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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	Descriptions of all code used to collect the electrophysiology data analyzed in this study are available in the original studies and repositories from which the data were obtained. Diffusion tensor imaging data were acquired using standard imaging platforms; no custom code was used for DTI acquisition.
Data analysis	Multiple software packages and custom algorithms were used. Commercial software: MATLAB with FieldTrip toolbox for EEG preprocessing, Seurat v3.1.1 for R v3.4 for single-cell RNA-seq analysis, FSL (BET, FLIRT, probtrackx2) for MRI preprocessing and tractography, ANTs for image registration, DTIPrep for diffusion data preprocessing, DSI Studio for deterministic tractography visualization. Open source tools: Java Information Dynamics Toolkit (JIDT) for transfer entropy calculations, Cell Ranger v5 and v7.0.0 for single-cell sequencing data processing. Custom code: Deep convolutional neural networks implemented with RMSprop optimizer and Bayesian hyperparameter optimization, genetic algorithm for mean-field model parameter optimization (194 batches with 50 parallel runs each), biophysically realistic mean-field model of basal ganglia-thalamo-cortical system based on van Albada and Robinson framework, phase-amplitude coupling analysis using modulograms with Hilbert transforms, chaos analysis via stochastic largest Lyapunov exponent calculation, entropy measures (permutation entropy, multiscale sample entropy, Lempel-Ziv complexity), and various preprocessing pipelines for multi-modal electrophysiology data.

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 electrophysiological datasets used in this study were obtained from previously published sources. Full details, including citations and links to repositories or supplementary materials, are provided in the Methods and Supplementary Information. The diffusion tensor imaging (DTI) data collected from patients with disorders of consciousness are not publicly available due to patient privacy restrictions but may be shared upon reasonable request and subject to approval by the institutional ethics committee.

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	Sex was reported in the human datasets analyzed in this study, and the proportion of male and female participants is summarized in the Methods. In our group-level analyses of DTI data, we performed a rank-based ANCOVA and included sex as a covariate to account for potential confounding effects. Gender identity beyond binary sex categories was not collected.
Reporting on race, ethnicity, or other socially relevant groupings	Race, ethnicity, and other socially relevant variables were not available in the datasets used in this study, which were primarily drawn from previously published sources. For the subset of new imaging data collected, such demographic information was not recorded. Therefore, no race- or ethnicity-based analyses were conducted.
Population characteristics	The human participants included in this study were patients with disorders of consciousness (DOC), including those in vegetative and minimally conscious states. Participants varied in etiology (e.g., traumatic brain injury, anoxic injury) and chronicity, but were otherwise selected based on clinical diagnosis rather than demographic or genetic criteria. Specific covariates such as age are detailed in the Methods section.
Recruitment	Most datasets analyzed were obtained from previously published studies and open-access repositories. Eligibility was determined based on clinical diagnosis, and no demographic selection criteria were applied. There is a potential for referral or institutional selection bias, which is a common limitation in studies of rare clinical populations.
Ethics oversight	All datasets used in this study received approval from the relevant institutional review boards or ethics committees, as detailed in the Methods. Each dataset was collected in accordance with the ethical standards of the institution and informed consent procedures at the time of data acquisition.

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	Sample sizes were determined based on available clinical datasets and previous studies in consciousness research. For TBI acute coma patients, 22 patients were included based on GCS scores <9 or GCS 9-14 with CT evidence of intracranial bleeding. For chronic DOC patients, 14 patients were included (0.97-6.8 years since injury). Animal studies used established sample sizes: 2 African green monkeys, 12 PD patients, 10 ET patients, and 7 GAERS rats. Independent validation used 20 healthy participants and 455 cardiac arrest patients from the I-CARE database. No formal statistical power calculations were performed; sample sizes were based on data availability and previous consciousness studies showing similar effect sizes.
Data exclusions	Multiple exclusion criteria were applied across datasets. For TBI patients: excluded those with non-significant head injuries, prior neurological disease, or brain death. For all EEG/ECoG data: excluded segments with significant motion artifacts after visual inspection, outlier standard deviations (>2.5 SD from mean), and channels with persistently high noise. For cardiac arrest patients: excluded EEGs with <60 seconds of usable data, recordings where most ICA components appeared pathological, and patients with brain deterioration obscuring ROI delineation. Exclusion criteria were pre-established based on standard electrophysiology preprocessing protocols and clinical inclusion criteria.
Replication	The study incorporated multiple forms of validation across datasets, species, and recording modalities. The consciousness detection network was trained on acute coma data and validated on chronic DOC patients, healthy controls, and animal models. Cross-species validation

included human patients and animal models (monkeys, rats). Independent test datasets included separate cohorts of healthy participants and cardiac arrest patients not used in training. All neural network training used standard validation procedures with 20% data holdout.

Randomization

For neural network training, data were randomly divided into training (80%) and validation (20%) subsets. For genetic algorithm optimization, random initial conditions and noise inputs were used across parallel runs. Clinical patient data represented naturalistic variation rather than experimental randomization. For synthetic data generation in discriminator training, parameters were randomly varied across 500 instances per signal type. Covariate control was achieved through standardized preprocessing (z-score normalization, common average referencing) and matching of recording parameters across datasets where possible.

Blinding

Investigators were not blinded to group allocation during data collection as this was a retrospective analysis of existing clinical and research datasets with known consciousness states. Clinical assessments (GCS, CRS-R scores) were performed by trained clinicians as part of standard care, independent of the research analysis. For neural network training and genetic algorithm optimization, automated procedures were used that did not require subjective assessment. Blinding was not relevant for this computational modeling study as the primary outcomes were objective neural network classifications and biophysical model parameters rather than subjective assessments.

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

Animals and other research organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research, and Sex and Gender in Research

Laboratory animals

The study involved multiple laboratory animal species. African green monkeys (Chlorocebus aethiops): 2 animals used for simultaneous intracranial electrophysiology recordings from frontal cortex and globus pallidus externa (GPe) during waking and propofol anesthesia states. Long-Evans rats: used for thalamic and cortical recordings during propofol anesthesia. Seven Genetic Absence Epilepsy Rats from Strasbourg (GAERS): used for spontaneous 6-8 Hz spike-and-wave seizure recordings with implanted stainless steel ECoG electrodes in somatosensory cortex. Seba's short-tailed bats (Carollia perspicillata): LFP recordings from dorsal striatum during spontaneous communication calls (reanalyzed from existing dataset).

Wild animals

The study did not involve wild animals. All animal data were obtained from laboratory animals in controlled research settings or from previously published datasets of laboratory animals.

Reporting on sex

Sex information was provided where available in the source datasets. For human participants: TBI patients (18 males, 4 females), chronic DOC patients (7 females, 7 males), healthy controls dataset 1 (6 females, 4 males), PD patients (3 females out of 12 total), ET patients (6 females, 4 males), cervical dystonia patients (4 females, 2 males), and DOC DTI cohort (30 males, 20 females). For animal studies, sex information was not consistently reported in the original datasets and was not a factor in the analyses performed. With the exception of the rank-based ANCOVA in the DTI analysis, which included sex as a covariate, sex-based analyses were not performed as the primary focus was on consciousness states rather than sex differences.

Field-collected samples

The study did not involve field-collected samples. All biological samples and recordings were obtained in clinical or laboratory settings under controlled conditions.

Ethics oversight

Multiple institutional approvals were obtained: UCLA Ronald Reagan Medical Center for TBI patient data, Casa Colina Hospital and Centers for Healthcare and UCLA IRBs for chronic DOC patients, The Hebrew University (MD-18-15449-5) for African green monkey studies, UCLA institutional review board for ET patient recordings, Regierungspräsidium Darmstadt, Germany (permit FU1126) for bat recordings, and University Hospital of Liège Ethics Committee for DOC patient DTI data. Human studies followed Declaration of Helsinki guidelines, and all participants or legal guardians provided written informed consent.

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

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. DOC patients underwent structural and diffusion MRI scanning without task performance or stimulation paradigms.

Design specifications

Single session per patient with structural T1-weighted and diffusion-weighted imaging acquisition. No experimental blocks or trials - continuous resting state scanning was performed.

Behavioral performance measures

No behavioral tasks were performed during MRI acquisition. Clinical consciousness assessment was conducted separately using Coma Recovery Scale-Revised (CRS-R) for patient classification into vegetative state (VS), minimally conscious state (MCS+), and emergence from MCS (EMCS) groups.

Acquisition

Imaging type(s)

Structural (T1-weighted) and diffusion-weighted imaging (DWI).

Field strength

3 Tesla

Sequence & imaging parameters

T1-weighted: 120 slices, TR = 2300 ms, TE = 2.47 ms, voxel size = 1 × 1 × 1.2 mm, flip angle = 9°. Diffusion-weighted imaging: 64 non-collinear directions at b-value = 1000 s/mm², repeated twice, 45 axial slices, TR = 5700 ms, TE = 87 ms, voxel size = 1.8 × 1.8 × 3.3 mm, flip angle = 90°, plus one b=0 image.

Area of acquisition

Whole brain scan was used for both structural and diffusion imaging to enable basal ganglia ROI analysis and tractography.

Diffusion MRI ☒ Used ☐ Not used

Parameters

Specify # of directions, b-values, whether single shell or multi-shell, and if cardiac gating was used.

Preprocessing

Preprocessing software

DTIPrep for denoising and motion/eddy current correction, BET for brain extraction of diffusion images, optiBET for T1-weighted brain extraction, ANTs for registration, FLIRT for coordinate transformations, FSL probtrackx2 for tractography.

Normalization

Data were transformed from MNI standard space to subject T1 space using ANTs, then to native diffusion space using FLIRT. ROIs from Keuken and Forstmann probabilistic atlas were transformed to individual subject spaces rather than normalizing subjects to standard space.

Normalization template

Keuken and Forstmann probabilistic basal ganglia atlas in MNI space was used as the source template for ROI definition, transformed to individual subject spaces.

Noise and artifact removal

DWI data were denoised and corrected for motion and eddy currents using DTIPrep. CSF masks were generated and intersected with ROIs to eliminate spurious voxels. Patients with brain deterioration obscuring ROI delineation were excluded.

Volume censoring

No explicit volume censoring was described. Quality control was performed through visual inspection of all masks and manual refinement as necessary.

Statistical modeling & inference

Model type and settings

ROI-based analysis examining structural connectivity between striatum and globus pallidus (GPe and GPi). Probabilistic tractography with up to three fiber orientations per voxel modeled using FSL's probtrackx2.

Effect(s) tested

Effect(s) tested

Group differences in structural connectivity strength (streamline counts) and microstructural properties (fractional anisotropy) between consciousness level groups (VS, MCS+, EMCS). Geometric normalization applied by dividing streamline counts by square root of seed × target mask sizes.

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

Anatomical location(s) Striatum, GPe, GPi

Statistic type for inference

(See Eklund et al. 2016)

ROI-based analysis using streamline counts and fractional anisotropy measures. No voxel-wise or cluster-wise statistical testing was performed. Analysis focused on region-of-interest comparisons between consciousness groups using probabilistic tractography metrics.

Correction

FDR correction was applied for testing across two hemispheres.

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

Probabilistic tractography analysis with geometric normalization of connectivity metrics. Independent variables: consciousness level groups (VS, MCS+, EMCS). Features extracted: streamline counts between striatum and pallidal regions (GPe, GPi), fractional anisotropy along tracts. Evaluation metrics: structural connectivity strength quantified as total streamlines reaching target, normalized by square root of seed × target mask sizes. Analysis performed separately for left and right hemispheres with bilateral ROI extraction from Keuken and Forstmann probabilistic atlas.