

1 **Many Pipelines, One Dataset: Analytic Flexibility and Its Impact in EEG**
2 **Research**

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4 **Authors**

5 *The list of authors and their affiliations appear at the bottom of the manuscript (page 30).*

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9 *Cesnaite, E., Algermissen, J., Vinding, M. C., Vitale, A., Pascarella, A., Fischer, N. L., Yang, Y.-*
10 *F., Trübutschek, D., Gianelli, C., Marshall, C. R., Abbasi, O., Adamovich, T., Adel, L., Agarwal,*
11 *N., Aguado-López, B., Ajmeria, U., Al, E., Aldeen, H., Alejandro, R. J., ..., Nilsson, G., Busch, N.*
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14
15 **Abstract**

16 *The EEGManyPipelines initiative included 396 scientists (168 teams) who independently*
17 *analyzed the same dataset to test the same hypotheses, mapping the full landscape of analytical*
18 *decisions. This captured an underexamined source of variability in research results: data*
19 *processing choices needed to arrive at an analyzable dataset. Considering full analysis pipelines,*
20 *ERP variability across teams was equivalent to variability across participants, suggesting that who*
21 *analyses the data is as important as who provides it. In contrast to prior many-analyst projects,*
22 *typically explaining less than 10% of variance in estimates, our granular codings of researcher*
23 *choices explained 53%, 75%, and 51% of the variance in difference waves across three*
24 *hypotheses, with unusual results partly attributable to deviations from the prototypical pipeline.*
25 *Despite the heterogeneity in approaches and estimates, teams reached a substantial consensus*
26 *on effect presence. By being transparent across all analysis stages, researchers can identify*
27 *uncertainty and still draw meaningful inferences.*

28
29
30 Scientific inquiry involves many steps between ideation and realization in the form of empirical
31 results. Each of these steps requires researchers to make choices—often with a diversity of
32 justifiable approaches—which can shape the ultimate outcome. Variability in the results of studies
33 attempting to address a given research question may arise at many levels, from (a) participant
34 characteristics and population differences, (b) features of the study design and method, (c) data
35 preprocessing and preparation steps, and (d) the statistical inference and interpretation of
36 results¹. In the normal course of science, carried out by small teams of investigators, the roles of
37 these factors are difficult to disentangle from one another. Traditional research approaches, such
38 as meta-analysis, have limited ability to identify such sources of heterogeneity. Individual
39 investigations differ across all of these dimensions simultaneously, data are often not available
40 for re-analysis²⁻⁴, and the mapping of analytic choices in published work is limited⁵.

41 Crowd science initiatives, organized by numerous partner laboratories around the world, can start
42 to isolate these influences by holding nearly all of them constant while allowing one to vary
43 naturally^{6–12}. Many Labs consortia repeat the same study methods across research sites,
44 revealing surprisingly limited population heterogeneity in replication results^{7,13,14}. In contrast, in
45 many-analyst initiatives, independent researchers analyze the same dataset to answer the same
46 set of hypotheses, rendering transparent differences in statistical approaches and empirical
47 estimates^{1,12,15–17}. With the sole exception of Botvinik-Nezer et al. (2020) in the fMRI domain, such
48 projects have presented the crowd of participating scientists not with the raw data, but with
49 processed and prepared data ready to analyze, potentially imposing artificial homogeneity and
50 preventing the full diversity of research pipelines from emerging naturally. For example, Aczel et
51 al.¹⁸ provided analysts with datasets from the replication packages of published papers, which
52 already had embedded within them numerous decisions by the original team. In addition, previous
53 many-analyst projects have typically explained less than 10% of the variability in empirical
54 estimates (e.g.,^{8,12,16,19}). This limited explanatory power may partly reflect their reliance on
55 relatively coarse codings of analysis characteristics, rather than detailed mappings of the full
56 analytic decision process. Finally, although they recruited far more perspectives on the data than
57 a standard small science investigation, the number of independent analyses was often small in
58 absolute terms (e.g., 29 teams in¹², and 23 individual analysts in¹⁹). This calls for even larger-
59 scale projects recruiting more analysts as well as new quantitative approaches featuring granular
60 codings of the full stream of researcher decisions, including the precise ordering of pipeline steps.

61 The EEGManyPipelines project was designed to investigate preprocessing and analysis pipelines
62 “in the wild”—that is, how researchers process and interpret the same raw data using their usual
63 workflows²⁰. Electroencephalography (EEG) is a core method in cognitive neuroscience valued
64 for its fine-grained temporal resolution and broad accessibility. EEG analysis involves a cascade
65 of interdependent decisions^{21–23}, which vary across researchers and laboratories and can affect
66 results^{24–27}. Before comparing brain responses between two conditions, researchers must decide
67 how and in what order to filter the data, detect and remove artifacts, reference the signal, segment
68 it into time windows, and select electrodes and time windows in which they want to test for the
69 presence of an effect. Even preprocessing steps thus span a broad parameter space and can
70 include epistemic as well as procedural considerations. At the same time, statistical modeling
71 likewise differs widely across researchers^{25,26}.

72 The goals of this six-year-long initiative, involving 431 participating researchers (396 of whom
73 analysed the initial dataset) at 358 institutions in 40 countries, were threefold. First, we sought to
74 capture variability in the full set of researcher decisions from raw EEG data to statistical inference,
75 as well as variability in the eventual results. As a benchmark, we quantitatively compared
76 variability in research results attributable to analysis pipelines relative to a better known source of
77 variability in results: the participants themselves. If cross-analyst variability matches cross-
78 participant variability in magnitude, this confirms that researcher decisions about what to do with
79 raw data profoundly shape research results – and thus warrant much greater consideration,
80 transparency, and scrutiny than has been forthcoming to date. Second, we aimed to
81 systematically map and link variability in researcher choices across their workflow to variability in
82 their results – and by doing so address the “parsing problem”²⁸ that has frustrated past many-
83 analyst projects in which most of the heterogeneity in estimates remained unaccounted for. As a

84 part of this effort, we quantified the extent to which specifications departed from the norm, both in
85 the choices made and the precise ordering of those choices, and tested whether uncommon
86 approaches account for uncommon results^{29,30}. Finally, we explored whether quantitative
87 dispersion of results can co-occur with qualitative convergence in scientific conclusions. Even if
88 EEG research teams differ greatly in the magnitude of their estimates from the time-series data,
89 they could ultimately agree on the presence or absence of a phenomenon. If so, scientific
90 transparency and the increased uncertainty that can go along with it can coexist with meaningful
91 collective conclusions.

92 Results

93 The Steering Committee of the EEGManyPipelines project selected a dataset representative of a
94 typical EEG experiment, comprising EEG data from 33 human participants who performed a long-
95 term memory task. We originally planned to test eight hypotheses, but narrowed our focus to the
96 three primary ones due to time and resource constraints. We selected the three event-related
97 potential (ERP) hypotheses (see Box 1), related to scene category (hypothesis 1), novelty
98 (hypothesis 2), and recognition memory (hypothesis 3), including early and late ERP components,
99 to assess how generalizable the results are across established hypotheses. These include two
100 hypotheses with specific formulations (hypotheses 1 and 2), and one with a more open-ended
101 formulation (hypothesis 3), which did not restrict the time window or electrode location, allowing
102 us to explore whether hypothesis specificity influences analytic variability. Below, we report the
103 results from 168 teams who completed the data analysis for the three hypotheses. We examine
104 variability in analysis pipelines, variability in reported results, and the link between the two.

Hypotheses analyzed by analyst teams

1. 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.
2. There are effects of image novelty (i.e., between images shown for the first time/new vs. repeated/old images) within the time-range 300-500 ms on EEG voltage at fronto-central channels.
3. 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]) on EEG voltage at any channels, at any time.

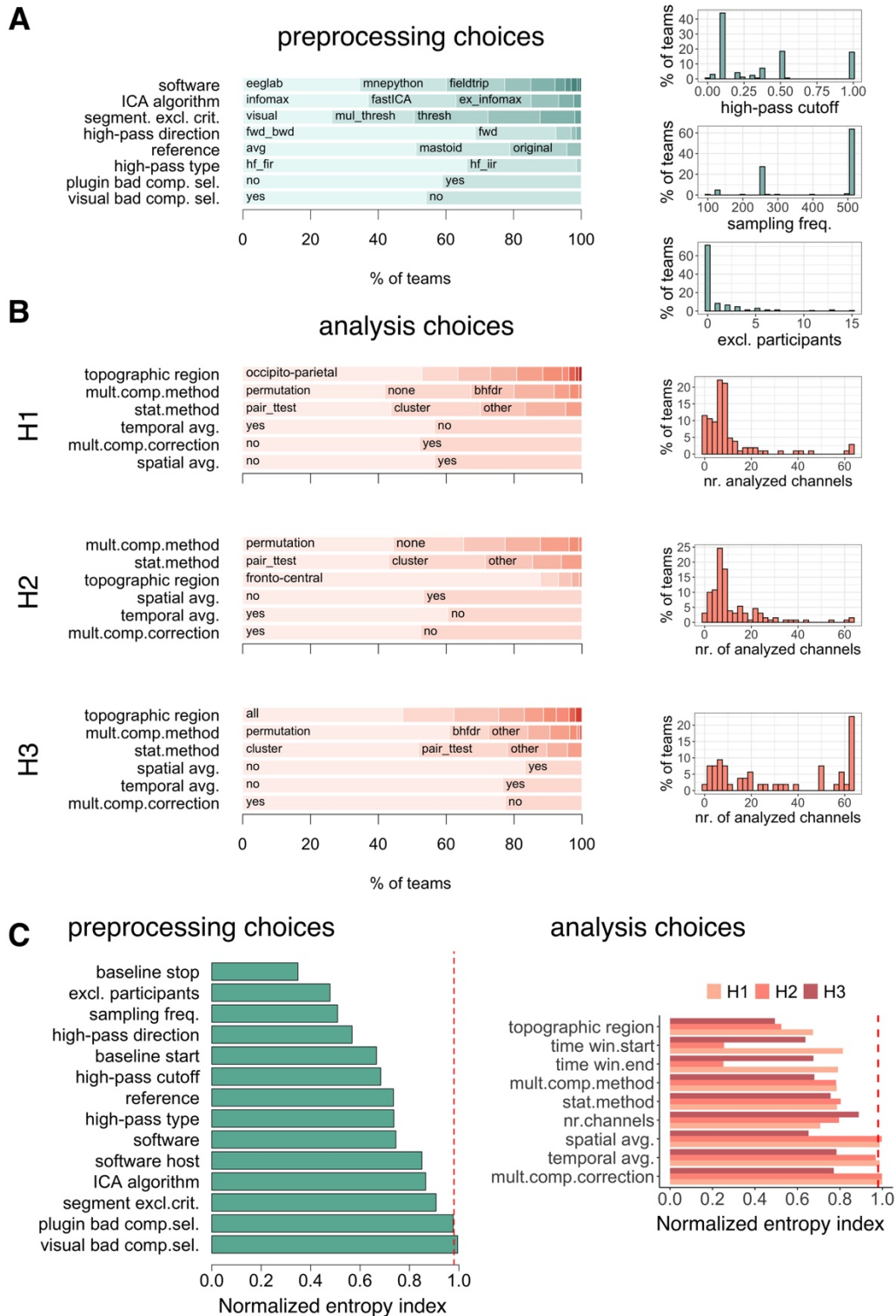
105 **Box 1.** Hypotheses analyzed by analyst teams whose results are presented in this paper.

106 **2.1. Quantifying divergence in approaches across teams**

107 Several recent studies attempted to map the variability of EEG analysis practices based on
108 published reports^{26,31}. Yet there is currently no empirical reference framework for evaluating the
109 observed diversity of real-life analysis pipelines applied to the same dataset. The
110 EEGManyPipelines project addresses this gap by providing the first data-driven characterization
111 of how EEG data are analyzed in practice, based on complete analysis pipelines implemented by
112 independent research teams analyzing the same dataset. At the same time, categorizing analysis
113 choices into discrete pipeline components necessarily involved some loss of granularity, as the
114 richness and nuance of real-world processing decisions cannot be fully captured by predefined
115 categories.

116 No two submitted pipelines were identical in their preprocessing and analysis choices. Teams
117 used a range of common EEG analysis packages (the most common were EEGLAB, MNE-
118 Python, and FieldTrip), and different reference schemes and high-pass filter cutoff values (Figure
119 1A). Pipelines included manual and automated procedures. Forty-eight teams excluded varying
120 numbers of participants from their analysis (Supplementary Figure S1). Statistical analysis
121 choices also varied considerably across teams (Figure 1B).

122 We quantified the overall agreement across teams using a normalized entropy index (NE) for
123 each preprocessing step (constant across hypotheses) and for each analysis choice (often
124 different across the three hypotheses). NE index values range from 0 to 1, where 0 indicates
125 perfect agreement across teams and 1 reflects a uniform distribution of choices, corresponding
126 to complete disagreement. For one of the 14 preprocessing steps (visual artifact-related
127 component selection), the distribution of choices was consistent with a uniform distribution
128 (NE=0.99, Figure 1 C). For two out of the nine analysis steps (averaging across channels, and
129 correcting for multiple comparisons), the distribution of choices was consistent with a uniform
130 distribution for both hypotheses 1 and 2 (both NE = 0.99). For hypothesis 2, but not others,
131 averaging across time window bins yielded the NE of 0.99. These results suggest very high
132 (almost maximal) variability even for these more specific hypotheses. In contrast, for hypothesis
133 3, no analysis step was consistent with a uniform distribution, indicating that, for this more open
134 hypothesis, pipeline choices were actually more homogeneous. One possible explanation for this
135 pattern is that, in the case of a more open-ended hypothesis without predefined time windows or
136 channels, there may be greater consensus about appropriate exploratory statistical approaches,
137 for instance, cluster statistics.



138

139 **Figure 1. Variability in EEG preprocessing and analysis steps.** A. Variability in choices for
 140 preprocessing steps for categorical (left) and continuous (right) variables. B. Variability in choices for each
 141 analysis step, separately for the three hypotheses. Variables are ordered by the number of different choice
 142 options. The colour gradient for categorical variables reflects the frequency of each response, with lighter

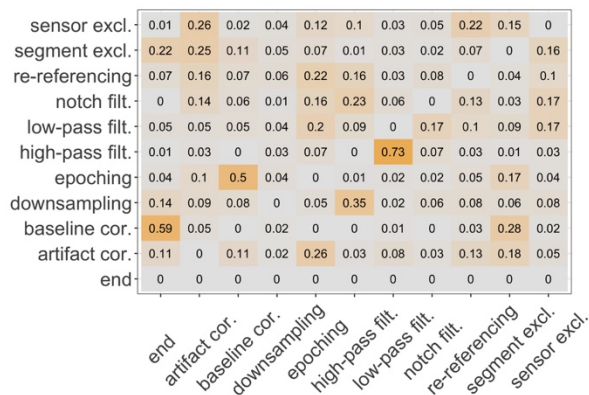
143 shades indicating most common choice per category. **C.** Standardized entropy index for both preprocessing
 144 and analysis steps (analysis steps split across the three hypotheses, each with a different colour). The
 145 vertical red dashed line marks the normalized entropy cutoff of 0.98. Abbreviations: ICA - independent
 146 component analysis; freq. - frequency; avg - averaging, ex_infomax - extended infomax; mul_thesh -
 147 multiple threshold; fwd - forward; bwd - backward; hf - high-pass filter; fir - finite impulse response; iir -
 148 infinite impulse response; bhfd - Benjamini-Hochberg false discovery rate; pair_ttest - paired t-test.

149

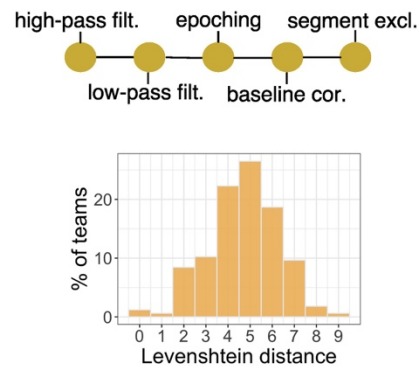
150 To compare variability in the pipeline order, we created a transition probability matrix that contains
 151 the probability of performing step B (columns) after step A (rows, Figure 2A). We identified a team
 152 whose step sequence had the highest mean transition probability across all analyst teams and
 153 used their order of steps as the prototypical order. The prototypical order of steps was 1) high-
 154 pass filtering, 2) low-pass filtering, 3) epoching, 4) baseline correction, and 5) segment exclusion
 155 (Figure 2B). We then scored each team's preprocessing sequence based on its distance from the
 156 prototypical order of steps using the Levenshtein similarity metric³². The distance score reflects
 157 the minimum number of operations—insertions, deletions, or substitutions—required to transform
 158 one team's pipeline into the prototypical order: larger values indicate greater deviation from the
 159 prototype. On average, teams differed from the prototype by 4.69 operations (SD = 1.59; see
 160 Figure 2B). Given the short length of the prototypical sequence, this represents high divergence,
 161 indicating that most teams used a different ordering or diverged in the majority of preprocessing
 162 steps relative to the prototype.

163

A Transition probability matrix



B Prototypical order of steps



164

165 **Figure 2. Variability in EEG pipeline sequences.** **A.** Transition probability matrix: values in each cell
 166 depict how likely it is to move from one step to another (from steps shown in rows to steps in columns). The
 167 darker colours indicate higher agreement across teams. **B.** Steps included in the prototypical pipeline
 168 sequence. The Levenshtein distance was calculated between this sequence and each team's reported
 169 pipeline to quantify deviations in processing order. Abbreviations: excl. - exclusion; filt. - filter; cor. -
 170 correction.

171

172 **2.2. Variability in hypothesis testing outcomes and effect sizes**

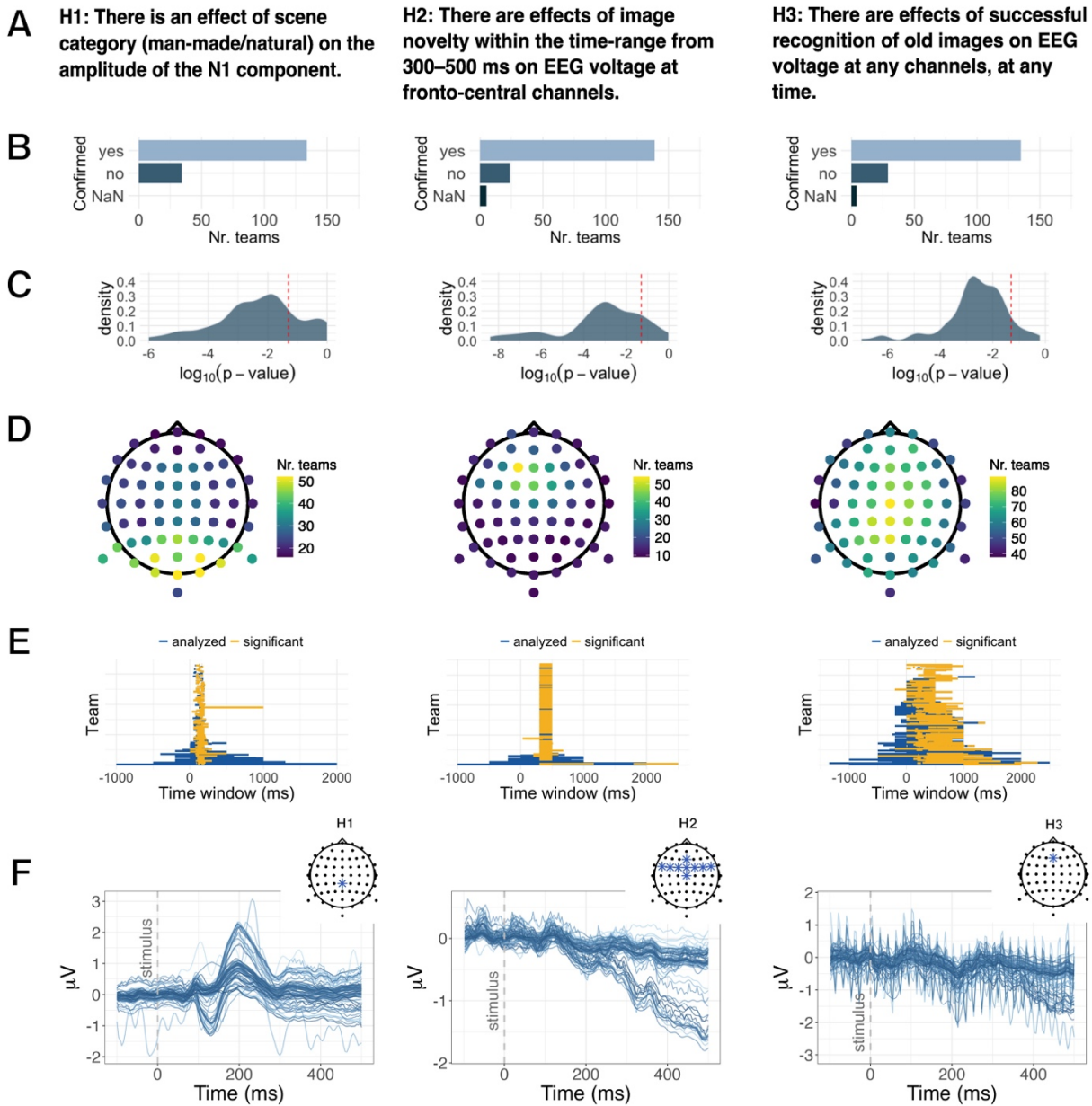
173 **2.2.1 Agreement on binary hypothesis outcomes masks divergence in effect sizes**

174 Analyst teams reported binary decisions on whether each hypothesis was confirmed (Figure 3B).
175 Confirmation rates were high for the three ERP hypotheses: on average 76.9% of teams
176 confirmed a given hypothesis.

177 The binary decision whether a statistical test was significant may hide underlying heterogeneity
178 in effect sizes. Thus, we further inspected the distribution of reported p -values (Figure 3C). P -
179 values are hard to compare across studies due to different sample sizes. However, in our case,
180 all analyst teams processed the same data, making the p -values comparable (with minor
181 deviations in data based on which the p -value is based, i.e., differences in excluded epochs or
182 participants).

183 The reported results and their locations in time and space varied between teams. Significant
184 effects for hypothesis 3 were reported in a larger number of channels and broader time windows
185 than for hypotheses 1 and 2 (Figure 3, D–E). This might be due to the open hypothesis
186 formulation: in contrast to hypotheses 1 and 2, we did not specify the location of an effect in
187 hypothesis 3. However, even for hypothesis 1, which addressed condition differences in the N100
188 ERP component, the chosen time window of interest and channel locations differed despite this
189 specification. Hypothesis 2 predefined a time window (300–500ms) and region of interest (fronto-
190 central electrodes). A number of teams diverged from these parameters: Nine teams (5%)
191 examined regions beyond the fronto-central area, 38 teams (23%) did not report a specific region
192 of interest, and 19 teams (11%) analyzed data outside the time window.

193 As a more direct measure of effect size, we computed ERP difference waves based on the
194 preprocessed data submitted by each team. For each team and for each condition, we computed
195 the mean wave across trials, subtracted the conditions from each other, and then averaged across
196 participants. These aggregated difference waves showed substantial variability (Figure 3F).



197

198 **Figure 3.** Results from the testing of the three ERP-based hypotheses. **A.** Hypothesis formulation. **B.**
 199 Hypothesis confirmation rates across teams. The 'NaN' column indicates the number of teams that did not
 200 indicate whether a hypothesis was confirmed. **C.** Density plots of \log_{10} transformed reported p-values. The
 201 red dashed line represents a p-value threshold of 0.05. **D.** Location of the reported channels that showed
 202 a significant effect. **E.** Analyzed time windows and time windows where a significant relationship was
 203 reported for every team. **F.** Difference waves and corresponding EEG channels used for ERP difference
 204 calculations. One line corresponds to one team. Note that some difference waves contain a prominent high-
 205 frequency component, which might be a result of an absence of a notch filter or a small number of epochs
 206 for one of the conditions.

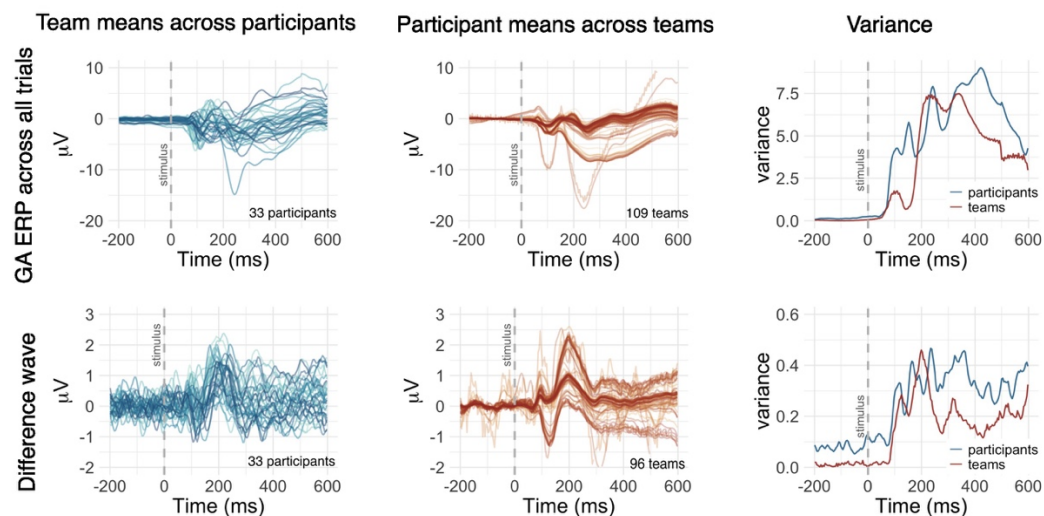
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208 2.2.2 Variability in results across teams was comparable to variability across 209 research participants

210 We compared variability in difference waves to a familiar benchmark in EEG research: variability
211 across participants, typically accounted for in second-level analysis (denominator of statistical
212 tests). Comparing the magnitudes of these two sources of variance is informative because EEG
213 researchers have strong intuitions about between-participants variance, which serves as an
214 important parameter in most statistical tests, while much less is known about the between-
215 pipelines variance.

216 First, we computed the average ERPs across all trials (independent of conditions) for each
217 participant and team. We then computed both (a) the average for each team, allowing us to
218 quantify variability across participants (Figure 4, left column), and (b) the average for each
219 participant, allowing us to quantify variability across teams (Figure 4, middle column). In addition,
220 we applied the same procedure to the difference waves for hypothesis 1 (splitting trials by
221 condition and subtracting conditions from each other).

222 Grand-average ERP and difference waves varied across both participants and teams (Figure 4),
223 with variability on a comparable scale across the two levels of analysis. Especially for late-latency
224 components of the hypothesis 1 difference wave (components above 300 ms post-stimulus), the
225 across-teams variance was lower than the across-participants variance (mean team variance =
226 0.19; mean participant variance = 0.34).



227

228 **Figure 4. Grand average (GA) event-related potentials (ERP) (top) and hypothesis 1 difference wave**
229 **(bottom) at the CPz channel across teams and across participants.** The left column shows the
230 variability across participants (each line is data from one participant averaged across teams). The middle
231 column shows the variability across teams (each line is data from one team averaged across participants).
232 The right panel shows the variance calculated across teams and across participants. For visualisation
233 purposes we baseline corrected the GA ERPs and difference waves prior to variance analyses.

234

235 **2.3. Association between results and analysis choices**

236 **2.3.1 Few pipeline choices predicted p-value size; most of the variance remained** 237 **unaccounted for**

238 We used regression models to test whether specific pipeline choices predicted the results. Given
239 that linear models assume normally distributed residuals, and that the distribution of p -values was
240 strongly right-skewed, we transformed p -values into z -values using the inverse normal quantile
241 function and used this metric as a dependent variable in linear models and pipeline choices as
242 independent variables. Due to the high number of pipeline steps, we used an automated model
243 comparison tool, which performed stepwise forward-and-backwards variable selection based on
244 Bayesian Information Criterion (BIC, for more details see Methods section 4.7).

245 **Hypothesis 1.** A model including the number of channels ($\beta = -0.31 \pm 0.12$, CI = [-0.55, -0.07], p
246 = 0.011), baseline time window length ($\beta = 0.35 \pm 0.14$, CI = [0.07, 0.63], $p = 0.015$), and correction
247 for multiple comparisons (a binary variable; $\beta = -0.89 \pm 0.26$, CI = [-1.40, -0.39], $p < 0.001$) yielded
248 the lowest BIC (BIC = 158.28). This model explained $R^2 = 0.13$ of the variance in p -values for
249 hypothesis 1. These results suggest that a larger number of analyzed channels, a shorter baseline
250 window length, and correction for multiple comparisons are linked to smaller p -values (Figure S2).
251 The counterintuitive finding that correction for multiple comparisons is linked to smaller p -values
252 might be explained by the observation that most of the teams used permutation tests as a method
253 of multiple comparison correction for hypothesis 1 (see Figure 1). Note that these coefficient
254 estimates and associated p -values are conditional on the BIC-selected model and are interpreted
255 as descriptive indicators of relative predictor importance rather than formal significance tests.

256 We also tested interactions between the baseline window length and correction for multiple
257 comparisons, and between the number of channels and correction for multiple comparisons. The
258 interaction between the baseline window length and correction for multiple comparisons was
259 statistically significant ($\beta = -0.95 \pm 0.35$, CI = [-1.64, -0.26], $p = 0.007$, Figure S2). This means
260 that the baseline window length was more strongly positively associated with p -values in teams
261 that did *not* correct for multiple comparisons relative to those that did. It may indicate that in the
262 absence of multiple comparisons, the larger baseline window length may inflate the likelihood of
263 a false-negative statistical result.

264 **Hypothesis 2.** Stepwise model selection using the BIC did not identify any subset of predictors
265 that improved fit compared to the null model. This suggests that none of the analysis steps
266 significantly explain variation in the p -value size.

267 **Hypothesis 3.** Stepwise model selection using the BIC identified a single predictor: averaging
268 across the spatial domain (a binary predictor; $\beta = -0.54 \pm 0.23$, CI = [-0.98, -0.09], $p = 0.019$; BIC
269 = -21.18, see Figure S3). This model explained 4% of the variance in p -values for hypothesis 3.
270 This finding suggests that teams that averaged across the spatial domain tended to report lower
271 p -values.

272 In summary, associations between analysis choices and team-reported p -values were
273 inconsistent across hypotheses and were overall sparse; most preprocessing and analysis
274 choices were not systematically or strongly related to the obtained p -value. This dependent
275 variable, notably utilized as the primary outcome in some prior many analyst projects (e.g.,¹⁹),
276 may have contributed to the limited variance successfully explained.

277 **2.3.2 Reference schemes, filtering, and component selection accounted for** 278 **substantial variance in ERP difference waves**

279 To test how processing pipelines affect the actual ERPs, we compared the preprocessed EEG
280 data submitted by the analyst teams. Effects derived from these data are directly comparable
281 across teams, as they are not contingent on team-specific statistical modelling or inference
282 choices. We obtained these effect sizes by creating an ERP difference wave (see Methods
283 section 4.5.2). A model comparison with BIC was used to select the optimal model predicting the
284 difference wave values from preprocessing steps.

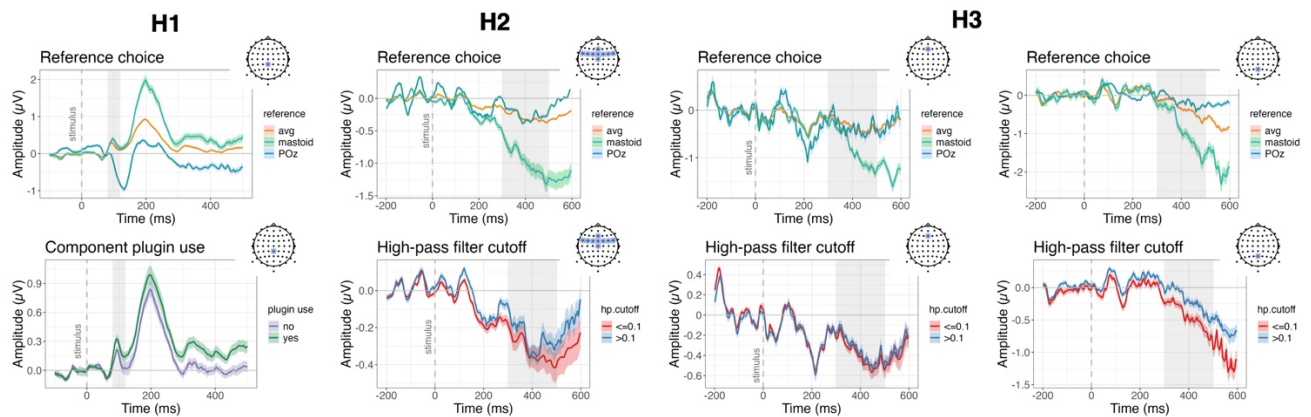
285 **Hypothesis 1.** We averaged the difference wave from 80–120 ms (a prototypical time window for
286 N100 effects) at the CPz channel for each team. A model including the reference channel and the
287 use of a bad-component selection plugin (a binary choice) as predictors yielded the lowest BIC
288 (BIC = -305.33). The model explained 53% of the variance in the size of the difference waves.
289 Depending on choice of the reference scheme, the sign of the N100 difference wave flipped:
290 While it was positive in teams who used an average or a mastoid reference ($n = 74$), suggesting
291 larger ERP amplitudes for man-made than natural stimuli, it was negative in teams who used a
292 POz reference ($n = 25$), suggesting larger ERP amplitudes for natural than man-made stimuli
293 categories. Difference waves were significantly smaller for teams with POz as reference
294 compared to the teams with an average reference ($\beta = -0.45 \pm 0.05$, CI = [-0.55, -0.34], $p < 0.001$,
295 Figure 5). Furthermore, the difference wave was slightly larger for teams with a mastoid reference
296 than teams with an average reference ($\beta = 0.07 \pm 0.04$, CI = [-0.018, 0.16], $p = 0.118$).

297 In addition, teams that used a plugin-based implementation to select bad components had larger
298 ERP difference waves for hypothesis 1 testing as compared to teams that did not ($\beta = 0.09 \pm 0.04$,
299 CI = [0.01, 0.17], $p = 0.031$, Figure 5). Of the 70 teams that used a plugin-based implementation,
300 34 used ICLabel³³.

301 **Hypothesis 2.** We averaged the difference waves from 300–500 ms (as indicated in the
302 hypothesis formulation) at a cluster of fronto-central channels. The model including reference
303 channel and high-pass filter cutoff value choice as predictors yielded the lowest BIC (BIC = -
304 259.43). This model explained 75% of the variance in the size of the difference waves. Teams
305 who used a mastoid reference found a larger difference between the two conditions than teams
306 who used an average reference ($\beta = -0.7 \pm 0.07$, CI = [-0.84, -0.56], $p < 0.001$) or a POz reference
307 (POz compared to average reference: $\beta = -0.03 \pm 0.03$, CI = [-0.09, 0.02], $p = 0.24$, Figure 5).
308 Furthermore, teams with a lower high-pass filter cutoff found a larger difference than teams with
309 a higher cutoff ($\beta = 0.07 \pm 0.01$, CI = [0.03, 0.10], $p < 0.001$, Figure 5).

310 **Hypothesis 3.** We averaged the difference waves from 300–500 ms (a prototypical window of
311 the late positive complex). Since hypothesis 3 did not specify a channel, a component, or a time

312 window for the analyses (and therefore is the most open of the hypotheses that were tested in
 313 this paper), we selected two locations: the Fz and Pz channels. Since the effects were
 314 comparable, we report the results obtained from the Fz channel in the text and the results for Pz
 315 in Table S7. The model containing the choice of reference channel and high-pass filter cutoff as
 316 predictors yielded the lowest BIC (BIC = -241.9). The model explained 51% of the variance in the
 317 size of the difference waves. Teams who used a mastoid reference found a larger difference wave
 318 compared to teams who used an average reference ($\beta = -0.45 \pm 0.07$, CI = [-0.59, -0.32], $p <$
 319 0.001) or POz reference ($\beta = -0.10 \pm 0.05$, CI = [-0.20, 0.001], $p = 0.05$). Furthermore, teams with
 320 a lower high-pass filter cutoff found a larger difference compared to teams with a higher cutoff (β
 321 = 0.06 ± 0.03 , CI = [0.002, 0.11], $p = 0.043$, Figure 5).



322

323 **Figure 5. Median difference waves for the three hypotheses for different pipeline choices.** The
 324 difference wave is plotted for the reference choice and component plugin use for hypothesis 1 (H1). The
 325 difference waves of hypotheses 2 (H2) and 3 (H3) are plotted for the reference choice and high-pass filter
 326 cutoff values at different channels. The scalp topographies show the locations of channels from which the
 327 difference waves were extracted. The shaded grey areas represent the time window over which the
 328 difference wave was averaged. Note that the high-pass filter cutoff value is grouped into two classes for
 329 visualisation. Abbreviations: avg - average; hp. - high-pass filter.

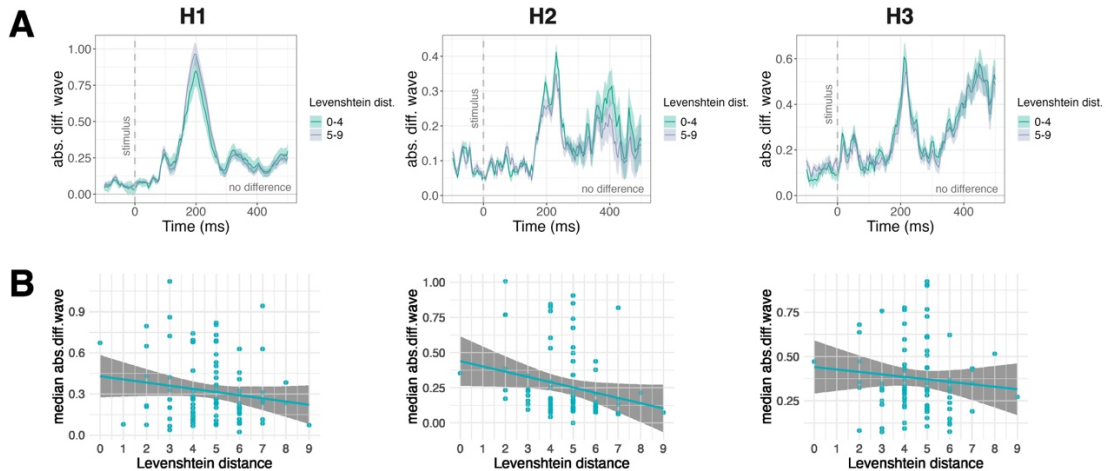
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331 2.3.3 More unusual pipelines are associated with flatter difference waves for 332 hypothesis 2

333 To quantify the unusualness of a team's pipeline, we calculated (a) the step-order prototypicality
 334 by using Levenshtein distance score (described in 2.1 and 4.5.1), and (b) the parameter-choice
 335 prototypicality, defined as the mean probability of the specific choices made by a team across
 336 preprocessing steps.

337 We then correlated the median absolute amplitude of the difference waves, reflecting the
 338 unusualness of the preprocessed EEG data (see Methods section 4.6), with the two metrics
 339 quantifying the unusualness of the corresponding analysis pipelines (step-order prototypicality
 340 and parameter-choice prototypicality indices). We observed directionally negative correlations
 341 between the difference waves and the Levenshtein distance scores regarding step-order

342 prototypicality (Figure 6), indicating that pipelines closer to the prototypical sequence tended to
 343 yield larger amplitudes, whereas more atypical step orders were associated with flatter difference
 344 waves. This relationship reached statistical significance only for hypothesis 2 ($\rho = -0.28$, $p =$
 345 0.009). For hypotheses 1 and 3, the association was in the same direction but did not reach
 346 significance ($\rho = -0.09$, $p = 0.38$, and $\rho = -0.10$, $p = 0.35$, respectively). For the parameter-choice
 347 prototypicality index, we found no statistically significant relationships with the unusualness of the
 348 difference waves for any hypothesis.



349
 350 **Figure 6. Associations between the unusualness of the order of steps and difference waves. A.**
 351 *Absolute amplitudes of difference waves of three hypotheses, color-coded based on the team's Levenshtein*
 352 *distance score (denoting the distance to the prototypical order of steps, also see Figure 2). The shaded*
 353 *area around the lines shows the standard error. For hypothesis 1 we used channel CPz, and for hypotheses*
 354 *2 and 3 we used channel Fz. B. Correlations between the median absolute difference wave amplitude in*
 355 *the time window between 100-600ms post stimulus and Levenshtein distance.*

356

357 Discussion

358 In the EEGManyPipelines project, 168 teams totalling 396 individual researchers analyzed the
 359 same dataset, enabling a meta-scientific investigation into how differences in analysis pipelines
 360 shape research outcomes. All teams tested the same hypotheses, thereby eliminating several
 361 major sources of variability when comparing across different research investigations. Despite this,
 362 pipelines differed in included channels, time windows, statistical models, and reported metrics.
 363 This large-scale, coordinated effort provides the first systematic quantification of differences in
 364 EEG preprocessing and analysis choices, variability in outcomes, and how these relate to one
 365 another, sampling realistic pipelines from a large group of active EEG researchers. At the same

366 time, it provides insights for any scientific discipline and investigation that grapples with
367 ambiguities in complex data.

368 Critically, our crowd of analysts started from the raw observations, allowing us to capture not only
369 heterogeneity in analytic specifications, but also in data preprocessing steps (see also¹⁵). The
370 latter remains an almost entirely shrouded aspect of researcher decision-making, with publicly
371 posted and shared datasets taking the form of processed data in the vast majority of cases.
372 Examining full research pipelines, including the precise ordering of pipeline steps, is especially
373 important in fields such as EEG research, where investigators regularly work with large amounts
374 of nested time-series data. For this purpose, our crowd of analysts submitted preprocessed data,
375 which allowed us to quantify variation in effect sizes attributable to the subsequently chosen data-
376 handling approach. Our findings reveal that choices regarding preprocessing parameters, such
377 as the reference channel, high-pass filter cutoff, and the way components associated with noise
378 are selected, predicted difference wave magnitude (i.e., the ERP difference between two
379 conditions). Comparing different sources of variability in ERP difference waves, cross-analyst
380 variability matched cross-participant variability in magnitude in this data, a descriptive benchmark
381 for variability in results attributable to researcher choices that we introduce into the literature here.
382 It is important to note that this comparison may depend heavily on several factors, including data
383 quality, the nature of the research question, and specific analytic contexts. However, at least in
384 this setting, who analyses the data is just as important as who provided the data—a testament to
385 the power of researchers' degrees of freedom to shape the outcomes of scientific investigations.

386 Despite variability in the difference waves, results for the three ERP hypotheses revealed a
387 majority agreement across teams: 76.9% of teams on average agreed on the presence of a
388 statistically significant effect. The hypotheses in question targeted well-established ERP effects
389 related to scene category (hypothesis 1), novelty, and recognition memory (hypotheses 2 and
390 3)^{34,35}. Notably, agreement rates were comparable across hypotheses, despite differences in how
391 specifically the ERP effects were defined, suggesting that the level of constraint in the hypothesis
392 did not substantially influence overall consensus. It is conceivable that agreement across teams
393 would look different in projects addressing novel or controversial hypotheses or relying on less
394 established experimental paradigms. Regardless, simple binary judgments of whether an ERP
395 hypothesis was confirmed or not camouflaged divergence in the underlying data patterns.
396 Difference waves not only varied in magnitude, but in some cases reversed in polarity. For
397 example, for hypothesis 1, while most teams identified a positive-going ERP for pictures of man-
398 made scenes, twenty-five teams found a directionally opposite pattern, with a larger amplitude for
399 pictures depicting natural scenes. Thus, two papers addressing the same question and analyzing
400 the same dataset could plausibly report ERP difference waves that lead to opposing conclusions.
401 To facilitate collectively adjudicating such issues, researchers should share their underlying
402 preprocessed data and code in an accessible format post-publication.

403 Similar to past many-analyst projects, which typically explain under 10% of the dispersion in
404 approaches and estimates (e.g.,^{16,19}), we found that variation in results based on transformed p -
405 values could hardly be explained by pipeline choices. Because all teams analyzed the same raw
406 data, the full variability in reported effects necessarily arose from differences in analysis pipelines.
407 Rather, the low explained variance may reflect the coarse nature of the outcome measure and

408 the exclusion of some idiosyncratic analytic decisions, such as trial or participant rejection criteria.
409 This underscores the importance of not only providing granular codings of researcher approaches
410 but also precise measurement of outcomes to solving the parsing problem²⁸ posed by radical
411 dispersion in estimates.

412 Indeed, we found that pipeline choices for the three hypotheses could be used to quantitatively
413 explain the majority of the variability in ERP difference waves derived from analysts' submitted
414 preprocessed data—53%, 75%, and 51% of the variance, respectively. The reference channel
415 emerged as the pipeline choice that explained the largest proportion of variance in all difference
416 waves^{36,37}. The influence of the specific reference location was hypothesis-dependent. For
417 hypothesis 1, teams using POz as the reference channel produced numerically larger N100
418 difference waves than those using mastoid or average references. However, the direction of the
419 effect was reversed for POz-referenced teams: they observed larger ERP amplitudes for natural
420 stimuli than for man-made stimuli, whereas teams using other reference schemes showed the
421 opposite pattern. Given that ERP effects in experiments using visual stimuli typically have a
422 posterior topography, and that most researchers chose to re-reference the data, keeping the
423 original reference might be considered a questionable choice. However, note that participating
424 EEG laboratories were asked to use their standard pipeline, that keeping the original reference
425 resulted in a plausible difference wave, and that the choice of this particular reference scheme
426 could have gone unnoticed in regular journal publications²⁶. Still, the question of defensibility or
427 quality of different pipeline choices remains an important one. Alternative branches of choices
428 should be weighted by methodological quality and parsed with regard to their theoretical
429 implications^{29,30}.

430 For hypotheses 2 and 3, the high-pass filter cutoff value was also a significant predictor of the
431 difference wave magnitude: higher cutoff frequencies were associated with smaller difference
432 waves, suggesting that the distinction between the two conditions became less pronounced. This
433 observation corroborates previous findings that higher filter cutoff can compromise ERP waves^{38–}
434 ⁴⁰. In addition, the use of an automated plugin to detect artifact-containing components was linked
435 to the size of the difference wave of hypothesis 1: teams that used the plugin-based
436 implementation reported larger ERP difference waves as compared to teams that did not use the
437 plugin. The effectiveness of independent component analysis critically depends on the quality of
438 source separation, which can be influenced by upstream preprocessing and data-cleaning
439 practices. However, the automated independent component classifiers, which are trained on
440 expert-labelled component examples, may outperform visual inspection conducted by a single
441 analyst, because they provide more standardized and experience-informed artifact identification.
442 This conclusion would have to be further corroborated by projects using simulated data sets (with
443 known artifact components) and by explicitly evaluating automated plugins in their ability to filter
444 out artifactual components.

445 The complex, multi-purpose nature of EEG preprocessing and analysis pipelines means that
446 many variables are needed to describe heterogeneity in these pipelines. Testing for the
447 moderating effects of a specific analytic choice across specifications may mask the extent to
448 which a combined set and ordering of choices are normative vs. deviates from common practice.
449 Therefore, we defined the step-order prototypicality and parameter-choice prototypicality, and

450 quantified the deviation of each team’s pipeline from these prototypes. Linking the step-order
451 prototypicality metric to the difference wave, we observed that teams with more unusual pipelines
452 (i.e., larger deviation from the prototypical order of steps) tended to observe weaker effects (i.e.,
453 smaller deviations of the difference waves from zero) for one of three hypotheses. Partly
454 supporting some prior critiques of crowd science^{29,30}, use of prototypicality metrics confirms that
455 unusual pipelines can contribute to unusual results. However, the prototypical pipeline does not
456 necessarily reflect the best pipeline to use in a given analysis. Future research using simulated
457 data in which the true underlying effect size is known is needed to determine whether an overall
458 assessment of a pipeline as “typical” vs. “atypical” is a good first indicator for its validity.

459 It is also important to emphasize that the generalizability of the conclusions from this project could
460 be limited to the shared particular dataset. Despite this caveat, we believe this first
461 EEGManyPipelines initiative represents a sufficiently striking “existence proof” regarding the
462 potential impact of researcher choices to hold some implications for routine EEG research
463 practice. First, analytic pipelines should be conceptualized as central components of study design.
464 Second, key preprocessing decisions, particularly reference schemes and filter settings, should
465 be subjected to robustness checks. Third, reliance on binary statistical judgments may obscure
466 meaningful variability in underlying waveform patterns; complementing such judgments with
467 continuous effect measures may therefore improve transparency and interpretability.

468 For the broader scientific community, our findings indicate that efforts to meaningfully explain
469 variability in results and reach collective conclusions should take into account full analysis
470 pipelines. This necessarily includes data preprocessing steps and their order, currently left
471 shrouded as a matter of routine research practice. Achieving this level of transparency requires
472 the widespread sharing of raw and preprocessed data, code, and sufficiently detailed
473 documentation—ideally through machine-readable, structured reporting tools such as ARTEM-
474 IS⁴¹. To streamline this documentation process, analysis software should actively support
475 transparent reporting by automatically generating ready-to-use, guideline-compliant method
476 descriptions that accurately reflect the analytic procedures employed. Finally, we recommend that
477 individual research teams routinely assess the robustness of their findings to variation in key data
478 preprocessing and analysis decisions (e.g., reference schemes, filter cutoff values, tools for
479 artifact correction), and transparently report how such choices influence their results.

480 Methods

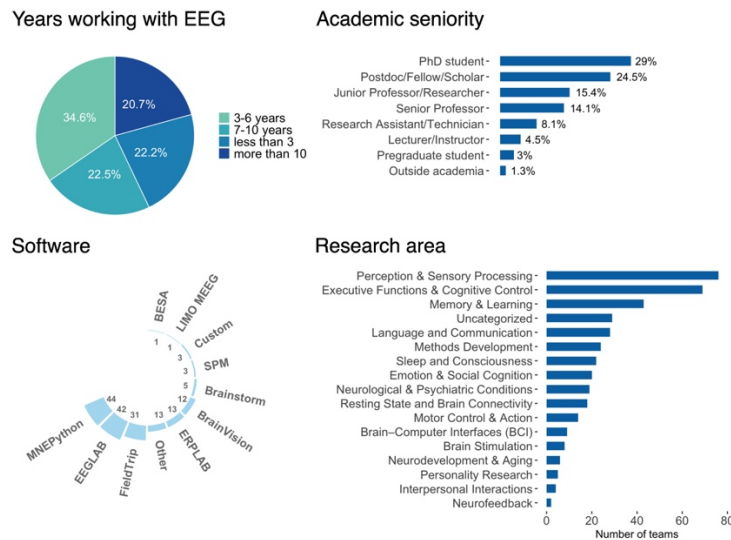
481 The steering committee of the EMP project was formed online, in a bottom-up grass-roots
482 fashion²⁰, in the summer of 2020. They selected a dataset to be analyzed, specified target
483 hypotheses that could be tested given the data, and recruited teams of analysts with certain
484 stipulations⁴². Analyst teams were asked to test hypotheses using their laboratory’s typical
485 analysis pipeline on the provided dataset. The steering committee analyzed the collective meta-
486 scientific data to map variability in pipelines, heterogeneity in results, and possible links between
487 analytic decisions and results. In recognition of their contributions, all participating analysts were
488 offered co-authorship on the resulting many-analyst journal articles.

489 Data was submitted in different formats. The steering committee transformed it into a consistent
 490 format for easier data analysis. The steering committee also checked the submitted descriptions
 491 of teams' analysis pipelines against the submitted code, identified discrepancies, and resolved
 492 any such discrepancies (relying on the code). All processed data, scripts, and response data
 493 provided by the analysts are available at <https://brainlife.io/project/6863bf5c1521e536327bfea7>
 494 and described in ⁴³.

495 The study was approved by the ethics committee of the Faculty of Psychology and Sports
 496 Sciences at the University of Münster, Germany (#2021-06-NB and #2021-52-NB-FA).

497 4.1 Enrolment and characteristics of analyst teams

498 Analysts were recruited via mailing lists, social media, and word-of-mouth from April to October
 499 2021. A total of 327 teams registered for the project before the start of the analysis phase. Teams
 500 could consist of one to three researchers, but were required to feature at least one member who
 501 had previously published an EEG study in a peer-reviewed journal to be eligible. The final
 502 EEGManyPipelines sample comprised 168 teams who submitted complete analyses and results
 503 for all eight hypotheses. These teams included 396 individual researchers (mean age 33.7 ± 7.5
 504 years; 150 women, 223 men, 2 gender-diverse, 21 undisclosed), representing diverse
 505 nationalities, career stages, and subfields of neuroscience (including memory, attention, and
 506 related areas, see Figure 7). More details on sample characteristics and dropout rates at different
 507 project stages are provided in the accompanying data descriptor paper⁴³.



508

509 **Figure 7. Demographic profile of analyst teams.** Details include years of experience with EEG,
 510 academic seniority, preferred software for data analysis, and primary research areas.

511 **4.2 EEG dataset**

512 EEG data were recorded from 33 participants (22 female; 4 left-handed; mean age: 27 years)
513 performing a continuous recognition memory task^{44,45}. Participants viewed a stream of scene
514 images (man-made: highways, buildings; natural: forests, beaches), some of which repeated, and
515 indicated whether each image was “new” (first presentation) or “old” (repeated) by lifting a finger
516 from one of two response keys (left/right CTRL). Response category assignments (old/new) were
517 counterbalanced across participants. Each image was displayed for 0.5 seconds on a black
518 background, followed by a blank screen presented until a response was generated. Feedback
519 was given via a green fixation cross for correct responses and a red cross for incorrect responses,
520 each displayed for 0.2 seconds. This dataset was selected because it comprises multiple
521 experimental conditions, making it suitable for testing a range of effects of interest, including
522 perceptual effects of scene category^{46,47} and cognitive effects related to memory^{34,35}.

523 EEG was recorded using a BioSemi ActiveTwo amplifier with 64 Ag/AgCl electrodes positioned
524 according to the International 10–10 system, as well as two mastoid electrodes and horizontal
525 and vertical electro-oculograms. Horizontal and vertical electro-oculograms were recorded from
526 electrodes at the lateral canthi and below the eyes, respectively. The Common Mode Sense and
527 Driven Right Leg electrodes were placed on the left and right sides of electrode POz. EEG was
528 recorded in DC mode at a sampling rate of 1,024 Hz with a 200 Hz low-pass filter and 24-bit AD
529 conversion. EEG was recorded in an acoustically shielded recording booth. Continuous EEG data
530 were only minimally preprocessed prior to sharing: data were re-referenced to the POz electrode,
531 downsampled to 512 Hz, and formatted according to the BIDS standard⁴⁸. Crucially, no attempts
532 were made to improve or modify data quality. The shared dataset thus represents a realistic range
533 of signal quality and typical EEG artifacts.

534 Additional technical details regarding the behavioral task and EEG dataset, including a detailed
535 explanation of the task structure, experimental conditions, and data organization, were provided
536 to analysts in an accompanying documentation file and are further described in the data descriptor
537 paper⁴³.

538 **4.3 Hypotheses**

539 Given the task design, the steering committee initially specified eight hypotheses to be tested
540 based on the provided data set⁴². Due to time and resource constraints, these were narrowed to
541 three established ERP hypotheses concerning visual stimulus processing and long-term
542 recognition memory. Hypothesis 1 asked whether different categories of scenes were processed
543 differently at an early time point (N100 component; note that scene categories were not matched
544 for low-level visual features, and hence, such features could likely drive differences in EEG signal
545 across categories). Hypothesis 2 asked which brain processes are involved in detecting image
546 novelty. Hypothesis 3 concerned which EEG features distinguished correct recognition decisions
547 from false alarms. According to their formulation, these hypotheses varied in terms of specificity:
548 Hypotheses 1 and 2 provided a predefined ERP component or range of channels, and time
549 windows to investigate, while hypothesis 3 was more open-ended without mentioning a particular
550 spatial or temporal region of interest.

551 **4.4 Instructions for analyst teams**

552 Analyst teams were instructed to analyze the EEG dataset and test the hypotheses using the
553 same analysis pipelines they would typically apply in their own research. The instructions outlined
554 the project's goals, described the dataset, listed the hypotheses, and specified the submission
555 requirements for results, analysis code, and processed data. The full instructions sent to the
556 analyst teams are available in the data descriptor paper⁴³ and at <https://osf.io/xfrbe/files/4nhck>.

557 Analyst teams were required to submit a comprehensive set of results and documentation. This
558 included: (1) binary decisions and confidence ratings for each hypothesis (prior and posterior
559 questionnaires), (2) a concise free-text report of their results, formatted like a typical results
560 section of a scientific paper, (3) detailed responses to an analysis questionnaire documenting all
561 preprocessing and analysis steps, (4) all analysis scripts needed to reproduce their pipeline,
562 including code documentation or stepwise descriptions for GUI-based analyses, and (5)
563 preprocessed trial-by-trial EEG data for each participant, along with documentation of bad
564 channels, rejected trials, and independent components removed during preprocessing.

565 **4.5 Estimating variability in pipelines and results**

566 It is important to note that we could not fully prevent cases of missing components of reports (e.g.,
567 incomplete result reports for each tested hypothesis) or missing parts of the files (e.g.,
568 incomplete/partial scripts, empty EEG data within a file, and missing event markers).

569 **4.5.1 Pipeline variability**

570 Based on the scripts provided by the teams, we revised both the individual values and the order
571 of steps in the analysis questionnaire reports and used the corrected values in the variability
572 analyses.

573 For each analysis step and decision, we quantified decision variability by normalized Shannon
574 entropy, based on the distribution of teams across all decision options. The normalized entropy
575 index is defined as:

$$576 \quad H_{norm}(X) = \frac{H(X)}{H_{max}} = \frac{-\sum_{i=1}^n p_i \log_2(p_i)}{\log_2 n},$$

577 where $H(X)$ is the Shannon entropy of the distribution of each of the processing step choices, n
578 is the total number of categories within the step, and p_i is the proportion of the category i .

579 This measure approaches 0 when one option is chosen with overwhelming consistency and 1
580 when all options are chosen equally often (uniform distribution). Because entropy is insensitive to
581 sample size, we supplemented it with exact binomial tests against a 0.5 null. In cases where
582 normalized entropy exceeded 0.98 threshold, we generally observed no statistically significant
583 deviation from uniformity.

584 To assess the prototypicality of pipelines, we introduced the parameter-choice prototypicality
585 index, which measured how common analysis choices were among teams. For each processing
586 step s , we computed the proportion of teams that made each possible choice. For a given team
587 t , let $p_{t,s}$ denote the proportion of teams that made the same choice as team t at step s . The
588 parameter-choice prototypicality index for team t was then calculated as:

$$589 \quad CTI_t = \frac{1}{S} \sum_{s=1}^S p_{t,s} ,$$

590 where S is the total number of processing steps. Lower values indicate that a team tended to use
591 rarer choices, whereas higher values indicate more common choices.

592 To quantify the sequence of processing steps, we defined 12 commonly used ERP analysis steps
593 and asked analyst teams to indicate the order in which they performed each one. Steps not used
594 by the team were left blank. Each step corresponded to a specific operation (e.g., high-pass or
595 low-pass filtering, segment rejection, etc.) and the sequence preserved the order of application.
596 Steps used by fewer than 25% of teams were removed (i.e., “Detrending”, “Spatial transform”).
597 To quantify how frequently one preprocessing step followed another, pipelines were encoded as
598 a transition probability matrix: rows correspond to preceding steps, and columns correspond to
599 subsequent steps (see Figure 2A). Each cell value reflects the probability that a given step
600 (column) immediately follows another step (row), calculated as the number of times a given
601 transition occurred across all pipelines. One team did not report the order of steps and one team
602 reported the order of only one step and were consequently excluded from the transition probability
603 matrix.

604 To estimate the prototypical order of steps, we identified the team whose step sequence had the
605 highest average probability from the transition probability matrix. According to this procedure, the
606 order of the prototypical pipeline was high-pass filtering, low-pass filtering, epoching, baseline
607 correction, and segment exclusion. To compute the distance of the pipelines submitted by all
608 teams with this prototypical order of steps, a letter code was assigned to each preprocessing
609 operation, and the entire pipeline was converted into a string. The Levenshtein string similarity³²
610 was then calculated by comparing character-by-character each pipeline sequence to the
611 prototypical string: based on the number of insertions, deletions, or substitutions needed to
612 transform one string into another, a distance score from the prototypical pipeline was assigned to
613 each team. The Levenshtein score was used to estimate each teams’ distance to the step-order
614 prototypicality.

615 **4.5.2 EEG time series data**

616 We were unable to process the time-series data from 51 teams for the following reasons: the data
617 were not epoched ($n = 23$), the files could not be opened ($n = 18$), or essential information—such
618 as channel labels, time points, data dimensions, or supporting files—was missing ($n = 10$; a more
619 detailed description can be found in ⁴³). The EEGManyPipelines steering committee brought data
620 from 117 teams into a matched format: EEG time-series data were transformed to the same epoch
621 window length (-200 to 600 ms), number and order of channels, and sampling rate (256 Hz). If
622 the data had a shorter epoch length or a varying number of participants (due to participant

623 exclusions), we added NaN values to standardize the format across teams. Thirty-four teams
624 provided their data in volts, which we converted to microvolts.

625 **Difference waves**

626 Out of 117 teams whose data was available, for hypothesis 1 the difference waves could be
627 extracted from 109 teams due to problems with event markers ($n = 4$), empty data for one of the
628 conditions ($n = 2$), preprocessing reference to a different hypothesis ($n = 1$), or problems with
629 channel labels ($n = 1$). For hypotheses 2 and 3, data from 115 teams were initially available (two
630 datasets from the 117 referred to different hypotheses); a further 27 teams were excluded due to
631 problems with event markers and 3 teams were excluded due to empty data structures, leaving
632 88 teams whose data could be used for further analyses.

633 Difference waves were calculated by subtracting the averaged ERPs of the two conditions that
634 are contrasted in each of the three hypotheses. For hypothesis 1, the difference wave was
635 obtained by subtracting the grand-average ERP for natural stimuli from that for man-made stimuli.
636 For hypothesis 2, the grand-average ERP for previously seen ('old') pictures was subtracted from
637 that for new pictures. For hypothesis 3, the grand-average ERP for 'misses' (old pictures falsely
638 identified as new) was subtracted from that for 'hits' (old pictures correctly recognized as old).

639 **Comparing signal variability across teams and participants**

640 To quantify the variability in results induced by different analytic decisions (i.e., across analyst
641 teams) relative to the variability typically observed across the participants in an EEG study (e.g.,
642 due to differences in skull size and thickness, brain anatomy, etc.), we computed grand-average
643 ERPs and difference waves for hypothesis 1 across teams and across participants. This was
644 completed to provide an overall representation of the neural responses used to compare EEG
645 signal variability across teams and participants.

646 To compute variability across participants, we averaged the ERPs and difference waves across
647 analysis teams for each participant and computed the variance of the participant averages. Next,
648 to compute variability across analysis teams, we calculated the grand-average ERPs (average
649 across participants) and difference waves for each analysis team, and computed the variance
650 across analysis teams (see Figure 4). Variance was calculated using an implementation of the
651 *var* function in R that uses the unbiased sample variance estimator, defined as the average
652 squared deviation from the mean with $n - 1$ as denominator, where n is the number of
653 observations.

654 **4.6 The link between prototypical pipelines and the results**

655 To answer whether unusual pipelines were associated with unusual results, we estimated the
656 average difference wave across teams for each hypothesis. For each hypothesis, we computed
657 the median absolute difference wave and averaged it within a 100–600 ms time window. For
658 hypothesis 1 we used channel CPz, and for hypotheses 2 and 3 we used channel Fz. Outliers
659 were identified as mean amplitude below $Q1 - 3 * IQR$ or above $Q3 - 3 * IQR$ and excluded

660 from further analysis. We then correlated these values with the step-order prototypicality
661 (Levenshtein distance between each team's step order and the prototypical step order) and
662 parameter-choice prototypicality index, using Spearman's Rank correlations.

663 4.7 Linking analysis choices to results

664 We used the corrected values from the analysis questionnaire as independent variables in linear
665 models. The dependent variables were derived from the reported p -values and difference waves
666 from three hypotheses. Unfortunately, we were unable to use standardized effect sizes as
667 dependent variables due to the high heterogeneity in the reports. Even within the same statistical
668 test (e.g., cluster-based statistics), the measures of the effect can differ, for example, by referring
669 to the range (e.g., t -min to t -max), the mean (e.g., t -mean), or the sum of test statistics (e.g., t -
670 sum).

671 Because the distribution of test statistics was skewed, we transformed p -values into z-scores
672 using the inverse normal quantile function in R version 4.4.1⁴⁹ to approximate a standard normal
673 distribution. If a team reported multiple significant p -values across electrodes and time windows,
674 we took the median p -value across their significant findings. In the models that used the
675 transformed p -values, model specifications were:

676 - **Hypothesis 1.** Out of 168 teams that completed the analysis, 14 teams did not report a
677 p -value, one team did not report if they corrected for multiple comparisons, and one team
678 was removed from the analysis as an outlier identified by studentized residual exceeding
679 an absolute value of 3. We included 152 teams in the linear model. We excluded
680 information on software host, method of multiple comparisons, and high-pass filter
681 direction from linear models due to high collinearity among these variables, as indicated
682 by the variance inflation factor (VIF). For hypothesis 1, independent variables were:
683 software, high-pass cutoff frequency, filter type, reference, sampling frequency, number
684 of excluded subjects, analyzed topographic region, analyzed number of channels,
685 averaging over the channels (a binary outcome, yes/no), segment exclusion criteria,
686 statistical method, correction for multiple comparisons (a binary outcome, yes/no),
687 analyzed time window length and whether it was averaged or not (a binary outcome,
688 yes/no), independent component analysis (ICA) algorithm, bad-component selection
689 visual or plugin based (a binary outcome, yes/no), and baseline window length.

690 - **Hypothesis 2.** Of the 168 teams that completed the analysis, 20 did not report a p -value,
691 23 teams did not report a p -value with the necessary precision, and one team did not
692 report whether they averaged across channels. A total of 124 teams provided full reports
693 that were included in the linear model. We excluded information on software host, multiple-
694 comparison method, and high-pass filter direction from linear models due to high
695 collinearity among these variables (based on VIF scores). The independent variables
696 were the same for hypothesis 2 as for hypothesis 1, except for the analyzed time window,
697 as it was already specified in hypothesis 2, and only a small fraction of teams deviated
698 from it.

699 - **Hypothesis 3.** Out of 168 teams that completed the analysis, 52 teams did not report a
700 *p*-value, one team did not report if they averaged across the sensors, one team did not
701 report if they averaged across the time window, and one team was removed from the
702 analysis based on studentized residual exceeding an absolute value of 3. In total, 113
703 teams submitted full reports and were included in the linear model. We excluded
704 information on software host, software, and high-pass filter direction from linear models
705 due to high collinearity associated with these variables (based on VIF scores). For
706 hypothesis 3, the independent variables were the same as for hypothesis 1, except for
707 software, the number of analyzed channels, and the topographic region. We did not
708 include the last two variables due to missing information.

709 We used difference waves of the hypothesis-specific conditions as dependent variables in linear
710 models. The model specifications for the three hypotheses were:

711 - **Hypothesis 1.** The mean difference wave from the CPz channel representing the N100
712 component (80–120 ms) served as the independent variable in the linear models for
713 hypothesis 1. Of the 109 teams with available data, eight lacked the CPz channel and
714 were excluded, and one team was removed as an outlier due to exceptionally high mean
715 amplitude values (above 10 μ V). From the remaining 100 teams, four were further
716 excluded based on studentized residuals (exceeding 3). Data from 96 teams were used
717 in the linear model. The independent variables were: software, high-pass cutoff- and type,
718 reference, sampling frequency, number of excluded subjects, segment exclusion criteria,
719 ICA algorithm, visual- or plugin-based bad-component selection (a binary outcome,
720 yes/no), and baseline window length.

721 - **Hypothesis 2.** The mean difference wave from Cz, Fz, FCz, FC1, FC2, FC3, FC4, FC5,
722 and FC6 channels in the time window between 300 and 500 ms was used as the
723 independent variable in linear models for hypothesis 2. Of the 88 teams for which
724 difference waves were available, two teams were excluded based on studentized
725 residuals (exceeding 3), two teams were excluded due to exceptionally high mean
726 amplitude values (above 10 μ V), and one team due to extreme leverage, which led to
727 numerical instability in the HC3 robust variance estimation. Data from 83 teams were used
728 in the linear model. The independent variables were: software, high-pass cutoff, type, and
729 direction, reference, sampling frequency, number of excluded subjects, segment
730 exclusion criteria, ICA algorithm, visual- or plugin-based bad-component selection, and
731 baseline window length.

732 - **Hypothesis 3.** The mean difference wave from Fz channels in the time window between
733 400 and 600 ms was used as the independent variable in the linear model for hypothesis
734 3. Of the 88 teams for which difference waves were available, two teams were excluded
735 due to exceptionally high mean amplitude values (above 10 μ V), one team was excluded
736 based on studentized residuals (exceeding 3), one team was excluded due to extreme
737 leverage, which led to numerical instability in the HC3 robust variance estimation, and one
738 team was excluded due to missing data points. Data from 83 teams were used in the linear
739 model. The independent variables were: software, high-pass cutoff, type, and direction,

740 reference, sampling frequency, number of excluded subjects, segment exclusion criteria,
741 ICA algorithm, visual- or plugin-based bad-component selection, and baseline window
742 length. To assess the generalizability of the findings, we also tested the mean difference
743 wave in the Pz channel using the same linear model specifications.

744 For all of linear models, we also included 4 variables representing the order of steps (all teams
745 received a binary score, yes/no, for each category): epoching before high-pass filtering, low-pass
746 filtering before artifact correction/rejection, re-referencing before artifact correction/rejection, and
747 artifact correction before artifact rejection. These categories were chosen based on prior
748 literature⁵⁰.

749 Missing reports from the analysis questionnaire detailing the data processing and analysis
750 pipelines were filled in as a mean score across teams for continuous variables, and as 'unknown'
751 for categorical ones to preserve other pipeline responses in the specified model. Continuous
752 variables were standardised to z-scores (mean = 0, SD = 1).

753 Because the initial linear model included many predictors, there was a risk of overfitting. To
754 identify the most parsimonious model, stepwise model selection was performed in both directions
755 using the Bayesian Information Criterion (BIC). The stepwise procedure was implemented using
756 the stepAIC() function, with the penalty parameter adjusted as $k = \log(n)$ to approximate the
757 BIC for more conservative model selection. The final model was selected using the BIC score,
758 which identifies the model expected to provide the best balance between fit and simplicity.
759 Subsequent coefficient estimates and p -values are conditional on this selected model and should
760 be interpreted descriptively rather than as confirmatory tests.

761 Model assumptions were evaluated prior to interpretation. Influential observations were examined
762 using studentized residuals. Observations with absolute studentized residuals greater than 3 were
763 identified and further assessed for undue influence using leverage and Cook's distance criteria.
764 Linearity was evaluated by examining the relationship between fitted values and residuals; no
765 systematic patterns were observed. Residual normality was assessed using the Shapiro–Wilk
766 and Kolmogorov–Smirnov tests. Homoscedasticity was evaluated using the Breusch–Pagan test.
767 Models that included the difference waves from hypotheses 2 and 3, and the p -values from
768 hypothesis 1 as dependent variables, showed evidence of heteroscedasticity. To account for
769 heteroscedasticity, robust standard errors were estimated using the HC3 heteroscedasticity-
770 consistent covariance matrix.

771 Data availability

772 The EEGManyPipelines dataset can be downloaded from the brainlife.io platform
773 (<https://brainlife.io/project/6863bf5c1521e536327bfea751>) under the Creative Commons
774 Attribution (CC-BY) license. The instructions for the analysts detailing the EEG dataset and task,
775 the questionnaires, and forms can also be found at the EEGManyPipelines Open Science
776 Framework repository (<https://osf.io/c5hyt>). For information on the data structure and usability, we
777 refer the reader to the accompanying data descriptor paper⁴³.

778 **Code availability**

779 https://github.com/EEGManyPipelines/Main_Paper/tree/main

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- 925

List of authors

927 Elena Cesnaite¹, Johannes Algermissen^{2,3,4}, Mikkel C. Vinding^{5,6}, Andrea Vitale⁷, Annalisa
 928 Pascarella⁸, Nastassja L. Fischer^{9,10}, Yu-Fang Yang¹¹, Darinka Trübutschek^{12,13}, Claudia
 929 Gianelli¹⁴, Charlotte R. Marshall¹⁵, Omid Abbasi¹⁶, Timofey Adamovich¹⁷, Lena Adel¹⁸, Nikita
 930 Agarwal^{19,20}, Blanca Aguado-López²¹, Uma Ajmeria²², Esra Al²³, Hannah Aldeen²⁴, Ricardo J.
 931 Alejandro²⁵, Evgeniia A. Alenina²⁶, Meera Alex²⁷, Ettore Ambrosini²⁸, Douglas J. Angus²⁹,
 932 Alessandra Anzolin³⁰, Stefan Appelhoff³¹, Giorgio Arcara^{32,33}, Yana Arkhipova³⁴, Maria
 933 Azanova^{23,35}, Chiara Bagattini³⁶, Daniel H. Baker³⁷, Christoph Bamberg³⁸, Francesca M.
 934 Barbero³⁹, Ceren Battal^{40,39}, Anna-Katharina R. Bauer⁴¹, Burcu Bayram⁴², Paulo R. Bazán⁴³,
 935 Henry Beale⁴⁴, Elena Belanova⁴⁵, Zara M. Bergström⁴⁶, Giulio Bernardi⁴⁷, Martina Berto⁴⁷, Monica
 936 Betta⁴⁷, Isabelle Blanchette⁴⁸, Marta Bortoletto⁴⁷, Davide Bottari⁴⁷, Claire Braboszcz⁴⁹, Daniel E.
 937 Bradford⁵⁰, Joseph L. Brooks⁵¹, Chloe M. Brunskill⁵², Florian Bublitzky^{53,54}, Daniel Büchel⁵⁵,
 938 Roberta P. Calce^{56,39}, Mariagrazia Capizzi^{21,57}, Raymundo Cassani⁵⁸, María Concepción
 939 Castellanos²¹, Luigi Cattaneo⁵⁹, Xim Cerda-Company^{60,61}, Lixiang Chen⁶², Xinyuan Chen⁶³, Yiyu
 940 Chen⁶⁴, Yoojeong Choo^{65,66}, Hu Chuan-Peng⁶⁷, Karan Chugani⁴⁹, Radoslaw Martin Cichy⁶⁸,
 941 Barbora Cimrová⁶⁹, Simon Ciranka³¹, Oren Civier⁷⁰, Carlotta Cogoni⁷¹, Michel-Pierre Coll⁴⁸, Julie
 942 Coloigner⁷², Angela Conejero²¹, Martin Constant^{73,74}, César E. Corona-González^{75,76}, Antonio
 943 Criscuolo⁷⁷, Damian Cruse⁷⁸, Claire Cury⁷², Artur Czeszumski⁷⁹, Martin J. Dahl⁸⁰, Matthew
 944 Davidson⁸¹, Ingmar E. J. de Vries^{59,3}, M. Dolores del Castillo⁸², Vincent DeLuca⁸³, Gianpaolo
 945 Demarchi⁸⁴, Kobe Desender⁸⁵, Marcelo Dias⁸⁶, Darcy Waller⁸⁷, Martin Dietz⁸⁸, Olaf Dimigen⁸⁹, Hao
 946 Ding^{90,91}, Li Dong⁹², Linda Drijvers^{3,93}, Brandi Lee Drisdelle^{94,95}, Gian Marco Duma⁹⁶, Guillaume
 947 Dumas⁹⁷, Benedikt Ehinger⁹⁸, Alexandra K. Emmendorfer⁹⁹, Alexander Enge¹⁰⁰, Stefanie
 948 Evas^{101,102}, Tommaso Fedele¹⁰³, Alessandra Federici⁴⁷, Gordon B. Feld¹⁰⁴, Lauren K. Fink¹⁰⁵, Shai
 949 Fischer¹⁰⁶, Emilia Fló^{107,108}, Silvia Formica¹⁰⁹, Norman Forschack¹¹⁰, Bettina Forster¹¹¹, Marcel
 950 Franz¹¹², Léon Franzen¹¹³, Cassidy M. Fry¹¹⁴, Alejandro Galvez-Pol¹¹⁵, Haydee G. García-
 951 Lázaro^{116,117}, José Carlos García Alanis¹¹⁸, Patricia Garrido-Vásquez¹¹⁹, Billy Gerdfeldter¹²⁰,
 952 Georgia Gerike^{121,122}, Magdalena Gippert²³, Carlos González-García²¹, Dario Gordillo¹²³, Anna
 953 Grabowska^{124,125}, Lisa-Marie Greenwood¹²⁶, Benjamin J. Griffiths²², Demetrio Grollero¹²⁷, Joachim
 954 Gross¹⁶, Danièle A. Gubler¹²⁸, Pierre Guilleminot¹²⁹, Berna Güler¹³⁰, Christopher Gundlach¹¹⁰, Eren
 955 Günsel¹³⁰, Mingqian Guo¹³¹, Malte R. Güth¹³², Céline Haciahmet¹³³, Itay Hadas¹³⁴, Jarmo
 956 Hämäläinen¹²¹, Sizhu Han¹³⁵, Anthony M. Harris⁴⁴, Mahmoud Hassan^{136,137}, Stefan Haufe^{138,19,139},
 957 Anibal S. Heinsfeld¹⁴⁰, Peer Herholz¹⁴¹, Mario Hervault¹⁴², Aron T. Hill¹⁴³, Alice Hodapp³⁴,
 958 Maximilian Hommelsen¹⁴⁴, Hanna Honcamp¹⁴⁵, Thomas J. Hosang¹⁴⁶, Chun-Hsien Hsu¹⁴⁷, Tzu-
 959 Yu Hsu^{148,147}, Changrun Huang¹⁴⁹, Christoph Huber-Huber⁵⁹, Matthew Hughes⁷⁰, Agustín
 960 Ibanez^{150,151,152,153,154}, Behzad Iravani¹⁵⁵, Kylie Isenburg³⁰, Bradley N. Jack¹²⁶, Mina Jamshidi
 961 Idaji^{23,156}, Oskar H. Jepsen¹⁵⁷, El Jeong¹⁵⁸, Fang Jiang¹⁵⁹, Ann-Kathrin Joechner⁸⁰, Matthew R.
 962 Johnson¹⁶⁰, Ki-Young Jung¹⁶¹, Neda Kaboodvand¹⁵⁵, Daniel Kaiser^{162,163,164,165}, Patrycja
 963 Kałamała¹²⁵, Taeho Kang¹⁶⁶, Nikolai Kapralov^{167,168}, Hamid Karimi-Rouzbahani^{169,170}, Mikolaj
 964 Kegler¹⁷¹, Nicholas J. Kelley¹⁷², Simon Kern¹⁰⁴, Casper Kerrén²³, Songhee Kim¹⁷³, Alina
 965 Kiseleva¹⁰³, Laura-Isabelle Klatt¹⁷⁴, Felix Klotzsche²³, Daniel S. Kluger¹⁷⁵, Peter König^{176,177}, Bruno
 966 Kopp¹⁷⁸, Julian Q. Kosciessa^{3,31}, Maciej Kosilo⁷¹, Boris Kotchoubey¹⁷⁹, Layla Kouara¹⁸⁰, Sander
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 969 Lenc^{39,190}, Cédric Lenoir³⁹, Wanru Li¹⁹¹, Zefeng Li¹⁹², Anna M. Liesefeld¹⁹³, Heinrich R. Liesefeld¹⁹⁴,
 970 Maxim Likhanov¹⁹⁵, Evan N. Lintz¹⁹⁶, Giulia Lioi¹⁹⁷, Vladimir Litvak¹⁹⁸, Xiaoyi Liu¹⁹⁹, Yikang Liu⁶⁷,
 971 Yu-Hui Lo²⁰⁰, Eduardo López-Caneda^{201,202}, David López-García²¹, Corinna Lorenz²⁰³, Andreas
 972 Löw¹⁴⁶, Runhao Lu^{169,204}, Zitong Lu²⁰⁵, Alicia Luque²⁰⁶, David Lydon-Staley²⁰⁷, Oskar
 973 MacGregor²⁰⁸, Antonio Maffei^{209,210}, Martin E. Maier²¹¹, Lisa M. Makowski²¹², Francesco
 974 Mantegna^{213,214}, Eleonora Marcantoni²¹⁵, María Carmen Martín-Buro²¹⁶, Ana Martinovici²¹⁷, Anna

975 Marzecova²¹⁸, Fabio Masina³³, Jason B. Mattingley⁴⁴, Sara Mazzini⁹³, Takfarinas Medani²¹⁹, Ting
976 Mei¹³¹, David Melcher²²⁰, Qingqing Meng²²¹, Nick S. Menger²²², Ahmad Mheich^{136, 223}, Milan
977 Mitka⁶⁹, Claire Monroy⁵¹, Maria Montefinese²²⁴, David Moreau²²⁵, Quentin Moreau²²⁶, Liad
978 Mudrik²²⁷, Faisal Mushtaq¹⁸⁰, Nicholas E. Myers²², Norberto E. Naal-Ruiz⁷⁵, Foroogh Najafi²²⁸,
979 Hong-Viet V. Ngo²²⁹, Lu Nie²³⁰, Martin Nilsson²³¹, Guiomar Niso^{232, 233}, Erika Nyhus²³⁴, Joyce
980 Oerlemans²⁵, Emanuele Olivetti²³⁵, Joan Orpella^{213, 236}, Eduard Ort²¹⁸, Ana F. Palenciano²¹,
981 Kyoungun Park²³⁷, Bernhard Pastötter²³⁸, Zita Patai^{239, 240}, Katharina Paul²⁴¹, Artur José M.
982 Paulo⁴³, Giovanni Pellegrino²⁴², Sergio M. Pereira Soares⁹³, Franco Pestilli²⁴³, Rachele Pezzetta³²,
983 Daniela M. Pfabigan²⁴⁴, Anna Plachti²⁴⁵, Ulrich Pomper²⁴⁶, Tzvetan Popov¹⁸⁶, Pavel Prado²⁴⁷,
984 Andrea B. Protzner²⁴⁸, Yanina Prystauka²⁴⁹, Haoyue Qian²⁵⁰, Milena Rabovsky³⁴, Janir Ramos da
985 Cruz^{251, 252}, Manuel Rausch^{253, 254, 255}, Amit Rawal^{256, 257}, Stefan Repplinger²⁵⁸, Danielle R. Rice²⁵⁹,
986 Igor Rieckensky⁶⁹, Pavel Riha¹⁸⁵, Johannes Rodrigues²⁶⁰, M. Paula Roncaglia²⁶¹, Michael Rose²⁶²,
987 Marlene Rösner^{263, 264}, Jason Rothman^{265, 266, 267}, Simon Ruch²⁶⁸, Philipp Ruhnau²⁶⁹, Adi Sarig
988 Golan²⁷⁰, Arkaprovo Sarkar²⁷¹, Akul Satish¹⁶⁹, Cristina Scarpazza^{33, 32}, Christoph Scheffel¹⁸², Judith
989 Schepers²⁷², Antonio Schettino^{273, 274}, Barbara Schmidt²⁷⁵, Fabian Schmidt³⁸, Anna-Lena
990 Schubert¹¹⁸, Anna-Lisa Schuler^{32, 23}, Catriona L. Scrivener²⁷⁶, Magdalena Senderecka¹²⁵, Ulrike
991 Senftleben²⁷⁷, Fatih Serin¹⁶⁹, J. Ignacio Serrano⁸², Mehran Shabanpour²⁷⁸, Veronika Shamova¹³⁹,
992 Idris Shareef¹⁵⁹, Dmitry Sherbina¹⁸⁷, Cassie Ann Short²⁷⁹, Carine Signoret²⁸⁰, Esaú V. P.
993 Sirius^{281, 43}, René Skukies²⁸², Aureli Soria-Frisch⁴⁹, Firat Soylu²⁸³, Sebastian Speer²⁸⁴, Tim Paul
994 Steinfath^{23, 168}, Robert Steinhauser²¹¹, Simon R. Steinkamp²⁴⁵, Tilman Stephani^{3, 23}, Alexander
995 Strobel¹⁸², Dawid Strzelczyk¹⁸⁶, Pheobe Sun²⁸⁵, Yanan Sun²⁸⁶, Caroline Surrey¹⁸², Nikolay
996 Syrov^{287, 288}, Marco Tagliaferri⁵⁹, Siddharth Talwar²⁸⁹, Vincenza Tarantino²⁹⁰, Alessandro
997 Tavano^{291, 292}, Jason R. Taylor²⁹³, Carsten Thiele²⁹⁴, Nivethida Thirugnanasambandam²⁹⁵, Lara
998 Todorova¹³⁰, Aleksandra Tomić⁸³, Stefan J. Troche²¹², Lin-Yuan Tseng²⁹⁶, Sarah Tune²⁹⁷, Gözem
999 Turan²⁹⁸, Luca Turella⁵⁹, José Luis Ulloa²⁹⁹, Michael Valiadis³⁰⁰, Antonino Vallesi³⁰¹, Gwen van der
1000 Wijk²⁴⁸, Marijn van Vliet³⁰², Marijn van Wingerden²⁶¹, Enrico Varano¹⁷¹, Mohith M. Varma^{169, 303},
1001 Margarida Vasconcelos³⁰⁴, Yoana Vergilova³⁰⁵, Adrià Vilà-Balló³⁰⁶, Antonino Visalli³⁰⁷, Giada
1002 Viviani²¹⁰, Robin Vloeberghs⁸⁵, Jan Wacker³⁰⁸, Ya-Jie Wang³⁰⁹, Meng-Yun Wang^{310, 3}, Tianlu
1003 Wang³¹¹, Duan Wei³¹², Markus Werkle-Bergner⁸⁰, David White³¹³, Simon Whitton³¹⁴, Kristina
1004 Wiebels²²⁵, Stefan Wiens¹²⁰, Christoph A. Wittkamp²⁶², Maren-Isabel Wolf²⁶², Audrey Wong-Kee-
1005 You¹¹⁶, Will Woods⁷⁰, Franz Wurm^{315, 316}, Syanah C. Wynn²³⁴, Jiushu Xie⁶⁷, Alba Xifra-Porxas⁴⁵,
1006 Weiyong Xu¹²¹, Lev Yakovlev³¹⁷, Jinbiao Yang⁹³, Mustafa Yavuz³¹⁸, Vahab Youssofzadeh¹⁷³,
1007 Rongjun Yu³¹⁹, Talha Zafar²⁴⁸, Sara Zago³², Ilya Zakharov³²⁰, Marta Z. Zakrzewska³²¹, Juanli
1008 Zhang^{322, 23}, Zhen Zhang¹³¹, Shanshan Zhen³²³, Xinqi Zhou³²⁴, Judy D. Zhu³²⁵, Siyu Zhu³²⁶, Qian
1009 Zhuang³²⁷, Catharina Zich³²⁸, Reza Zomorodi³²⁹, Camila Zugarramurdi¹⁰⁷, Muhammad S.
1010 Navid^{330, 331}, Tuomas Puoliväli³³², Mehdi Senoussi^{25, 333, 25}, Jeremy D. Yeaton³³⁴, Balazs Aczel³³⁵,
1011 Mike X. Cohen³³⁶, Arnaud Delorme^{337, 338}, Anna Dreber³³⁹, Jörg Hipp³⁴⁰, Felix Holzmeister³⁴¹,
1012 Magnus Johannesson³³⁹, Vanja Ković³⁴², Robert Oostenveld^{3, 6}, Yuri G. Pavlov³⁴³, Cyril Pernet³⁴⁴,
1013 Russell A. Poldrack³⁴⁵, Aina Puce³⁴⁶, Tom Schonberg^{347, 270}, Martin Schweinsberg³⁴⁸, Anđela
1014 Šoškic³⁴², Barnabas Szasz^{349, 350}, Eric L. Uhlmann³⁵¹, Gustav Nilsson^{155, 120 *}, Niko A. Busch^{1 *}

1015 *shared last authorship

1016 Correspondence and requests for materials should be addressed to Gustav Nilsson or Niko A. Busch.

1017

1018 ¹Institute of Psychology, University of Muenster, Muenster, Germany.

1019 ²Department of Experimental Psychology, University of Oxford, Oxford, United Kingdom.

1020 ³Donders Institute for Brain, Cognition and Behaviour, Radboud University, Nijmegen, The
1021 Netherlands.

- 1022 ⁴Zurich Center for Neuroeconomics, Department of Economics, University of Zürich, Zurich,
1023 Switzerland.
- 1024 ⁵Department of Psychology, University of Copenhagen, Copenhagen, Denmark.
- 1025 ⁶NatMEG, Department of Clinical Neuroscience, Karolinska Institutet, Stockholm, Sweden.
- 1026 ⁷Department of Psychology and Cognitive Science, University of Trento, Italy.
- 1027 ⁸Institute for Applied Mathematics "Mauro Picone" (IAC), CNR, Italy.
- 1028 ⁹Centre for Research in Pedagogy and Practice (CRPP), National Institute of Education (NIE),
1029 Singapore.
- 1030 ¹⁰Science of Learning Centre (SoLEC), National Institute of Education (NIE), Singapore.
- 1031 ¹¹Division of Experimental Psychology and Neuropsychology, Department of Education and
1032 Psychology, Freie Universität Berlin, Berlin, Germany.
- 1033 ¹²Department of Cognitive Neuroscience, Faculty of Psychology and Neuroscience, Maastricht
1034 University, Maastricht, The Netherlands.
- 1035 ¹³Research Group Neural Circuits, Consciousness and Cognition, Max Planck Institute for
1036 Empirical Aesthetics, Frankfurt/Main, Germany.
- 1037 ¹⁴Department of Clinical and Experimental Medicine, University of Messina, Italy.
- 1038 ¹⁵Centre for Human Brain Health, School of Psychology, University of Birmingham, Birmingham,
1039 United Kingdom.
- 1040 ¹⁶Institute for Biomagnetism and Biosignal Analysis, University of Muenster, Germany.
- 1041 ¹⁷Federal Scientific Center for Psychological and Interdisciplinary Research, Russian Federation.
- 1042 ¹⁸McGill University, Canada.
- 1043 ¹⁹Physikalisch-Technische Bundesanstalt, Germany.
- 1044 ²⁰Technische Universität Berlin, Berlin, Germany.
- 1045 ²¹Mind, Brain and Behavior Research Center (CIMCYC), University of Granada, Granada, Spain.
- 1046 ²²University of Nottingham, United Kingdom.
- 1047 ²³Max Planck Institute for Human Cognitive and Brain Sciences, Leipzig, Germany.
- 1048 ²⁴University of Nebraska - Lincoln, United States.
- 1049 ²⁵Department of Experimental Psychology, Ghent University, Ghent, Belgium.
- 1050 ²⁶Affective Psychophysiology Laboratory, Institute of Health Psychology, HSE University, Saint
1051 Petersburg, Russian Federation.
- 1052 ²⁷American University of Sharjah, Sharjah, United Arab Emirates.
- 1053 ²⁸Department of Neuroscience, University of Padova, Italy.
- 1054 ²⁹School of Psychology, Bond University, Gold Coast, Australia.
- 1055 ³⁰Department of Physical Medicine and Rehabilitation, Spaulding Rehabilitation Hospital, Harvard
1056 Medical School, Boston, MA, United States.
- 1057 ³¹Max Planck Institute for Human Development, Berlin, Germany.
- 1058 ³²IRCCS San Camillo Hospital, Venice, Italy.
- 1059 ³³Department of General Psychology, University of Padova, Italy.
- 1060 ³⁴Department of Psychology, University of Potsdam, Germany.

- 1061 ³⁵Max Planck School of Cognition, Leipzig, Germany.
- 1062 ³⁶Department of Neuroscience, Biomedicine and Movement Sciences, University of Verona,
1063 Verona, Italy.
- 1064 ³⁷Department of Psychology, University of York, United Kingdom.
- 1065 ³⁸Center for Cognitive Neuroscience, University of Salzburg, Salzburg, Austria.
- 1066 ³⁹Institute of Neuroscience (IoNS), University Catholic of Louvain (UCLouvain), Brussels,
1067 Belgium.
- 1068 ⁴⁰Faculty of Psychology and Education Sciences, University of Coimbra, Coimbra, Portugal.
- 1069 ⁴¹Department of Psychology, Royal Holloway University of London, Egham, United Kingdom.
- 1070 ⁴²Department of Cognition, Emotion, and Methods in Psychology Faculty of Psychology University
1071 of Vienna Liebiggasse 5 1010 Vienna, Austria.
- 1072 ⁴³Hospital Israelita Albert Einstein, São Paulo, Brazil.
- 1073 ⁴⁴Queensland Brain Institute & School of Psychology, The University of Queensland, St Lucia,
1074 Australia.
- 1075 ⁴⁵School of Human Sciences, University of Greenwich, London, United Kingdom.
- 1076 ⁴⁶School of Psychology, University of Kent, United Kingdom.
- 1077 ⁴⁷MoMiLab, IMT School for Advanced Studies Lucca, Lucca, Italy.
- 1078 ⁴⁸School of Psychology, Laval University, Quebec City, Canada.
- 1079 ⁴⁹Starlab Barcelona S.L., Spain.
- 1080 ⁵⁰School of Psychological Science, Oregon State University, Corvallis, Oregon, United States.
- 1081 ⁵¹School of Psychology, Keele University, Keele, United Kingdom.
- 1082 ⁵²University of York, United Kingdom.
- 1083 ⁵³Department of Psychosomatic Medicine and Psychotherapy, Central Institute of Mental Health
1084 Mannheim, Medical Faculty Mannheim/Heidelberg University, Germany.
- 1085 ⁵⁴German Center for Mental Health, partner site Mannheim-Heidelberg-Ulm, Germany.
- 1086 ⁵⁵Exercise Science & Neuroscience, Department Exercise & Health, Paderborn University,
1087 Germany.
- 1088 ⁵⁶Institute of Research in Psychology (IPSY), University Catholic of Louvain (UCLouvain),
1089 Brussels, Belgium.
- 1090 ⁵⁷Department of Experimental Psychology, University of Granada, Granada, Spain.
- 1091 ⁵⁸Montreal Neurological Institute, McConnell Brain Imaging Centre, McGill University, Montreal,
1092 Quebec, Canada.
- 1093 ⁵⁹Center for Mind/Brain Sciences (CIMeC), University of Trento, Italy.
- 1094 ⁶⁰Computer Science Department, Universitat Autònoma de Barcelona, Cerdanyola del Valles,
1095 Spain.
- 1096 ⁶¹Bridging Research in AI and Neuroscience, Computer Vision Center, Cerdanyola del Valles,
1097 Spain.
- 1098 ⁶²Freie Universität Berlin, Berlin, Germany.
- 1099 ⁶³Donders Institute for Brain, Cognition, and Behaviour, Radboud University, Nijmegen, the
1100 Netherlands.

- 1101 ⁶⁴Korea University, Republic of Korea.
- 1102 ⁶⁵University of Iowa, Iowa City, IA, United States.
- 1103 ⁶⁶University of Maryland, College Park, MD, United States.
- 1104 ⁶⁷School of Psychology, Nanjing Normal University, China.
- 1105 ⁶⁸Department of Education and Psychology, Freie Universität Berlin, Berlin, Germany.
- 1106 ⁶⁹Centre of Experimental Medicine, Slovak Academy of Sciences, Slovak Republic.
- 1107 ⁷⁰Swinburne University of Technology, Melbourne, Australia.
- 1108 ⁷¹Instituto de Biofísica e Engenharia Biomédica, Faculdade de Ciências da Universidade de
1109 Lisboa, Portugal.
- 1110 ⁷²University of Rennes, CNRS, Inria, Inserm, France.
- 1111 ⁷³University of Bremen, Germany.
- 1112 ⁷⁴Faculty of Psychology and Educational Sciences, University of Geneva, Geneva, Switzerland.
- 1113 ⁷⁵Tecnologico de Monterrey, School of Humanities and Education, Monterrey, N.L., México.
- 1114 ⁷⁶Department of Physics and Mathematics, Universidad de Monterrey, Nuevo León, Mexico.
- 1115 ⁷⁷Faculty of Psychology and Neuroscience, Maastricht University, Maastricht, The Netherlands.
- 1116 ⁷⁸School of Psychology, University of Birmingham, Birmingham, United Kingdom.
- 1117 ⁷⁹Faculty of Philosophy, University of Warsaw, Warsaw, Poland.
- 1118 ⁸⁰Center for Lifespan Psychology, Max Planck Institute for Human Development, Berlin, Germany.
- 1119 ⁸¹Discipline of Psychology, University of Technology Sydney, Sydney, Australia.
- 1120 ⁸²Center for Automation and Robotics (CAR), Spanish National Research Council (CSIC), Spain.
- 1121 ⁸³UiT The Arctic University of Norway, Norway.
- 1122 ⁸⁴Center for Cognitive Neuroscience and Department of Psychology, University of Salzburg,
1123 Salzburg, Austria.
- 1124 ⁸⁵Brain & Cognition, KU Leuven, Belgium.
- 1125 ⁸⁶Behavior and Metabolism Laboratory, Champalimaud Research, Champalimaud Foundation,
1126 Lisbon, Portugal.
- 1127 ⁸⁷Department of Neuroscience, Brown University, Providence, RI, United States.
- 1128 ⁸⁸Centre for Functionally Integrative Neuroscience, Institute of Clinical Medicine, Aarhus
1129 University, Denmark.
- 1130 ⁸⁹University of Groningen, The Netherlands.
- 1131 ⁹⁰Academic Unit of Neurology, Trinity College Dublin, Dublin, Ireland.
- 1132 ⁹¹Department of Neurology, Universitätsklinikum Würzburg, Würzburg, Germany.
- 1133 ⁹²University of Electronic Science and Technology of China, School of Life Science and
1134 Technology, Chengdu, China.
- 1135 ⁹³Max Planck Institute for Psycholinguistics, Nijmegen, The Netherlands.
- 1136 ⁹⁴University of Bristol, Bristol, United Kingdom.
- 1137 ⁹⁵Birkbeck, University of London, London, United Kingdom.
- 1138 ⁹⁶Scientific Institute IRCCS E.Medea, Conegliano (TV), Italy.

- 1139 ⁹⁷CHU Sainte-Justine Azrieli Research Center, Department of Psychiatry and Addictology,
1140 University of Montréal, Montréal, Québec, Canada.
- 1141 ⁹⁸University of Stuttgart, Germany.
- 1142 ⁹⁹Section Teaching and Innovation of Learning, Faculty of Psychology and Neuroscience,
1143 Maastricht University, Maastricht, The Netherlands.
- 1144 ¹⁰⁰Department of Psychology, Humboldt-Universität zu Berlin.
- 1145 ¹⁰¹School of Psychology, University of Adelaide, Adelaide, Australia.
- 1146 ¹⁰²Human Health, Commonwealth Scientific and Industrial Research Organisation (CSIRO),
1147 Adelaide, Australia.
- 1148 ¹⁰³Institute of Cognitive Neuroscience, Higher School of Economics, Russian Federation.
- 1149 ¹⁰⁴Department of Clinical Psychology, Central Institute of Mental Health Mannheim, Medical
1150 Faculty Mannheim/Heidelberg University, Germany.
- 1151 ¹⁰⁵Department of Psychology, Neuroscience & Behaviour, McMaster University, Hamilton, ON,
1152 Canada.
- 1153 ¹⁰⁶School of Psychological Sciences, Tel Aviv University, Tel Aviv, Israel.
- 1154 ¹⁰⁷Facultad de Psicología, Universidad de la República, Montevideo, Uruguay.
- 1155 ¹⁰⁸Institut du Cerveau et de la Moelle Épinière, Paris, France.
- 1156 ¹⁰⁹Department of Psychology, Humboldt-Universität zu Berlin, Berlin, Germany.
- 1157 ¹¹⁰Wilhelm Wundt Institute for Psychology, Leipzig University, Germany.
- 1158 ¹¹¹City St George's, University of London, Centre for Clinical, Social and Cognitive Neuroscience
1159 Research, London, United Kingdom.
- 1160 ¹¹²Department of Clinical Psychology, Friedrich Schiller University Jena, Jena, Germany.
- 1161 ¹¹³Department of Psychiatry and Psychotherapy, University of Lübeck, Lübeck, Germany.
- 1162 ¹¹⁴Department of Human Development and Family Studies, Pennsylvania State University,
1163 University Park, Pennsylvania, United States.
- 1164 ¹¹⁵University of the Balearic Islands, Psychology Department. Active Cognition, Embodiment, and
1165 Environment Lab, Spain.
- 1166 ¹¹⁶Smith-Kettlewell Eye Research Institute, United States.
- 1167 ¹¹⁷Cardiff University Brain Research Imaging Centre (CUBRIC), School of Psychology, Cardiff
1168 University, Cardiff, United Kingdom.
- 1169 ¹¹⁸Johannes Gutenberg University Mainz, Germany.
- 1170 ¹¹⁹Department of Psychology, University of Concepción, Concepción, Chile.
- 1171 ¹²⁰Department of Psychology, Stockholm University, Stockholm, Sweden.
- 1172 ¹²¹Department of Psychology, University of Jyväskylä, Jyväskylä, Finland.
- 1173 ¹²²Niilo Mäki Institute, Jyväskylä, Finland.
- 1174 ¹²³Brain Mind Institute, EPFL, Lausanne, Switzerland.
- 1175 ¹²⁴Doctoral School in the Social Sciences, Jagiellonian University, Cracow, Poland.
- 1176 ¹²⁵Centre for Cognitive Science, Jagiellonian University, Cracow, Poland.
- 1177 ¹²⁶Research School of Psychology, Australian National University, Canberra, Australia.

- 1178 ¹²⁷IMT School for Advanced Studies Lucca, Lucca, Italy.
- 1179 ¹²⁸University of Bern, Switzerland.
- 1180 ¹²⁹Institut de Neurosciences des Systèmes, INSERM, Marseille, France.
- 1181 ¹³⁰Department of Psychology, Sabancı University, Istanbul, Turkey.
- 1182 ¹³¹Radboud University, The Netherlands.
- 1183 ¹³²Center for Molecular and Behavioral Neuroscience, Rutgers University, Newark, NJ, United
1184 States.
- 1185 ¹³³Department of Cognitive Psychology, University Trier, Germany.
- 1186 ¹³⁴University of California San Diego, La Jolla, California, United States.
- 1187 ¹³⁵Department of Psychology, Philipps-Universität Marburg, Marburg, Germany.
- 1188 ¹³⁶MINDIG, F-35000, Rennes, France.
- 1189 ¹³⁷School of Science and Engineering, Reykjavik University, Reykjavik, Iceland.
- 1190 ¹³⁸Uncertainty, Inverse Modeling and Machine Learning Group, Technische Universität Berlin,
1191 Berlin, Germany.
- 1192 ¹³⁹Department of Neurology, Charité Universitätsmedizin Berlin, Berlin, Germany.
- 1193 ¹⁴⁰Department of Psychology, University of Texas at Austin, Texas, United States.
- 1194 ¹⁴¹NeuroDataScience - ORIGAMI laboratory, McConnell Brain Imaging Centre, The Neuro
1195 (Montreal Neurological Institute-Hospital), Faculty of Medicine and Health Sciences, McGill
1196 University, Montreal, Quebec, Canada.
- 1197 ¹⁴²Univ. Grenoble Alpes, Inserm U1216, CHU Grenoble Alpes, Grenoble Institut Neurosciences,
1198 France.
- 1199 ¹⁴³School of Psychology, Deakin University, Melbourne, Australia.
- 1200 ¹⁴⁴Cognitive Neuroscience, Institute of Neuroscience and Medicine (INM-3), Forschungszentrum
1201 Jülich, Jülich, Germany.
- 1202 ¹⁴⁵Department of Neuropsychology and Psychopharmacology, Faculty of Psychology and
1203 Neuroscience, Maastricht University, Maastricht, The Netherlands.
- 1204 ¹⁴⁶Experimental Psychology Unit, Helmut Schmidt University, Hamburg, Germany.
- 1205 ¹⁴⁷Institute of Cognitive Neuroscience, National Central University, Taiwan.
- 1206 ¹⁴⁸Graduate Institute of Mind, Brain and Consciousness, Taipei Medical University, Taipei,
1207 Taiwan.
- 1208 ¹⁴⁹Department of Psychology & Neuroscience, Duke University, Durham, NC, United States.
- 1209 ¹⁵⁰Latin American Brain Health Institute (BrainLat), Universidad Adolfo Ibáñez, Santiago de Chile,
1210 Chile.
- 1211 ¹⁵¹Global Brain Health Institute, Trinity College Dublin, Dublin, Ireland.
- 1212 ¹⁵²Department of Biophysics, School of Medicine, Istanbul Medipol University, Istanbul, Turkey.
- 1213 ¹⁵³Barcelonaβeta Brain Research Center (BBRC), Pasqual Maragall Foundation, Barcelona,
1214 Spain.
- 1215 ¹⁵⁴Cognitive Neuroscience Center (CNC), Universidad de San Andrés, Buenos Aires, Argentina.
- 1216 ¹⁵⁵Department of Clinical Neuroscience, Karolinska Institutet, Stockholm, Sweden.

- 1217 ¹⁵⁶The Berlin Institute for the Foundations of Learning and Data, Berlin, Germany.
- 1218 ¹⁵⁷Psychosis Research Unit, Aarhus University Hospital – Psychiatry, Denmark.
- 1219 ¹⁵⁸Seoul National University, Republic of Korea.
- 1220 ¹⁵⁹Department of Psychology, University of Nevada, Reno, United States.
- 1221 ¹⁶⁰Inciteful, LLC, United States.
- 1222 ¹⁶¹Seoul National University College of Medicine, Republic of Korea..
- 1223 ¹⁶²Neural Computation Group, Department of Mathematics and Computer Science, Physics,
1224 Geography, Justus Liebig University Giessen, Germany.
- 1225 ¹⁶³Center for Mind, Brain and Behavior, Universities of Giessen, Marburg, and Darmstadt,
1226 Germany.
- 1227 ¹⁶⁴Cluster of Excellence "The Adaptive Mind", Universities of Giessen, Marburg, and Darmstadt,
1228 Germany.
- 1229 ¹⁶⁵Center for Applied Computer Science and Data Science, Justus Liebig University Giessen,
1230 Germany.
- 1231 ¹⁶⁶Human-Machine Interaction Group, TU Wien, Vienna, Austria.
- 1232 ¹⁶⁷Department of Neurology, Max Planck Institute for Human Cognitive and Brain Sciences,
1233 Leipzig, Germany.
- 1234 ¹⁶⁸International Max Planck Research School NeuroCom, Leipzig, Germany.
- 1235 ¹⁶⁹MRC Cognition and Brain Sciences Unit, University of Cambridge, Cambridge, United
1236 Kingdom.
- 1237 ¹⁷⁰Queensland Brain Institute, University of Queensland, Brisbane, Australia.
- 1238 ¹⁷¹Department of Bioengineering, Imperial College London, London, United Kingdom.
- 1239 ¹⁷²University of Southampton, United Kingdom.
- 1240 ¹⁷³Neurology department, Medical College of Wisconsin, Milwaukee, WI, United States.
- 1241 ¹⁷⁴Leibniz Research Centre for Working Environment and Human Factors, Dortmund, Germany.
- 1242 ¹⁷⁵Institute for Biomagnetism and Biosignal Analysis, University of Muenster, Muenster, Germany.
- 1243 ¹⁷⁶University Osnabrück, Germany.
- 1244 ¹⁷⁷University Medical Center Hamburg-Eppendorf, Hamburg, Germany.
- 1245 ¹⁷⁸Hannover Medical School, Germany.
- 1246 ¹⁷⁹Institute of Medical Psychology and Behavioral Neurobiology, University of Tübingen,
1247 Tübingen, Germany.
- 1248 ¹⁸⁰School of Psychology, University of Leeds, Leeds, United Kingdom.
- 1249 ¹⁸¹Department of Psychology, Clinical Psychology and Psychotherapy, University of Regensburg,
1250 Germany.
- 1251 ¹⁸²Faculty of Psychology, TUD Dresden University of Technology, Germany.
- 1252 ¹⁸³Centre for Tactile Internet with Human-in-the-Loop (CeTI), TUD Dresden University of
1253 Technology, Germany.
- 1254 ¹⁸⁴University of Padova, Italy.

1255 185Brain and Mind Research Program, Central European Institute of Technology, Masaryk
1256 University, Brno, Czechia.

1257 186University of Zurich, Switzerland.

1258 187Research Centre for Neurotechnology, Southern Federal University, Rostov-on-Don, Russian
1259 Federation.

1260 188Center for Depression, Anxiety, and Stress Research, Mclean Hospital, Belmont, United States.

1261 189Department of Psychiatry, Harvard Medical School, Boston, MA, United States.

1262 190Basque Center on Cognition, Brain and Language (BCBL), Donostia-San Sebastian, Spain.

1263 191Peking-Tsinghua Center for Life Sciences, Peking University, Beijing, China.

1264 192Ghent University, Belgium.

1265 193Department of Psychology, Ludwig-Maximilians-Universität München, Germany.

1266 194Department of Psychology, University of Bremen, Germany.

1267 195Centre de Recherche en Psychologie et Neurosciences, Aix Marseille University, CNRS,
1268 CRPN, Marseille, France.

1269 196Sonoma State University, Rohnert Park, CA, United States.

1270 197IMT Atlantique, Lab-STICC UMR CNRS 6285, Brest, France.

1271 198UCL Queen Square Institute of Neurology, United Kingdom.

1272 199Princeton University, United States.

1273 200Department of Psychology, National Taiwan University, Taiwan.

1274 201Psychology Research Center (CIPsi), University of Minho, Braga, Portugal.

1275 202Department of Clinical Psychology and Psychobiology, Faculty of Psychology, Health Research
1276 Institute of Santiago de Compostela (IDIS), University of Santiago de Compostela, Spain.

1277 203Department of Psychology, University of Wuppertal, Wuppertal, Germany.

1278 204Montreal Neurological Institute, Department of Neurology and Neurosurgery, McGill
1279 University, Montreal, Quebec, Canada.

1280 205MIT McGovern Institute for Brain Research, Boston, United States.

1281 206Department of Applied Language Studies and Nebrija Research Center in Cognition, Nebrija
1282 University, Madrid, Spain.

1283 207University of Pennsylvania, Philadelphia, PA, United States.

1284 208School of Informatics, University of Skövde, Skövde, Sweden.

1285 209Department of Developmental Psychology and Socialization (DPSS), University of Padova,
1286 Italy.

1287 210Padova Neuroscience Center (PNC), University of Padova, Italy.

1288 211Catholic University of Eichstätt-Ingolstadt, Germany.

1289 212Institute of Psychology, University of Bern, Bern, Switzerland.

1290 213Department of Psychology, New York University, New York, NY 10003, United States.

1291 214Department of Engineering Science, Oxford University, Oxford, Oxfordshire, United Kingdom.

1292 215Centre for Neurotechnology, School of Psychology and Neuroscience, University of Glasgow,
1293 Glasgow, United Kingdom.

- 1294 ²¹⁶Department of Psychology, Rey Juan Carlos University, Madrid, Spain.
- 1295 ²¹⁷Rotterdam School of Management, Erasmus University, The Netherlands.
- 1296 ²¹⁸Department of Biological Psychology of Decision Making, Institute of Experimental Psychology,
1297 Heinrich Heine University Düsseldorf, Düsseldorf, Germany.
- 1298 ²¹⁹Ming Hsieh Department of Electrical and Computer Engineering, University of Southern
1299 California, Los Angeles, CA, United States.
- 1300 ²²⁰New York University Abu Dhabi, United Arab Emirates.
- 1301 ²²¹National Acoustic Laboratory, Sydney, Australia.
- 1302 ²²²Institute of Medical Psychology and Behavioural Neurobiology, Eberhard Karls University of
1303 Tübingen, Germany.
- 1304 ²²³CHUV-Centre Hospitalier Universitaire Vaudois, Service des Troubles du Spectre de l'Autisme
1305 et apparentés, Lausanne University Hospital, Les Allières – Av. Beaumont 23, 1011, Lausanne,
1306 Switzerland.
- 1307 ²²⁴Department of Developmental Psychology and Socialisation (DPSS), University of Padova,
1308 Italy.
- 1309 ²²⁵School of Psychology, University of Auckland, New Zealand.
- 1310 ²²⁶CHU Sainte-Justine, Canada.
- 1311 ²²⁷School of Psychological Sciences and Sagol School of Neuroscience, Tel Aviv University, Tel
1312 Aviv, Israel.
- 1313 ²²⁸School of biomedical engineering, University of British Columbia, Vancouver, Canada.
- 1314 ²²⁹Department of Psychology, University of Essex, United Kingdom.
- 1315 ²³⁰School of Biomedical Engineering, Sun Yat-sen University, China.
- 1316 ²³¹Aging Research Center, Department of Neurobiology, Care Sciences, and Society, Karolinska
1317 Institutet and Stockholm University, Stockholm, Sweden.
- 1318 ²³²Psychological & Brain Sciences, Indiana University, Bloomington, IN, United States.
- 1319 ²³³Neuroimaging Group, Cajal Neuroscience Center, CSIC, Madrid, Spain.
- 1320 ²³⁴Department of Psychology and Program in Neuroscience, Bowdoin College, Brunswick, United
1321 States.
- 1322 ²³⁵Bruno Kessler Foundation, Italy.
- 1323 ²³⁶Department of Neuroscience, Georgetown University Medical Center, Washington, DC 20007,
1324 United States.
- 1325 ²³⁷Interdisciplinary Program in Bioengineering, College of Engineering, Seoul National University,
1326 Seoul, South Korea.
- 1327 ²³⁸Department of Liberal Arts and Social Sciences, University of Technology Nuremberg,
1328 Nuremberg, Germany.
- 1329 ²³⁹Dept. of Neuropsychology, Institute of Cognitive Neuroscience, Ruhr-Universität Bochum,
1330 Bochum, Germany.
- 1331 ²⁴⁰Institute of Behavioural Neuroscience, Department of Experimental Psychology, Division of
1332 Psychology and Language Sciences, University College London, United Kingdom.
- 1333 ²⁴¹Differential Psychology and Psychological Assessment, University of Hamburg, Germany.

- 1334 ²⁴²Clinical Neurological Science Department, Schulich School of Medicine and Dentistry, Western
1335 University, London, Ontario, Canada.
- 1336 ²⁴³Department of Psychology, The University of Texas at Austin, Texas, United States.
- 1337 ²⁴⁴Department of Clinical and Biological Psychology, University of Bergen, Bergen, Norway.
- 1338 ²⁴⁵Danish Research Centre for Magnetic Resonance, Department of Radiology and Nuclear
1339 Medicine, Copenhagen University Hospital - Amager and Hvidovre, Copenhagen, Denmark.
- 1340 ²⁴⁶Faculty of Psychology, University of Vienna, Austria.
- 1341 ²⁴⁷Facultad de Ciencias de la Rehabilitación y Calidad de Vida, Universidad San Sebastián, Chile.
- 1342 ²⁴⁸Department of Psychology, University of Calgary, Calgary, Canada.
- 1343 ²⁴⁹Department of Linguistic, Literary and Aesthetic Studies, University of Bergen, Bergen, Norway.
- 1344 ²⁵⁰Center for Excellence in Brain Science and Intelligence Technology, Chinese Academy of
1345 Sciences, China.
- 1346 ²⁵¹Wyss Center for Bio and Neuroengineering, Geneva, Switzerland.
- 1347 ²⁵²ABILITY Neurotech, Geneva, Switzerland.
- 1348 ²⁵³Philosophisch-pädagogische Fakultät, Katholische Universität Eichstätt-Ingolstadt, Eichstätt,
1349 Germany.
- 1350 ²⁵⁴Fakultät Gesellschaft und Ökonomie, Hochschule Rhein-Waal, Cleves, Germany.
- 1351 ²⁵⁵Institut für Psychologie, Universität Klagenfurt, Klagenfurt am Wörthersee, Austria.
- 1352 ²⁵⁶Ernst Strüngmann Institute (ESI) gGmbH of the Max Planck Society, Frankfurt, Germany.
- 1353 ²⁵⁷Faculty of Behavioural and Human Movement Sciences, Vrije Universiteit Amsterdam, The
1354 Netherlands.
- 1355 ²⁵⁸Otto-von-Guericke-University Magdeburg, Germany.
- 1356 ²⁵⁹Department of Human Development and Family Studies, The Pennsylvania State University,
1357 University Park, PA, United States.
- 1358 ²⁶⁰Department of Psychology V, Differential Psychology, Personality Psychology, and
1359 Psychological Diagnostics, Julius-Maximilians University of Würzburg, Germany.
- 1360 ²⁶¹Department of Cognitive Science & Artificial Intelligence, Tilburg School of Humanities and
1361 Digital Sciences, Tilburg University, Tilburg, the Netherlands.
- 1362 ²⁶²Department of Systems Neuroscience, University Medical Center Hamburg-Eppendorf,
1363 Hamburg, Germany.
- 1364 ²⁶³Institut für Psychologie, Otto-von-Guericke-University Magdeburg, Magdeburg, Germany.
- 1365 ²⁶⁴Centre for Human Brain Health, University of Birmingham, Birmingham, United Kingdom.
- 1366 ²⁶⁵UiT Center for Language, Brain and Learning (C-LaBL), the Arctic University of Norway,
1367 Tromsø, Norway.
- 1368 ²⁶⁶Linguistics and English Language, Lancaster University, Lancaster, United Kingdom.
- 1369 ²⁶⁷Nebrija Research Center in Cognition, Nebrija University, Madrid, Spain.
- 1370 ²⁶⁸Faculty of Psychology, UniDistance Suisse, Brig, Switzerland.
- 1371 ²⁶⁹School of Psychology and Humanities, University of Lancashire, United Kingdom.
- 1372 ²⁷⁰Sagol School of Neuroscience, Tel Aviv University, Tel Aviv, Israel.

- 1373 ²⁷¹Department of Biosciences and Bioengineering, Indian Institute of Technology Bombay, India.
- 1374 ²⁷²Institute for Visualization and Interactive Systems (VIS), University of Stuttgart, Stuttgart,
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- 1376 ²⁷³Engagement & Research Services, Erasmus University Rotterdam, The Netherlands.
- 1377 ²⁷⁴Institute for Globally Distributed Open Research and Education (IGDORE), Sweden.
- 1378 ²⁷⁵Universitätsklinikum Jena, Germany.
- 1379 ²⁷⁶School of Philosophy, Psychology and Language Sciences, University of Edinburgh,
1380 Edinburgh, United Kingdom.
- 1381 ²⁷⁷Department of Psychology, TUD Dresden University of Technology, Dresden, Germany.
- 1382 ²⁷⁸Concordia Institute for Information Systems Engineering (CIISE), Concordia University,
1383 Montreal, Canada.
- 1384 ²⁷⁹Department of Psychology, Carl von Ossietzky Universität Oldenburg, Germany.
- 1385 ²⁸⁰Linköping University, Sweden.
- 1386 ²⁸¹Center for Mathematics, Computing and Cognition, Federal University of ABC (UFABC), São
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- 1388 ²⁸²Center for Simulation Science, University of Stuttgart, Germany.
- 1389 ²⁸³University of Alabama, United States.
- 1390 ²⁸⁴Psychology Department, Princeton University, Princeton, NJ, United States.
- 1391 ²⁸⁵University College Dublin, Ireland.
- 1392 ²⁸⁶School of Psychological Sciences, Macquarie University, Sydney, Australia.
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- 1395 ²⁸⁹University Catholic of Louvain (UCLouvain), Brussels, Belgium.
- 1396 ²⁹⁰Department of Psychology, Educational Science and Human Movement, University of Palermo,
1397 Italy.
- 1398 ²⁹¹Institute of Psychology, Goethe University Frankfurt, Germany.
- 1399 ²⁹²Max-Planck-Institut für empirische Ästhetik, Germany.
- 1400 ²⁹³University of Manchester, Manchester, United Kingdom.
- 1401 ²⁹⁴Department of Neurology, University Clinic, Otto-von-Guericke University Magdeburg,
1402 Germany.
- 1403 ²⁹⁵Department of Biosciences and Bioengineering, Indian Institute of Technology Bombay,
1404 Mumbai, India.
- 1405 ²⁹⁶Department of Health Technology and Informatics, The Hong Kong Polytechnic University,
1406 Hong Kong.
- 1407 ²⁹⁷University of Lübeck, Germany.
- 1408 ²⁹⁸Goethe University Frankfurt, Germany.
- 1409 ²⁹⁹Programa de Investigación Asociativa (PIA) en Ciencias Cognitivas, Centro de Investigación
1410 en Ciencias Cognitivas (CICC), Facultad de Psicología, Universidad de Talca, Talca, Chile.
- 1411 ³⁰⁰University of Tübingen, Germany.

- 1412 ³⁰¹Department of Neuroscience, University of Padova, Padova, Italy.
- 1413 ³⁰²Department of Neuroscience and Biomedical Engineering, Aalto University, Espoo, Finland.
- 1414 ³⁰³Department of Management, Hong Kong Baptist University, Hong Kong.
- 1415 ³⁰⁴Research Center for Psychological Science, Faculty of Psychology, University of Lisbon,
1416 Lisbon, Portugal.
- 1417 ³⁰⁵KESS Kindliche Entwicklung und Sprache Stärken, Offenbach, Germany.
- 1418 ³⁰⁶Department of Psychology, University of Girona, Girona, Spain.
- 1419 ³⁰⁷Department of Biomedical, Metabolic and Neural Sciences, University of Modena and Reggio
1420 Emilia, Italy.
- 1421 ³⁰⁸University of Hamburg, Germany.
- 1422 ³⁰⁹Department of Psychology and Behavioral Sciences, Zhejiang University, Hangzhou, China.
- 1423 ³¹⁰Language and Genetics Department, Max Planck Institute for Psycholinguistics, Nijmegen, The
1424 Netherlands.
- 1425 ³¹¹Ernst Strüngmann Institute (ESI) for Neuroscience in Cooperation with the Max Planck Society,
1426 Frankfurt, Germany.
- 1427 ³¹²Social Science Laboratory of Reading and Development in Children and Adolescents, Ministry
1428 of Education, & Center for Studies of Psychological Application, School of Psychology, South
1429 China Normal University, China.
- 1430 ³¹³Centre for Mental Health and Brain Sciences, Swinburne University of Technology, Melbourne,
1431 Australia.
- 1432 ³¹⁴University of Nevada, Reno, United States.
- 1433 ³¹⁵Department of Health, Medical, and Neuropsychology, Leiden University, Leiden, The
1434 Netherlands.
- 1435 ³¹⁶Leiden Institute for Brain and Cognition, Leiden University, The Netherlands.
- 1436 ³¹⁷Faculty of Biology, Shenzhen MSU-BIT University, China.
- 1437 ³¹⁸Graduate School of Health Sciences, Istanbul University, Istanbul, Turkey.
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- 1440 ³²¹Bioeconomy division, RISE Research Institutes of Sweden, Stockholm, Sweden.
- 1441 ³²²Epilepsy Unit, Department of Clinical Neurosciences, University Hospitals and Faculty of
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- 1443 ³²³Department of Social and Behavioural Sciences, City University of Hong Kong, Hong Kong.
- 1444 ³²⁴Institute of Brain and Psychological Sciences, Sichuan Normal University, Chengdu, China.
- 1445 ³²⁵School of Psychological Sciences, Macquarie University, Australia.
- 1446 ³²⁶School of Sport Training, Chengdu Sport University, Chengdu, China.
- 1447 ³²⁷Center for Cognition and Brain Disorders/ Department of Neurology, The Affiliated Hospital of
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- 1451 ³²⁹CAMH-University of Toronto, Canada.

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1454 ³³¹Donders Institute for Brain, Cognition and Behaviour, Radboud University Medical Center,
1455 Nijmegen, The Netherlands.

1456 ³³²Faculty of Information Technology, University of Jyväskylä, Jyväskylä, Finland.

1457 ³³³CLLE, Université Toulouse Jean Jaurès, CNRS, Toulouse, France.

1458 ³³⁴Department of Language Science, University of California, Irvine, United States.

1459 ³³⁵ELTE, Eotvos Lorand University, Budapest, Hungary.

1460 ³³⁶Radboud University Medical Center, Donders Centre for Medical Neuroscience, The
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1465 ³³⁹Department of Economics, Stockholm School of Economics, Stockholm, Sweden.

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1467 Innovation Center Basel, F. Hoffmann–La Roche Ltd., Basel, Switzerland.

1468 ³⁴¹Department of Economics, University of Innsbruck, Innsbruck, Austria.

1469 ³⁴²Laboratory for Neurocognition and Applied Cognition, Faculty of Philosophy, University of
1470 Belgrade, Belgrade, Serbia.

1471 ³⁴³Department of Psychology, University of Alabama at Birmingham, United States.

1472 ³⁴⁴Neurobiology Research Unit, Copenhagen University Hospital, Rigshospitalet, Copenhagen,
1473 Denmark.

1474 ³⁴⁵Department of Psychology, Stanford University, Stanford, CA, United States.

1475 ³⁴⁶Department of Psychological & Brain Sciences, Indiana University, Bloomington, United States.

1476 ³⁴⁷School of Neurobiology, Biochemistry & Biophysics, Faculty of Life Sciences, Tel Aviv
1477 University, Tel Aviv, Israel.

1478 ³⁴⁸ESMT Berlin, Berlin, Germany.

1479 ³⁴⁹Institute of Operations and Decision Sciences, Corvinus Institute for Advanced Studies (CIAS),
1480 Corvinus University of Budapest, Budapest, Hungary.

1481 ³⁵⁰Institute of Psychology, ELTE Eötvös Loránd University, Budapest, Hungary.

1482 ³⁵¹Department of Organizational Behavior, INSEAD, Singapore.

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1666 Soria-Frisch, and Claire Braboszcz are employees of Starlab, Barcelona. Maximilian Hommelsen
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1668 Barcelona SL and is an advisor of Neuroelectrics. Mahmoud Hassan is the Founder and CEO of
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1678 Author contributions

1679 **Current EEGManyPipelines Steering Committee constitution:** Johannes Algermissen, Niko
1680 A. Busch, Elena Cesnaite, Nastassja L. Fischer, Claudia Gianelli, Gustav Nilsonne, Annalisa
1681 Pascarella, Darinka Trübutschek, Mikkel C. Vinding, Andrea Vitale, Yu-Fang Yang

1682 **Steering Committee members who initiated the project:** Johannes Algermissen, Niko A.
1683 Busch, Nastassja L. Fischer, Claudia Gianelli, Josh Koen, Charlotte R. Marshall, Muhammad
1684 Samran Navid, Gustav Nilsonne, Annalisa Pascarella, Tuomas Puoliväli, Mehdi Senoussi,
1685 Darinka Trübutschek, Mikkel C. Vinding, Andrea Vitale, Yu-Fang Yang, Jeremy Yeaton

1686 **Drafting the manuscript:** Johannes Algermissen, Niko A. Busch, Elena Cesnaite, Nastassja L.
1687 Fischer, Claudia Gianelli, Gustav Nilsonne, Annalisa Pascarella, Darinka Trübutschek, Mikkel C.
1688 Vinding, Andrea Vitale, Yu-Fang Yang, Eric L. Uhlmann

1689 **EEG dataset sent to the analysts (experiment design, data collection, and quality**
1690 **assurance):** Niko A. Busch

1691 **Experimental design of the EEGManyPipelines project:** Johannes Algermissen, Niko A.
1692 Busch, Elena Cesnaite, Nastassja L. Fischer, Claudia Gianelli, Charlotte R. Marshall, Muhammad
1693 Samran Navid, Gustav Nilsonne, Annalisa Pascarella, Tuomas Puoliväli, Darinka Trübutschek,
1694 Mikkel C. Vinding, Andrea Vitale, Yu-Fang Yang

1695 **Analysis team (recruitment, point of contact, and data management):** Johannes
1696 Algermissen, Niko A. Busch, Elena Cesnaite, Nastassja L. Fischer, Claudia Gianelli, Charlotte R.
1697 Marshall, Gustav Nilsson, Annalisa Pascarella, Tuomas Puoliväli, Darinka Trübtschek, Mikkel
1698 C. Vinding, Andrea Vitale, Yu-Fang Yang

1699 **Analysis team (data analysis and visualisation):** Johannes Algermissen, Elena Cesnaite,
1700 Nastassja L. Fischer, Annalisa Pascarella, Mikkel C. Vinding, Andrea Vitale

1701 **Participated as members of the advisory board and reviewed and edited the manuscript:**
1702 Balazs Aczel, Mike X. Cohen, Arnaud Delorme, Anna Dreber, Jörg Hipp, Felix Holzmeister,
1703 Magnus Johannesson, Vanja Ković, Robert Oostenveld, Yuri G. Pavlov, Cyril Pernet, Russell
1704 Poldrack, Aina Puce, Tom Schonberg, Martin Schweinsberg, Anđela Šoškić, Barnabas Szasz,
1705 Eric L. Uhlmann

1706 **Participated as members of analysis teams and reviewed and edited the manuscript:** Omid
1707 Abbasi, Timofey Adamovich, Lena Adel, Nikita Agarwal, Blanca Aguado-López, Uma Ajmeria,
1708 Esra Al, Hannah Aldeen, Ricardo J. Alejandro, Evgeniia A. Alenina, Meera Alex, Ettore Ambrosini,
1709 Douglas J. Angus, Alessandra Anzolin, Stefan Appelhoff, Giorgio Arcara, Yana Arkhipova, Maria
1710 Azanova, Chiara Bagattini, Daniel H. Baker, Christoph Bamberg, Francesca M. Barbero, Ceren
1711 Battal, Anna-Katharina R. Bauer, Burcu Bayram, Paulo R. Bazán, Henry Beale, Elena Belanova,
1712 Zara M. Bergström, Giulio Bernardi, Martina Berto, Monica Betta, Isabelle Blanchette, Marta
1713 Bortoletto, Davide Bottari, Claire Braboszcz, Daniel E. Bradford, Joseph L. Brooks, Chloe M.
1714 Brunskill, Florian Bublatzky, Daniel Büchel, Roberta P. Calce, Mariagrazia Capizzi, Raymundo
1715 Cassani, María Concepción Castellanos, Luigi Cattaneo, Xim Cerda-Company, Lixiang Chen,
1716 Xinyuan Chen, Yiyu Chen, Yoojeong Choo, Hu Chuan-Peng, Karan Chugani, Radoslaw Martin
1717 Cichy, Barbora Cimrová, Simon Ciranka, Oren Civier, Carlotta Cogoni, Michel-Pierre Coll, Julie
1718 Coloigner, Angela Conejero, Martin Constant, César E. Corona-González, Antonio Criscuolo,
1719 Damian Cruse, Claire Cury, Artur Czeszumski, Martin J. Dahl, Matthew Davidson, Ingmar E. J.
1720 de Vries, M. Dolores del Castillo, Vincent DeLuca, Gianpaolo Demarchi, Kobe Desender, Marcelo
1721 Dias, Darcy Waller, Martin Dietz, Olaf Dimigen, Hao Ding, Li Dong, Linda Drijvers, Brandi Lee
1722 Drisdelle, Gian Marco Duma, Guillaume Dumas, Benedikt Ehinger, Alexandra K. Emmendorfer,
1723 Alexander Enge, Stefanie Evas, Tommaso Fedele, Alessandra Federici, Gordon B. Feld, Lauren
1724 K. Fink, Shai Fischer, Emilia Fló, Silvia Formica, Norman Forschack, Bettina Forster, Marcel
1725 Franz, Léon Franzen, Cassidy M. Fry, Alejandro Galvez-Pol, Haydee G. García-Lázaro, José
1726 Carlos García Alanis, Patricia Garrido-Vásquez, Billy Gerdfeldter, Georgia Gerike, Magdalena
1727 Gippert, Carlos González-García, Dario Gordillo, Anna Grabowska, Lisa-Marie Greenwood,
1728 Benjamin J. Griffiths, Demetrio Grollero, Joachim Gross, Danièle A. Gubler, Pierre Guilleminot,
1729 Berna Güler, Christopher Gundlach, Eren Günseli, Mingqian Guo, Malte R. Güth, Céline
1730 Haciaahmet, Itay Hadas, Jarmo Hämäläinen, Sizhu Han, Anthony M. Harris, Mahmoud Hassan,
1731 Stefan Haufe, Anibal S. Heinsfeld, Peer Herholz, Mario Hervault, Aron T. Hill, Alice Hodapp,
1732 Maximilian Hommelsen, Hanna Honcamp, Thomas J. Hosang, Chun-Hsien Hsu, Tzu-Yu Hsu,
1733 Changrun Huang, Christoph Huber-Huber, Matthew Hughes, Agustin Ibanez, Behzad Iravani,
1734 Kylie Isenburg, Bradley N. Jack, Mina Jamshidi Idaji, Oskar H. Jepsen, El Jeong, Fang Jiang, Ann-
1735 Kathrin Joechner, Matthew R. Johnson, Ki-Young Jung, Neda Kaboodvand, Daniel Kaiser,
1736 Patrycja Kałamała, Taeho Kang, Nikolai Kapralov, Hamid Karimi-Rouzbahani, Mikolaj Kegler,

1737 Nicholas J. Kelley, Simon Kern, Casper Kerrén, Songhee Kim, Alina Kiseleva, Laura-Isabelle
1738 Klatt, Felix Klotzsche, Daniel S. Kluger, Peter König, Bruno Kopp, Julian Q. Kosciessa, Maciej
1739 Kosilo, Boris Kotchoubey, Layla Kouara, Sander Krewinkel, Leon O. H. Kroczeck, Corinna Kührt,
1740 Sara Lago, Martin Lamoš, Nicolas Langer, Dmitry Lazurenko, Pierre Le Denmat, Ty Lees, Tim
1741 Lehmann, Tomas Lenc, Cédric Lenoir, Wanru Li, Zefeng Li, Anna M. Liesefeld, Heinrich R.
1742 Liesefeld, Maxim Likhanov, Evan N. Lintz, Giulia Lioi, Vladimir Litvak, Xiaoyi Liu, Yikang Liu, Yu-
1743 Hui Lo, Eduardo López-Caneda, David López-García, Corinna Lorenz, Andreas Löw, Runhao Lu,
1744 Zitong Lu, Alicia Luque, David Lydon-Staley, Oskar MacGregor, Antonio Maffei, Martin E. Maier,
1745 Lisa M. Makowski, Francesco Mantegna, Eleonora Marcantoni, María Carmen Martín-Buro, Ana
1746 Martinovici, Anna Marzecova, Fabio Masina, Jason B. Mattingley, Sara Mazzini, Takfarinas
1747 Medani, Ting Mei, David Melcher, Qingqing Meng, Nick S. Menger, Ahmad Mheich, Milan Mitka,
1748 Claire Monroy, Maria Montefinese, David Moreau, Quentin Moreau, Liad Mudrik, Faisal Mushtaq,
1749 Nicholas E. Myers, Norberto E. Naal-Ruiz, Foroogh Najafi, Hong-Viet V. Ngo, Lu Nie, Martin
1750 Nilsson, Guiomar Niso, Erika Nyhus, Joyce Oerlemans, Emanuele Olivetti, Joan Orpella, Eduard
1751 Ort, Ana F. Palenciano, Kyoungun Park, Bernhard Pastötter, Zita Patai, Katharina Paul, Artur
1752 José M. Paulo, Giovanni Pellegrino, Sergio M. Pereira Soares, Franco Pestilli, Rachele Pezzetta,
1753 Daniela M. Pfabigan, Anna Plachti, Ulrich Pomper, Tzvetan Popov, Pavel Prado, Andrea B.
1754 Protzner, Yanina Prystauka, Haoyue Qian, Milena Rabovsky, Janir Ramos da Cruz, Manuel
1755 Rausch, Amit Rawal, Stefan Replinger, Danielle R. Rice, Igor Riečanský, Pavel Riha, Johannes
1756 Rodrigues, M. Paula Roncaglia, Michael Rose, Marlene Rösner, Jason Rothman, Simon Ruch,
1757 Philipp Ruhnau, Adi Sarig Golan, Arkaprovo Sarkar, Akul Satish, Cristina Scarpazza, Christoph
1758 Scheffel, Judith Schepers, Antonio Schettino, Barbara Schmidt, Fabian Schmidt, Anna-Lena
1759 Schubert, Anna-Lisa Schuler, Catriona L. Scrivener, Magdalena Senderecka, Ulrike Senftleben,
1760 Fatih Serin, J. Ignacio Serrano, Mehran Shabanpour, Veronika Shamova, Idris Shareef, Dmitry
1761 Sherbina, Cassie Ann Short, Carine Signoret, Esaú V. P. Sirius, René Skukies, Aureli Soria-
1762 Frisch, Firat Soyly, Sebastian Speer, Tim Paul Steinfath, Robert Steinhauser, Simon R.
1763 Steinkamp, Tilman Stephani, Alexander Strobel, Dawid Strzelczyk, Pheobe Sun, Yanan Sun,
1764 Caroline Surrey, Nikolay Syrov, Marco Tagliaferri, Siddharth Talwar, Vincenza Tarantino,
1765 Alessandro Tavano, Jason R. Taylor, Carsten Thiele, Nivethida Thirugnanasambandam, Lara
1766 Todorova, Aleksandra Tomić, Stefan J. Troche, Lin-Yuan Tseng, Sarah Tune, Gözem Turan,
1767 Luca Turella, José Luis Ulloa, Michael Valiadis, Antonino Vallesi, Gwen van der Wijk, Marijn van
1768 Vliet, Marijn van Wingerden, Enrico Varano, Mohith M. Varma, Margarida Vasconcelos, Yoana
1769 Vergilova, Adrià Vilà-Balló, Antonino Visalli, Giada Viviani, Robin Vloeberghs, Jan Wacker, Ya-
1770 Jie Wang, Meng-Yun Wang, Tianlu Wang, Duan Wei, Markus Werkle-Bergner, David White,
1771 Simon Whitton, Kristina Wiebels, Stefan Wiens, Christoph A. Wittkamp, Maren-Isabel Wolf,
1772 Audrey Wong-Kee-You, Will Woods, Franz Wurm, Syanah C. Wynn, Jiushu Xie, Alba Xifra-
1773 Porxas, Weiyong Xu, Lev Yakovlev, Jinbiao Yang, Mustafa Yavuz, Vahab Youssofzadeh,
1774 Rongjun Yu, Talha Zafar, Sara Zago, Ilya Zakharov, Marta Z. Zakrzewska, Juanli Zhang, Zhen
1775 Zhang, Shanshan Zhen, Xinqi Zhou, Judy D. Zhu, Siyu Zhu, Qian Zhuang, Catharina Zich, Reza
1776 Zomorodi, Camila Zugarramurdi.