nature portfolio

Corresponding author(s): Ning Liu

Last updated by author(s): Jul 6, 2026

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	no software was used
Data analysis	AFNI(21.0.04), ANTs (2.5.3) were used in the data preprocessing. The custom code writen in Matlab(2023b) was used in the data analysis.

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 data that support the findings of this study and the custom codes used for analyses are available from the corresponding author upon reasonable request.

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	For UWS group: 10 males and 4 females; For MCS group: 9 males and 3 females.
Reporting on race, ethnicity, or other socially relevant groupings	All patients involved in this study were Chinese.
Population characteristics	Patients were diagnosed based on the Coma Recovery Scale-Revised (CRS-R) scores collected at both the diagnostic (T0: 1-3 days after admission) and prognostic (T1: 6 months after T0) time points. The CRS-R score at each time point was derived from multiple assessments (typically 3-5 evaluations) conducted within a one-week period, and the highest score was retained for analysis. For UWS group: 44.00±14.25 years; For MCS group: 47.08±11.60 years.
Recruitment	A total of 48 patients from Beijing Tiantan Hospital, Capital Medical University, were recruited for the study. Patients were diagnosed based on the Coma Recovery Scale-Revised (CRS-R) scores collected at both the diagnostic (T0: 1-3 days after admission) and prognostic (T1: 6 months after T0) time points. The CRS-R score at each time point was derived from multiple assessments (typically 3-5 evaluations) conducted within a one-week period, and the highest score was retained for analysis. Twenty-two patients were excluded due to large local brain lesions (>30% of total brain volume), poor T1-Weighted image quality, or severe motion artifacts during MRI scanning (>40% of volumes censored). Finally, 26 patients were included in the present study: 14 with UWS and 12 with MCS.
Ethics oversight	All experimental procedures and study protocols were approved by the Ethics Committee of Beijing Tiantan Hospital (No. KY2022-094-02).

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	A total of 48 patients from Beijing Tiantan Hospital, Capital Medical University, were recruited for the study. Patients were diagnosed based on the Coma Recovery Scale-Revised (CRS-R) scores collected at both the diagnostic (T0: 1-3 days after admission) and prognostic (T1: 6 months after T0) time points. The CRS-R score at each time point was derived from multiple assessments (typically 3-5 evaluations) conducted within a one-week period, and the highest score was retained for analysis. Twenty-two patients were excluded due to large local brain lesions (>30% of total brain volume), poor T1-Weighted image quality, or severe motion artifacts during MRI scanning (>40% of volumes censored). Finally, 26 patients were included in the present study: 14 with UWS and 12 with MCS.
Data exclusions	Because a patient died before data collection at the T1 time point, the prognostic task in the SVM analysis was conducted with the remaining 25 patients.
Replication	In the power-law distribution analysis, we conducted replication tests by selecting different thresholds; in the Ising model analysis, we performed multiple Monte Carlo simulations to enhance reproducibility; and in the SVM analysis, we employed 10-fold cross-validation.
Randomization	It was not relevant to our study, because patient diagnosis was determined by the CRS-R score and the two study groups were of comparable size, there was no requirement for randomization.
Blinding	It was not relevant to our study, because patient diagnosis was determined by the CRS-R score and the two study groups were of comparable size, there was no requirement for blinding.

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

Clinical data

Policy information about clinical studies

All manuscripts should comply with the ICMJE guidelines for publication of clinical research and a completed CONSORT checklist must be included with all submissions.

Clinical trial registration	All experimental procedures and study protocols were approved by the Ethics Committee of Beijing Tiantan Hospital (No. KY2022-094-02).
Study protocol	Patients were diagnosed based on the Coma Recovery Scale-Revised (CRS-R) scores collected at both the diagnostic (T0: 1-3 days after admission) and prognostic (T1: 6 months after T0) time points. The CRS-R score at each time point was derived from multiple assessments (typically 3-5 evaluations) conducted within a one-week period, and the highest score was retained for analysis.
Data collection	Patients from Beijing Tiantan Hospital, Capital Medical University, were recruited for the study. Functional and anatomical MRI scanning was carried out in the Beijing Tiantan Hospital, Capital Medical University, at a 3-Tesla GE SIGNA PET/MRI scanner with a 20-channel head coil.
Outcomes	We conducted a analysis of the critical dynamics in the neural activity of patients with disorders of consciousness and compared the differences between the UWS and MCS groups. Furthermore, we investigated the potential applications of brain criticality in patient diagnosis and prognosis.

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, mosiacism, off-target gene editing) were examined.*

Magnetic resonance imaging

Experimental design

Design type	Resting state.
Design specifications	N/A
Behavioral performance measures	N/A

Acquisition

Imaging type(s)	Functional, structural, and PET
Field strength	3 T
Sequence & imaging parameters	For anatomical scans, T1-weighted (T1w) structural images were obtained with the following parameters: voxel size = 1.0 × 0.5 × 0.5 mm3; repetition time (TR) = 8.49 ms; echo time (TE) = 3.25 ms; flip angle (FA) = 12º; field of view (FOV) = 256 × 256 mm2. Functional images were acquired using T2*-weighted gradient multiband accelerated echo-planar imaging (EPI) sequences with the following parameters: voxel size = 3.4 × 3.4 × 3.8 mm3; TR = 2000 ms; TE = 30 ms; FA =

72º; FOV = 64 × 64 mm2. The original voxel size of 18F-FDG PET images was 1.6 × 1.6 × 2.8 mm3. The resting-state fMRI run consisted of 200 volumes (TR = 2.0 s), corresponding to a total scan duration of 6.7 minutes.

Area of acquisition: A whole brain scan.

Diffusion MRI ☐ Used ☒ Not used

Preprocessing

Preprocessing software: AFNI(21.0.04) and ANTs (2.5.3).

Normalization: The EPI volumes were co-registered to Montreal Neurological Institute (MNI) space with the anatomical scan using antsregistrationsyn in ANTs.

Normalization template: Montreal Neurological Institute (MNI 152) space.

Noise and artifact removal: The initial five volumes were discarded to ensure that the BOLD signal had reached a stable equilibrium before further analysis. After removing large transients with 3dDespike, volumes were slice-time corrected using 3dTshift. To minimize changes in EPI signals, anatomical volumes were aligned to EPI volumes with 3dAllineate. The EPI volumes were then motion-corrected using six parameters (3 translations and 3 rotations) in 3dvolreg and co-registered to Montreal Neurological Institute (MNI) space with the anatomical scan using antsregistrationsyn in ANTs. To improve the signal-to-noise ratio (SNR) and limit the effect of smoothness, EPI volumes were spatially smoothed with a 3.5-mm full-width at half-maximum Gaussian kernel using 3dmerge and then normalized by the mean signal. Signals were detrended, and artifacts were controlled by regressing out motion parameters, which included 12 motion regressors consisting of the six demeaned motion parameters and their temporal derivatives, and global signals (3dDeconvolve) from the BOLD signals.

Volume censoring: Motion was quantified as the Euclidean norm of the six motion parameters between consecutive TRs, commonly referred to as framewise displacement (FD). FD exceeding 0.5 mm were flagged as excessive, leading to the censoring (scrubbing of high-motion frames from the time series) of both the affected volume and the preceding volume to account for potential spin-history effects. Additionally, volumes with more than 10% voxels deviating from the base volume were identified as outliers and also excluded from subsequent analyses.

Statistical modeling & inference

Model type and settings: Differences in critical metrics between the UWS and MCS groups were assessed using independent t-tests.

Effect(s) tested: N/A

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

Anatomical location(s): Schaefer 400 brain atlas.

Statistic type for inference (See Eklund et al. 2016): N/A

Correction: N/A

Models & analysis

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

Multivariate modeling and predictive analysis: To assess whether the identified critical metrics could serve as potential biological markers for clinical categorization (MCS or UWS) and prognosis, we trained support vector machine (SVM) classifiers using the libSVM toolbox. At the whole-brain level, the power-law scaling exponent, Ising energy, and mean phase synchronization were normalized and used as input features. At the ROI level, the phase synchronization of 400 ROIs was normalized and treated as input features. Model accuracy was evaluated using 10-fold cross-validation, and receiver operating characteristic (ROC) curves were generated to calculate the area under the curve (AUC).