| Study file | Feature | Columns | Encoding | | |
|-------------------------|---|--|---|--|--|
| Demographics | Race | "RAWHITE", "HISPLAT", "RAINDALS", "RABLACK", "RAASIAN", "RAHAWOPI", "RANOS" | 7 features, encoded as 1 if the participant was considered from this ethnic origin, 0 if not. | | |
| | Sex | "SEX" | Encoded as 0 if the participant was a woman, 1 if it was a man. | | |
| | Handedness | "HANDED" | 3 features: "RIGHT_HANDED", "LEFT_HANDED" and "AMBIDEXTROUS" with 0 or 1 depending on the handedness of the participant. | | |
| Social | Years of educa- tion | "EDUCYRS" | Float corresponding to the n. of years of education of the participant. | | |
| Age | Age | "AGE" | Float corresponding to the age of the participant. | | |
| Parkinson's features | Presence of tremor, rigidity, or postural instability at baseline | "DXTREMOR", "DXRIGID", "DXBRADY", "DXPOSINS" | 4 features encoded as 0 if the participants didn't have this symptom, 1 if so. Bradyki- nesia was not mentioned in the paper but was used in the code, so we added this feature in our model. | | |
| | Dominant dis- ease side | "DOMSIDE" | "DOMSIDE" feature column was used and split into 3 features: "DOMSIDE_LEFT", "DOMSIDE_RIGHT" and "DOMSIDE_BOTH" with 0 or 1 depending on the dominant side of disease for the participant. | | |
| | Symptom dura- tion and disease duration | "INFODT", "SXDT", "PDDXDT" | Symptom duration and disease duration: we respectively computed the number of days between the columns "INFODT" and "SXDT" and between the columns "INFODT" and "PDDXDT". Dates were first converted to "Month-Year" before computing the number of days between the two dates. | | |
| MoCA scores file | Baseline MoCA score | "MCATOT" | Integer value corresponding to the score of the participant. Missing values were replaced by the mean value across other participants. This information was not mentioned in code or paper. | | |
| GDS score file | Baseline GDS to- tal score | "GDSSATIS", "GDSDROPD", "GDSEMPTY", "GDSBORED", "GDSGSPIR", "GDSAFRAD", "GDSHAPPY", "GDSHLPLS" ,"GDSHOME", "GDSMEMRY", "GDSALIVE", "GDSWRTLS", "GDSENRGY", "GDSHOPLS", "GDSBETER" | We computed the total score by summing all the columns containing "GDS" in the GDS short version study file. Missing values were replaced by the mean value across other participants. | | |

Table 1. Demographics and clinical features set as input for the machine learning models. For baseline MDS-UPDRS scores included for prediction at 1year, 2 years and 4 years, see section Outcome measurement.

| Experiments | Cohort | Image preprocessing | ALFF/ReHo computation | Selection of input features | Workflow name |
|--|----------------------------|--|-----------------------------------|-----------------------------------|--|
| Reproduction | Closest-to- paper: n=82 | Reproduction with AFNI segmentation | Z-score | All | Reproduction pipeline closest-to-original cohort |
| Variations of cohorts | Ours: n=102 | Reproduction with AFNI segmentation | Z-score | All | Reproduction pipeline replication cohort |
| Variations of image pre- processing | Closest-to- paper: n=82 | Reproduction with FSL segmentation | Z-score | All | Reproduction pipeline FSL segmentation |
| | Closest-to- paper: n=82 | Reproduction without anatomic priors | Z-score | All | Reproduction pipeline no anatomic priors |
| | Closest-to- paper: n=82 | fMRIprep pipeline | Z-score | All | fMRIprep pipeline |
| Variations of image feature processing | Closest-to- paper: n=82 | Reproduction with AFNI segmentation | Not z-scored im- ages | All | Reproduction pipeline no z-score |
| | Closest-to- paper: n=82 | Reproduction with AFNI segmentation | ALFF instead of fALFF, Z-score | All | Reproduction pipeline ALFF |
| Variations of sets of input features | Closest-to- paper: n=82 | Reproduction with AFNI segmentation | Z-score | No dominant disease side | Reproduction pipeline no domside |
| | Closest-to- paper: n=82 | Reproduction with AFNI segmentation | Z-score | No baseline UPDRS | Reproduction pipeline no UPDRS |
| | Closest-to- paper: n=82 | Reproduction with AFNI segmentation | Z-score | Only imaging features | Reproduction pipeline only imaging features |
| | Closest-to- paper: n=82 | | Z-score | No imaging features | No imaging features |

Table 2. Terminology of the experiments in the current paper. Blue text denotes cohort or analysis variations that are closest to the original study, green text indicates variations due to unknown information, while red text indicates variations that are less similar to the original study.