Supplemental Online Content

Table S1. Literature overview of studies performing shape analysis in Parkinson's disease between 2012-2022

*data obtained from the publicly available Parkinson's Progression Markers Initiative (PPMI)

**as observed on DA transporter single-photon emission tomography

Abbreviations: DAT-SPECT, DA transporter single-photon emission tomography; DLB, Lewy Body Dementia; EDS, excessive daytime sleepiness; HC, healthy controls; MCI, mild cognitive impairment; PD, Parkinson's Disease; PDD, Parkinson's Disease Dementia; PIGD, postural instability and gait disorder; TD, tremor dominant; UPDRS-3, Unified Parkinson's Disease Rating Scale, part 3.

Table S2. Demographics complete sample per cohort

Abbreviations: N, sample size; sd, standard deviation; MoCA, Montreal Cognitive Assessment; MDS-UPDRS3, Movement Disorders Society sponsored revision of the Unified Parkinson's disease rating scale part 3; HC, healthy controls; PD, Parkinson's disease.

Table S3. Comparison complete sample PD vs controls

Corrected for age, sex and intracranial volume as fixed factors, and cohort as random intercept.

Table S4. Sample size by ROI and number of excluded failed segmentations

Abbreviations: ROI; Region Of Interest, PD; Parkinson's Disease, L; Left, R; Right.

Table S5. Hoehn & Yahr Stage Characteristics

n (%); Mean ± SD; * Significantly different from other Hoehn & Yahr stage groups on Mann-Whitney test at *p* < 0.001

Table S6. MatchIT controls selection and overlap between Hoehn and Yahr stage analyses

Abbreviations: HY; Hoen and Yahr.

Table S7A-D. Results HY-control comparison

Corrected for age, sex and intracranial volume as fixed factors, and cohort as random intercept.

A - HY1 vs controls

B - HY2 vs controls

C - HY3 vs controls

D - HY4-5 vs controls

Abbreviations: MoCA, Montreal Cognitive Assessment; MDS-UPDRS3 OFF, Movement Disorders Society sponsored revision of the Unified Parkinson's disease rating scale part 3 assessed in OFF medication state.

Pearson's product-moment correlations were tested for subjects with both clinical variables for the test of interest available (MoCA, MDS-UPDRS-III, or time since diagnosis). Abbreviations: MoCA, Montreal Cognitive Assessment; MDS-UPDRS3 OFF, Movement Disorders Society sponsored revision of the Unified Parkinson's disease rating scale part 3 assessed in OFF medication state.

Table S10. Results time since diagnosis analysis

Corrected for age, sex and intracranial volume as fixed factors, and cohort as random intercept.

Corrected for age, sex and intracranial volume as fixed factors, and cohort as random intercept. Abbreviations: MoCA, Montreal Cognitive Assessment.

Table S12. Results MDS-UPDRS3 OFF analysis

Corrected for age, sex and intracranial volume as fixed factors, and cohort as random intercept. Abbreviations: MDS-UPDRS3 OFF, Movement Disorders Society sponsored revision of the Unified Parkinson's disease rating scale part 3 assessed in OFF medication state.

Table S13. Machine learning model comparison

Performance metrics for the One-against-All binary classification and Ordit ordinal classification models across Hoehn and Yahr stages. Abbreviations: HY, Hoehn and Yahr.

Table S14A-D. Results k-means clustering on thalamus vertices of HY1 + HY2 participants

Cluster differences were characterized by total volume of the thalamus and other subcortical structures, but not by age, sex, ICV, HY stage, time since diagnosis, age of onset, MDS-UPDRS3, MoCA and/or LEDD. Abbreviations: HY, Hoehn & Yahr; AO, Age of onset; MoCA, Montreal Cognitive Assessment; MDS-UPDRS3, Movement Disorders Society sponsored revision of the Unified Parkinson's disease rating scale part 3; LEDD, Levodopa equivalent daily dose; ICV, intracranial volume; L, left; R, right.

A - K=2 Sample descriptives

B - K=2 contribution of cohorts to cluster in percentages

C - K=3 Sample descriptives

D - K=3 contribution of cohorts to cluster in percentages

Table S15. Cohort characteristics

Scanner protocol information for each sample included in analyses. Abbreviations: PD = Parkinson's disease; HC = healthy controls; TR = Repetition Time; TE = Echo time; TI = Inversion time; FOV = field of view; FA = flip angle

Table S16A-H. Results Jacobian Determinant

Corrected for age, sex and intracranial volume as fixed factors, and cohort as random intercept. Abbreviations: MoCA, Montreal Cognitive Assessment; MDS-UPDRS3 OFF, Movement Disorders Society sponsored revision of the Unified Parkinson's disease rating scale part 3 assessed in OFF medication state.

A - Complete sample PD vs controls

B - HY1 vs controls

C - HY2 vs controls

D - HY3 vs controls

E - HY45 vs controls

F - Time since diagnosis in PD

G - MoCA in PD

H - MDS-UPDRS3 Off in PD

Figure S1. Flowchart of data inclusion.

Schematic overview of available datasets for each analysis, categorized by 'Mass Univariate Statistical Analysis' and 'Multivariate Predictive Models'. For the univariate analyses, we performed group comparison and correlation analysis on radial thickness. For the multivariate analyses, binary classification and multi-task classification were performed. Abbreviations: PD, Parkinson's disease; MoCA, Montreal Cognitive Assessment; MDS-UPDRS3, Movement Disorder Society sponsored revision of the Unified Parkinson's Disease Rating Scale part 3; HY, Hoehn and Yahr.

Figure S2A-F. Mass univariate analysis: significant vertex-wise differences in thickness between people with PD and controls.

Effect maps are projected onto the subcortical regions showing (**A-B**) the PD versus controls and (**C-F**) subgroup comparisons. Positive b-values indicate that regions are thicker, negative b-values indicate that regions are thinner in PD compared to controls. All groups are sex- and age-matched (**A-F**). The models are corrected for intracranial volume and cohort in all panels, and additionally corrected for age and sex in panel **B**.

Figure S3A-B. Group differences in time since diagnosis and MoCA across HY stage.

(A) Time since diagnosis (in years) and (B) MoCA scores are shown for HY stages 1 to 4-5. Sample sizes are shown below the raincloud plots. *** indicates $p < .001$.

■HY3 ■HY45 ■ overlap

Figure S4A-C. Pattern coherence analysis with spin permutation tests.

Each panel shows the effect maps of two case-control mass univariate analyses are projected onto the subcortical regions to highlight overlapping patterns between the stages (purple), regardless of the direction of the effects. (**A**) HY1 vs controls (blue) and HY2 vs controls (pink), (**B**) HY2 vs controls (blue) and HY3 vs controls (pink), (**C**) HY3 vs controls (blue) and HY45 vs controls (pink).

Figure S5A-B. Hippocampal subregions on the ordinal classification maps.

For visualization purposes, we overlaid subregions of the hippocampus according to the FreeSurfer v.6.0 hippocampal subfield atlas (mirrored) onto the effect maps from the ordinal classification model (**A**). The color codes from the hippocampal subregions are shown in (**B**).

 $\mathbf c$ Classification HY1 vs HY345 Dorsal \times 10⁻⁵ Ventral

Figure S6A-C. Machine learning binary classification of HY stages versus each other based on the thickness of subcortical structures.

Classification maps of (**A**) HY1 vs HY2, (**B**) HY2 vs HY345, and (**C**) HY1 vs HY345 are shown. The color bars represent learned weights of the classification model, positive values (SD from the learned weights) in red, negative values in blue. More intense colors indicate stronger predictive power of the classification. Note that the right thalamus in panel **A** shows a biologically implausible pattern due to low signal.

Figure S7A-C. Machine learning: binary classification maps for HY stages versus controls.

Binary classification uses vertex-wise thickness information from all subcortical structures. The color bars represent learned weights of the classification model, positive values (SD from the learned weights) in red, negative values in blue. More intense colors indicate stronger predictive power of the classification. Displayed are the results of (**A-C**)

the binary classification of each of the HY stages versus controls. Note that the right thalamus in panel **C** shows a biologically implausible pattern due to low signal.

Figure S8A-C. Machine learning: One-against-All classifications of the HY stages.

One-against-All classification maps of (**A**) HY1, (**B**) HY2, and (**C**) HY345 are shown. The color bars represent learned weights of the classification model, positive values (SD from the learned weights) in red, negative values in blue. More intense colors indicate stronger predictive power of the classification. Note that all structures except for the left thalamus in panel **A** and the left globus pallidus and right amygdala in panel **C** show a biologically implausible pattern due to low signal.

Figure S9A-E. Machine learning: model comparison One-against-All and Ordit.

This figure features a comparison of the multi-task classification performance of One-against-All and Ordit models. It is noteworthy that although the two models' predictive performance scores are comparable (with chance performance of 0.33), Ordit results in a relatively more balanced confusion matrix (**AB**, Table 2) and balanced scores across all classification metrics (**C-E**, Table 2). The collection of anatomical maps representing the One-against-All model is more difficult to interpret than the single Ordit-TVL1 model map, in part because the grouping of different diagnostic categories together does not necessarily reflect the direction of PD-related anatomical change once the disease onset has occurred. Confusion matrices of the (**A**) One-against-All, and (**B**) Ordit models are shown. The ordinal model classifies the plurality of subjects in each HY stage correctly, unlike the One-against-All model. In each row the proportion of misclassified stages is approximately the same due to class-balancing. This is visualized by the diagonal carrying the biggest number. In the lower panels, (**C**) F-score, (**D**) precision, and (**E**) recall are compared between the two models for each HY stage. The corresponding values of performance parameters are provided in Table S13.

Figure S10A-D. Caudate nucleus medial curve discrepancies along its longitudinal axis.

The pattern of PD vs. controls shape differences in the caudate nucleus revealed by the binary classifiers suggests a "pancaking" effect: an apparent compression along the sagittal axis coupled with an apparent expansion along the axial direction in PD patients relative to controls (Figure 4A, Figure S6A-C). We performed a post hoc analysis to investigate whether this pattern could be caused by some bias in the medial curve. One plausible source of bias is possibly due to the curvature regularization used in fitting the curve. In general, if the overall shape of a region is curved, the medial curve will be pushed towards the concave side of the structure by the regularization. Thus, if the effect of PD were a curving of the caudate nucleus, or if there was bias in segmentation failure of the caudate nucleus in FreeSurfer, this could possibly result in an apparent flattening effect. To check this, we computed the difference between each point on the medial curve and the "true" medial point based on the cross-section of each subject's caudate nucleus shape at a given location. In this figure, medial curve discrepancies reflect the difference between the medial curve and "true" medial point along the caudate nucleus at 50 slice locations. The medial curve and "true" medial points are shown for (**A**) one subject (1-D "bias" map) and (**B**) did not differ significantly between sites, (**C**) PD and controls, or (**D**) the HY stages. The result was a 1-D "bias" map for each subject (**A**). These results give more credibility to the observed flattening effect in PD indicated by the shape map.

Silhouette analysis for KMeans clustering on sample data with n_clusters = 2

Silhouette analysis for KMeans clustering on sample data with n clusters = 3

Figure S11A-C. K-means clustering: determining optimal k

We performed k-means clustering (Python package scikit-learn 1.3.2) on the bilateral thalamus vertices in the combined HY1 and HY2 sample set to identify subgroups with shared morphological features. Ordinary least squares means was used to regress out explained variance of age, sex, ICV and cohort. Next, we applied the elbow and

Calinski-Harabasz method in KElbowVisualizer (package yellowbrick 1.5) and silhouette score (scikit-learn) to determine the optimal k clusters. Linear principal component analysis and k-means clustering was performed and identified clusters were statistically compared on clinical characteristics using t-tests and chi-squared tests. (**A**) Elbow method, (**B**) Calinsky-Harabasz method and (**C**) Silhouette method, including scatterplot of clustered data by the first and second principal component. The optimal k clusters indicated by the elbow method was two; and by the Calinski-Harabasz index and silhouette score three.

ENIGMA-Parkinson's Disease Datasets

Figure S12. World map of the ENIGMA-Parkinson's Disease Datasets.

Locations of collaborating sites are indicated by red location drops, locations of the Parkinson's Progressive Marker Initiative (PPMI) datasets are indicated by a yellow plus sign, and other open datasets are indicated by a blue circle.

Figure S13. The ENIGMA-Shape Pipeline.

1) The ENIGMA-Shape pipeline uses a template based on subcortical structures from 200 young adults and has been applied to various conditions like major depressive disorder $^!$, schizophrenia 2 2 , obsessive-compulsive disorder 3 3 , and 22q11.2 Deletion Syndrome^{[4](https://paperpile.com/c/nb8m4m/wfidg)}. Unlike cortical analysis, subcortical geometries remain relatively stable across ages in healthy adults, primarily varying by volume. Thus, we normalize features in subject-to-template registration to minimize age-related biases in the resulting shape descriptors. The first steps of the ENIGMA-Shape pipeline, including FreeSurfer parcellation^{[5,](https://paperpile.com/c/nb8m4m/Peyx)[6](https://paperpile.com/c/nb8m4m/VGRR)}, performed by all source institutes individually. For each participant, we used non-linear spherical registration to align the surface with the template, creating a mesh representing the outer boundaries of the structure. These meshes were then pooled for quality assessment and mega-analysis. 2) Quality assessment entailed visual inspection of the meshes according to the ENIGMA-Shape protocol to assure anatomical accuracy, with exclusion of poorly segmented regions from the analysis. Mean imputation was performed for failed segmentations. We adjusted the overall logistic loss function by the inverse of the diagnostic or staging label frequency, to account for the imbalance in PD/control and HY stage group size. 3) In previous work^{[2](https://paperpile.com/c/nb8m4m/bJMU3)}, we modified the searchlight FDR procedure^{[7,8](https://paperpile.com/c/nb8m4m/nbZz9+TAxT8)} for global application across all structures in each linear model. Distances between vertices were defined as the Euclidean distance, with those between different structures set to infinity. The correction is more conservative than one that accounts for correlations between different regions but less conservative than the original FDR approach $^{\circ}$, which ignores spatial correlation. 4) In this study, we focused on thickness as a shape morphometry measure as it offers intuitive interpretability in the context of neurodegeneration. We also analyzed the logarithm of the Jacobian determinant (Figure S14A-H), which reflects the ratio of two local surface areas: a surface patch on the participant and template surface^{[10,11](https://paperpile.com/c/nb8m4m/uYuM+X8ax)}. Log-Jacobian values below 1 indicate surface contraction and values above 1 indicate expansion. The two measures of shape morphometry are considered complementary to each other (Figure S15A-C).

Figure S14A-H. Mass univariate analysis: significant vertex-wise differences in Jacobian determinant between people with PD and controls.

The patterns observed in the thickness analyses partly aligned with those observed in the Jacobian determinant analyses. The Jacobian determinant results are also presented in Table S13A-H. Conceptually, the Jacobian determinant and thickness differ in interpretability; whereas the Jacobian is an indirect reflection of surface expansion or contraction, the thickness values directly represent the absolute difference in tissue thickness. A comparison of both measures of shape deformation is visualized in Figure S15A-C. Effect maps are projected onto the subcortical regions showing the (**A**) PD versus controls, and (**B-E**) subgroup comparisons, and (**F-H**) correlations with clinical

markers. Positive b-values indicate that regions are thicker, negative b-values indicate that regions are thinner in PD compared to controls. (**B-E**) All HY groups are sex- and age-matched. (**A-H**) The models are corrected for intracranial volume and cohort in all panels, and additionally corrected for age and sex in panel **H**.

Figure S15A-C. Comparison of log Jacobian versus thickness effects.

Comparing the effects of a volume-preserving deformation (**A**) on thickness (**B**) and log Jacobian (**C**) measures in a hippocampal surface model. Notably, the direction of effect is concordant between the two measures in areas of positive curvature and discordant in areas of negative curvature. Another example is to imagine a stretching of the hippocampus along the main axis. The thickness would remain unchanged, while the jacobian would increase. The arrows in panels **B** and **C** highlight similarities (green) and differences (red) between the two measures of shape deformation.

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