

Report Biomarkers

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Abstract

Abstract: introduce rationale of investing brain dopamine function and potential brain asymmetry in PD.

This study, which focuses on Parkinson's disease, aims to investigate the significance of left-right lateralization based on dopamine values using DAT-SPECT imaging data and their correlation with clinical symptoms in Parkinson's disease patient (PD) and healthy controls (HC). DAT-SPECT (Dopamine Transporter Single Photon Emission Computed Tomography) is an imaging technique primarily used to visualize and measure the density of dopamine transporters in the brain. Indeed, this technique is particularly useful in the diagnosis and evaluation of neurodegenerative diseases, such as Parkinson's disease and other forms of parkinsonism. The dataset, used to perform the analysis, consists of variables relating to demographic data, DAT-SPECT scores and finally the Neuropsychological (NP) tests which are a combination of clinical, neurological, and imaging test since there is no specific test for the diagnosis of Parkinson's disease.

ADD RESULTS

1 Introduction

Parkinson's disease is a chronic neurodegenerative disorder of the central nervous system primarily affecting motor control. It is characterized by the progressive loss of nerve cells in the brain region called the substantia nigra, which is responsible for producing a neurotransmitter called dopamine. Dopamine deficiency leads to motor symptoms such as tremors, muscle rigidity, bradykinesia (slowness of movement), and postural instability. In addition to motor symptoms, Parkinson's disease can cause a wide range of non-motor symptoms including sleep problems, depression, anxiety, fatigue, and cognitive difficulties. While the exact cause of Parkinson's disease is not fully understood, it is believed to result from a combination of genetic and environmental factors [1]. Currently, there is no cure for Parkinson's disease, but there are treatments available to manage symp-

toms and improve the patients' quality of life. However, studies conducted in recent years have shown that the lateralization of brain dopamine in Parkinson's disease (PD) is a significant and distinctive aspect of the pathology. In particular, during its development, the degeneration of dopaminergic neurons in the substantia nigra is not uniform. Generally, one side of the brain is more affected than the other, leading to marked asymmetry. This marked asymmetry is visible not only in motor symptoms, such as more pronounced tremors on one side of the body and greater use of one hand over the other, but it can also be evident in non-motor disturbances, including cognitive issues for example in the sleep behavior and or sense of smell [4].

In previous studies, the connection between dopamine lateralization and symptoms has already been examined. For example, in [3], it resulted that the motor symptoms on the less affected side were more correlated to striatal DAT

binding.

Therefore, the aim of this study is to further investigate this idea, analyzing a dataset containing information about patients' motor and cognitive symptoms and also their lateralization data obtained from DAT-SPECT scans. The dopamine degeneration is explored in three different Regions of Interests (ROIs) in the brain, divided in right and left: Caudate, Putamen and Putamen Anterior. This analysis aims to investigate the relationship (if present) between the lateralization of dopamine function in these brain areas and the symptoms showed by Parkinson's patients, and relationship (if present) between the lateralization of dopamine function in these brain areas and possible covariates showed by healthy controls.

Agreeing with what found in [3], the group expected to find a strong relation between the dopamine lateralization and the motor symptoms. Also the lateralization in different ROIs was expected to be related: a high lateralization in the Caudate was expected if both Putamen and Putamen Anterior were highly lateralized.

2 Material and Methods

2.1 Dataset description

The dataset used in this study was composed of 1556 subjects, of which 256 healthy controls and 1300 PD patients with different levels of symptoms' severity. Not all the variables given were interesting for the study. For example, all the data regarding the MRI acquisitions were discarded, because the analysis focused on the data from the DAT-SPECT scans, which were Striatal Binding Ratios (SBR) of the three ROIs (right and left sides), whether the scan was completed and its quality based on visual interpretation, as well as information regarding the date of the scan and the injection.

The dataset included a part of demographics data, like age, ethnicity, gender, family members affected by PD, height, weight and dominant hand. A total of 967 and 589 patients were males and females, respectively. The average age in the baseline was 62.69 ± 10.11 years

(range [29.3–86.5]).

There was then the data regarding the neuropsychological assessments of the patients using the Movement Disorder Society (MDS)-sponsored revision of the Unified Parkinson's Disease Rating Scale (MDS-UPDRS). The test is divided in 4 parts, concerning different classes of motor and cognitive symptoms, as specified in the PPMI Program Protocols (THE PARKINSON'S PROGRESSION...). Each answer could range from 0 (normal) to 4 (severe), and for each part there was a summing-up variable, that contained the sum of all the scores of that section. These variables were called NP1PTOT, NP1RTOT, NP2TOT, NP3TOT, NP4TOT. Some motor symptoms, especially in the third part, were divided in right and left, for example, the severity of tremor of the right or left upper limb. This was useful to investigate the different relation with the dopamine function lateralization.

Più aggiungere forse grafici con distribuzioni variabili iniziali, tipo grafici lateralizzazione

2.2 Cleaning e preprocessing

The first step was dividing the dataset in patients (PD, SWEDD, Prodromal) and HC.

In the preprocessing of the data, the patterns of missing values were analyzed, to determine the best course of action, through the VIM package in R.

In the HC, as shown in figure 1, GENETICS and FAMILIARITY are mostly empty fields, due to the nature of these variables: for healthy subjects, the chance of having relatives with a PD diagnosis and of having genetics history related to PD are low. On the opposite, for PD patients (figure 2), GENETICS is empty at the TOT %, while FAMILIRITY has the TOT % of NaNs. The reason for this missingness, is probably that patients didn't know if their relatives had history of Parkinson's, or they didn't take the genetics test.

In the complete dataset, NP4TOT is missing at the 73.9%; nearly all the HC didn't take the fourth part of the test, and also the partici-

pation of the PD was really low. This suggests that the fourth part of the test was taken by a few subjects. For this reason, the NP4 variables were not taken into account in the statistical analysis.

For all the test-related variables (NP1TOT, NP1RTOT, NP2TOT, NP3TOT), both in HC and PD, if a subject is missing a value for one test, also the other tests' results are missing. The pattern of missing data is considered to be MAR (Missingness At Random). For the statistical analysis, all the subjects that were missing at least one test result weren't considered.

For ETHNICITY, SEX, and HAND (dominant hand of the subject), there aren't miss-

ing values in the whole dataset. In the ENROLLAGE variable, the missing values were calculated using the DAT-SCAN date and the birth date of the subject.

Regarding HEIGHT and WEIGHT, the pattern of missing data is MAR, with a total of TOT % of NaNs.

The variable PRIM_DIAG described the primary diagnosis; the group found some subjects with the value of 97, that wasn't explained by the data dictionary, therefore it was removed both from the HC and from the PD.

In figures 3 and 4, all the combinations of missing values of the dataset have been represented, using the VIM package in R.

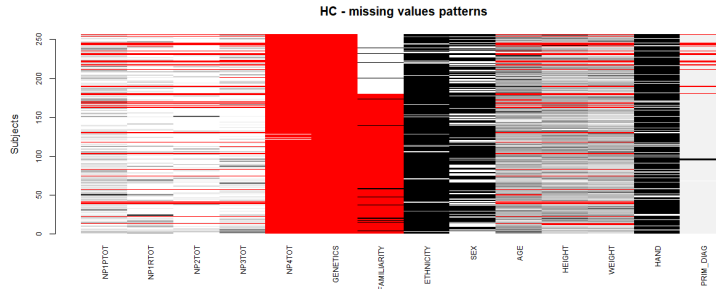


Figure 1: Pattern of missing values in HC

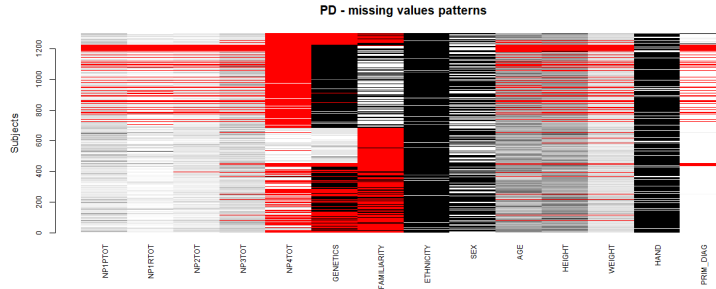


Figure 2: Pattern of missing values in PD

Another reason of exclusion from the analysis, was having an incomplete DAT-SCAN, a scan with poor quality, or, just for HC, a MoCA (Montreal Cognitive Assessment) score lower than 26. This test assesses the cognitive im-

pairment, and, under 26, the subjects couldn't be considered healthy.

The preprocessing step ended with the removal of some outliers from ENROLLAGE, HEIGHT and WEIGHT. (DA CONTROL-

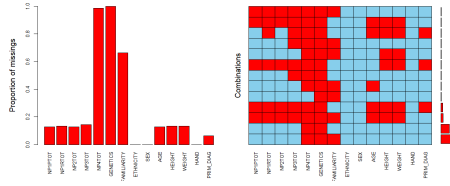


Figure 3: Missing values in HC

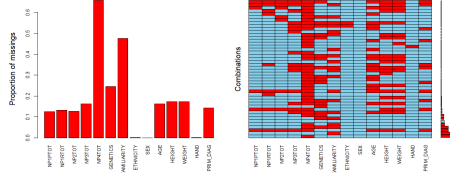


Figure 4: Missing values in PD

LARE)

Concerning the demographics data, the two datasets were compared, to see if they had the same distributions. The average values of age, height and weight were similar for the two groups, as well as the proportion of male and female was comparable.

(Abbiamo controllato che i hc e pd fossero simili (stessa pop di m/f età etc))

2.3 Feature extraction

In order to perform the statistical analysis to answer the study questions, the relevant features were extracted.

From the lateralization data, the group used a DAT binding asymmetry index found in [2]: $(\text{right} - \text{left SBR}) / (\text{right} + \text{left SBR})$.

- Come abbiamo trovato il lateralization index [REFERENCE] - Matrice di correlazione in base alla matrice di correlazione - $\hat{\rho}$ scelto le variabili più significative

2.4 Statistical methods

2- Che statistiche abbiamo usato, perchè Anova per vedere se c'è diff tra hc e pd [forse è meglio

sostituire con wilxcon?]

2.5 Linear regression

IMMAGINE linear regression + descrizione statistiche

3 Results

- A clear and concise description of the statistical results providing answers to the research questions
- A sensitivity analysis of the results to co-variables, group matching and data quality (e.g. missing data, data miss balance)

4 Discussion

- Direct answers to the research questions
- An overview of the limitations of the study
- A list of possible suggestions to improve the study in case someone will repeat it in future

References

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