Processing of analysis-ready image-derived phenotypes from the PPMI dataset

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Summary

We processed T1-weighted images of 1716 baseline PPMI participants through FreeSurfer and MRIQC pipelines. The output from the FreeSurfer pipeline was then further processed to extract analysis-ready image-derived-phonotypes based on standard brain atlases within the FreeSurfer package. We also tabulated the outputs of the MRIQC pipeline which provides a set of image-quality-metrics for the T1w images. These metrics can help with quality assurance and can be used in conjunction with the FreeSurfer output to define custom quality control criteria. Both FreeSurfer image-derived-phonotypes and MRIQC image-quality-metrics are shared in this release.
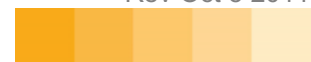
Method

Describe the methods used. Sufficient information should be provided to enable investigators to understand the methodology and interpret the data

Data curation: We downloaded T1-weighted images (DICOMs) from the baseline visit of participants in the Parkinson's progression markers initiative (PPMI) [1]. We followed the Nipoppy protocol [2] which adopts FAIR (i.e. Findability, Accessibility, Interoperability, and Reuse) data principles [4] for data curation and reproducible processing. Using Nipoppy bidsification tools (https://nipoppy.readthedocs.io/en/latest/user_guide/bids_conversion.html), we converted and organized these DICOMs into brain imaging data structure (BIDS) [4].

Data processing: We used Nipoppy processing tools (https://nipoppy.readthedocs.io/en/latest/user_guide/processing.html) run containerized FreeSurfer-v7.3.2 [5] and MRIQC-v23.1.0 [6] pipelines. For efficiency and reliability reasons, we used anatomical sub-workflow within the fMRIPrep-v23.1.3 container to run the FreeSurfer pipeline. Nipoppy tracks all the run-time parameters ensuring reproducibility and enabling identical processing of new subjects and subsequent visits.

Image-derived-phenotype (IDP) extraction: We used Nipoppy feature extraction tools (https://nipoppy.readthedocs.io/en/latest/user_guide/extraction.html) to generate analysis-ready IDPs from outputs of the processing pipelines. For FreeSurfer, we used default Desikan-Killiany (DK) and ASEG atlases to calculate regional cortical thickness (CTh), surface area (SA) and subcortical volumes. For MRIQC, we tabulated a set of image-quality-metrics for the T1w images which can be used to define quality control criteria suitable for a given study.

Data sharing: We share data in multiple CSV files as follows.
MRIQC
loni_mriqc23_anat_IQM.csv: This file contains the set of calculated IQMs for the T1-weighted images by the MRIQC pipeline.

FreeSurfer
loni_fs7_aseg_volumes.csv: This file contains the subcortical volumes calculated based on the default FreeSurfer ASEG atlas.
loni_fs7_aparc_cth.csv: This file contains the cortical thickness values calculated based on the default FreeSurfer DK (APARC) atlas.
loni_fs7_aparc_sa.csv: This file contains the cortical surface area values calculated based on the default FreeSurfer DK (APARC) atlas.

References

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