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	Data were acquired with Philips Achieva DStream release 5.7 software
Data analysis	Data was processed with Excel (office 365); Image j v1.54g (NIH software); Fiji v1.54f (NIH software); ITK-Snap v4.0.1 (NIH software); FSL 6.0 ; and Phyton 3.12.2

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

Numerical data, code and materials used in this work are available at DOI: 10.5281/zenodo.14726926. Raw DICOM Images from subjects are available in NIFTI format (anonymized) upon request (contact: Pedro Ramos-Cabrer, pramos@cicbiomagune.es)

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 study was performed on eight men and two women as reported in the methods section. This is a pilot study on few subjects.
Reporting on race, ethnicity, or other socially relevant groupings	N/A
Population characteristics	Age, gender and particularities of the subjects under study have been described in the manuscript.
Recruitment	Subjects participated voluntarily in this study, as stated in the manuscript. Participants were recruited by contacting runners clubs, trainers and physiotherapists. All volunteers were included in the study without self selection bias or other biases.
Ethics oversight	Comité de Etica de Investigación de Euskadi (CEImE)

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	This is a pilot study, no sample size was calculated a priori
Data exclusions	No data were excluded from analysis
Replication	Replication was not applicable to this study as all measurements were normailized to pre-run values
Randomization	N/A. All subjects were grouped together, no groups were compared in data analysis.
Blinding	Image processing and data analysis were done blinded to group allocation during data collection

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	N/A
Novel plant genotypes	N/A
Authentication	N/A

Magnetic resonance imaging

Experimental design

Design type	Longitudinal MRI imaging of subjects before and after task performance
Design specifications	Longitudinal examination (repeated measurements) of the subjects
Behavioral performance measures	Behavior was not assessed in the study

Acquisition

Imaging type(s)	Multi-echo 3D gradient and spin echo sequence (GRASE); T1w anatomical image
Field strength	3 T
Sequence & imaging parameters	MRI scans were acquired on a 3T whole body MRI system (Achieva Dstream, Philips Medical System, Best, The Netherlands) using the internal quadrature body coil for transmission and a 32-channel phased array coil for reception. Each subject underwent an imaging protocol that included: 1) a multi-echo 3D gradient and spin echo sequence (Grase) for myelin water imaging, with the following parameters: TR = 2000 ms; 32 echoes with a minimum echo time of 9.3 ms and maximum of 298 ms; SENSE 2.5; flip angle 90º, band width in EPI frequency direction 2591; field of view (FOV) 230 mm2; 78 slices in transverse orientation; voxel size 1.2 x 1.2 x 1.8 mm; total scan time 7:08 min 2) a high-resolution T1w anatomical image in a sagittal orientation with the following parameters: TR=7.4 ms; TE=3.4 ms; matrix size 228 x 228; flip angle 9º; FOV 250 x 250 X180 mm; slice thickness 1.1 m; 300 slices, acquisition time 4:55 m.
Area of acquisition	whole brain

Diffusion MRI ☐ Used ☒ Not used

Preprocessing

Preprocessing software	FSL and Python
Normalization	Raw data were exported in DICOM format for off-line processing. First, data were converted into NIFTI format using dcm2niix. Anatomic brain images (skull stripped out) were obtained from T1-weighted images applying BET implementation from the FSL 6.0 distribution. Population distributions of T2 values were computed voxelwise from multitecho data using Julia implementation of DECAES software. For the analysis of interindividual and intraindividual changes in MWF maps, all MWF maps for subjects at different imaging sessions (pre-run, post-run, recovery and rest) were registered to a T2 weighted anatomical image of the brain of subject 1 (echo 8 of the echo train, with TE=74.48 ms) at session 1 using ANTS Syn registration. For image segmentation and assessment of MWF values in different regions of the brain, T1 weighted images were nonlinearly registered to the JHU DTI-based white matter atlas for white matter track segmentation and in parallel to the LPBA40 collection of the SRI24 brain atlas for segmentation of gray matter regions. Transformation matrices were later applied to the MWF maps, previously linearly registered to the corresponding T1W image.
Normalization template	JHU DTI-based white matter atlas for white matter track segmentation LPBA40 collection of the SRI24 brain atlas for Gray matter segmentation
Noise and artifact removal	No noise and artifact removal were done
Volume censoring	Anatomic brain images (skull stripped out) were obtained from T1-weighted images applying BET implementation from the FSL 6.0 distribution.

Statistical modeling & inference

Model type and settings	univariate
Effect(s) tested	student t-test

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

Anatomical location(s)	automatic segmentation of brain regions using the JHU DTI-based white matter atlas for white matter track segmentationand th LPBA40 collection of the SRI24 brain atlas for Gray matter segmentation
Statistic type for inference (See Eklund et al. 2016)	N/A, no fMRI data have been analyzed in this study
Correction	N/A, no fMRI data have been analyzed in this study

Models & analysis

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