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Making neuroscientific analyses replicable: An open science fMRI preprocessing pipeline

Abstract

Open science principles (such as sharing ideas, data, and results; Merton, 1973) have not yet been fully adopted by the neuroscientific community impeding replications of research results (e.g., Poldrack et al., 2017). Apart from the actual data analysis, analytical flexibility regarding preprocessing of the MRI data can lead to varying study results (Botvinik-Nezer, et al., 2020). To enable reproducibility of neuroimaging analyses from our group, we have implemented an open science MRI preprocessing pipeline, which connects several open-source neuroimaging software and scripts: 1) conversion to a standard data format with HeuDiConv (Halchenko et al., 2017), 2) basic preprocessing steps with fMRIPrep (motion correction, field unwarping, normalisation, bias field correction, and brain extraction; Esteban et al., 2019), and 3) quality control with MRIQC (Esteban et al., 2017). Besides ensuring a standard quality of our data and saving resources by automation of preprocessing steps, our openly available preprocessing pipeline can be used by other researchers to reproduce our results, and for their own neuroimaging data. As such, our pipeline exemplifies how open science can contribute to more robust and standardized research, which is especially relevant when translating complex neuroimaging analyses to clinical research.

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