The EEGManyPipelines Dataset: Metascientific Data on 168 Independent Analyses of a Single EEG Dataset

The list of authors and their affiliations appear in the Appendix at the end of the paper.

Abstract

There is a growing need for large-scale, global studies in response to the replication crisis, which has raised concerns across many scientific fields and prompted efforts to understand the sources of variability in research outcomes. Here we describe the EEGManyPipelines dataset: a many-analyst study aiming to examine how differences in electrophysiology (EEG) data analysis may contribute to differences in the results. We describe data shared and analyzed by 168 analyst teams. The original shared raw data consisted of behavioral data and EEG recordings of 33 participants performing a long-term memory task, together with 8 hypotheses regarding event-related potentials and time-frequency effects. Analyst teams also provided meta-scientific data detailing analysts' approach to hypotheses: processed EEG data, scripts, and answers to questionnaires. We propose this unique dataset for future use to study analytical flexibility, research culture, and scientific decision-making. It offers a valuable tool for meta-scientific, global and multicenter studies, EEG methodology, and reproducibility studies.

Background and Summary

In the last decade, many fields—including experimental psychology, cognitive neuroscience, and several biomedical, behavioral, and social sciences—have faced a replication crisis, with sometimes half or more of studies estimated to fail to replicate[1–4]. Among the explanations proposed, one key contributor may be variability in data processing and analysis[3,5,6]. Recently, several projects have used a many-analysts approach to systematically map variability in data analysis practices onto variability in research outcomes[7,8]. This approach involves independent teams analyzing the same dataset to answer the same research questions[9]. Under these controlled conditions, differences in results between analysts can only be attributed to variations in analysis choices. The EEGManyPipelines project was launched to explore the extent of this variability in real-world EEG analysis practices and their effect on research outcomes[10].

Neuroimaging data, including electroencephalography (EEG) data, allow considerable flexibility in data processing and analysis choices. Analytical variability in functional magnetic resonance imaging (fMRI) has been demonstrated to substantially affect scientific conclusions[7]. However, we do not know to what extent these results transfer to other neuroimaging modalities, such as EEG. Researchers' degrees of freedom for EEG data analysis practices are comparable to those in fMRI, both due to intrinsic data properties, the many available data analysis packages, published pipelines, and general reliance on custom code. However, EEG recordings are particularly susceptible to artifacts linked to experimental task design, such as sweating or involuntary facial muscle contractions during demanding tasks. Moreover, less technical support is required for EEG compared to fMRI, leading to limited support from specialized staff such as MR physicists.

To investigate variability in EEG data analysis practices and effects on results, the EEGManyPipelines project was launched at the end of 2020. Initially, 327 teams consisting of 1–3 analysts each signed up for the project (sign-up phase was July–September 2021) and received the same dataset to analyze with the methods they typically use. The EEG dataset consisted of a typical visual recognition memory experiment: a continuous recognition task, with some images repeating multiple times. Together with the data, analyst teams received a set of eight hypotheses to test (Box 1). The hypotheses varied in specificity, ranging from narrow hypotheses about condition-specific effects on EEG voltage at a specific set of channels within a specific time window, to more open-ended hypotheses about condition differences at any possible time point, channel location, or frequency band. Analyst teams had eight months to analyse the data (the data analysis phase lasted October 2021–May 2022).

A total of 168 teams out of 327 (51.4%) completed data analysis and submitted results. Teams reported the outcomes of their hypothesis testing in both a standardized format (by filling in a questionnaire form) and as a free-text results report. They also submitted processed EEG data, analysis scripts, a detailed description of their processing pipeline, and the results. Additionally, all individual analysts provided demographic information and rated their confidence in the evidence for each hypothesis tested before and after data analyses.

The EEGManyPipelines project aimed to link the variability in data analysis choices to the variability in results. Together with the original dataset sent to the analyst teams, we share the original meta-scientific data as submitted by the analysts and a version curated for consistency, which allows users to process all data using software of their own choice. This rich dataset can be used to address a wide range of questions, including how features of data analytic decisions affect reported results, different approaches to hypothesis testing and decision making. In addition, EEGManyPipelines provides a rich database of coding practices using different software tools with the added advantage of direct comparability (all code was developed to analyze the same dataset and answer the same research questions).

The data is available free of charge through the open-source brainlife.io cloud platform.[11] The following sections present our project, structured in three parts: first, we describe the data and information that was sent to analyst teams. Second, we describe the data collected after the analysis phase (referred to as meta-scientific data). Finally, we provide a description of the curation process and the curated meta-scientific data.

Methods

Overview

We shared the same EEG dataset, along with a set of hypotheses, with expert teams and asked them to analyze the data in line with their typical analysis practices. At the end of the data analysis phase, analyst teams submitted detailed responses for every tested hypothesis and provided cleaned EEG data as well as the code for processing it. Below, we provide a more detailed description of the analysts, procedures, and documentation, as well as of the data sent to and received from the analyst teams by the end of the analysis phase. We curated the EEG preprocessed data, the Analysis questionnaire, and the Result forms for convenient handling (i.e., we converted them to the same format).

Analysts

Analysts were invited to join the EEGManyPipelines project through advertisements in mailing lists, social media posts, presentations at conferences, and word-of-mouth. To be eligible to participate, each team was required to include at least one member who had published an EEG study in a peer-reviewed journal before the registration deadline. The EEGManyPipelines study was approved by the ethics committee of the Faculty of Psychology and Sports Sciences at the University of Münster, Germany (#2021-06-NB and #2021-52-NB-FA).

A total of 327 eligible teams signed up, but 57 teams cancelled participation (Figure 1, panel A). Teams could consist of up to three individual researchers. An analyst could not join multiple teams. All team members signed a participation agreement permitting their data and results to be shared online under CC-BY license (see the participation agreement at https://osf.io/zq3ca). Every team could choose a team identifier themselves, or allow the Steering Committee (members of the Steering Committee are listed in the *Author contributions* section) to pick a random identifier consisting of letters and numbers.

The analysis phase lasted from October 2021 to May 2022. Upon request, 34 teams were granted a 15-day deadline extension, and nine teams were granted a one-month extension. In total, 168 teams submitted processed data, scripts, answers to questionnaires, and results for all eight hypotheses—these teams are the final EEGManyPipelines analyst teams who contributed to the shared data. These 168 teams comprised 396 individual researchers (mean age 33.7 ± 7.5 years; 150 female, 223 male, 2 self-identified as diverse, 21 did not give an answer). The demographics are summarized in Figure 1, panels B-E (further details can be found in Trübutschek et al. (2024)). Analysts who completed the assignment were invited as co-authors on this and the main EEGManyPipelines paper.

The geographical distribution of the analysts is comparable with that of the broader EEG research community, based on the geographical distribution of PubMed-indexed EEG articles published 2017—2022. The geographical distribution of EEGManyPipelines analysts included Europe (69%), North and South Americas (14%), Asia (12%), and Oceania (5%). In comparison, PubMed analyses revealed that most published research based on authors' affiliation comes from Europe (48%), North and South Americas (24%), Asia (24%), Oceania (4%), and African countries (<1%) (see Trübutschek et al. (2024), Figure 1 for details).

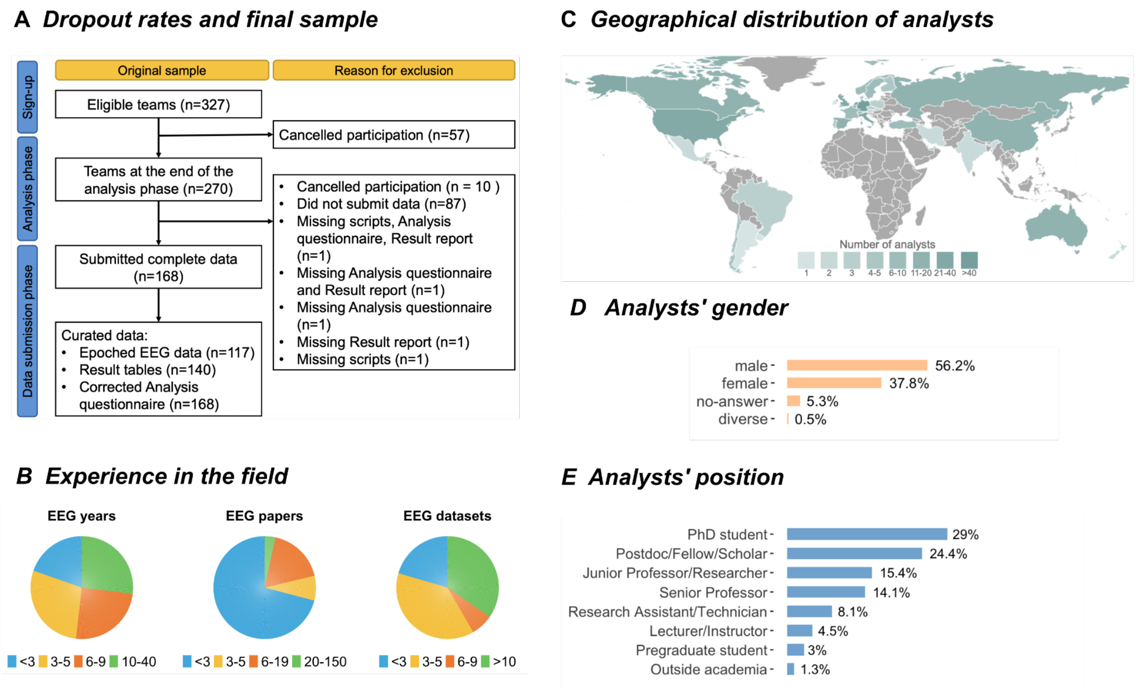

Figure 1. Inclusion flowchart and demographic information of participating analysts (n=168). A. Flow diagram indicating team numbers at different stages and reasons for dropout. **B.** Expertise in performing EEG, the number of published EEG papers, and the number of collected EEG datasets. **C.-E.** Charts summarize demographic data of the participating analysts: geographical distribution of analysts (**C**), gender (**D**), and self-reported job position grouped into categories (**E**). The figure in panel C was adapted from Trübutschek et al. (2024).

Analysis task and data shared with the analysts

Acquisition of the EEG dataset

The EEG dataset sent to the analysts was recorded from 33 participants (22 female; 4 left-handed; mean age 27 years) with normal or corrected-to-normal vision who participated for course credit or financial compensation. Although a relatively small sample size increases the possibility of diverging results when testing the same hypotheses, it represents a typical sample used in similar research. Clayson et al. (2019) suggested that an average sample size for event-related potentials (ERP) research was 21 participants. The dataset sent to analyst teams was collected for a different pilot long-term memory study; however, no results using this data had been previously published.

The EEG experiment was approved by the Ethics Committee of the Faculty of Psychology and Sports Sciences at the University of Münster, Germany (#2016-22-NB). Participants received written information about the aims and procedures before participating in the study. All participants gave written informed consent and agreed to have the data and results shared openly.

The data were recorded in two distinct laboratory locations. The first 17 participants were recorded in a Faraday cage, while the last 16 participants were recorded in a different soundproof booth lacking electrical shielding.

Experimental design and stimuli

Participants performed a continuous visual recognition task[12,13]. They viewed a stream of images (see Figure 2) where some images were repeated, and were asked to judge if each image was seen for the first time (“new”), or had been seen before (“old”) in the experimental session by lifting a finger from one of two response keys (left/right CTRL). Images were displayed for 500 milliseconds, followed by a blank screen until a response was made (self-paced). Feedback was provided via a color change of the fixation cross: the grey cross turned green or red for 200 milliseconds, indicating correct and incorrect responses, respectively. Releasing both keys together initiated a variable inter-trial interval (1000-3000 milliseconds) followed by the next trial. A gray fixation cross was displayed at the center of the screen during a response period and inter-stimulus intervals. The experimental conditions (scene category, number of presentations, correct/incorrect responses, reaction times) are coded in the EEG trigger markers. The experiment was programmed in MATLAB (The MathWorks, Natick, MA, USA) using the PsychToolbox[14].

The experiment included 600 unique images: 300 were presented only once, and 300 were presented three times, totaling 1,200 trials. Stimuli were presented in a pseudo-randomized order such that repeated images reappeared after 10 to 60 intervening trials. The stimuli consisted of 600 grayscale images from four scene categories (forests, highways, beaches, and buildings) sourced via Google Image Search. Each image measured 10 x 7.5 (horizontal x vertical) degrees of visual angle (dva) and was presented on a black background. Stimuli were presented on a calibrated LCD monitor (VIEWPixx/EEG) with 1920 × 1080 pixel resolution and a refresh rate of 100 Hz, positioned 86 cm from the participants’ eyes. Head position was stabilized using a chin rest.

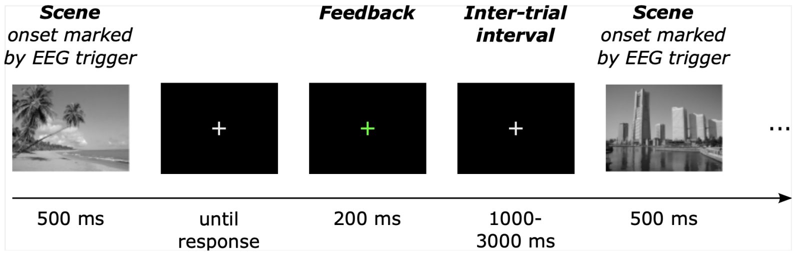

Figure 2. Timeline of an example trial in the EEG continuous visual recognition memory experiment. Participants viewed images of natural (i.e., beaches, forests) and man-made (i.e., highways, buildings) scenes. The task was to indicate whether they had been shown this image previously. Feedback (correct/incorrect) was indicated by a green/red cross.

EEG recordings

EEG was recorded using a 64-channel BioSemi Active-Two amplifier system with 64 Ag/AgCl electrodes, arranged according to the international 10-10 system. Two additional electrodes were placed on the mastoids. Horizontal and vertical electro-oculograms (EOG) were recorded from electrodes at the lateral canthi and below the eyes, respectively. The Common Mode Sense (CMS) and Driven Right Leg (DRL) electrodes were placed on the left and right sides of electrode POz. EEG was recorded in DC mode at a sampling rate of 1024 Hz with a 200 Hz low-pass filter and 24-bit AD conversion. EEG was recorded in an acoustically shielded recording booth. The onset time of scene images was marked and recorded in the EEG data by a trigger sent from the stimulus computer to the BioSemi ActiView recording software.

EEG preparation

The EEG data underwent minimal preprocessing, which included: (i) re-referencing to electrode POz, which resulted in POz containing only zeros; (ii) vertical EOG computation by subtracting infra-orbital channels (IO1 and IO2) from super-orbital channels (Fp1 and Fp2), (iii) horizontal EOG computation by subtracting the right channel (AFp10) from the left channel (AFp9), (iv) downsampling to 512 Hz by using the EEGLAB[15] function *pop_resample,* which uses an anti-alias filter to 0.9 of the Nyquist frequency, (v) simplification of event codes (to retain only information relevant for the eight hypotheses).

Hypotheses

Analysts tested the eight hypotheses presented in Box 1, featuring questions about ERP and time-frequency effects. "EEG voltage" refers to the conventional time-domain signal. “Spectral power” refers to the result of a (time-)frequency transform (e.g., fast-fourier-transform, wavelets, multitapers, etc.). All timing-related specifications are relative to image onset as indicated by the trigger markers in the EEG data.

The hypotheses were formulated by steering committee members, who have extensive experience in memory research. Only hypotheses that were typically studied in memory research and that would allow for a binary comparison were selected. The terms and concepts in the hypotheses (e.g., N1 component, spectral power, theta power) should be familiar to most EEG researchers. We did not specify the definitions of the concepts used in the hypotheses. For example, "theta power" and "alpha power" refer to the response within the canonically defined alpha and theta frequency bands in the EEG literature, but exact frequency ranges (e.g., 7–12 Hz for alpha) were left unspecified in the instructions to accommodate analysts using their own definitions.

Hypotheses were arranged in order of approximate specificity or ambiguity regarding “when” and “where” to test for an effect. For the comparatively ambiguous hypotheses, there were a priori a larger number of justifiable approaches to analyze the data. The comparatively ambiguous hypotheses (i.e., hypotheses 3a, 3b, 4a, 4b, see Box 1) invited for different methodological approaches (the selection of channels, time window, or frequency ranges were left open) to testing the same idea as compared to specific hypotheses (i.e., hypotheses 1, 2a–c, see Box 1), which specified an ERP component, time window, or channel locations.

Box 1. Hypotheses sent to the analyst teams.

H1. There is an effect of scene category (i.e., a difference between images showing man-made vs. natural environments) on the amplitude of the N1 component, i.e. the first major negative EEG voltage deflection.

H2. There are effects of image novelty (i.e., between images shown for the first time/new vs. repeated/old images) within the time-range from 300–500 ms …

a. ... on EEG voltage at fronto-central channels.

b. ... on theta power at fronto-central channels.

c. ... on alpha power at posterior channels.

H3. There are effects of successful recognition of old images (i.e., a difference between old images correctly recognized as old [hits] vs. old images incorrectly judged as new [misses]) …

a. ... on EEG voltage at any channels, at any time.

b. ... on spectral power, at any frequencies, at any channels, at any time.

H4. There are effects of subsequent memory (i.e., a difference between images that will be successfully remembered vs. forgotten on a subsequent repetition) …

a. ... on EEG voltage at any channels, at any time.

b. ... on spectral power, at any frequencies, at any channels, at any time.

Instructions for analysts

At the beginning of the analysis phase, teams received instructions describing the dataset and hypotheses, along with guidance on how to approach the data. Instructions were intentionally kept open, giving analysts freedom to choose how to process the data and test the hypotheses. Analysts were instructed to analyze the data with pipelines corresponding as closely as possible to the pipelines that they would use to analyze their own data. Analysts were not expected to analyze the data beyond what was required for testing the hypotheses provided. In addition, analysts were given instructions on how to report results, as well as guidelines for submitting code and processed EEG data. Below, we detail instructions for the meta-scientific data we collected (more details about the questionnaires in A, B, and C sections can be found below, in the *Raw meta-scientific data* section):

A) *Instructions for the Prior and Posterior expectations questionnaire*. In the instructions document, we asked analysts to fill in the questionnaires before and after hypothesis testing. We informed them that they would have to provide a binary response stating their subjective belief about each hypothesis test and their confidence rating to the indicated result (both before and after having analyzed the data). Within the instructions document, the Posterior expectations questionnaire is also referred to as the Results questionnaire.

B) *Instructions for the Free-text results report.* The analyst teams were asked to report their results for each hypothesis in a free-text format. We asked for the report to be concise and formatted similarly to the results section of a scientific journal article (about one paragraph per hypothesis).

C) *Instructions for the Analysis questionnaire*. Here, we asked for as many details as possible in response to a comprehensive list of questions about EEG processing steps and statistical procedures. We recommended taking notes and documenting the analysis steps.

D) *Instructions for submitting analysis scripts.* We asked analysts to use the same analysis pipelines as they would apply to data they collected themselves. Analyst teams were instructed to submit the code used and/or generated during their analysis of the EEG data. They were asked to provide all scripts needed to reproduce their analyses. Instructions included a recommendation to clearly indicate the order of processing (e.g., by using a separate text file or by numbering the scripts). Analysts were encouraged to comment and document scripts. If analysts used a graphical user interface (GUI) analysis software, they were asked to provide GUI screenshots or a text file (e.g., in *.txt*, *.docx*, or *.pdf formats*) detailing the steps. If the software packages allowed for exporting an ordered list of functions (with all the input settings), analysts were asked to export and submit such documentation. The instructions included examples for the most common EEG analysis software.

E) *Instructions on how to submit processed EEG data.* Analyst teams were asked to submit the trial-by-trial pre-processed EEG data for each participant (i.e., after any data cleaning and processing steps but before averaging and inference). Data had to be arranged in separate folders for each participant (e.g., subj01, subj02, ...), even if participants were excluded from further analysis. All processed data of one participant had to be stored within a single file. There were no restrictions on file formats. Teams were asked to submit data in the native format used by their chosen analysis software. Additionally, teams had to include: (i) a tabular file (*.txt* or *.csv*) with the numbers/labels of channels that were identified as "bad channels" (e.g., channels that were removed and/or eventually interpolated) for each subject, (ii) a tabular file (*.txt* or *.csv*) with indices of rejected trials during pre-processing for each participant (while retaining consistent trial indices relative to all trials), (iii) a text file description (in *.txt*, *.pdf*, or. *docx* formats) detailing the total number of independent components (ICs) obtained after independent component analysis (ICA) decomposition and the number of ICs selected for removal, and the reason for their removal.

Raw meta-scientific data

Raw meta-scientific data comprises the data as submitted by analyst teams. It contains their demographic data, answers to questionnaires, results from hypothesis testing, processed EEG data, and scripts with documentation.

Demographic data. Analysts provided demographic information that included their age, gender, country of residence, highest degree obtained, and number of years since obtaining that degree, job position, number of years in that position, EEG-related research areas and topics, years of experience with EEG, number of EEG datasets analyzed, and number of published EEG papers. To reduce the possibility of linking team identifiers to persons, we split the demographic table into two: one without information on country of residence and gender, and a separate table containing only the country and gender information with a randomly assigned team number.

Prior expectations questionnaire. Before being given access to the EEG data, each analyst was asked to complete a questionnaire about their prior expectations concerning each hypothesis. They were asked to indicate the expected outcome (confirmation or rejection of the hypothesis), their confidence level based on their current understanding of the topic (on a scale from 0 to 100%, with 1% increments), and to indicate what percentage of teams they believed would confirm each hypothesis. Finally, analysts were asked to rate their expertise in all topics related to the hypotheses. The questionnaire can be found at https://osf.io/p9kda[16].

Analysis questionnaire. Each analyst team completed the Analysis questionnaire detailing their data processing steps. The questionnaire consisted of three parts: (i) analysis software, (ii) preprocessing, and (iii) inferential statistics. If analysts used different processing pipelines for different hypotheses, they were asked to report the pipeline they used for testing hypothesis 4b (i.e., the most open or unspecified one; Box 1). They were also asked to use the free-text options of the subsections of the questionnaire to report any deviation in this step for the other hypotheses. The questionnaire can be found at *https://osf.io/cemb6*[16].

Free-text results report. Analyst teams provided free-text reports of their findings for each hypothesis, similar to the results sections of peer-reviewed journal articles. We asked them to include the statistical parameters in the reports (e.g., test-statistic, p-value, or other decision criterion) that guided the decisions on whether the hypotheses were confirmed or not. We asked them to report numerical values with a high level of precision (e.g., 7–8 digits after the comma or a numerically exact fraction). Analysts were encouraged to include additional relevant information, for instance, when and where any condition differences were found, how strong they were, and to briefly discuss their findings. The form can be found at *https://osf.io/zdpu7*[16].

Processed EEG data and scripts. Analyst teams submitted processed EEG data for each participant, along with text files that detailed participant-level information, including removed channels, removed bad trials, and specifics of the independent component analysis and component rejection. Analyst teams were also asked to submit all scripts with the code used to process and analyze EEG data in a separate folder. The document with the instructions sent to the analysts can be found at https://osf.io/4nhck[16].

Posterior expectations questionnaire. At the end of the analysis phase, analysts were asked to report the results for each hypothesis. We asked analysts to rate their confidence in the reported result (on a scale from 0 to 100%, with 1% increments) and to indicate their beliefs on what percentage of teams will confirm the hypothesis. The Posterior expectations questionnaire was formulated in a similar way to the Prior expectations questionnaire. The *questionnaire* can be found at *https://osf.io/7x9jp*[16].

Curated meta-scientific data

The Steering Committee curated the data submitted by analyst teams for the following reasons: to match the format across teams for more efficient data handling (i.e., *Curated processed EEG data*), to aggregate and harmonize the level of detail in the original meta-scientific data (i.e., *Curated result forms*), and to correct possible reporting errors (i.e., *Corrected analysis questionnaire*). Specifically, the curated meta-scientific data included:

A) *Curated processed EEG data.* The processed EEG data (described in the section *Raw meta-scientific data*) were submitted in various file formats with differing names, data structures, channel orders, and epoch lengths. To facilitate data analysis across multiple teams, we converted the epoched EEG data into a common format, matching the data files in terms of their sampling rate (250 Hz), epoch length (from -200 to 600 ms relative to image onset), and number and order of channels.

B) *Curated result forms.* The free-text result forms submitted by some analyst teams (described in more detail in the section *Raw meta-scientific data*) lacked sufficient detail for statistical analyses and comparison between the teams. To acquire sufficient detail in the result reports, we asked all analyst teams to fill in a report form with predefined sections several months after the end of the analysis phase. Analysts were asked to fill in information about the time window of the effect, sensor or channel locations, frequency range (if applicable), effect size, statistical significance, corrected statistical significance (if correction for multiple comparisons was used), and interpretation of the result (significant or not) for each hypothesis separately.

C) *Corrected analysis questionnaire.* We compared the responses from the Analysis questionnaire (described in more detail in the section *"Raw meta-scientific data"*) with the data processing scripts. We developed a semi-automatic procedure to scan through the scripts and generate a report for each analyst team, listing the functions and steps detected in the scripts (a more detailed description is provided under the *Technical validation* section). We then compared these reports to the responses in the Analysis questionnaire. Responses in the Analysis questionnaire were revised, taking the information found in the scripts as the correct answer whenever a mismatch was detected through the script check procedure. The template for comparing the Analysis questionnaire responses to the processing scripts can be found at *https://osf.io/4237v*[16].

Data Records

The EEGManyPipelines dataset is available through the brainlife.io platform: https://brainlife.io/project/6863bf5c1521e536327bfea7[17]. Everyone can access and download the data after registering on brainlife.io[17] platform and agreeing to the brainlife.io *Acceptable Use Policy* and *Privacy Policy*. The data is available under the Creative Commons Attribution (CC-BY 4.0) license, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

The data can be downloaded through the web interface. When using a web interface, in the *Files* section, select the desired files or folders by checking the box next to each item. A green *Download* button will then appear in the lower-right corner of the interface, allowing you to download either individual files or entire folders.

The instructions for the analysts detailing the EEG dataset and task, questionnaires, and forms can also be found at the EEGManyPipelines Open Science Framework repository[16].

Dataset structure

The complete EEGManyPipelines dataset is arranged in three main folder structures: *Data shared with analysts*, *Raw meta-scientific data*, and *Curated meta-scientific data* (see Figure 3). The *Data shared with analysts* folder contains data from 33 subjects, information on channel locations, and documentation that was sent to the EEGManyPipelines analyst teams. The *Raw meta-scientific data* folder contains data collected from the analyst teams: demographic data, preprocessed EEG data, scripts, and questionnaires. The *Curated meta-scientific data* folder contains data from the *Raw meta-scientific data* folder that was brought to a uniform format across teams (i.e., preprocessed EEG data, curated result forms) or corrected based on information found in the scripts (i.e., corrected analysis questionnaire). Dropout rates for analyst teams at each data curation stage are shown in Figure 1A.

```
ROOT
 ¦--Data shared with analysts                                         18.7 GB
 ¦   ¦--eeg_BIDS                                                      18.7 GB
 ¦   ¦   ¦--sub-001
 ¦   ¦   ¦   °--eeg
 ¦   ¦   ¦       ¦--Sub-001_task-xxx_channels.tsv
 ¦   ¦   ¦       ¦--Sub-001_task-xxx_eeg.eeg
 ¦   ¦   ¦       ¦--Sub-001_task-xxx_eeg.json
 ¦   ¦   ¦       ¦--Sub-001_task-xxx_eeg.vhdr
 ¦   ¦   ¦       ¦--Sub-001_task-xxx_eeg.vmrk
 ¦   ¦   ¦       ¦--Sub-001_task-xxx_events.json
 ¦   ¦   ¦       °--Sub-001_task-xxx_events.tsv
 ¦   ¦   °--...
 ¦   ¦--channel_locations                                                7 KB
 ¦   ¦   ¦--chanlocs_besa.txt
 ¦   ¦   °--chanlocs_ced.txt
 ¦   ¦--events                                                          1.9 MB
 ¦   ¦   ¦--EMP01_events.csv
 ¦   ¦   ¦--...
 ¦   ¦   °--EMP33_events.csv
 ¦   °--documentation                                                   718 KB
 ¦       ¦--EMP_dataset_documentation.pdf
 ¦       ¦--EMP_instructions_for_analysts.pdf
 ¦       °--TriggerTable.csv
 ¦--Raw metascientific data                                             4.3 TB
 ¦   ¦--Demographics                                                     68 KB
 ¦   ¦   ¦--demographic_final_sample_teamID_reduced.csv
 ¦   ¦   °--demographic_country_gender.csv
 ¦   ¦--Questionnaires                                                  3.8 MB
 ¦   ¦   ¦--Analysis questionnaire
 ¦   ¦   ¦   ¦--Analysis_questionnaire.csv
 ¦   ¦   ¦   ¦--Analysis_questionnaire_code_questions.csv
 ¦   ¦   ¦   °--Raw
 ¦   ¦   ¦--Free-text results
 ¦   ¦   ¦   ¦--manypipelines_table_freetext_result.csv
 ¦   ¦   ¦   °--txt files
 ¦   ¦   ¦       ¦--Results_freetxt_h1.txt
 ¦   ¦   ¦       °--...
 ¦   ¦   °--Prior and posterior beliefs
 ¦   ¦       ¦--manypipelines_table_prior_questionnaire.csv
 ¦   ¦       °--manypipelines_table_posterior_questionnaire.csv
 ¦   °--Preprocessed EEG data and scripts
 ¦       ¦--543a674af51b043
 ¦       ¦   ¦--Data
 ¦       ¦   ¦   ¦--subj01
 ¦       ¦   ¦   ¦   ¦--Preprocessed time-series data
 ¦       ¦   ¦   ¦   ¦--Excluded sensors
 ¦       ¦   ¦   ¦   ¦--Excluded trials
 ¦       ¦   ¦   ¦   °--Removed ICA components
 ¦       ¦   ¦   °--...
 ¦       ¦   °--Scripts
 ¦       °--...
 °--Curated metascientific data                                         303 GB
     ¦--Curated preprocessed EEG data                                 302.8 GB
     ¦   ¦--standart_0a0e092a0c1e6c8f.mat
     ¦   °--...
     ¦--Curated result forms                                          215.6 MB
     ¦   ¦--result_form_d5c8ed05b7af02a3.xlsx
     ¦   ¦--...
     ¦   °--Other
     °--Curated analysis questionnaire                                  1.6 MB
         ¦--Analysis_questionnaire_corrected.csv
         °--Analysis_questionnaire_script_order_corrected.csv
```

Figure 3. File structure of the EEGManyPipelines dataset. Schematic representation of data shared with analysts, raw meta-scientific data, curated meta-scientific data, and the sub-folders included in the datasets (i.e., EEG files, preprocessing scripts, and questionnaires). The size of files and folders is listed on the right.

Data shared with the analysts

The folder *Data shared with analysts* contains the EEG data and instructions as it was shared with the analysts. The EEG data is provided in 32-bit BrainVision format files (.dat, .vhdr, and .vmrk); the data files are formatted consistent with the BIDS specification[18].

In addition to the BIDS-formatted EEG data, the folder has additional subfolders that contain information about channel locations, trigger events in the EEG data, and documentation. Channel coordinates are stored in the *chanlocs_ced.txt* file (using polar, cartesian, and spherical coordinates) and in the text file *chanlocs_besa.txt* (using BESA notation). All trigger values and their associated experimental conditions are stored in the *TriggerTable.csv* file. Information about each trial was provided as a text file for each participant. All data files included information about timing and type of relevant experimental events in the form of triggers in the data. The files with a file extension task-xxx_*events.tsv* accompanying each EEG data set also describe the trigger codes (trigger onset time, data sample, trigger channel, and trigger value), which have been extracted from the trigger channel in the corresponding EEG data file as per the BIDS standard.

Raw meta-scientific data

Demographics. Demographic information about the analysts can be found in the two comma-separated files *demographic_final_sample_teamID_reduced.csv* and *demographic_country_gender.csv*. The file *demographic_final_sample_teamID_reduced.csv* contains information on team identifier, age, job position, years in their current job position, highest degree, years since obtaining the degree, EEG field, EEG topics, years working with EEG, number of EEG datasets, and number of EEG papers published. The file *demographic_country_gender.csv* contains information on the analyst's country of residence and gender with a randomly assigned team number.

Questionnaires. The *Questionnaires* folder contains data from four questionnaires that analyst teams submitted after the data analysis phase:

- *Prior and posterior beliefs.* The folder contains files of *Prior expectations* and *Posterior expectations* questionnaires for each team. The data for the *Prior expectations questionnaire* is stored in the comma-separated file *manypipelines_table_prior_questionnaire.csv*. The data contains analysts' beliefs (confirmation or rejection) and confidence ratings for each hypothesis, along with their predictions of other teams' outcomes. The data for the *Posterior expectations questionnaire* is stored in the comma-separated file *manypipelines_table_posterior_questionnaire.csv*. The data contains information on analysts' reports, including whether their team confirmed or rejected each hypothesis, their confidence rating, and their beliefs on the percentage of teams that confirmed/rejected each hypothesis. Both files contain responses from every team member coded in the 'id' column with values ranging from 1-3 depending on the team's size.

- *Analysis questionnaire.* The analyst teams documented their analysis pipelines and the rationale behind each step. Their responses can be found in the *Analysis_questionnaire.csv* file. The columns contain codes for each question from the questionnaire. The list of questions and the corresponding column code can be found in the file *Analysis_questionnaire_code_questions.csv*.

- *Free-text results report.* The Free text results are shared in the *manypipelines_table_freetext_result.csv* file as well as in separate text files, one file for each hypothesis (see Figure 3). The documents contain information on team identifiers and team responses to the results of each hypothesis test.

Processed EEG data and scripts. Processed EEG data and scripts that were submitted at the end of the analysis phase are stored in folders named with team identifiers. Each folder contains *Data* and *Scripts* subfolders (see Figure 3). Within the Data folder, processed EEG data are stored together with complementary files for the participant (e.g., sub-001) in four folders:

- *Preprocessed time-series data*. The preprocessed EEG data and its supplementary files for each subject. The file formats depend on the software the team used.

- *Excluded sensors*. A text file containing information about the number or a label of channels excluded from the original dataset.
- *Excluded trials*. A text file with indices of the trials rejected during the preprocessing of each subject's EEG data.
- *Removed ICA components*. A *.txt*, *.docx*, or *.pdf* file with a full-text description of the total number of ICs retained in the ICA decomposition, the overall number of ICs selected for removal, and a breakdown of the number of ICs identified as pertaining to non-brain signal.

The *Scripts* folder contains the script files with the code each team used to process the EEG data. The file formats depend on the software used to process the data. If a team used GUI-based software, the *Scripts* folder will contain a *.txt* or *.pdf* file with a description of the steps and values used.

Curated meta-scientific data

Curated analysis questionnaire. The curated analysis questionnaire file format is identical to the analysis questionnaire file (described in more detail in the section *"Raw meta-scientific data"),* except that individual values have been corrected based on the provided scripts (for more details, see the *Technical Validation* section). The information can be found in the *Analysis_questionnaire_corrected.csv* file. The order of steps was not corrected in this file, but the corrected version can be found in the *Analysis_questionnaire_script_order_corrected.csv* file.

Curated result forms. Curated results forms were shared by 140 out of 168 teams, either as separate Excel files, as a single Excel file containing separate sheets for each hypothesis, as a *.ods*, .csv, *.pdf,* or *.html* file. In cases where separate files were submitted to the project, we combined them into a single Excel file (by adding results from different hypotheses to separate sheets) to facilitate file handling. If a team submitted a result form in a PDF or HTML format, we left the format intact.

Curated preprocessed EEG data. All curated processed EEG data files (n=117) are provided as a single *.mat* file per team in the typical FieldTrip structure format[19]. Each team file contains data on every participant that was included in the analysis. The trial-by-trial EEG data have the same epoch duration from -200 to 600 ms relative to image onset. All of the files contain the same number and order of channels. In case a team submitted shorter epochs or fewer channels than our defined standard, we filled the missing time points and channels with NaN values. Each file contains a prefix '*standart_*' and a team identifier, followed by a file *.mat* extension. Files contain the following fields: a time vector for every epoch, channel labels, epoched EEG data, sampling frequency, configuration structure, the order of dimensions, and trial info. More details about the curated preprocessed EEG data and data exclusion criteria can be found in the *Technical Validation* section.

Technical Validation

Data shared with the analysts

To confirm data integrity and verify that the dataset contained all necessary information for analysis, the EEGManyPipelines steering committee members conducted an ERP analysis following the same instructions given to the analysts. These results were not available to analysts. Specifically, we compared man-made scenes with natural scenes, old with new items, hits with misses, and subsequently remembered with forgotten items (see hypotheses 1-4 in Box 1). No statistical tests were carried out on these data. The condition effects identified in this analysis (Figure 4) are closely aligned with published findings in the memory literature (e.g.,[20]). This analysis was conducted solely for the purposes of verifying data integrity and illustration. It should not be regarded as a ground truth against which the analysts' results can be compared.

Besides the minimal processing of the data described above in section *EEG recordings and preprocessing*, the EEG data were provided as "raw data" without any corrections to bad channels or artifacts, as the purpose of EEGManyPipelines was to gather information on the different ways researchers would carry out these types of analyses.

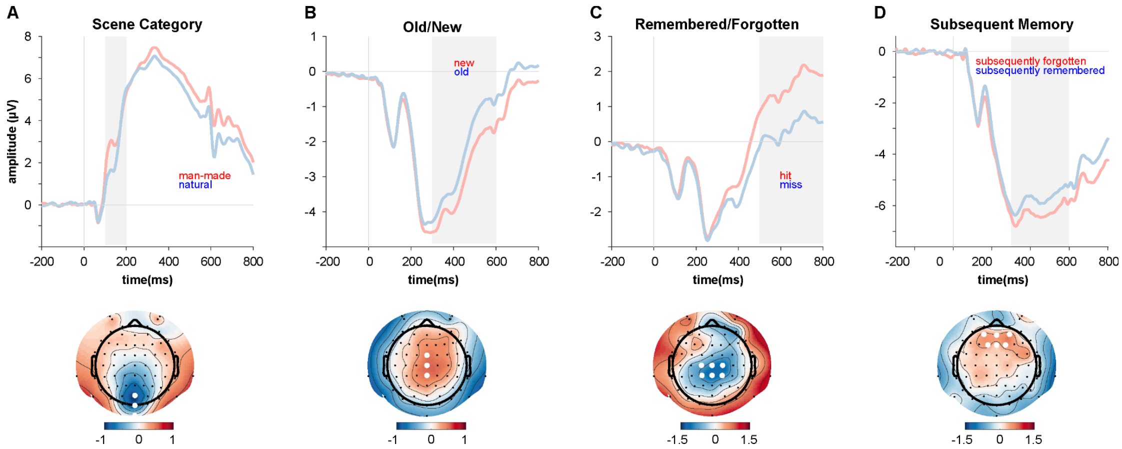

Figure 4. Analyses of four hypotheses by the EEGManyPipelines steering committee for data validation. ERP results as processed and analyzed by the lab that collected the original data. ERP analysis comparing (A) man-made vs. natural scenes (H1), (B) old vs. new items (H2), (C) remembered vs. forgotten items (H3), and (D) subsequently remembered vs. forgotten items (H4). The shaded grey areas represent intervals of mean amplitude values used to compute topographies. ERP time series are averaged across electrodes indicated by white markers in the topographies. No statistical tests were used in these analyses.

Note that the data were recorded in two distinct laboratory locations. The consistency of the trigger-to-image-onset offset between recordings from the two laboratories was tested using a photodiode, and it was consistent in both setups. Although the EEG setup, presentation software, and stimulation script were identical, the data were collected using two different computer and monitor systems, and we cannot entirely rule out the possibility that differences in acquisition setup introduced minor variations in the collected data, beyond the expected electrical interference at 50 Hz. In particular, one analyst team conducted a detailed comparison of the two sub-groups and reported a delay of ~16 ms in the first negative peak to visual stimulus onset at occipital channels between participants 1–17 (N1 mean peak latency = 71 ms) and participants 18–33 (N1 mean peak latency = 87 ms).

Raw meta-scientific data

We did not modify the data uploaded by the analyst teams. However, we checked the data for completeness by confirming successful upload of the results (listed in the *Raw meta-scientific data* part of the *Methods* section) to the provided platform. It is important to note that this nevertheless could not prevent cases of missing parts of the reports (e.g., the completeness of result reports for each tested hypothesis) or missing parts of the files (e.g., missing parts of the scripts, empty EEG data within a file, and missing markers). We did not exclude any team based on the findings or procedures.

Curated meta-scientific data

Corrected analysis questionnaire. To correct the Analysis questionnaire for possible errors as well as empty responses, we developed a semi-automatic procedure, which included the following steps:

1. We used an automated procedure to identify the functions used by each team in their submitted code. We identified function names for MATLAB-based toolboxes as strings before a bracket. For Python-based toolboxes, we used the AST (Abstract Syntax Tree) module to systematically extract function names along with their input parameters.

2. We visually inspected the list of all unique function names found in step 1 and determined whether the function was relevant for data processing (based on function names found in toolboxes for EEG data processing).

3. We grouped all function names into 12 categories representing different processing steps based on all identified functions found in the scripts (i.e., filtering, re-referencing, downsampling, subject exclusion, trial exclusion, artefact correction, baseline correction, epoching, interpolation, detrending, sensor exclusion, and multiple classes for functions that were used for multiple processing steps, including the aforementioned ones).

4. We used the relevant function list from step 2 to scan the codes again, but this time, we looked for the parameters passed to the functions.

5. We created a list of all function names and function arguments, as well as their class (based on step 3), for each team.

6. We compared the list from step 5 to the self-report of each team in the Analysis questionnaire, correcting mismatches (taking the information found in the scripts as the correct answer) or filling in missing data. These steps included choices associated with downsampling, segment exclusion, channel exclusion, interpolation, participant exclusion, high-pass, low-pass, and notch filters, re-referencing, method of artifact correction and selection, detrending, spatial transformation, order of steps, baseline correction, and epoching. These selected steps encompassed 59 questions on the data processing choices and 15 questions on the order of steps (and an additional 16 clarification questions) from the Analysis questionnaire that were checked in 165 teams (totalling 12,210 entries). Entries of three teams could not be corrected due to difficulties in opening files containing code.

Based on this procedure, we corrected 281 entries (44 empty responses and 237 mismatches, a total of 2.9% of the responses) from the selected 59 fields in the Analysis questionnaire. Reports from 104 teams were adjusted based on this procedure. We did not include counts of errors or misses in the reported order of steps. This was due to ambiguities in the reports, as several teams described steps that were not specified in the *order of steps* section of the *Analysis questionnaire*. A corrected version of the step order, with the number of steps held constant, is provided in the file *Analysis_questionnaire_script_order_corrected.csv*.

Curated preprocessed EEG data. We validated that the data could be opened and loaded into MATLAB software. We also confirmed that all data in the *Curated preprocessed EEG data* folder has the same epoch length, aligned to the image onset, and has a matching order of channels, and has the same sampling rate. We curated the data of 117 teams. Data from 51 teams could not be brought to the common format due to the following reasons: non-epoched data (n=23), failure to open the data (n=18), missing channel or time information (n=8), mismatch in data dimensions (n=1), and a part of the files missing (n=1). Data submitted in volts were converted to the same scale (microvolts) for 34 teams.

Curated results forms. Out of 140 teams, two teams submitted the result forms in a .pdf file format, two teams submitted .ods files, one team submitted a .csv file, and one team submitted an HTML file. Six teams submitted files that could not be aggregated within a single file and were added to the *Other* subfolder.

Usage Notes

Data shared with the analysts

The EEG dataset shared with the analysts may be used just as any other EEG dataset. The data can be used to investigate research questions on neural dynamics underlying different memory processes.

Raw and curated meta-scientific data

At the time of releasing the EEGManyPipelines dataset, we analyzed the processed EEG data and statistical test outcomes submitted by the analysts for three hypotheses (hypotheses 1, 2a, and 3a, see Box 1). The main findings concerning the results of these hypotheses will be published under the same project name. All three hypotheses concerned EEG voltage differences between different conditions and were analyzed by linking EEG data processing steps (from the corrected analysis questionnaire) to the obtained p-value and ERP difference waves. Other hypotheses, including hypotheses regarding the effects of the time-frequency distribution and power of two oscillatory bands, have not yet been analyzed. In addition to the hypotheses not yet analyzed, we suggest several other lines of research worthy of further investigation from a metascience perspective. Below, we outline a few potential uses for the data.

The EEGManyPipelines dataset contains a comprehensive comparative database of code from researchers who were asked to analyze the same data and address the same research questions. A single dataset comprising 168 pipelines enables the systematic mapping of tool choice, pipeline complexity, and adherence to best-practice guidelines. Since the task and data are the same for all analysis teams, it offers better comparability and more reliable options for estimating variability compared to scraping scripts and code from researchers' repositories (e.g., GitHub), which are typically developed to answer different questions and applied to various datasets.

The scripts collected in the database provide a unique sample of coding practices in cognitive neuroscience that allows not only to explore questions that are specific to the task given in the EEGManyPipelines project, but also to go beyond the original task and focus more generally on coding practices and technical implementation. The scripts could be used, for example, to guide the teaching of neuroscience students or to test the robustness of pipelines by investigating how well the code performs across different systems and platforms. They can also be analyzed using text mining or other approaches that quantify aspects of the scripts themselves—for example, investigating which functions or tools were used across teams to study variability in coding style. The scripts can also be used to explore how accessible the code is or to evaluate how well the coding practices follow established recommendations for building analysis pipelines (e.g., Van Vliet, 2020 [21]).

The EEG data shared with the analysts can serve as a reference for comparing data before and after processing for each of the datasets submitted by the analysts. This is useful for further analyses that seek to compare the impact of specific analysis steps identified in EEG pipelines, e.g., testing if and how a given processing step reduces variability or noise by comparing raw to processed data (e.g., Delorme, 2023[22]). The raw data can also be used to replicate the processing by the analysts by applying their scripts to the data. Note that the submitted processed data includes different file formats, depending on the software that was used to analyze the data. While most EEG analysis software supports cross-format reading of EEG data files, there may be cases where specific software is needed. In such cases, please refer either to (i) the analysis questionnaire where the analysts reported what software they used, (ii) the code provided by the analysts, or (iii) to the code used to read and aggregate curated EEG data. This can also be used to explore specific technical details about the data, such as file formats used, the size of data files, or similar questions.

Finally, the EEGManyPipelines dataset is rich in unrestrained qualitative reports of tests of different hypotheses. The free-text results sections, submitted by analyst teams in addition to their binary hypothesis test outcomes, offer a unique opportunity to study how reporting practices and scientific conclusions are influenced by sociological factors other than data and hypotheses. The free-text forms provide both a qualitative description of the results and a window into how the analysts chose to summarise their findings – it can be used for qualitative analyses or quantified with various text mining approaches. Findings such as these could be relevant not only to the EEG community but also to cognitive neuroscientists at large.

Limitations

We would like to outline a few limitations of the collected data. Although the analyst teams constitute an expert sample, they varied in familiarity with the hypotheses. High variability in reporting practices within Free-text results reports can make it challenging to automatically extract distinct information (e.g., channels included in the analyses) across all reports. Advanced text mining techniques may be required to address these challenges. Furthermore, the Free-text results report might lack details about the statistical outcome and conclusion for each hypothesis (e.g., the location of an effect is often under-reported). Finally, collected data does not allow addressing replication problems related to differences in hardware (e.g., different montages, amplifiers, impedances).

Ethical considerations in data use

As a comprehensive metascience repository, the EEGManyPipelines dataset can be used to explore numerous metascience questions. It is shared with the intent of Findability, Accessibility, Interoperability, and Reuse of digital assets (FAIR, https://www.go-fair.org/fair-principles/) for researchers to pursue their metascience analyses. This can encompass testing a metascience hypothesis not covered by the initial intent of the EEGManyPipelines project, for instance, by exploring associations between the demographic data, analysis questionnaire, or scripts used to process EEG data. We encourage researchers to use the dataset to its fullest to boost the emerging field of metascience and provide new insight into scientific practices. However, we discourage analyses that seek to single out specific individuals or demographic groups. The EEGManyPipelines project is a large collaborative project built on trust between all involved researchers and dedication to sharing one's analysis choices and processed data. To be part of many analyst studies requires a certain open-mindedness and willingness to put one's research practice under scrutiny for the betterment of science.

Data Availability

The EEGManyPipelines dataset can be downloaded from the brainlife.io platform (https://brainlife.io/project/6863bf5c1521e536327bfea7[17]) under the Creative Commons Attribution (CC-BY) license. The instructions for the analysts detailing the EEG dataset and task, the questionnaires, and forms can also be found at the EEGManyPipelines Open Science Framework repository[16].

Code Availability

The code for the curated EEG data, as well as plots for the data descriptor paper, can be found at https://github.com/EEGManyPipelines/Dataset_paper.

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Acknowledgements

We would like to thank Russell Poldrack for his valuable feedback to the study design and execution. We would also like to thank Joshua D. Koen, Maryam Alimardani, Dani Bassett, Matthias Franken, David Lydon-Staley, Amanda L. McGowan, Ting Mei for taking part in the initial stages of the project.

Funding Acknowledgements

The EEGManyPipelines project is supported by grants from German Research Foundation (DFG; BU 2400/11-1) to Niko A. Busch, by the DFG priority program "META-REP: A Meta-scientific Programme to Analyse and Optimise Replicability in the Behavioural, Social, and Cognitive Sciences" to Niko A. Busch and Elena Cesnaite, and Riksbankens Jubileumsfond (grant number: P21-0384) to Gustav Nilsonne, together with Mikkel C. Vinding and Niko A. Busch. Annalisa Pascarella acknowledges the Gruppo Nazionale Calcolo Scientifico-Istituto Nazionale di Alta Matematica (GNCS-INdAM). Darinka Trübutschek was supported by the European Union's Horizon 2020 research and innovation program under the Marie Sklodowska-Curie grant number 101023805. Alessandra Anzolin was funded by National Institutes of Health (NIH), National Center for Complementary and Integrative Health (NCCIH), Award Number R21-AT013513 and the Logan University-Martinos Center-Spaulding Integrative Neuroimaging Training Fellowship. Yana Arkhipova was supported by the German Research Foundation DFG via SFB 1287, project B03. Maria Azanova was supported by the German Federal Ministry of Education and Research (BMBF) and the Max Planck Society. Ceren Battal was supported by The Portuguese Foundation for Science and Technology (FCT). Giulio Bernardi was supported by an ERC Starting Grant (TweakDreams; Grant agreement ID: 948891). Claire Braboszcz was funded by the European Union's Horizon 2020 research and innovation programme under Marie Skłodowska-Curie grant agreement No. 801342 (Tecniospring INDUSTRY) and the Government of Catalonia's Agency for Business Competitiveness (ACCIÓ). Florian Bublatzky was funded by Deutsche Forschungsgemeinschaft (DFG, German Research Foundations) – Project-ID 290032019. Xim Cerda-Company was supported by a project (PID2023-151083NA-I00) funded by MICIU/AEI/10.13039/501100011033 and FEDER, UE. Karan Chugani was funded by the European Union's Horizon 2020 research and innovation programme under grant agreement No. 945307 (Emotional Cities). Oren Civier, Matthew Hughes, Tom Johnstone, William Woods and David White acknowledge the facilities and scientific and technical assistance of the National Imaging Facility, a National Collaborative Research Infrastructure Strategy (NCRIS) capability, at Swinburne Neuroimaging, Swinburne University of Technology. César E. Corona-González expresses sincere gratitude to SECIHTI for the financial support received during the PhD program (reference number: 894658). Martin Dietz was supported by the Lundbeck Foundation (ref. R322-2019-2711). M. Dolores del Castillo was funded by the MICIU/AEI/ 10.13039/501100011033 (Spanish Ministry of Science, Innovation and Universities, Spanish State Research Agency; grant PID2023-150271NB-C21), and iRoboCity2030-CM (grant TEC-2024/TEC-62). Anna Dreber was funded by the Knut and Alice Wallenberg Foundation. Linda Drijvers was funded by the Max Planck Society through a Minerva Fast Track Fellowship awarded to Linda Drijvers. Brandi Lee Drisdelle was funded by the Natural Sciences and Engineering Research Council of Canada (NSERC) Postdoctoral Fellowships program and the Fonds de recherche du Québec – Nature et technologies (FRQNT) Postdoctoral research scholarship program. Gian Marco Duma was funded by Ricerca Corrente from Italian Ministry of Health. Guillaume Dumas was funded by the Institute for Data Valorization, Montreal (IVADO; CF00137433), the Fonds de recherche du Québec (FRQ; 285289), the Natural Sciences and Engineering Research Council of Canada (NSERC; DGECR-2023-00089), the Canadian Institute for Health Research (CIHR 192031; SCALE). The computational analyses were enabled in part by support provided by Calcul Québec (www.calculquebec.ca) and Digital Research Alliance of Canada (www.alliancecan.ca). Benedikt

Ehinger was funded by Deutsche Forschungsgemeinschaft (DFG, German Research Foundations) in the Emmy Noether Programme - Project-ID 538578433. Stefanie Evas was funded by an Industry PhD award comprising an Australian Government Research Training Program Stipend (RTPS) administered by the University of Adelaide, together with funding from the Commonwealth Scientific and Industrial Research Organisation (CSIRO, Australia) and Fonterra Co-operative Group Limited (New Zealand). Gordon B. Feld was funded by Deutsche Forschungsgemeinschaft (DFG, German Research Foundations) in the Emmy Noether Programme - 404679789. Norman Forschack was supported by the Deutsche Forschungsgemeinschaft (DFG grants: FO 1615/1-1, MU 972/29-1). Haydée G. García Lázaro was supported by the Smith-Kettlewell Eye Research Institute's C.V. Starr Fellowship Fund and the E. Matilda Ziegler Foundation for the Blind. Carlos González-García was supported by Project PID2023-149428NB-I00 funded by MCIN/AEI/10.13039/501100011033 and by FEDER, EU, and Grant RYC2021-033536-I funded by MCIN/AEI/10.13039/501100011033 and by the European Union NextGeneration EU/PRTR. Benjamin J. Griffiths was funded by a Leverhulme Trust Early Career Fellowship (ECF-2021-628). Anthony M. Harris was supported by the Australian Research Council (DE220101019). Stefan Haufe was supported by an ERC Starting Grant (TrueBrainConnect; Grant agreement ID: 758985). Alice Hodapp was funded by the German Research Foundation DFG Emmy Noether grant RA 2715/2-1. Chun-Hsien Hsu was funded by National Science and Technology Council, Taiwan (MOST-108-2636-H-008-001 & 114-2410-H-008 -042). Christoph Huber-Huber was supported by a Marie Skłodowska-Curie Individual Fellowship (No. 846392) and by the Ministry of Universities and Research Italy (MUR) within the NextGenerationEU/PNRR framework (grant number 0000027). Augustin Ibanez was supported by the Multi-Partner Consortium to Expand Dementia Research in Latin America (ReDLat), supported by the Fogarty International Center (FIC), the National Institutes of Health, the National Institute on Aging (R01 AG057234, R01 AG075775, R01 AG21051, R01 AG083799, CARDS-NIH 75N95022C00031), the Alzheimer's Association (SG-20-725707), the Rainwater Charitable Foundation – The Bluefield Project to Cure FTD, and the Global Brain Health Institute. AI is also supported by ANID/FONDECYT Regular (1250091, 1210176, 1220995) and ANID/FONDAP/15150012. Bradley N. Jack was funded by the Australian Research Council (DE220100739). Taeho Kang was partially funded by the Institute of Information & Communications Technology Planning & Evaluation (IITP) Grants from the Korean government (No. 2017-0-00451), partially funded by the Austrian Science Fund (FWF) 10.55776/I6222. Hamid Karimi-Rouzbahani was supported by Newton International Fellowship (NIF\R1\192608) and follow-on fundings (AL231037 & AL24100035) from the Royal Society and Australian Research Council DECRA Fellowship DE230100608. Bruno Kopp was funded by Karlheinz-Hartmann Stiftung, Hannover. Daniel S. Kluger was funded by the European Union (ERC StG No. 101162169) and the Innovative Medical Research (IMF) programme of the University of Münster (grant ID KL 1 2 22 01). Corinna Kührt was funded by the German Research Foundation (DFG, Deutsche Forschungsgemeinschaft) as part of the Collaborative Research Centre "Volition and Cognitive Control" – SFB 940/2 – and Germany's Excellence Strategy – EXC 2050/1 – Project ID 390696704 – Cluster of Excellence "Centre for Tactile Internet with Human-in-the-Loop" (CeTI) of Technische Universität Dresden. Martin Lamoš was supported by the core facility MAFIL supported by MEYS CR (LM2023050 Czech-BioImaging), part of the Euro-BioImaging (www.eurobioimaging.eu) ALM and Medical Imaging Node (Brno, CZ). Vladimir Litvak was supported by core funding from Wellcome Centre for Human Neuroimaging (203147/Z/16/Z). Alicia Luque was supported by the César Nombela Talent Attraction Grant (2023-T1/PH-HUM-29098), funded by the General Directorate of Research and Technological Innovation of the Regional Government of Madrid (Spain). Radek Marecek was supported by the core facility MAFIL supported by MEYS CR (LM2023050 Czech-BioImaging), part of the Euro-BioImaging (www.eurobioimaging.eu) ALM and Medical Imaging Node (Brno, CZ). Anna Marzecova was funded by the Deutsche Forschungsgemeinschaft (DFG) grant JO-787/6-1 and Research Foundation Flanders (FWO) postdoctoral fellowship (12V5620 N). Jason B. Mattingley was funded by an Investigator Grant awarded by the Australian National Health and Medical Research Council (NHMRC, GNT2010141). Sara Mazzini was funded by the Max Planck Society through a Minerva Fast Track Fellowship awarded to Linda Drijvers. Maria Montefinese was funded by the

Investment line 1.2 “Funding projects presented by young researchers” (CHILDCONTROL) from the European Union -NextGenerationEU. Faisal Mushtaq was supported by funding from UKRI BBSRC (BB/X008428/1), the National Institute for Health and Care Research (NIHR) Leeds Biomedical Research Centre (NIHR203331) and the EEG101 European COST Action (CA24148). Guiomar Niso was supported by the Spanish Government RYC2021-033763-I and PID2023-150034OA-I00. Norberto E. Naal-Ruiz was supported by Tecnologico de Monterrey and the Secretariat of Science, Humanities, Technology, and Innovation (SECIHTI). Robert Oostenveld was funded by the European Union through the SIESTA project (Horizon Europe) under Grant number 101131957. Andrea B. Protzner was supported by a Natural Sciences and Engineering Research Council of Canada Discovery Grant (05299–2020). Milena Rabovsky was supported by the German Research Foundation DFG Emmy Noether grant RA 2715/2-1. Pavel Riha was supported by the Czech Health Research Council AZV NU22-04-00661 and the core facility MAFIL supported by MEYS CR (LM2023050 Czech-BioImaging), part of the Euro-BioImaging (www.eurobioimaging.eu) ALM and Medical Imaging Node (Brno, CZ). Johannes Rodrigues was funded by Deutsche Forschungsgemeinschaft (DFG, German Research Foundations) – Project-ID 540631605 and the European Union through the project “Hyperautomation Ökosystem (Hyko)“ (1.2-StMWKF.4-UFR-002) in the European fonds for regional development (ERDF). Judith Schepers was supported by the International Max Planck Research School for Intelligent Systems (IMPRS-IS). Noor Seijdel was funded by the Max Planck Society through a Minerva Fast Track Fellowship awarded to Linda Drijvers. Magdalena Senderecka was supported by the National Science Centre of Poland (2020/38/E/HS6/00490). J. Ignacio Serrano was supported by the MICIU/AEI/ 10.13039/501100011033 (Spanish Ministry of Science, Innovation and Universities, Spanish State Research Agency; grant PID2023-150271NB-C21), and iRoboCity2030-CM (grant TEC-2024/TEC-62). Cassie Ann Short was supported by the Deutsche Forschungsgemeinschaft (DFG, German Research Foundations) grant WA2593/9-1. Esaú V. Sirius was funded by São Paulo Research Foundation (FAPESP) (grant number 2019/06423-7). René Skukies would like to thank the Deutsche Forschungsgemeinschaft (DFG, German Research Foundation) for supporting this work by funding - EXC2075 – 390740016 under Germany's Excellence Strategy. We acknowledge the support by the Stuttgart Center for Simulation Science (SimTech). Aureli Soria-Frisch was funded by the European Union’s Horizon 2020 research and innovation programme under grant agreement No. 945307 (Emotional Cities). Simon R. Steinkamp was funded by a Novo Nordisk Foundation Exploratory Interdisciplinary Synergy Grant, ref NNF20OC0064869. Alessandro Tavano was supported by the Deutsche Forschungsgemeinschaft (DFG) Grant number 510229904 and the Max Planck Society. Nivethida Thirugnanasambandam was supported by DBT/Wellcome Trust India Alliance Fellowship (IA/CPHI/16/1/50264)). Luca Turella was supported by the European Union – Next Generation EU, in the framework of the project MNESYS - A MULTISCALE INTEGRATED APPROACH TO THE STUDY OF THE NERVOUS SYSTEM IN HEALTH AND DISEASE (Prot. n. PE00000006). Luca Turella was also supported by the European Union - Next Generation EU PRIN 2022 (DD 104 02/02/22) – PNRR – M4 – C2 – INV1.1 – PRIN –Project Title [COMPArative charACTterization of the parietal lobe: a multimodal approach (COMPAACT project)] – project identifier code [2022JT852C] – CUP [E53D23022180006]. The views and opinions expressed are solely those of the authors and do not necessarily reflect those of the European Union, nor can the European Union be held responsible for them. Eric Luis Uhlmann was supported by funding from the INSEAD R&D Committee. José Luis Ulloa was supported by the Programa de Investigación Asociativa (PIA) en Ciencias Cognitivas of the Cognitive Science Research Center at Universidad de Talca and the FONDEQUIP-ANID project EQM190153. Adrià Vilà-Balló was funded by MICIU/AEI (10.13039/501100011033), FEDER, EU (project PID2023-151083NA-I00), the Dirección General de Ordenación del Juego, Ministerio de Derechos Sociales, Consumo y Agenda 2030 (project SUBV24/00014), and the European Union’s Horizon Europe programme (grant agreement No. 101155881; HORIZON-HLTH-2024-DISEASE-03-two-stage). Marijn van Vliet was funded by the Research Council of Finland, (RCF) grant #343385. Ingmar E. J. de Vries was supported by a Marie Skłodowska-Curie Postdoctoral Fellowship (No. 101060807). Gwen van der Wijk was supported in her work through a Mamdani Family Foundation Graduate Scholarship and Alberta Graduate Excellence

Scholarship (AGES: International). Audrey Wong-Kee-You was supported by the Rachel C. Atkinson Postdoctoral Fellowship. Judy D. Zhu was supported by the Australian National Imaging Facility, a National Collaborative Research Infrastructure Strategy (NCRIS) capability, at the KIT-Macquarie Brain Research (MEG) Laboratory, Macquarie University.

Competing interests

Omid Abbasi is the CEO of Virgobit GmbH, a company that creates healthcare software solutions.nPaulo Rodrigo Bazán started working at Brain Products GmbH in March 2024. Karan Chugani, Aureli Soria-Frisch, and Claire Braboszcz are employees of Starlab, Barcelona. Aureli Soria-Frisch works at Starlab Barcelona SL and is an advisor of Neuroelectrics. Mahmoud Hassan is the Founder and CEO of MINDIG. Jörg Hipp is a full-time employee of F. Hoffmann-La Roche Ltd. Agustin Ibanez is supported by the Multi-Partner Consortium to Expand Dementia Research in Latin America (ReDLat), supported by the Fogarty International Center (FIC), the National Institutes of Health, the National Institute on Aging (R01 AG057234, R01 AG075775, R01 AG21051, R01 AG083799, CARDS-NIH 75N95022C00031), the Alzheimer's Association (SG-20-725707), the Rainwater Charitable Foundation – The Bluefield Project to Cure FTD, and the Global Brain Health Institute. Agustin Ibanez is also supported by ANID/FONDECYT Regular (1250091, 1210176, 1220995) and ANID/FONDAP/15150012. Muhammad Samran Navid is associated with Brain Products GmbH since December 2025. All other authors declare no competing interests.

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Appendix

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