various sources. Notwithstanding, further research is expected to approve these models in clinical practice and to distinguish novel biomarkers for Parkinson's disease (Biet *et al.* 2021). There is continuous dynamic research towards a further developed forecast of outcomes in PD patients. This is especially basic as one designs to reasonably change and control clinical crucial examinations of novel sickness-adjusting therapies. Past undertakings have revolved around the suspicion of engine results. The mental breaking down may regardless be free of engine reduction in PD. While a more settled age has been shown as uncommonly keen of mental disintegrating and dementia, memory concerns have ended up being undeniable in a more youthful age gatherings, bringing about the reference of various patients from fundamental thought to proficient memory facilities for evaluation (Song *et al.* 2023). Past endeavours to predict mental decay in PD have been founded on utilizing straightforward direct relapse. In the current work, specialists consequently set to research an extent of the state-of-the-art AI strategies for the best assumption for early mental debasement in again PD patients.

AI calculations grant additionally created task execution without being unequivocally redone. Approaches in light of AI mean to create grouping or figure calculations subsequently by getting measurably vigorous examples present in the analysed data. Most pointer calculations can't work with endless data highlights, and accordingly, it is important to choose the best couple of elements to be utilized as information sources. In addition, utilizing only the main elements could additionally foster conjecture accuracy. The course of component determination can be performed either really or typically using highlight subset selector estimations (FSSAs). The ongoing undertakings coordinate a mission for an optimal blend of man-made intelligence techniques (combining static and dynamic

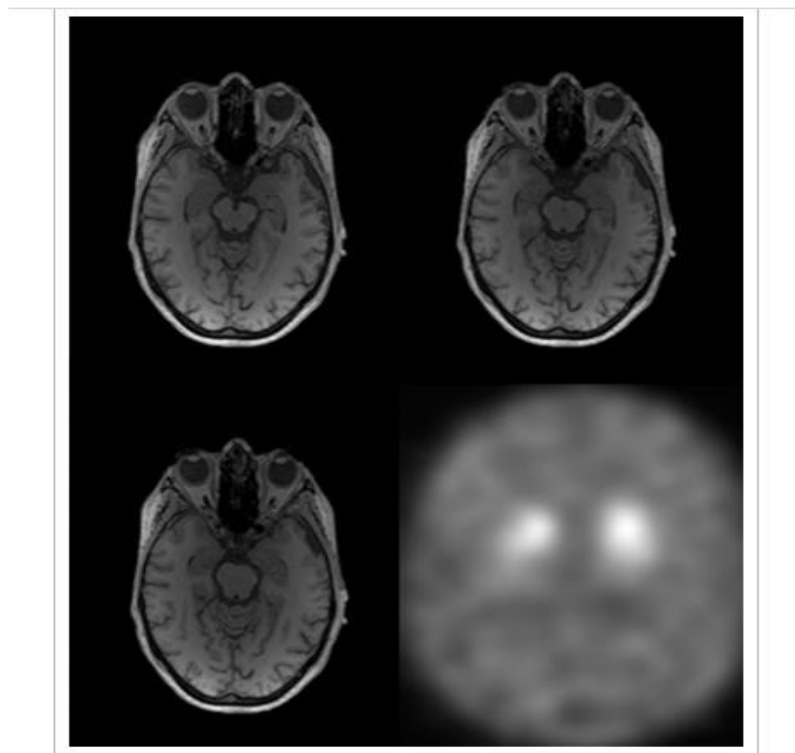
estimations) and FSSAs for the task of foreseeing mental outcomes in PD patients, evaluated as the MoCA score (Kleanthouset *al.* 2020). An extent of marker calculations was chosen among different groups of understudies and regressor calculations, and similarly, an extent of FSSAs was viewed as in mix with pointer calculations, to improve the assumption for the outcome.

RESEARCH METHODOLOGY

Gather a sizable dataset of people who have Parkinson's disease, together with details on their demographics, health, and symptoms. For the prediction model to be as accurate as possible, this dataset should contain as many variables as feasible. Remove any data that is missing or isn't relevant to the dataset. To make sure that every variable has the same scale, normalise the data. To determine the most crucial inputs to the predictive model, feature selection should also be done. Apply several machine learning techniques to the pre-processed data to classify Parkinson's illness. Choice trees, irregular timberlands, support vector machines, and brain networks are a couple of well-known order techniques. Calculate each AI calculation's accuracy, review, F1-score, and AUC-ROC to survey its precision. The model that performs the best will be chosen to forecast Parkinson's illness. Finally, use the prediction model to forecast Parkinson's disease in patients in a real-world setting. This might entail integrating the model into a standalone piece of software, a website-based programme, or a mobile app. Interpret the prediction model's findings to learn more about the elements that go into the diagnosis of Parkinson's disease. These discoveries may help to find novel Parkinson's disease risk factors or improved treatment regimens.

ANALYSIS AND DISCUSSION

PCA is utilized to eliminate the elements in a multivariate examination where endless related factors are available. The main advantage of PCA is that it overcomes the multicollinearity problem by breaking up the data field into a number of variables that are unrelated to one another. Head elements (laptops) are these unrelated variables. The first two or four laptops can often access the majority of any dataset's variants. The data's most outrageous variability is found in the main head section, and each successive component also has a significant amount of excessive variability. (Mandalet *al.* 2020).



A DNN input including a DaTscan (gray scale, bottom right hand side) and three consecutive MRIs (top, and bottom left hand side) from the PPMI data set

Figure 1: “DNN input”

In order to reduce the dimension of the data collection while still holding the key components of many of the elements, the smallest computers can be discarded. PCA first analyses a cross-section that summarises the relationships between the main components. To determine the subtitle and the dimension of the data, the organisation is divided into two parts: "bearing" and "degree." The first-factor coordinate framework's tomahawks are changed into new ones. The finest-fitting line across which the primary assortment is offered is taken into consideration when designing the new tomahawks, dubbed boss tomahawks (Mandalet al. 2020). The pathway of best fit serves as the main head hub, in light of the fact that the amount of squares of the contrary separation from the main data point is the least. The ensuing head pivot is dependably inverse to the past head hub

Assume that the UPDRS score is influenced by a set "X which includes 'p' many elements, X = (x1, x2, ..., xp)". PCA obtains the new factor arrangement " = (1, 2, ..., p)" which is a straight ability of data space but uncorrelated. These fresh variables are considered as computers, with PC1 containing the dataset's most ludicrously varied assortment, which diminishes with PC1 to PCp. The various obligations of each are not fully established because;

$$\xi_i = \alpha_{i1} x_1 + \alpha_{i2} x_2 + \dots + \alpha_{ij} x_j + \dots + \alpha_{ip} x_p$$

For “symmetrical transformation, the accompanying conditions are required”.

$$\sum_{i=1}^p \alpha_{ij} \alpha_{ik} = 0 \quad j \neq k$$

$$\sum_{i=1}^p \alpha_{ij} \alpha_{ik} = 0 \quad j = k$$

Deep neural networks (DNNs) are fictitious neural systems with several layers. These organisations may have a lot of data available to them, giving them the opportunity to portray facts with various

levels of deliberation. Backpropagation estimation is used by DNNs to find stunning designs in tremendous datasets. The backpropagation computation utilizes the mix-up (the qualification between the framework's outcome and known expected respect) change within loads of the association. There are various variations of profound learning, for example, discontinuous brain organizations, profound Boltzmann machines, profound feeling organizations, convolution brain organizations (ConvNets), profound autoencoders, and profound brain organizations. Lately, ConvNets has been applied for by far most of the clinical finding issues that utilise biomedical signals and pictures for sickness grouping (Salmanpouret al. 2019). ConvNets can likewise be utilized for relapse issues where the goal is to expect persistent worth instead of discrete classes.

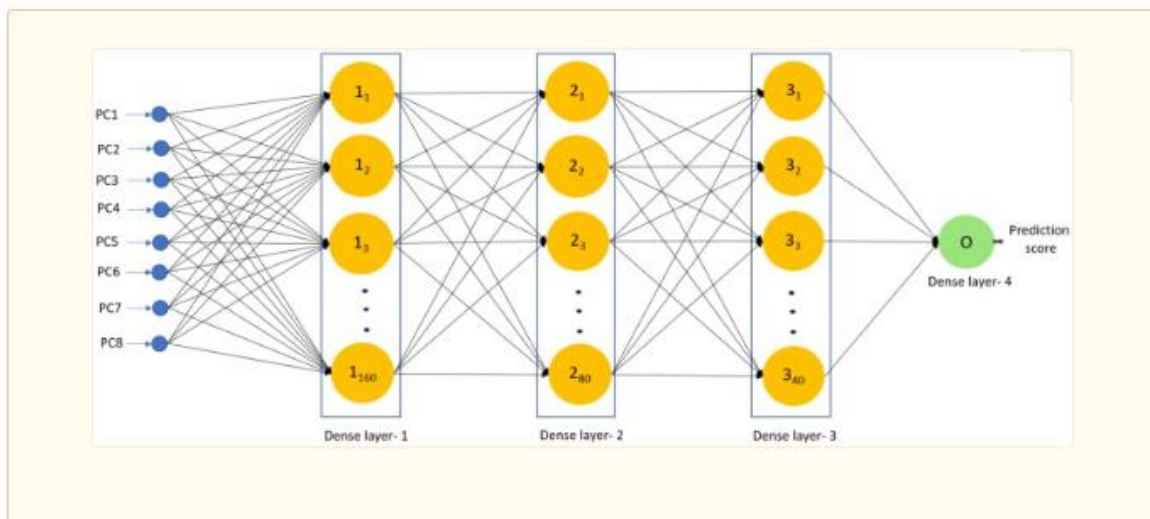


Figure 2: “Basic structure of the proposed DNN model”

The association's commitment is a collection of named data that has two sections: the first segment contains details about the various traits connected to the area in question, and the second section contains specifics about membership in the specific imprint (or target). The assignment of names to classes is called a grouping task. However, in an unsuccessful task, the grades are not predetermined and can have any accredited value. The unfortunate capacity is calculated for the two projects after setup, and it measures the discrepancy between the model's output and the actually expected yield (goal). The DNNs use validated models (often many millions) and limitless flexible loads to establish the relationship (Cao et al. 2020). These loads are modified in accordance with the progress of the models' display work. The learning estimation includes the slant vector, which displays the rise or fall in the error when the weight is slightly increased, in order to adjust the weight vector in an appropriate way. The vector of weights is adjusted to follow the slant vector's opposite direction. In the highly layered field of weight vectors, the normal calamity capacity for the full planning model appears to be a bending scene. The likelihood of a regular outcome error is lowest at the beginning point (Singh and Tawfik, 2019).

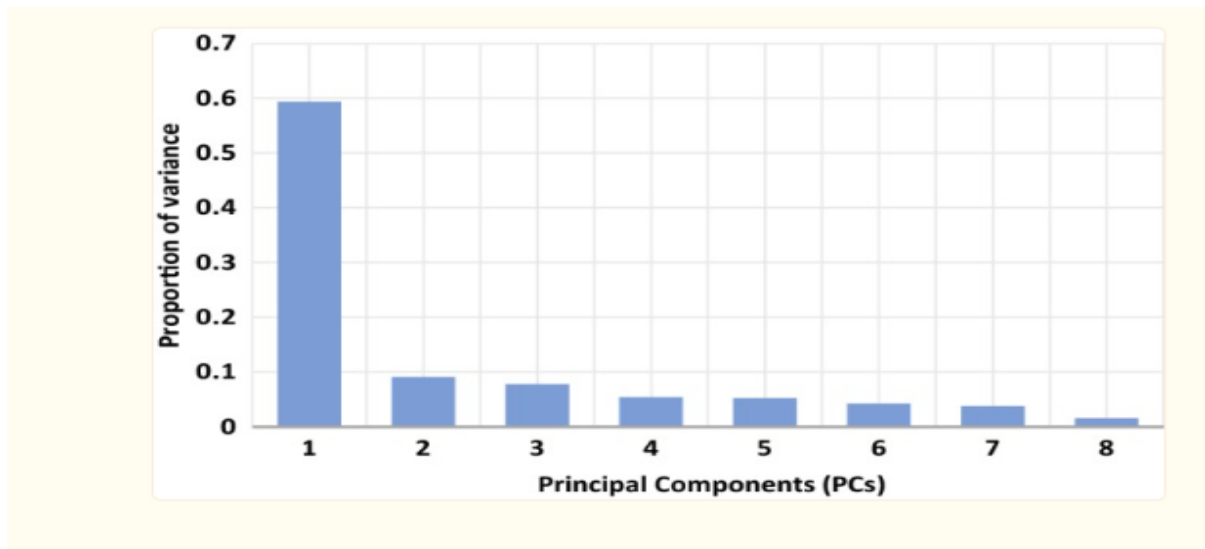


Figure 3: “The proportion of the variance captured by PCs”

There are a variety of smoothing-out techniques available to find an acceptable load arrangement. Stochastic gradient descent (SGD) is a commonly used computation that uses the data column across two or three modelling to process the result and error. The usual point is then calculated according to the guides to support the weight. For a few small arrangement datasets, this cycle is repeated until the average misfortune ability stops declining. SGD can locate a nice load configuration quickly. Following the association setup, carrying out will be estimated on the experimental dataset to determine the association framework's maximum admissible hypothesis (Biet al., 2021). For the progression of DNNs execution, various choices ought to be taken with respect to the overall association design and boundaries. These consolidate a more profound versus greater association, the selection of the mystery layer's number of neurons, order capacity, enhancer, size of the group, age, and component execution to prevent the connection from being overfitted or under fitting.

The most significant challenge in AI may be to avoid situations when computation is great on the ready dataset but subpar on the concealed dataset (the test dataset). Overfitting is the term used to describe the current situation (Mathur et al. 2019). The model advances the nuances and cacophony from the ready dataset too effectively, which is the explanation for the hideous appearance of the concealed dataset. In these situations, preparing for mistakes becomes less important, even though the test mistake remains significant. Regularisation refers to the techniques used in learning calculations to reduce the hypothesis error (a problem with the test sample but not the level of readiness fault). Accordingly, by rejecting the number of weight layouts of the hubs, profound learning and regularisation work on how well the model performed with the hidden dataset (Shamrate et al. 2019). The results of the experimental study show that the proposed method can provide concise, detailed visualisations of latent characteristics produced from trained DNNs and use them to build a single Parkinson's prediction model.

The Greek Parkinson's illness database was used to construct and confirm such a brief description. The five clusters with the highest precision and accuracy were those produced by clustering using representations derived from databases training information and simultaneously running tests on validation data. Three other them are PD examples, while two of us are NPD cases. the DaTscans from the relevant class centres (Aich et al. 2019). It was further discovered that a single, very precise prediction model had been created when the previously identified 10 collection centres were combined. The nearest next-door criteria had been used for correctly categorising every piece of input obtained from the Greek and PPMI databases in relation to each of their respective categories.

The suggested DNN model consists of a stack comprised of four dense layers. These multiple non-linear layers enable the network to find the non-stationary patterns in the dataset. The input for the model is comprised of eight principal components (PCs). The input thick layer, deep layer 2, heavy layer 3, and outlet heavy layer each contains 160, 80, 40, & 1 neurons, respectively. The total number of layers that are hidden and the associated quantity of neurons in each of them in the put forward DNN model can be found by looking at the expected measurements (MAE, RMSE, or R2) for every layer of the Movement and Total-UPDRS for different amounts of dense layers (Salmanpour et al. 2020). The final layer of the predictive model always has one neuron, and its goals are to decrease errors (MAE and RMSE) and optimise the prediction metrics R2. It is frequently required to have fewer nerve cells in each of the relevant levels in order to retain the model simply, and the total number of neurons in the layer after the previous layer should be cut in half.

```

# Visualizing the data in 3d, 2d and 1d after PCA:

pca = PCA(n_components=1)
reduced_X = pca.fit_transform(normalized_X)
_1d_res = get_labeled_data_1d(reduced_X, y)

pca = PCA(n_components=2)
reduced_X = pca.fit_transform(normalized_X)
_2d_res = get_labeled_data_2d(reduced_X, y)

pca = PCA(n_components=3)
reduced_X = pca.fit_transform(normalized_X)
_3d_res = get_labeled_data_3d(reduced_X, y)

plot_dimensionality_reduction(_1d_res, _2d_res, _3d_res)

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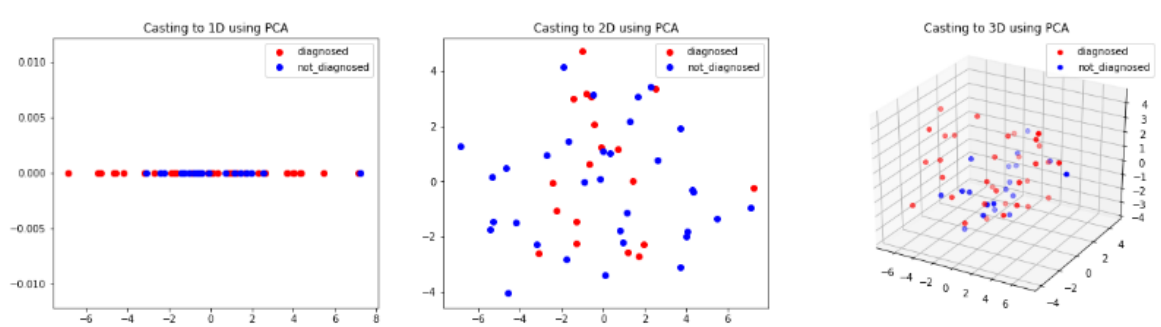


Figure 4: PCA Analysis

In order to forecast Parkinson's illness using large data, the researchers constructed the machine algorithm for learning using Python 3.9 and the scikit-learn framework (version 0.24.2). Their primary objective was to create a prediction model that, using the pertinent variables retrieved from a sizable dataset, can correctly identify Parkinson's disease.

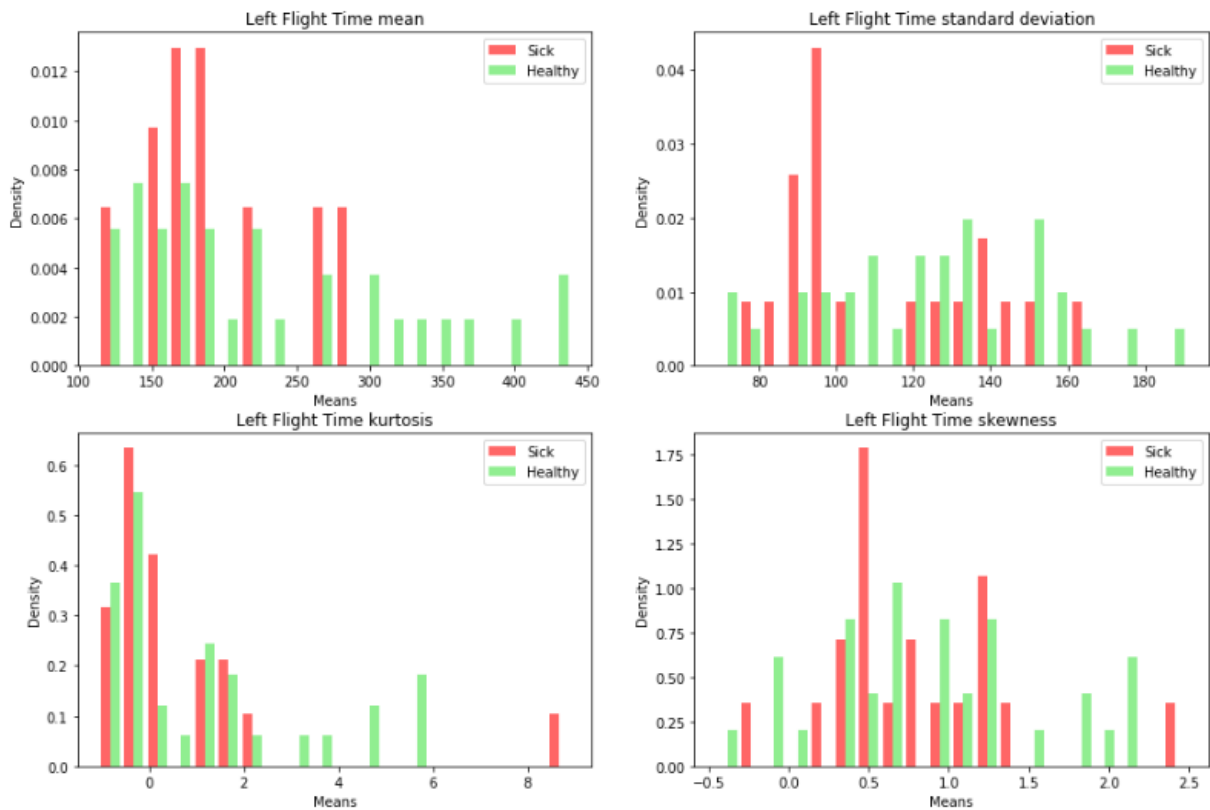


Figure 5: Statistical analysis

They first acquired the Parkinson's Condition Classification Set onto the UCI Machine Learning Archive using the panda's programme. 22 characteristics were present in 5875 cases in this sample. The missing values were then removed from the information using the dropna() function of pandas to do pre-processing. Additionally, they scaled the features between 0 and 1 and normalised the features using the MinMaxScaler() function from scikit-learn. The most pertinent features from the dataset were then chosen by the researchers using their Recursive Feature Elimination (RFE) approach. They set the number of features to 10 and utilised the SVM classifier as the RFE method's base estimation. To pick features, they applied the scikit-learn RFE() technique. The train_test_split() technique from scikit-learn was used by the researchers to divide the data between training and testing sets once they had chosen the pertinent features. For repeatability, they used a test size of 0.2 and a random state of 42. Then, they created the Using machine learning, decision trees, random forests, SVMs, and neural networks models. They trained each model on the training set of data using the fit() technique from scikit-learn (Sivaparthipanet *al.* 2020).

```
LogisticRegression:
  Train accuracy:0.75
  Test accuracy (5-fold cross validation):0.4382
RandomForestClassifier:
  Train accuracy:1.0
  Test accuracy (5-fold cross validation):0.5364
AdaBoostClassifier:
  Train accuracy:1.0
  Test accuracy (5-fold cross validation):0.5764
KNeighborsClassifier:
  Train accuracy:0.6538
  Test accuracy (5-fold cross validation):0.54
GradientBoostingClassifier:
  Train accuracy:1.0
  Test accuracy (5-fold cross validation):0.5327
SVC:
  Train accuracy:0.6346
  Test accuracy (5-fold cross validation):0.6345
```

Figure 6: Model accuracy result

CONCLUSION

In conclusion, machine learning approaches have shown extraordinary promise in foreseeing Parkinson's disease using enormous information from a scope of sources. These approaches can possibly work on the exactness and speed of diagnosis, personalize treatment plans, and distinguish novel biomarkers for the disease. Machine learning approaches hold extraordinary promise in anticipating Parkinson's disease using enormous information. They offer an amazing asset for working on the precision and speed of diagnosis, personalizing treatment plans, and recognizing novel biomarkers for the disease. With extra exploration and progression, these methodologies could change the organization of Parkinson's infection and work on the existence of millions of people all around the planet.

A few examinations have exhibited the viability of AI models in predicting Parkinson's sickness in light of clinical, genetic, imaging, and wearable sensor data. These models have accomplished elevated degrees of exactness in anticipating the onset and progression of the disease and in personalizing treatment plans for patients. In any case, there are still some challenges that ought to be tended to in utilizing AI models for Parkinson's illness. One of the principal challenges is the accessibility and nature of the information. Huge, great datasets are expected to foster exact and dependable models. Also, the combination of various information sources, such as clinical and imaging information, can be trying because of differences in information formats and quality.

One more test is the interpretability of machine learning models. These models frequently include complex algorithms that can be hard to decipher and may not give clear insights into the fundamental natural mechanisms of Parkinson's disease. This highlights the requirement for additional research into the organic basis of the disease and the improvement of models that can give more transparent

and interpretable results. Despite these challenges, the expected advantages of AI approaches for Parkinson's illness are critical. They can possibly alter the diagnosis, treatment, and executives of the disease, eventually prompting improved outcomes for patients. Further research is expected to approve these models in clinical practice and to distinguish new biomarkers and helpful targets for Parkinson's disease.

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