nature portfolio

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Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our Editorial Policies and the Editorial Policy Checklist.

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a	Confirmed
☐	☒ The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☐	☒ A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒ The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☐	☒ A description of all covariates tested
☐	☒ A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☐	☒ A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☐	☒ For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☒	☐ For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☐	☒ For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☐	☒ Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated

Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection	Stimulus responses were collected via Psychtoolbox v3 on MATLAB R2017B. Imaging data collected 3T GE Discovery MR750 onto Flywheel.
Data analysis	Imaging data were preprocessed and analyzed with the following tools: fmriprep, MATLAB2023B, SPM12 toolbox (https://www.fil.ion.ucl.ac.uk/spm/), CANLab toolbox (https://github.com/canlab), NeuroSynth (decoder only), HumanConnectome Workbench (for visualization only), R version 4.2.1 (2022-06-23)

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

The processed data generated in this study have been deposited in the OSF database under accession code cs3km [https://osf.io/cs3km/] (https://

doi.org/10.17605/osf.io/cs3km). The raw fMRI data are available on OpenNeuro under accession code ds006111 [https://openneuro.org/datasets/ds006111] (doi:10.18112/openneuro.ds006111.v1.0.0).

Research involving human participants, their data, or biological material

Policy information about studies with human participants or human data. See also policy information about sex, gender (identity/presentation), and sexual orientation and race, ethnicity and racism.

Reporting on sex and gender	We report gender (not sex). Participants were asked to self-identify as Male or Female in a self-report questionnaire, and had the option to not respond (59 Women, 37 Men, 4 No Response). We balanced the gender of storytellers, who made up the stimuli in this study, and sought to balance Gender representation in our participant recruitment. We did not intend to analyze gender effects in this study. At the request of the editor, we performed a post hoc gender analysis that confirmed results do not differ by gender.
Reporting on race, ethnicity, or other socially relevant groupings	Participants self-identified their race and ethnicity in a questionnaire (see Supplementary Figure 1A). We sought to collect a sample that was representative of the city where our participants were recruited (Palo Alto, CA). We did not expect race or ethnicity effects, and did not conduct race or ethnicity-specific analyses. The current study is not sufficiently powered to analyze these effects in a meaningful way.
Population characteristics	Participants (N = 100; 59 Women, 37 Men, 4 No Response) were required to be between the ages of 18 and 65, and could not have contraindications for the MRI environment (i.e., claustrophobia or metal implants in the body). The average age of our participants was 25.23 (standard deviation = 9.96). Informed consent was obtained from all participants and participants were financially compensated via an Amazon gift card.
Recruitment	Participants were recruited on the Stanford University campus and surrounding area (Palo Alto) via flyers and online advertisements. Recruitment is skewed towards college-aged students as a result. Participant demographics are representative of Palo Alto, however, Palo Alto is not fully representative of the United States-- it skews towards high levels of socioeconomic status. Targets (who made up the video stimuli) were recruited in the same way and were mostly students.
Ethics oversight	This study was approved by the Stanford University Institutional Review Board. Informed consent was taken from all participants.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☒ Life sciences ☐ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	100 participants (59 Women, 37 Men, 4 No Response, average age = 25.23 STD = 9.96) were recruited and analyzed. This sample size was determined by previous studies conducted by the PI (Dr. Jamil Zaki). No statistical method was used to predetermine sample size.
Data exclusions	Participants were not excluded from the analysis. A technical error occurred for one participant where this participant experienced some redundant trials. Redundant trials were excluded from that analysis of the one participant, no other data were excluded from the analyses.
Replication	We sought to (1) validate the machine learning model results within 'validation' trials collected per participant and (2) test the 'sensitivity' and 'specificity' of our brain-based models for "ground truth" emotion and emotion inference by comparing our models' weights with existing brain patterns of social and emotion processing in the literature. These results are described in the manuscript and Supplementary figures.
Randomization	Participants were randomly assigned to an order when they signed up for the experiment.
Blinding	The Investigators were not blinded to allocation during experiments and outcome assessment.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☒	☐ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☐	☒ MRI-based neuroimaging

Plants

Seed stocks — *Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.*

Novel plant genotypes — *Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.*

Authentication — *Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosiacism, off-target gene editing) were examined.*

Magnetic resonance imaging

Experimental design

Design type	Event-related
Design specifications	24 unique trials (stories) that ranged 1 - 3 minutes in length
Behavioral performance measures	Participants provided moment-by-moment ratings via button pressing in the MRI. We ensured participants made ratings by (1) giving them a practice session with the button box, (2) inspecting each rating trace to ensure that there was movement throughout the stimulus presentation, and (3) conducting a post-experiment comprehension test. The experimenter also checked in with the participant between functional runs to ensure they were comfortable and alert.

Acquisition

Imaging type(s)	functional and structural
Field strength	3T
Sequence & imaging parameters	gradient echo sequence (BOLD EPI, TR = 2 s, TE = 25 ms, FOV = 23.3, Flip Angle = 77)
Area of acquisition	Whole Brain Acquisition (46 slices at 2.9 mm thickness, voxel size = 29.mm^3, interleaved order of acquisition)

Diffusion MRI ☐ Used ☒ Not used

Preprocessing

Preprocessing software	FMRIPREP version 1.4.1-2019, FreeSurfer v6.0.1, AFNI v16.2.07
Normalization	spatial normalization vis nonlinear registration with antsRegistration tool of ANTs v2.1.0
Normalization template	Spatial normalization to the ICBM 152 Nonlinear Asymmetrical template v 2009c using brain-extracted versions of both the T1w volume and template
Noise and artifact removal	Functional data were slice time corrected using 3dTshift and motion corrected using mcflirt; physiological noise regressors were extracted using CompCor. 36 nuisance regressors were ultimately extracted via FMRIPREP (including CSF and white matter regressors and their derivatives as well as 3D motion regressors and their derivatives, as well as spike/motion outliers). Nuisance regressors were included in first-level models.
Volume censoring	framewise displacement was calculated per functional run via Nipype in FMRIPREP

Statistical modeling & inference

Model type and settings	At the first-level we used univariate fixed effects general linear models. The brain-based models of "ground truth" and inference were derived using a multivariate machine learning regression technique-- cross-validated least absolute shrinkage and selection operator-regularized principal components regression (LASSO-PCR; lasso number = 120, error type = MSE, LOO-CV)
Effect(s) tested	Participant-derived intensity ratings which were reduced to 5 levels of intensity

Specify type of analysis: ☐ Whole brain ☐ ROI-based ☒ Both

Anatomical location(s)	272 brain regions from the Brainnetome Atlas use in functional connectivity analysis; Harvard-Oxford Atlas for a priori ROIs
Statistic type for inference (See Eklund et al. 2016)	voxel-wise (within grey matter mask)
Correction	FDR (two-tailed q < 0.05)

Models & analysis

n/a	Involved in the study
☐	☒ Functional and/or effective connectivity
☒	☐ Graph analysis
☐	☒ Multivariate modeling or predictive analysis

Functional and/or effective connectivity	Functionary connectivity with extracted with pdist 'correlation' in MATLAB which is one minus the sample linear correlation between observations (treated as sequences of values). Degree centrality was calculated over that matrix.
Multivariate modeling and predictive analysis	The feature sets included all voxels in the brain (no feature selection but LASSO-PCR has a penalization method built in). The models were trained to predict intensity rating levels as specified via a leave-one-whole-subject-out cross-validation procedure.