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<br>*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<br>*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 | Human behavioral performance was recorded using Presentation software (version 20.1, Neurobehavioral Systems, 371 Berkeley, CA, USA) through LumiTouch keypads (Photon Control Inc., Burnaby, BC, Canada). Human fMRI data was collected using a multi-band echo-planar imaging (EPI) sequence with a multi-band acceleration factor of 2 on a Philips Achieva 3.0 T scanner using a 32-channel head coil. The human diffusion weighted imaging (DWI) data was collected using a 3T whole-body MRI scanner (Prisma Fit, Siemens.Medical Solutions) using a 64-channel whole-head coil. For mice behavior, investor relations barriers (Digikey, Thief River Falls, MN) was used to detect the nose poke. |
| Data analysis | Human behavioral data was analysed in Matlab R2022b using custom codes. The preprocessing, GLM, and DCM analysis of fMRI data was performed using SPM12 (Wellcome Department of Imaging Neuroscience, University College London, UK; http://www.fil.ion.ucl.ac.uk/spm) implemented in Matlab R2022b (MathWorks Inc). The representational similarity analysis of fMRI data was implemented using the RSA toolbox available on GithHub (https://github.com/rsagroup/rsatoolbox) and custom codes developed in Matlab R2022b. The psychophysiology interaction analysis of fMRI data was performed using the generalized PPI (gPPI) toolbox (https://www.nitrc.org/projects/gppi). The fMRI results were presented using MRIcron (https://www.nitrc.org/projects/mricron). The white-matter pathways between MD seeds and PFC were estimated using the Reproducible Tract Profiles 2 (RTP2) pipeline. The comparison of streamline density between the MD and PFC pathways was performed using 3dttest++ in AFNI. The CogLink Modeling were performed in Python 3.12.3 |

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 raw behaviors, processed fMRI data and group-level fMRI data have been deposited on the Open Science Framework (OSF) (https://osf.io/6n7db/). The raw imaging data is not publicly available due to restrictions related to the individual information that could compromise the privacy of research participants. The processed fMRI data may be requested to the corresponding author. The data used to generate the CogLink results was deposited in Mendeley with DOI: 10.17632/2jbbvcdwy7.1. Source data are provided in this paper.

## 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 | The sex was considered in study design, and we matched both female and male participants. The sex data was determinted based on the biological characteristics observed by the experimenter. The information to disaggregate sex data has not been collected. No sex-based analyses were performed because sex is not the factor we focused in our study. |
| Reporting on race, ethnicity, or other socially relevant groupings | We didn't use any socially constructed or socially relevant categorization variables in our manuscript |
| Population characteristics | For the fMRI data collection, female and male participants (mean age ± SD: 24.5 ± 3.3 years) were recruited. For the tractography, a separate dataset of 113 healthy human participants (mean ± SD = 24.5 ± 4.33 years; 65 females) was collected. All participants were right-handed and had normal or corrected to normal vision. Participants with a history of psychiatric or neurological disorders as well as any those taking regular medication or presented contradictions to MRI scanning (i.e., metal implants, pregnancy, breast feeding, claustrophobia) were excluded. |
| Recruitment | We posted our advertisement on the virtual blackboard of the Ruhr-University Bochum. All participants who meet the criterion mentioned above were included. There was no self-selection bias. |
| Ethics oversight | The study was approved by the local ethics committee of the medical faculty at the Ruhr-University Bochum. |

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 | The human sample size was assessed with the free-source software G*Power 3.1.9.2. The required sample size was calculated using the two-tailed t-test between two dependent samples with effect size 0.7 and error probability 0.05. The predicted sample size was 29. Considering possible exclusions of participants, we recruited 40 participants in total. |
| Data exclusions | Participants who failed during the training session were excluded from fMRI scanning because they were unable to correctly identify the tactile patterns. Participants who performed the task during fMRI scanning but failed to learn the correct associations between tactile stimuli and responses were excluded from further data analysis. |
| Replication | For the human results, we tested the reproducibility of switch-related MD and PFC signals using a different human study sample from a previously published paper (Wang and Pleger, 2020, Cerebral Cortex). For the animal results, the data from previous studies in Halassa's group (Schmitt et al., 2017, Rikhye et al., 2018, Mukherjee et al., 2021) was also used to test the replication of the results of optogenetic manipulation on MD in mice. |
| Randomization | Our study consisted only of one experimental group. Randomization was not applicable. |
| Blinding | No blinding was performed as this is not relevant to this study. |

# 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 |

## Animals and other research organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research, and Sex and Gender in Research

| | |
|---|---|
| Laboratory animals | Two male C57Bl/6 mice (aged 1.5-5 months) obtained from The Jackson Laboratory were used in this study |
| Wild animals | No wild animals were involved in our study |
| Reporting on sex | Only male mice were used in this study. |
| Field-collected samples | The study did not involve samples collected from the field |
| Ethics oversight | All animal experiments were performed according to the guidelines of the US National Institutes of Health and the Institutional Animal Care and Use Committee at the Tufts University School of Medicine |

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

## Plants

| | |
|---|---|
| Seed stocks | n/a |
| Novel plant genotypes | n/a |
| Authentication | n/a |

## Magnetic resonance imaging

### Experimental design

| | |
|---|---|
| Design type | Event-related task design |
| Design specifications | The fMRI experiment consisted of 540 trials in total, which were split into 3 runs. Each run lasted ~16 mins and consisted of 4 blocks. Each block contained 45 trials and each trial's duration was ~3 seconds. Trials were presented with randomized intertrial intervals ranging between 1500 and 3000ms, in 100ms steps. |
| Behavioral performance measures | Behavioral responses (i.e., Go or No-Go) were recorded, and the percentage of correct responses at different stages of the task were used to assess whether participants performed as expected |

## Acquisition

Imaging type(s): Functional MRI and diffusion-weighted MRI

Field strength: 3T

Sequence & imaging parameters: Functional scans were collected using a multi-band echo-planar imaging (EPI) sequence with a multi-band acceleration factor of 2. Thirty eight transaxial slices parallel to the anterior-posterior commissure (AC-PC) covering the whole brain were acquired with a voxel size of 2 x 2 x 3 mm3, TR = 2,200 ms, TE = 24 ms, flip angle =90, the field of view 224 mm, and no interslice gap. High-resolution T1-weighted structural images were also acquired using isotropic T1 TFE sequence (176 transversally oriented slices, voxel size: 1 x 1 x1 mm3, field of view 240 x 176 mm2).

Area of acquisition: whole brain scan

Diffusion MRI ☒ Used ☐ Not used

Parameters: For the tractography dataset, the MRI acquisitions included one T1-weighted (T1w) structural image and diffusion-weighted imaging (DWI) sequences. High-resolution MPRAGE T1-weighted structural images were collected with the following parameters: TR = 2530 ms; TE = 2.36ms; flip angle = 7°; field of view = 256 mm; voxel size = 1 mm isotropic; 176 slices.

## Preprocessing

Preprocessing software: The DWI data were preprocessed using MRtrix54 functionsThe functional scans were preprocessed using the Statistical Parametric Mapping software SPM12 (Wellcome Department of Imaging Neuroscience, University College London, UK; http://www.fil.ion.ucl.ac.uk/spm) implemented in Matlab R2017b (MathWorks Inc). The DWI data were preprocessed using MRtrix54 functions

Normalization: The individual T1w image was normalized to the Montreal Neurological Institute (MNI) reference space using the unified segmentation approach and parameters were next applied to the BOLD-sensitive EPI scans.

Normalization template: MNI-space standard templates in SPM was used for normalization

Noise and artifact removal: Data were high pass filtered at 1/128 Hz to remove low-frequency signal drifts. Motion-correction parameters were included into the GLM, which allows movements effects to be discounted when looking for brain activations

Volume censoring: The first five volumes in each run were removed

## Statistical modeling & inference

Model type and settings: For the first level of univariate GLM analysis, the contrast ( "Switch > Steady State") were assessed to reveal changes of BOLD responses after the reversal. The contrast images were next applied to the second-level one-sample t-test to reveal group results (thresholded at p=0.05, small volume FWE corrected)

Effect(s) tested: Using the GLM for univariate analysis, we compared Steady State to Switch trials (Switch > Steady State) to assess whole brain responses to reversal. Using the univariate GLM, we also analyzed the modulatory effect of model-free and model-based RL variables during Switch trials.

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

Anatomical location(s): Automated Anatomical Labelling (AAL) atlas

Statistic type for inference: voxel-wise

(See Eklund et al. 2016)

Correction: Whole brain peak-level FWE correct at $p < 0.05$, and small-volume FWE peak-level correction at $p < 0.05$

## 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: Regression coefficient of the psycho-physiological Interaction (PPI) term, Dynamic causal modelling (DCM)

Multivariate modeling and predictive analysis: Independent variables were voxel-wise fMRI responses to outcomes; The response pattern to outcomes in MD, dmPFC and caudate after the reversal (Switch period) of Keep and Change trials were compared using Pearson's correlations to establish the representational dissimilarity matrix (RDM) for representational similarity analysis (RSA).