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Advances in the Clinica software platform for clinical neuroimaging studies

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Introduction:

Carrying out neuroimaging studies often involves multiple steps requiring different tools. As such it can be difficult to reproduce an experiment. Clinica (Routier et al., 2021) is a software platform that aims at empowering users with an environment to make reproducibility possible. In this abstract, we present the new pieces of functionality and improvement that have been integrated to Clinica to improve the overall user experience and extend Clinica's reach to other datasets.

Methods:

Clinica is built around three main axes: BIDS (Gorgolewski et al., 2016) converters, neuroimaging processing, and statistics and machine learning workflows.

Considering this, new functionalities and improvements can be divided in two parts:

On the one hand, improvement and new features added to the converters, which enable normalization of raw data from public databases to the community-driven standard BIDS. As such, existing converters have been optimized following coding best-practices and metadata information has been updated as per community feedback. Besides, BIDS converters for two new public datasets (OASIS3 (LaMontagne et al., 2019) and HABS (Dagley et al., 2017)) have been added to our pipelines. OASIS3 is a retrospective study containing over 30 years of data. It provides a large database (over 1000 participants) currently converted only for T1 and PET modalities. The second converter is for HABS, a converter for the Harvard dataset (with 290 participants), which aims at finding out whether changes seen on scans of patients are related to early memory changes.

On the other hand, a general effort was made to improve the preprocessing pipelines. In particular, we have added the possibility to use custom atlases with our *t1-freesurfer* and *t1-freesurfer-longitudinal* pipelines. These atlases enable researchers who wish to work on particular brain areas to do so, and to explore regions which may not be covered in FreeSurfer's (Fischl et al., 2012) built-in atlases.

On top of these changes, the core of Clinica has undergone considerable change. The continuous integration has been reworked to be more robust. The logging and command line parsing modules have been completely revised to use state-of-the-art libraries and practices. Finally, dependency management is now handled by poetry for more robust deployment.

Results:

The new functionalities available through Clinica aim to address the needs of a larger audience: access to public datasets through standardized format and easy execution of preprocessing pipelines to support and encourage reproducible neuroimaging studies. The source code of Clinica is hosted on Github and the software is distributed under an MIT license. A comprehensive user guide accompanies the software platform (available from www.clinica.run).

Conclusion:

Clinica is an open-source software platform for clinical neurosciences. It tackles most of the challenges found in the neuroscience research environment and facilitates more reproducible and trustworthy research. Community feedback resulted in the development of new functionalities including those presented in this abstract.

In the near future, we are looking to extend the functionalities of Clinica to further improve reproducibility and user experience. Indeed, for reproducibility, a future version of Clinica will integrate a provenance module that allows users to record the history and relationships associated with each resource. This is currently under development and discussed with associated working groups in the community. Further, a cloud version of Clinica will allow users to interact with Clinica through a web interface and visualize the results interactively. Besides these two projects, Clinica is continuously improving through community feedback.

References:

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Figures:

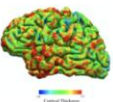
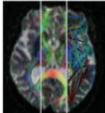
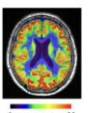
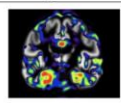
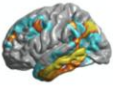

Anatomical MRI	Diffusion MRI	PET
<ul style="list-style-type: none"> t1-linear: Bias field correction, affine registration and cropping t1-volume: Tissue segmentation (GM, WM, CSF), inter-subject registration using Dartel, spatial normalization to standard space (MNI) t1-freesurfer/t1-freesurfer-longitudinal: Cortical surface extraction, segmentation of subcortical structures, cortical thickness estimation, spatial normalization to standard space (FSAverage) 	<ul style="list-style-type: none"> dwi-preprocessing: Correction of raw DWI data dwi-dti: Extraction of DTI-based measures, normalization to standard space (MNI) dwi-connectome: Tractography & connectome 	<ul style="list-style-type: none"> pet-linear: Affine registration, intensity normalization and cropping pet-volume: Registration to T1 MRI, partial volume correction, spatial normalization to standard space (MNI), intensity normalization pet-surface/pet-surface-longitudinal: Registration to T1 MRI, intensity normalization, partial volume correction, projection to cortical surface, spatial normalization to standard space (FSAverage) 
Machine Learning	Statistics	Converters
<ul style="list-style-type: none"> machinelearning-prepare-spatial-svm: Preparation of T1 MRI and PET data for spatially regularized SVM 	<ul style="list-style-type: none"> statistics-volume: Voxel-based mass-univariate analysis with SPM statistics-surface: Surface-based mass-univariate analysis with SurfStat 	Several pipelines to convert public neuroimaging datasets into the BIDS Standard. <ul style="list-style-type: none"> adni-to-bids nfd-to-bids alibi-to-bids habs-to-bids oasis-to-bids oasis3-to-bids 

Figure 1 List of the main functionalities currently available in Clinica: converters of public neuroimaging datasets to BIDS; neuroimaging processing pipelines for structural MRI, diffusion MRI and PET; and statistics and machine learning workflows.