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.
     
     No statistical tests were used to predetermine the sample size, but this sample size is within the standard range in the field.

  2. **Data exclusions**
     
     Describe any data exclusions.
     
     Established exclusion criteria (Online Methods, section "Participants") were applied for excessive head motion (n=1) and lack of variability in confidence (n=1).

  3. **Replication**
     
     Describe whether the experimental findings were reliably reproduced.
     
     Computational and behavioural findings were reliably reproduced across behavioural and fMRI testing sessions. All attempts at replication were successful.

  4. **Randomization**
     
     Describe how samples/organisms/participants were allocated into experimental groups.
     
     Participants were not grouped and hence no randomization was performed. Trial order was fully randomized for each subject.

  5. **Blinding**
     
     Describe whether the investigators were blinded to group allocation during data collection and/or analysis.
     
     Data collection and analysis were not performed blind to the conditions of the experiments.

     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

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

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

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

The task was programmed in MATLAB 2014b using Psychtoolbox (version 3.0.12). Behavioural data and fMRI ROI data were analysed using hierarchical mixed-effects regression using lme4 in R (Version 3.3.3). P-values for linear regression coefficients were obtained using the car package in R (version 2.1) as Wald type III chi-squared tests. Computational models were implemented in STAN (rstan, Version 2.6.0).

fMRI data were analysed using SPM 12 (v6225), AFNI (version compiled September 2015) and custom scripts in MATLAB. Mediation analyses were carried out with the Mediation Toolbox in MATLAB (https://canlabweb.colorado.edu/wiki/doku.php/help/mediation/m3_mediation_fmri_toolbox). MRI images were visualised using FSL (version 5.0.8) and Surfice.

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 unique materials are readily available from the authors or freely available online.

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 cell lines were used

b. Describe the method of cell line authentication used.

No cell lines were used

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

No 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 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.

Twenty-five healthy participants were included in the analysis of behavioural data (14 females, mean age 24.0, SD = 3.6); of these, twenty-two healthy participants were included in the analysis of fMRI data (12 females, mean age 24.1, SD = 3.4).
## MRI Studies Reporting Summary

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

### Experimental design

1. Describe the experimental design.  
   - Event-related, randomized trial sequence

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.
   - 4 blocks, 90 trials per block, 5.9s per trial, 2s inter-trial interval

3. Describe how behavioral performance was measured.
   - Button press, response time, confidence rating. Performance was assessed via hierarchical mixed-effects regression of the effects of motion coherence on accuracy and confidence.

### Acquisition

4. Imaging
   - a. Specify the type(s) of imaging.  
     - Functional and structural
   - b. Specify the field strength (in Tesla).  
     - 3 Tesla
   - c. Provide the essential sequence imaging parameters.
     - BOLD-sensitive echo-planar images (EPI) were acquired using a Siemens epi2d BOLD sequence (42 transverse slices, TR = 2.34s; echo time = 30ms; 3 x 3 x 3 mm resolution voxels; flip angle = 90 degrees; 64 x 64 matrix; slice tilt -30deg T > C; interleaved acquisition).
   - d. For diffusion MRI, provide full details of imaging parameters.
     - N/A

5. State area of acquisition.
   - Whole-brain

### Preprocessing

6. Describe the software used for preprocessing.
   - SPM12 v6225

7. Normalization
   - a. If data were normalized/standardized, describe the approach(es).
     - Each participant’s structural image was segmented into gray matter, white matter and cerebral spinal fluid images using a nonlinear deformation field to map it onto a template tissue probability map. These deformations were applied to both structural and functional images to create new images spatially normalized to Montreal Neurological Institute space and interpolated to 2x2x2 mm voxels.
   - b. Describe the template used for normalization/ transformation.
     - SPM12’s MNI template

8. Describe your procedure for artifact and structured noise removal.
   - Motion correction parameters estimated from the realignment procedure and their first temporal derivatives were entered as nuisance covariates.

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.
- First-level mass univariate; second-level random effects

### 11. Specify the precise effect tested.
- Positive/negative interaction of post-decision motion strength x choice accuracy (GLM1); positive/negative parametric effects of confidence (GLM2).

### 12. Analysis

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<td>a.</td>
<td>Specify whether analysis is whole brain or ROI-based.</td>
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<td>b.</td>
<td>If ROI-based, describe how anatomical locations were determined.</td>
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<td>Whole-brain and ROI-based</td>
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<td>The pMFC ROI was an 8mm sphere around peak coordinates (MNI coordinates [x, y, z] = [0 17 46]) obtained from Fleming et al. (2012). Anterior prefrontal ROIs were obtained from the right-hemisphere atlas of Neubert et al. (2014) and mirrored to the left hemisphere to create bilateral masks (area 46, FPM, FPl). The vmPFC ROI was an 8mm sphere around peak coordinates [-1 46 -7] obtained from a meta-analysis of value-related activity (Bartra et al. 2013). The ventral striatum ROI was specified anatomically from the Oxford-Imanova Striatal Structural atlas included with FSL.</td>
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### 13. State the statistic type for inference.
- (See Eklund et al. 2016.)

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<td>For all analyses except multilevel mediation, statistical inference was conducted using Gaussian random field theory as implemented in SPM12 to obtain clusters satisfying P&lt;0.05, family-wise error (FWE) corrected at a cluster-defining threshold of P&lt;0.001 uncorrected. To apply multiple comparisons correction to the multilevel mediation model output we took a non-parametric approach due to second-level images already comprising bootstrapped P-values. The cluster extent threshold for FWE correction was estimated based on Monte Carlo simulation (100,000 iterations) using the 3dClustSim routine in AFNI (version compiled September 2015), cluster-defining threshold P&lt;0.001 uncorrected. Numerical simulations and tests of empirical data collected under the null hypothesis show that both methods provide appropriate control over false positives (Eklund et al. 2016).</td>
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### 14. Describe the type of correction and how it is obtained for multiple comparisons.
- FWE and Monte-Carlo

### 15. Connectivity

| a. | For functional and/or effective connectivity, report the measures of dependence used and the model details. |
| b. | For graph analysis, report the dependent variable and functional connectivity measure. |
| N/A | N/A |

### 16. For multivariate modeling and predictive analysis, specify independent variables, features extraction and dimension reduction, model, training and evaluation metrics.
- N/A