nature research

Corresponding author(s): H. Hannah Nam (hannah.nam@stonybrook.edu)

☐ Initial submission ☐ Revised version ☒ Final submission

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.

Sample sizes were determined by available funding and subject recruitment response. In Study 1, subjects were pre-selected from a larger battery of questionnaires to increase ideological representativeness and therefore the sample size was 49. A post hoc power analysis for Study 1's effect size of r=.29 reveals achieved power of .54. Study 2 was conducted as a replication and a post hoc power analysis for effect size of r=.49 for N=45 reveal achieved power of .96, suggesting that together, the samples obtained were sufficient.

2. Data exclusions

Describe any data exclusions.

We pre-selected Study 1 subjects from a larger battery of questionnaires to establish ideological representativeness, and we also deliberately used an ethnically homogeneous sample of White/European-American subjects to minimize potential group differences (following a similar example from Kanai, Feilden, Firth, & Rees, 2011*). One subject did not meet these pre-established criteria and was therefore excluded from Study 1's analysis. Study 2 included a more ethnically diverse sample in order to increase representativeness and did not exclude subjects from analysis.

* Kanai, R., Feilden, T., Firth, C. & Rees, G. Political orientations are correlated with brain structure in young adults. Curr. Biol. 21, 677-680 (2011).

3. Replication

Describe whether the experimental findings were reliably reproduced.

Study 2 was a confirmatory replication study of Study 1 and the experimental findings were reproduced.

4. Randomization

Describe how samples/organisms/participants were allocated into experimental groups.

The primary analyses in both studies did not involve assignment into experimental groups. In Study 1, we explored whether the experience of being in the MRI scanner would affect self-reports of political ideology and system justification. For this analysis, we randomly assigned subjects to fill out the questionnaire before or after the MRI scan.

5. Blinding

Describe whether the investigators were blinded to group allocation during data collection and/or analysis.

In both Studies 1 and 2, the experimenter was blinded to subjects' political ideology and system justification.

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).

n/a	Confirmed
☐	☒ The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.)
☐	☒ A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒ A statement indicating how many times each experiment was replicated
☐	☒ 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)
☐	☒ A description of any assumptions or corrections, such as an adjustment for multiple comparisons
☐	☒ The test results (e.g. *P* values) given as exact values whenever possible and with confidence intervals noted
☐	☒ A clear description of statistics including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)
☒	☐ Clearly defined error bars

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

Software

Policy information about availability of computer code

7. Software

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

For structural MRI data processing and regression modeling, we used SPM8 as implemented in Matlab. For multiple regression modeling using extracted ROI values, we used SPSS statistical software. We did not use custom algorithms for analyses.

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.

Materials and reagents

Policy information about availability of materials

8. Materials availability

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

All behavioural questionnaire materials used were drawn from previous literature and are publicly available at https://osf.io/p7vmw/

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.

Animals and human research participants

Policy information about studies involving animals; when reporting animal research, follow the ARRIVE guidelines

11. Description of research animals

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

No animals were 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.

In both Studies 1 and 2, human subjects were healthy (with no history of neurological disorders) and right-handed. In Study 1, the mean age was 19 years (SD = 1.16), comprised 28 female and 20 male subjects, and all subjects identified their race/ethnic background as White. In Study 2, mean age was 20 (SD = 1.66), comprised 30 females and 15 males, and the sample identified their race/ethnic background as 27% White, 9% Black, 16% Latino/Hispanic, 44% Asian, and 4% other.

Corresponding Author: H. Hannah Nam (hannah.nam@stonybrook.
Date: 2017/09/30

Reporting Summary for MRI studies

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

Experimental design

1. Describe the experimental design.	Resting state scan
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.	1 structural scan (MPRAGE)
3. Describe how behavioral performance was measured.	No task was administered in the scanner.

Acquisition

4. Imaging	
a. Specify the type(s) of imaging.	Structural
b. Specify the field strength (in Tesla).	3T
c. Provide the essential sequence imaging parameters.	T1-weighted high-resolution anatomical images (MPRAGE, repetition time = 2500 ms; echo time = 4.35 ms; field of view = 256 × 256 mm; voxel size = 1 × 1 × 1 mm) were acquired for each subject, with slices collected manually aligned to be parallel to the anterior commissure- posterior commissure line.
d. For diffusion MRI, provide full detail on imaging parameters.	n/a
5. State area of acquisition	Whole brain scan

Preprocessing

6. Describe the software used for preprocessing.	We segmented T1-weighted MR images into grey matter and white matter using the segmentation tools in Statistical Parametric Mapping 8 (SPM8; Wellcome Department of Imaging Neuroscience, London UK, http://www.fil.ion.ucl.ac.uk/spm). Then we performed diffeomorphic anatomical registration through exponentiated lie algebra (DARTEL) in SPM8 for intersubject registration of the grey matter images. We smoothed the registered images with a Gaussian kernel of 12 mm full-width half-maximum and then transformed them to Montreal Neurological Institute (MNI) stereotactic space using affine and nonlinear spatial normalization implemented in SPM8. We ensured that the total amount of grey matter was retained before and after spatial transformation by modulating the transformed images by the Jacobian determinants of the deformation field.
7. Normalization	
a. If data were normalized/standardized, describe the approach(es).	Affine and nonlinear spatial normalization (as implemented in SPM8) were applied to the grey matter images. We ensured that the total amount of grey matter was retained before and after spatial transformation by modulating the transformed images by the Jacobian determinants of the deformation field.
b. Describe the template used for normalization/transformation.	MNI stereotactic space as implemented in SPM8

8. Describe your procedure for artifact and structured noise removal.	n/a
9. Define your software and/or method and criteria for volume censoring and state the extent of such censoring.	n/a

Statistical modeling & inference

10. Define your model type and settings.	Multivariate regression group analysis including covariates of age, sex, global volume, and focal predictor of system justification.
11. Specify the precise effect tested.	We specified a t-contrast for the continuous variable of self-reported measure of system justification (within the factorial design of multiple regression), such that significant voxels would be positively related to system justification scores.
12. Analysis	
a. Specify whether analysis is whole brain or ROI-based.	The focal analyses are ROI-based. We also report more exploratory whole brain analyses.
b. If ROI-based, describe how anatomical locations were determined.	We specified the amygdala ROI within left and right amygdala masks based on the Harvard-Oxford subcortical structural atlas implemented in the Oxford University Centre for Functional MRI of the Brain Software Library (www.fmrib.ox.ac.uk), such that voxels within the mask had a 20% or greater chance of being classified as the amygdala.
13. State the statistic type for inference. (See Eklund et al. 2016.)	We report peak voxel statistics (as well as the cluster size in Supplementary Tables 1-2).
14. Describe the type of correction and how it is obtained for multiple comparisons.	Exploratory whole brain analyses were thresholded at $p < .001$ and minimum cluster of 20 voxels. For small volume corrected analyses we report FWE-corrected statistics.
15. Connectivity	
a. For functional and/or effective connectivity, report the measures of dependence used and the model details.	n/a
b. For graph analysis, report the dependent variable and functional connectivity measure.	n/a
16. For multivariate modeling and predictive analysis, specify independent variables, features extraction and dimension reduction, model, training and evaluation metrics.	Multivariate regression model included the independent variables of age, sex, global brain volume, and system justification.