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Reporting Summary

Nature Research 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 Research 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	MR data was acquired as described in the Methods and sequence parameters are listed in the MRI section below. For comparison with the existing state-of-the art, data from publicly available sources as described in the Methods (MR inputs and parameters for the model) were used including a tissue probability map in SPM and data from the BraVa database.
Data analysis	MIDAS (v2.35), MATLAB (R2019b), and neuTube (v1.0) software was used for data analysis. MATLAB code used for brain temperature model is built upon the VaPor Model (Blowers et al., 2018) which is publicly available. SPM12 was used for tissue segmentation and co-registration of all MR images in MATLAB.

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 Research 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 list of figures that have associated raw data
- A description of any restrictions on data availability

Raw MR data are available from the corresponding author on reasonable request.

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	For this pilot study, sample size was chosen based on previous studies in the MRI community for proof-of-concept demonstration using data from human subjects.
Data exclusions	No data was excluded.
Replication	Replication was performed across subjects, i.e., the model was used in three unique subjects to demonstrate proof-of-concept.
Randomization	No randomization was performed.
Blinding	Blinding was not relevant as all subjects were healthy volunteers for this pilot 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
☐	☒ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

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

Human research participants

Policy information about studies involving human research participants

Population characteristics	Three healthy human volunteers participated in this study, 1 male and 2 female, ages 36, 28, and 26.
Recruitment	Volunteers were recruited through the local community at Emory University and the greater Atlanta area.
Ethics oversight	Emory University Institutional Review Board.

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

Magnetic resonance imaging

Experimental design

Design type	No functional or resting state MRI was acquired. Images acquired include non-contrast T1-weighted imaging, magnetic resonance angiography, magnetic resonance venography, and echo planar spectroscopic imaging.
Design specifications	One scan of each type (listed above) was acquired from each volunteer. No functional or resting state MRI was acquired.
Behavioral performance measures	No tasks were required and no behavioral input was used for any of the subjects.

Acquisition

Imaging type(s)	Structural, spectroscopy, angiography, venography
Field strength	3 Tesla
Sequence & imaging parameters	T1-weighted images: magnetization-prepared rapid gradient echo (MPRAGE) sequence (repetition time (TR)/inversion time (TI)/echo time (TE) = 2300/900/3.39 ms, flip angle = 9°, field of view (FOV) = 256 × 256 mm^2, matrix size = 192 × 192, 160 slices, slice thickness = 1 mm). MR angiography (MRA): 3D time-of-flight (TOF) sequence (TR/TE = 22/3.86 ms; flip angle = 15°, FOV = 200 × 200 mm^2, matrix size = 256 × 256, slice thickness = 0.62 mm). MR venography (MRV): 2D TOF sequence (TR/TE = 18/3.79 ms, flip angle = 60°, FOV = 220 × 220 mm^2, matrix size = 256 × 256, slice thickness = 3.0 mm). MR spectroscopy: whole brain echo planar spectroscopic imaging (TR1/TR2/TE = 1551/511/17.6 ms, flip angle = 71°, FOV = 280 × 280 mm^2, and interpolated resolution = 64 × 64 × 32).
Area of acquisition	Whole brain

Diffusion MRI ☐ Used ☒ Not used

Preprocessing

Preprocessing software	For arterial and venous vessel segmentation, neuTube 1.0 (Feng et al., 2015) was used. For co-registration of MR images to T1-weighted image space as well as tissue segmentation, SPM12 was used in MATLAB (v. R2019b). MIDAS (Metabolite Imaging and Data Analysis System; Maudsley et al., 2006) was used for preprocessing of EPSI data.
Normalization	MRA, MRV, and EPSI data were registered to T1-weighted image space for each subject
Normalization template	T1-weighted image for each subject (no normalization or registration across subjects or to a standard template)
Noise and artifact removal	N/A
Volume censoring	Spectral quality control of EPSI data was performed in MIDAS with following criteria: metabolite linewidth (<13Hz), water linewidth (<12Hz), Cramer-Rao lower bounds of water (<2%), and frequency shift of the metabolites or water peaks (<20Hz). All other images were used in their entirety.

Statistical modeling & inference

Model type and settings	Whole brain temperatures were compared on a voxel-wise basis using difference mapping.
Effect(s) tested	None

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

Statistic type for inference (See Eklund et al. 2016)	Voxel-wise
Correction	NA

Models & analysis

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