

Reporting Summary

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Please do not complete any field with "not applicable" or n/a. Refer to the help text for what text to use if an item is not relevant to your study. For final submission: please carefully check your responses for accuracy; you will not be able to make changes later.

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 (<i>n</i>) 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 <i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>
☐	☒ 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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>
☒	☐ 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 <i>d</i> , Pearson's <i>r</i>), 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	Visual stimuli and video content were displayed using PsychoPy2 (Peirce et al., 2019) and projected onto a screen 80 cm from the eyes through an angled mirror mounted on top of the head coil using a digital light processing projector (Hyperion MRI Digital Projection System, Psychology Software Tools, Sharpsburg, PA, USA) with a resolution of 1920 x 1080 pixels at 60 Hz. Data were preprocessed using FMRIPREP version 23.0.0. T1-weighted volumes were corrected for intensity nonuniformity using N4BiasFieldCorrection v2.1.0 (Tustison et al., 2010) and skull-stripped using the OASIS template in antsBrainExtraction.sh v2.1.0. Spatial normalization through nonlinear registration to the ICBM 152 Nonlinear Asymmetrical template version 2009c (https://nist.mni.mcgill.ca/icbm-152-nonlinear-atlases-2009/) was completed using the antsRegistration tool (Avants et al., 2008). Brain tissue segmentation of cerebrospinal fluid (CSF), white-matter (WM) and gray-matter (GM) using Fast (Zhang et al., 2001) was performed on extracted T1w images. Functional data were slice time corrected using 3dTshift from AFNI v16.2.07 (Cox, 1996) and motion corrected using mcflirt (FSL v5.0.9) (Jenkinson et al., 2002). Flirt (FSL) performed boundary-based registration with six degrees of freedom to co-register the corresponding T1w images to functional data (Greve & Fischl, 2009). Motion correcting transformations, BOLD-to-T1w transformation, and T1w-to-template Montreal Neurological Institute (MNI) warp were concatenated and applied in a single step using antsApplyTransforms (ANTs v2.1.0) using Lanczos interpolation. All functional images were high-passed (0.007) using Nilearn's signal cleaning function (https://nilearn.github.io/stable/modules/generated/nilearn.signal.clean.html). For further description of fMRIPrep's preprocessing pipeline see: https://fmriprep.readthedocs.io/en/latest/workflows.html.
Data analysis	All code and software packages used for data analysis is available here: https://github.com/isaacrc/metaawareness-and-default-states

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](#)

All anonymized data are publicly available online (<https://github.com/isaacrc/metaawareness-and-default-states>)

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

Forty healthy human volunteers (aged 18-21, normal or corrected to normal vision, 37 right handed, 17 female) were recruited from the community and from a subject pool sponsored by Princeton University. All subjects provided consent and received course credit for participation or monetary compensation. One subject was excluded due to scanner malfunction. All procedures were approved by the Princeton Institutional Review Board.

Reporting on race, ethnicity, or other socially relevant groupings

Not available

Population characteristics

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Recruitment

subjects were recruited from the community and from a subject pool sponsored by Princeton University

Ethics oversight

Princeton Institutional Review Board

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](https://www.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

40

Data exclusions

fMRI Scanner malfunction

Replication

All data and software used to generate results are available online

Randomization

Participants completed three runs of the external attention condition and three runs of the internal attention condition. For each run, a unique video clip was used. All participants viewed the same six videos, but the attention condition (external, internal) and order of video presentation were randomized for each subject. The six video clips were pseudo-randomly sorted into two groups, with two high salience videos and one low salience video assigned to group A, and one high salience and two low salience videos assigned to group B. Half of participants completed the external condition using the three video clips in group A and the internal condition using the three video clips in group B. The other half of participants did the opposite, completing the internal condition using the three video clips in group A and completing the external condition using the three video clips in group B. Within each set of three videos, the order of video clips was randomly varied between subjects. Finally, half of participants began the experiment performing three runs of the external attention condition followed by three runs of the internal condition, and the other half began with the internal attention condition followed by the external condition.

Blinding

None

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, mosaicism, off-target gene editing) were examined.

Magnetic resonance imaging

Experimental design

Design type

Event-based

Design specifications

All subjects participated in two attention conditions. In the external attention condition, a video clip was presented on screen. Participants were instructed to pay attention to the video and press the button if they noticed that their mind had wandered from the video content. Mind-wandering was explicitly defined as content on mind that was unrelated to the content of the video, such as thinking about potential dinner plans or memories about the previous weekend. Participants repeated this task four times in a row, sequentially viewing the same video clip and indicating any lapses of attention to the video with button presses. Once they finished four repetitions, participants were given an optional 30 s of rest and an opportunity to communicate with the experimenter. In the second condition, the internal attention condition, participants viewed another video clip (different from the video seen during the external attention condition), and this time were tasked with ignoring the video content and instead focusing on the rhythmic sensation of their breathing, silently reciting "breathe in, breathe out" while keeping their eyes open and on screen. Once again, subjects were instructed to press the button if they noticed that their mind had wandered from their breathing, for example if their mind had wandered to the content of the video. The internal attention task was completed four times, with the same video clip presented each time. Thus one complete run of the external attention condition consisted of focusing on a video clip for four repetitions, and one complete run of the internal condition consisted of focusing on breath and ignoring an external video clip for four repetitions. Participants completed three runs of the external attention condition and three runs of the internal attention condition. For each run, a unique video clip was used. All participants viewed the same six videos, but the attention condition (external, internal) and order of video presentation were randomized for each subject. The six video clips were pseudo-randomly sorted into two groups, with two high salience videos and one low salience video assigned to group A, and one high salience and two low salience videos assigned to group B. Half of participants completed the external condition using the three video clips in group A and the internal condition using the three video clips in group B. The other half of participants did the opposite, completing the internal condition using the three video clips in group A and completing the external condition using the three video clips in group B. Within each set of three videos, the order of video clips was randomly varied between subjects. Finally, half of participants began the experiment performing three runs of the external attention condition followed by three runs of the internal condition, and the other half began with the internal attention condition followed by the external condition.

Behavioral performance measures

Button presses

Acquisition

Imaging type(s)	functional, structural
Field strength	3T
Sequence & imaging parameters	Functional imaging data were collected using a 3T MAGNETOM Skyra scanner (Siemens Healthineers AG, Erlangen, Germany), equipped with a 64-channel head/neck coil. Gradient-echo T2*-weighted echo-planar images (EPI) with blood oxygen level dependent (BOLD) contrast were used as an index of brain activity (Logothetis et al., 2001). Functional image volumes were composed of 40 near-axial slices with no interslice gap and an in-plane acceleration factor of 2 using Generalized Autocalibrating Partially Parallel Acquisition (GRAPPA), with slice thickness = 3.0 mm, field of view (FOV) = 200 mm, 80 x 80 matrix, 2.5 mm x 2.5 mm in-plane resolution, echo time (TE) = 30 ms, flip angle = 70°, and bandwidth of 1690 Hz/Px. A full functional volume was collected every 1.5 seconds (TR = 1500 ms). Before functional runs, matching spin-echo EPI pairs with reversed phase-encode blips produced pairs of images with distortions going in opposite directions for blip-up/blip-down susceptibility distortion correction. An additional high-resolution structural image was collected for each participant, with 3D magnetization-prepared rapid acquisition gradient echo (MPRAGE) sequence, voxel size = 1 mm isotropic, FOV = 256 mm, matrix size = 256 x 256, 176 slices, TR = 2300 ms, TE = 2.96 ms, inversion time (TI) = 1000 ms, flip angle = 9°, iPAT GRAPPA = 2, bandwidth = 240 Hz/Px, anterior-posterior phase encoding, and ascending acquisition.
Area of acquisition	State whether a whole brain scan was used OR define the area of acquisition, describing how the region was determined.
Diffusion MRI	☐ Used ☒ Not used

Preprocessing

Preprocessing software	Data were preprocessed using FMRIPREP version 23.0.0.
Normalization	Spatial normalization through nonlinear registration to the ICBM 152 Nonlinear Asymmetrical template version 2009c (https://nist.mni.mcgill.ca/icbm-152-nonlinear-atlases-2009/) was completed using the antsRegistration tool (Avants et al., 2008). Brain tissue segmentation of cerebrospinal fluid (CSF), white-matter (WM) and gray-matter (GM) using Fast (Zhang et al., 2001) was performed on extracted T1w images.
Normalization template	MNI152NLin2009cAsym
Noise and artifact removal	Nuisance regressors were defined as the first 5 principal components for CSF and WM masks as well as 3 translation and 3 rotation time series.
Volume censoring	None

Statistical modeling & inference

Model type and settings	General Linear Model, within-subject functional connectivity, inter-subject correlation, ANOVA, mixed-linear effects, t-test
Effect(s) tested	All statistical tests were two-tailed with $\alpha = 0.05$. Behavioral data were analyzed using mixed-design ANOVAs, independent-samples t-tests, and linear regression; ISC data were analyzed using nonparametric bootstrapping and linear mixed-effects models; connectivity data were analyzed using sign-flip permutation tests; and GLM results were assessed using nonparametric permutation-based inference. Multiple comparisons were controlled using Benjamini-Hochberg FDR correction where applicable (ISC voxel-wise tests; connectivity network-pair tests). Effect sizes are reported throughout as Cohen's d for pairwise comparisons, partial η^2 for ANOVA terms, ΔR^2 for linear mixed-effects model fixed effects, and R^2 for regression analyses.
Specify type of analysis:	☒ Whole brain ☐ ROI-based ☐ Both
Statistic type for inference	First level regression was performed using Nilearn's FirstLevelModel function. The result was 12 beta maps for each subject, 6 for the period prior to the button press in each of the six videos, and 6 for the period following the button press in each of the six videos. We then averaged the beta maps of the three videos belonging to the internal attention condition and separately averaged the three videos belonging to the external condition. Thus, for each subject, there were two whole-brain beta maps for the meta-awareness period right before the button press (one for the external attention condition, one for the internal attention condition), and two beta maps for the period when the focus of attention shifted after the button press (again, one for the external and one for the internal attention condition). A second-level model was fit using Nilearn's SecondLevelModel, with the first-level contrasts of interest (external, internal, external minus internal) entered as input. To assess statistical significance while controlling for multiple comparisons, we applied a nonparametric permutation-based two-sided t-test (nilearn.glm.second_level.non_parametric_inference). This approach performs 10,000 random sign-flip permutations on whole-brain beta maps to generate a null distribution of voxelwise t-statistics under the null hypothesis of no effect. A voxelwise cluster-forming threshold of $p < 0.001$ was used. The resulting z-statistic map reflects the distribution of group-level effects corrected using permutation testing.
Correction	Benjamini-Hochberg FDR correction

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

Within-subject functional connectivity is a way to measure correlations between the BOLD time courses of two different brain regions within the same individual. We used the Schaefer 200-parcel atlas (https://nilearn.github.io/dev/modules/description/schaefer_2018.html) to divide the cortex into regions, and averaged region-level connectivity values within each of the 34 cortical networks defined by the atlas to produce a 34x34 network-level connectivity matrix of Fisher-z transformed values. In principle, for each subject, a separate matrix could be computed for each of the 4 repetitions, for each of the 6 videos, resulting in 24 matrices.

To understand how connectivity may have changed as subjects experienced the same videos in repetition, we directly compared the first and last repetitions in the following way. For each subject, we averaged together the three videos from the internal condition and the three videos from the external condition; then we averaged across subjects, averaging together all matrices for the internal attention condition and all matrices for the external attention condition. Finally, the aggregate matrices from the first repetition were subtracted from the aggregate matrices from the fourth repetition. This subtraction yielded two group-level difference matrices. One showed how, in the internal attention condition, connectivity changed from the first to the last repetition; the other showed the same but for the external attention condition.

To assess statistical significance, we used a permutation-based approach. Prior to group-level averaging, we applied sign-flipping across subject-level matrices: a random vector of 1s and -1s (equal in length to the number of subject-video matrices) was multiplied element-wise across matrices, flipping the sign of correlations for a subset of subjects. We then averaged these permuted matrices across subjects and videos to generate one null matrix per iteration. Repeating this process 10,000 times produced a null distribution of correlation matrices. We performed two-sample t-tests between each cell of the original group-level matrix and its corresponding distribution from the 10,000 permuted matrices. Resulting p-values were false-discovery-rate (FDR) corrected across all unique network pairs.