Life Sciences Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form is intended for publication with all accepted life science papers and provides structure for consistency and transparency in reporting. Every life science submission will use this form; some list items might not apply to an individual manuscript, but all fields must be completed for clarity.

For further information on the points included in this form, see Reporting Life Sciences Research. For further information on Nature Research policies, including our data availability policy, see Authors & Referees and the Editorial Policy Checklist.

- Experimental design

1. Sample size
   Describe how sample size was determined.
   Because data from multiple datasets were combined in a multi-study framework, balanced subsampling was performed (n = 15 per study) to help equate statistical power for comparisons between studies.

2. Data exclusions
   Describe any data exclusions.
   No data were excluded from the analysis.

3. Replication
   Describe whether the experimental findings were reliably reproduced.
   Although replication was not attempted, the main findings reflect effects that are reliable across 6 different studies.

4. Randomization
   Describe how samples/organisms/participants were allocated into experimental groups.
   This was not a randomized study, it was a mega-analysis of multiple studies. Contrasts were constructed within subjects and the goal was to compare effects across studies. Participants were recruited independently for each of the 18 studies being analyzed. A posteriori group assignment was based on the goals of each study and experimental manipulation being used (e.g., studies involving thermal stimulation of the forearm were considered members of the 'pain' domain).

5. Blinding
   Describe whether the investigators were blinded to group allocation during data collection and/or analysis.
   Investigators were not aware of group comparisons during data collection. No blinding was performed for data analysis.

Note: all studies involving animals and/or human research participants must disclose whether blinding and randomization were used.
6. Statistical parameters

For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or in the Methods section if additional space is needed).

<table>
<thead>
<tr>
<th>Item</th>
<th>Status</th>
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</thead>
<tbody>
<tr>
<td>□ The exact sample size ( n ) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.)</td>
<td>Confirmed</td>
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<tr>
<td>□ A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly</td>
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<td>□ A statement indicating how many times each experiment was replicated</td>
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<tr>
<td>□ The statistical test(s) used and whether they are one- or two-sided (note: only common tests should be described solely by name; more complex techniques should be described in the Methods section)</td>
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<tr>
<td>□ A description of any assumptions or corrections, such as an adjustment for multiple comparisons</td>
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<tr>
<td>□ The test results (e.g. ( P ) values) given as exact values whenever possible and with confidence intervals noted</td>
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<tr>
<td>□ A clear description of statistics including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)</td>
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<tr>
<td>□ Clearly defined error bars</td>
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</table>

See the web collection on statistics for biologists for further resources and guidance.

7. Software

Policy information about availability of computer code

Describe the software used to analyze the data in this study.

Analysis was conducted using CANLab and SPM software implemented in MATLAB. Code for implementing all analyses is available at https://github.com/canlab/ and www.fil.ion.ucl.ac.uk/spm/software/.

For manuscripts utilizing custom algorithms or software that are central to the paper but not yet described in the published literature, software must be made available to editors and reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). Nature Methods guidance for providing algorithms and software for publication provides further information on this topic.

8. Materials availability

Policy information about availability of materials

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a for-profit company.

No unique materials were used.

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).

No antibodies were used.

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.

No eukaryotic cell lines were used.

b. Describe the method of cell line authentication used.

No eukaryotic cell lines were used.

c. Report whether the cell lines were tested for mycoplasma contamination.

No eukaryotic cell lines were used.

d. If any of the cell lines used are listed in the database of commonly misidentified cell lines maintained by ICLAC, provide a scientific rationale for their use.

No commonly misidentified cell lines were used.

11. Description of research animals

Provide details on animals and/or animal-derived materials used in the study.

Non-human animals were not used.
Policy information about studies involving human research participants

12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants.

270 healthy human participants were involved in the research. The age and gender of participants in each of the 18 studies are detailed in Supplementary Table 7.
MRI Studies Reporting Summary

Form fields will expand as needed. Please do not leave fields blank.

- **Experimental design**
  1. Describe the experimental design.
     - Multiple methods are used, depending on the study. Our approach aims to generalize across these methodological factors.
  2. Specify the number of blocks, trials or experimental units per session and/or subject, and specify the length of each trial or block (if trials are blocked) and interval between trials.
     - The number of trials per subject ranged from 8 to 768. Stimulus durations ranged from 2s to 18s. Scan length ranged from 5 min to 13.5 min. Details for each study are listed in Supplementary Table 7 and the original publications for each study.
  3. Describe how behavioral performance was measured.
     - Behavioral data are not presented.

- **Acquisition**
  4. Imaging
     - a. Specify the type(s) of imaging.
       - BOLD fMRI
     - b. Specify the field strength (in Tesla).
       - 1.5 and 3 Tesla
     - c. Provide the essential sequence imaging parameters.
       - EPI (standard and multiband) and spiral in-out sequences were used for data acquisition. Readers are referred to the original publications for more details.
     - d. For diffusion MRI, provide full details of imaging parameters.
       - Diffusion MRI was not collected.
  5. State area of acquisition.
     - Whole brain scans were used.

- **Preprocessing**
  6. Describe the software used for preprocessing.
     - SPM and custom code were used for preprocessing, the particular version depending on the study. Readers are referred to the original publications for more details.
  7. Normalization
     - a. If data were normalized/standardized, describe the approach(es).
       - Non-linear normalization to MNI space was performed.
     - b. Describe the template used for normalization/ transformation.
       - The templates used depend on the study, but all are in ICBM152 space.
  8. Describe your procedure for artifact and structured noise removal.
     - Regression of motion parameters was performed in all studies (either 6 parameters based on translation and rotation or 24 with the inclusion of their derivatives, successive differences, and squared successive differences).
  9. Define your software and/or method and criteria for volume censoring, and state the extent of such censoring.
     - Outlier timepoints were excluded in some studies. These were identified based on Mahalanobis distance using a chi-square test.
10. Define your model type and settings. Multivariate RSA models were specified and fitted using least squares regression. Subject was treated as a random effect.

11. Specify the precise effect tested. Dissimilarity between brain activity (1 - Pearson’s correlation coefficient) was modeled as a function of study, psychological subdomain, and domain.

12. Analysis
   a. Specify whether analysis is whole brain or ROI-based. ROI-based and whole brain searchlight
   b. If ROI-based, describe how anatomical locations were determined. Existing parcellations were used for ROI-based analyses.

13. State the statistic type for inference. (See Eklund et al. 2016.) Voxel-wise statistics were used.

14. Describe the type of correction and how it is obtained for multiple comparisons. FDR correction was used.

15. Connectivity
   a. For functional and/or effective connectivity, report the measures of dependence used and the model details. Connectivity analysis was not performed.
   b. For graph analysis, report the dependent variable and functional connectivity measure. Graph analysis was not performed.

16. For multivariate modeling and predictive analysis, specify independent variables, features extraction and dimension reduction, model, training and evaluation metrics. For multivariate models, the independent variables comprised dissimilarity matrices (1 - Pearson’s correlation coefficient) estimated on data from all subjects (n = 270). Feature extraction was done in three ways: using local searchlights in the medial frontal cortex (MFC), using a priori ROIs in the MFC (Vogt parcellation), and using a set of ROIs that spans the whole brain (Brainnetome atlas). No dimension reduction was performed. RSA-based models were estimated using least squares regression. Partial Least Squares regression was also used to predict psychological domains from patterns of brain activity. Inferences were made on parameter estimates using bootstrap and Monte Carlo methods.