

1 Re-awakening the brain: Forcing transitions in disorders of  
2 consciousness by external *in silico* perturbation

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## Abstract

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A fundamental challenge in neuroscience is accurately defining brain states and predicting how and where to perturb the brain to force a transition. The ability to promote a transition from one brain state to another by externally driven stimulation could significantly impact rehabilitation and treatments for patients suffering from complex brain injury cases. Thus, it is crucial to find therapeutic interventions able to re-balance the dynamics of brain disorders towards more healthy regimes. Here, we investigated resting-state fMRI data of patients suffering from disorders of consciousness (DoC) after coma (minimally conscious and unresponsive wakefulness states) and healthy controls. We applied model-free and model-based approaches to help elucidate the underlying brain mechanisms of patients with DoC. The model-free approach allowed us to characterize brain states in DoC and healthy controls as a probabilistic metastable substate (PMS) space. The PMS of each group was characterized by a repertoire of unique patterns (i.e., metastable substates) with different probabilities of occurrence. In the model-based approach, we adjusted the PMS of each DoC group to a causal whole-brain model. This allowed us to explore optimal strategies for promoting a transition to the PMS of the control group by applying off-line *in silico* probing. Furthermore, this approach enabled us to evaluate the impact of all possible local perturbations in terms of their global effects and sensitivity to stimulation, which is a biomarker providing a deeper understanding of the mechanisms underlying DoC. Our results show that transitions from DoC to more healthy regimes were obtained in a synchronous protocol, in which areas from the motor and subcortical networks were the most sensitive to perturbation. This motivates further work to continue understanding brain function and treatments of disorders of consciousness by external stimulation.

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**Keywords:** brain states, resting-state fMRI, whole-brain modelling, brain dynamics, disorders of consciousness, off-line *in silico* probing

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## Author summary

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We studied disorders of consciousness by defining a brain state as a repertoire of metastable substates with different probabilities of occurrence. We created whole-brain computational models of DoC to uncover the causal mechanisms underlying recovery. These models allowed us to transition from DoC to a control healthy state by studying the effects of artificial individual local perturbations under different protocol regimes. We demonstrated successful transitions in the synchronization protocol and showed that the most sensitive areas were located in the motor network and subcortical regions. We believe this could be very valuable for developing clinical treatments and has a great deal for future therapies.

## 56 Introduction

57 The brain is a dynamical, complex, and self-organized system with spontaneous activity emerging  
58 from non-linear interactions of billions of neurons (Sporns, 2011). This gives rise to an ample  
59 discrete repertoire of metastable patterns (i.e., substates) around critical points between order and  
60 chaos (Cabral et al., 2017b; Deco et al., 2017c). The lifetimes and stabilities of specific substates  
61 govern the dynamics of a particular brain state (Deco and Kringelbach, 2016; Tognoli and Kelso,  
62 2014). Current research is increasing our understanding of the causal dynamics underlying many  
63 different brain states, such as wakefulness, sleep, anesthesia, and disorders of consciousness (DoC).  
64 Nevertheless, such mechanisms still remain elusive and a deeper comprehension would facilitate  
65 the design of novel interventions for brain disorders and possibly for the loss of consciousness like  
66 coma. Recently, directly perturbing the brain *in silico* has been proposed and investigated as a  
67 possible intervention that could contribute to a deep understanding of the dynamical mechanisms  
68 of brain states in health and disease (Escrichs et al., 2022; Vohryzek et al., 2022a; Deco et al.,  
69 2019). Furthermore, such perturbations could be used to force transitions between different brain  
70 states in a translational clinical context, for example, to promote transitions from brain disorders  
71 to health (Fox et al., 2014; Thibaut et al., 2014; Schiff et al., 2007).

72 A healthy brain relies on the brain's flexibility and capacity to integrate information and main-  
73 tain rich dynamics in an evolving environment across time and space (Deco et al., 2015). By  
74 contrast, brain disorders present disruptions in the normal range of brain activity (Du et al.,  
75 2018). In the specific clinical domain of DoC, it has been found that their characteristic brain  
76 patterns present disruptions of long-range cortical correlations typical in a healthy state (Demertzi  
77 et al., 2019). Such post-coma states are distinguished into the minimally conscious state (MCS)  
78 and unresponsive wakefulness syndrome (UWS). The former MCS is identified when patients are  
79 awake and respond with limited awareness, and the latter UWS corresponds to patients who do not  
80 respond to stimulation in a conscious manner (Giacino et al., 2018, 2002). DoC patients present  
81 lower flexibility and efficiency of information processing and a limited broadcast of information,  
82 which coexists with a reduced neural propagation and responsiveness to events (Panda et al.,  
83 2023). Furthermore, UWS shows reduced metastability and repertoire of functional networks in  
84 comparison to MCS (Panda et al., 2022).

85 In recent years, different definitions of brain states have been proposed using empirical neu-  
86 roimaging and electrophysiological data. Approaches based on functional magnetic resonance imag-  
87 ing (fMRI) have implemented static analysis such as long-range temporal dependence via Hurst  
88 exponent (Tagliazzucchi et al., 2013) and attractors between brain regions (Gu et al., 2018; Deco  
89 and Jirsa, 2012). Considering brain activity is multi-dimensional and ever-changing, these ap-  
90 proaches have been further examined from a more realistic and richer viewpoint considering brain  
91 dynamics, which reveals the different brain patterns evolving during a scanning period (Escrichs  
92 et al., 2021b; Sanz Perl et al., 2022; Deco and Kringelbach, 2020; Preti et al., 2017; Hansen et al.,  
93 2014; Allen et al., 2014; Hutchison et al., 2013). Nevertheless, a universal, formal, robust, and  
94 quantitative definition of brain states, and a deep comprehension of the effects of perturbations  
95 to force recovery, remains unknown (Deco et al., 2019, 2017c). Stemming from recent progress in

96 these areas, and given the difficulty of predicting the final collective emergent activity even if the  
97 building blocks are known (Deco et al., 2019), we could still benefit from a better understanding  
98 of brain dynamics and optimal strategies for a recovery towards healthy brain states (Vohryzek  
99 et al., 2022a; Escrichs et al., 2022; Kringelbach and Deco, 2020; Edlow et al., 2020; Deco et al.,  
100 2017a; Keilholz et al., 2017).

101 There is a long tradition of perturbative approaches for brain research. Clinical techniques  
102 for stimulation exist, such as the non-invasive transcranial direct current stimulation (tDCS)  
103 (Knotkova et al., 2019; Ruffini et al., 2018; Siebner et al., 2009) and transcranial magnetic stim-  
104 ulation (TMS) (Litvak et al., 2007; Pascual-Leone, 1999), and the minimally invasive technique  
105 deep brain stimulation (DBS) (Mohseni et al., 2012; Kringelbach et al., 2007). Still, research in  
106 lesioned humans is rare, only undertaken when the disease is severe, and accompanied by ethical  
107 constraints (Deco and Kringelbach, 2017; Clausen, 2010). Massimini and colleagues developed  
108 the perturbational complexity index (PCI), which has been used to distinguish brain states by  
109 calculating the lempel-ziv complexity from the electroencephalography response to TMS pertur-  
110 bation (Casarotto et al., 2016; Casali et al., 2013; Massimini et al., 2009). The PCI measures the  
111 perturbation-elicited variations in intrinsic global brain activity and has shown to be successful  
112 in distinguishing between awake vs. sleep, awake vs. anesthesia, and MCS vs. UWS (Casarotto  
113 et al., 2016; Casali et al., 2013; Ferrarelli et al., 2010; Massimini et al., 2009). However, given  
114 the ethical restrictions of empirical neurostimulation approaches, causal whole-brain models based  
115 on *in silico* perturbation protocols are fundamental to understanding the underlying mechanisms  
116 of brain dynamics (Escrighs et al., 2022). This promising tool allows experimenting in unprece-  
117 dented unlimited scenarios (e.g., perturbing one brain area at a time) without exposing real brains  
118 (Kringelbach and Deco, 2020; Breakspear, 2017; Deco et al., 2015; Deco and Kringelbach, 2014).

119 Recently, Deco et al. (2019) proposed the awakening framework that consists of model-free  
120 and model-based approaches to force transitions from deep sleep to awake. In particular, the  
121 model-free approach based on Leading Eigenvector Dynamics Analysis (LEiDA) (Cabral et al.,  
122 2017b) uses the concept of metastability, defined as the characteristic of a system to maintain an  
123 equilibrium in a temporal window although being slightly perturbed (Freyer et al., 2012; Kelso,  
124 2012; Freyer et al., 2011). The nature, duration, and arrangement of existent metastable substates  
125 (i.e., patterns) give rise to a probabilistic metastable substate (PMS) space typifying each brain  
126 state (Deco et al., 2017c). LEiDA has been shown to be robust and successful in identifying brain  
127 states in healthy aging (Escrighs et al., 2021a; Cabral et al., 2017b), depression (Figueroa et al.,  
128 2019) and different states of consciousness (Kringelbach and Deco, 2020; Lord et al., 2019; Deco  
129 et al., 2019). The model-based approach consists in building whole-brain models composed of a  
130 network of coupled local nodes (Botvinik-Nezer et al., 2020; Deco et al., 2019) to simulate the  
131 empirical PMS and perturb the resulting PMS model to force the transition to a desired control  
132 state. This elegant framework has been extended to promote transitions from aging (Escrighs  
133 et al., 2022), patients with depression (Vohryzek et al., 2022b) and schizophrenia (Mana et al.,  
134 2023) towards more healthy regimes.

135 Here, we aimed to study the dynamical complexity and causal mechanisms of brain activity in  
136 DoC by using the aforementioned framework. Firstly, we applied LEiDA to define the PMS of DoC

137 patients and healthy controls. Secondly, we built Hopf whole-brain models fitted and optimized to  
138 the empirical PMS of DoC at the bifurcation point, representing a state of criticality in which the  
139 two regimes (oscillatory and noisy) cannot be differentiated. This generative whole-brain model  
140 linked structural anatomy with functional dynamics on the basis of effective connectivity (Deco  
141 et al., 2019). Finally, we applied off-line *in silico* external unilateral and localized probing to force  
142 the transition from the PMS obtained in MCS and UWS, separately, to the PMS of healthy controls.  
143 In this way, employing offline *in silico* probing, we could evaluate candidate regions for stimulation  
144 aiming to recover DoC patients. Nevertheless, this innovative approach not only allowed us to  
145 assess the effects of all potential local perturbations but also provided valuable insights into their  
146 mechanistic global effects and sensitivity to stimulation.

## 147 Materials and Methods

### 148 Ethics statement

149 The study was approved by the Ethics Committee of the Faculty of Medicine of the University  
150 of Liège according to the Helsinki Declaration on ethical research. Written informed consent was  
151 obtained from controls and the patients' legal surrogates.

### 152 Participants

153 A total of 23 controls and 46 non-sedated patients with DoC were selected from a dataset  
154 previously described in Escrichs et al. (2021b); López-González et al. (2021); Demertzi et al. (2019).  
155 Trained clinicians carried out the clinical assessment and Coma Recovery Scale-Revised (CRS-R)  
156 scoring to determine the patients' state of consciousness. The CRS-R diagnosis was made after  
157 at least 5 CRS-R, and the highest level of consciousness was taken as the final diagnosis, which  
158 was also confirmed using positron emission tomography (PET) (i.e., patients in MCS presented  
159 a relatively preserved metabolism in the frontoparietal network, whilst patients with UWS had  
160 a bilateral hypometabolism in this network). Thus, 30 patients in MCS and 16 in UWS were  
161 included.

### 162 MRI Data Acquisition

163 MRI data were acquired on a 3T Siemens TIM Trio scanner (Siemens Inc, Munich, Germany).  
164 Resting-state fMRI data were obtained using a gradient echo-planar imaging (EPI) sequence (300  
165 volumes, 32 transversal slices, TR= 2000 ms, TE=30 ms, flip angle = 78°, voxel size = 3x3x3 mm,  
166 FOV = 192 mm). After fMRI acquisition, a structural T1 magnetization-prepared rapid gradient-  
167 echo (MPRAGE) sequence was acquired (120 slices, TR = 2300 ms, voxel size = 1.0x1.0x1.2 mm,  
168 flip angle = 9°, FOV = 256 mm). Finally, diffusion-weighted MRI (DWI) was acquired with 64  
169 directions (b-value =1,000 s/mm<sup>2</sup>, voxel size = 1.8 × 1.8 × 3.3 mm<sup>3</sup>, FOV = 230 × 230 mm<sup>2</sup>,  
170 TR/TE= 5,700/87 ms, 45 transverse slices, 128 × 128 voxel matrix) preceded by a single b0 image.

## 171 Resting state fMRI preprocessing

172 The pre-processing of resting-state fMRI data was performed using MELODIC (Multivariate  
173 Exploratory Linear Optimized Decomposition into Independent Components) version 3.14 (Beck-  
174 mann and Smith, 2004) from FMRIB's Software Library (FSL, <http://fsl.fmrib.ox.ac.uk/fsl>)  
175 as described in our previous studies (Escrichs et al., 2021b; López-González et al., 2021). The  
176 following steps were performed: discarding the first 5 volumes, motion correction motion using  
177 MCFLIRT (Jenkinson et al., 2002), non-brain removal using BET (Brain Extraction Tool) (Smith,  
178 2002), spatial smoothing with a 5 mm Gaussian Kernel, rigid-body registration, high pass filter  
179 (with a cutoff of 100 s) and single-session Independent Component Analysis (ICA) with automatic  
180 dimensionality estimation. Then, noise components and lesions-driven artifacts (for patients) were  
181 manually classified and removed for each subject by looking at the spatial map, time series, and  
182 power spectrum (Griffanti et al., 2017; Salimi-Khorshidi et al., 2014) using FIX (FMRIB's ICA-  
183 based X-noiseifier) (Griffanti et al., 2014). Finally, FSL tools were used to co-register the images  
184 and extract the time series between 214 cortical and subcortical brain areas for each subject in  
185 MNI space from the Shen resting-state atlas (without the cerebellum) (Shen et al., 2013).

## 186 Probabilistic Tractography preprocessing

187 A whole-brain structural connectivity (SC) matrix was computed for each subject of the control  
188 group and then averaged in a two-step process as described in previous studies (Muthuraman  
189 et al., 2016; Cao et al., 2013; Gong et al., 2009). We used the resting-state atlas mentioned above  
190 to create a structural connectome in each individual's diffusion native space. In brief, DICOM  
191 images were converted to Neuroimaging Informatics Technology Initiative (NIfTI) using dcm2nii  
192 ([www.nitrc.org/projects/dcm2nii](http://www.nitrc.org/projects/dcm2nii)). The b0 image in DTI native space was co-registered to  
193 the T1 structural image by using FLIRT (Jenkinson and Smith, 2000). Then, the T1 structural  
194 image was co-registered to the standard space by using FLIRT and FNIRT (Andersson et al.,  
195 2007; Jenkinson and Smith, 2000). The transformations were inverted and applied to warp the  
196 resting-state atlas from MNI space to the native diffusion space by applying a nearest-neighbor  
197 interpolation method. Analysis of diffusion images was performed using the processing pipeline of  
198 the FMRIB's Diffusion Toolbox (FDT) in FMRIB's Software Library [www.fmrib.ox.ac.uk/fsl](http://www.fmrib.ox.ac.uk/fsl).  
199 Non-brain tissues were extracted using Brain Extraction Tool (BET) (Smith, 2002), eddy current-  
200 induced distortions and head movements were corrected using eddy correct tool (Andersson and  
201 Sotropoulos, 2016), and the gradient matrix was reoriented to correct for subject motion (Leemans  
202 and Jones, 2009). Then, Crossing Fibres were modeled using the default BEDPOSTX parameters,  
203 and the probability of multi-fibre orientations was computed to improve the sensitivity of non-  
204 dominant fibre populations (Behrens et al., 2007, 2003). Probabilistic Tractography was performed  
205 in native diffusion space using the default parameters of PROBTRACKX (Behrens et al., 2007,  
206 2003). The connectivity probability to each of the other 214 brain areas was estimated for each  
207 brain area as the total proportion of sampled fibres in all voxels in the brain area  $n$  that reached  
208 any voxel in the brain area  $p$ . Given that Human Diffusion Tensor Imaging (DTI) does not capture  
209 directionality, the  $SC_{np}$  matrix was symmetrized by computing its transpose  $SC_{pn}$  and averaging

210 both matrices. Finally, to obtain the structural probability matrix, the value of each brain area  
211 was divided by its corresponding number of generated tracts.

## 212 Leading Eigenvector Dynamics Analysis (LEiDA)

213 This first step aims to define the empirical brain states from a quantitative point of view, defined  
214 as a conjunction of substates, applying LEiDA method (Cabral et al., 2017b) as schematized in  
215 **Figure 1a**. For all subjects in all states, the blood oxygenation level-dependent (BOLD) time  
216 series of each brain area of the parcellation were filtered in the range 0.04-0.07 Hz and Hilbert-  
217 transformed to obtain the evolution of phase of the time series. A BOLD phase coherence matrix  
218  $dFC(t)$  was then calculated at any given repetition time (TR) between each brain area pair  $n$  and  
219  $p$  by calculating the cosine of the phase difference as:

$$220 \quad dFC(n, p, t) = \cos(\theta(n, t) - \theta(p, t)). \quad (1)$$

221 In this way, the interregional BOLD signal synchrony for all subjects was obtained at all time  
222 points. If nodes are temporarily aligned, the difference between their Hilbert transformed signal  
223 angle is  $0^\circ$  and the phase coherence is close to one [ $\cos(0^\circ)=1$ ]. When a pair of nodes develop  
224 orthogonal BOLD signals, then the phase coherence is close to zero [ $\cos(90^\circ)=0$ ]. The resulting  
225  $dFC(t)$  of each subject at each timepoint was a 3D matrix of size of  $N \times N \times T$ , being  $N$  the number  
226 of brain areas (214) and  $T$  the total time points (295). A total of 69 3D matrices were calculated,  
corresponding to all of the groups together (controls, MCS and UWS).

227 In order to facilitate the future classification process, the dominant connectivity pattern was  
228 obtained by reducing the dimensionality of the matrices into their leading eigenvectors  $V_1(t)$ . This  
229 can be applied since FC matrices are undirected and symmetric across the diagonal (Deco et al.,  
230 2019). The leading eigenvectors (of dimension  $N \times 1$ ) capture the dominant connectivity pattern  
231 at each time point  $t$  whilst explaining most of the variance, representing the contribution of each  
232 brain area to the whole structure and improving the signal-to-noise ratio (Cabral et al., 2017b).  
233 The dimensionality of the data was reduced from  $N \times N$  to  $N \times 1$ , and the dominant functional  
234 connectivity pattern  $dFC(t)$  could be observed by calculating the outer product of  $V_1(t)$  with its  
235 transpose ( $V_1 V_1^T$ ) (Lohmann et al., 2010).

236 The following step consisted of identifying recurrent FC patterns representing the substates.  
237 The leading eigenvectors  $dFC(t)$  for each TR and all subjects from all states ( $20355 = 69$  par-  
238 ticipants \* 295 timepoints) were clustered with K-means clustering, varying  $k$  from 3 to 8. This  
239 algorithm is an unsupervised method consisting of assigning the data to the closest cluster cen-  
240 troid iteratively and re-calculating the  $k$  centroids in each iteration until convergence. The resulting  
241 cloud centroids  $V_c(t)$  represent the dominant connectivity pattern in each cluster. The  $k$  discrete  
242 number of patterns of size  $N \times 1$  correspond to the substates obtained from all subjects in all col-  
243 lapsed groups of subjects. These cluster centroids  $V_c(t)$  represent the contribution of each brain  
244 area to the community structure and were rendered onto brain maps.

245 Upon computing the discrete number of FC patterns for each  $k$ , we calculated the resulting  
246 probability of occurrence in each group. This was computed as the ratio between the total number

247 of epochs assigned to a specific cluster (i.e., for each subject in each group divided by the total  
248 amount of epochs in the given group). This gave rise to the Probabilistic Metastable Substate  
249 Space (PMS), which typifies each brain state from the probability of occurrence of being in each  
250 particular substate from the substate repertoire.

251 **Whole-Brain Computational Model**

252 After characterizing the empirical PMS for the different profiles, a whole-brain Hopf compu-  
253 tational model was obtained for each DoC state (**Figure 1b**). The dynamics from functional  
254 interactions between each brain area were emulated based on the anatomical SC. In other words,  
255 the emergence of activity can be explained in a mechanistic way by merging anatomical connec-  
256 tivity, which determines structure, and functional connectivity that represents activity dynamics,  
257 with the inclusion of effective connectivity (EC) (Deco et al., 2015). The working point of each  
258 model was fitted to the empirical data and optimized by determining the specific parameters of  
259 the model (Deco et al., 2019).

260 The normal form of supercritical Hopf bifurcation (Landau-Stuart oscillator) was used to sim-  
261 ulate the BOLD activity for each of the 214 cortical and subcortical brain areas based in Shen  
262 parcellation. The Landau-Stuart oscillator has been used to study transitions from noisy to oscilla-  
263 tory regimes and, when coupled based on the brain's architecture, to replicate complex interactions  
264 in brain dynamics (Deco et al., 2015).

265 An uncoupled node  $n$  can be represented in Cartesian coordinates with the following pair of  
266 coupled equations:

$$\begin{aligned}\frac{dx_n}{dt} &= [a_n - x_n^2 - y_n^2]x_n - \omega_n y_n + \beta\eta_n(t), \\ \frac{dy_n}{dt} &= [a_n - x_n^2 - y_n^2]y_n + \omega_n x_n + \beta\eta_n(t),\end{aligned}\tag{2}$$

267 where  $x_n$  emulates the BOLD signal of the node and  $\eta_n(t)$  is the additive Gaussian noise with  
268 standard deviation  $\beta = 0.01$ . This normal form describes the noisy and synchrony scenarios and  
269 has a supercritical bifurcation in  $a=0$ . For  $a<0$ , the node is stable in a fixed point and represented  
270 by noise from asynchronous firing of neurons. For  $a>0$ , metastable oscillations are obtained due  
271 to the synchronized firing of neurons at a frequency of  $w/2\pi$  (Deco et al., 2017b). The transition  
272 from a noisy to a fully oscillatory scenario is called Hopf, and since it is the simplest way to model  
273 it mathematically, it is called normal form. Here, we chose a value of  $a_n=-0.02$  for each brain  
274 node  $n$  following previous findings (Deco et al., 2017c), near the brink of Hopf bifurcation, in the  
275 critical border between synchrony and desynchrony. The frequency of the system  $f_n = \omega_n/2\pi$  was  
276 estimated from the empirical data as the averaged peak frequency of the filtered BOLD signal in  
277 the 0.04- to 0.07-Hz band for each brain node  $n=1, \dots, 214$  (Deco et al., 2019).

278 The whole-brain dynamics were modelled by including an additive coupling term  $C_{np}$  which  
279 adjusts the input to node  $n$  from each of the rest of the nodes  $p$  based on the SC. This weighted  
280 matrix assumes different myelination densities across long-range connectivities. A global coupling  
281 weight  $G$  was also added to represent the strength between all nodes, corresponding to the control

282 parameter adjusted to fit the dynamical working region of the simulations to the empirical data.  
 283 It scales all of the connections allowing maximal fitting between simulations and empirical data,  
 284 assuming all axonal conductivity to be equal across the brain. The whole-brain dynamics at each  
 285 node  $n$  was thus defined by the following set of coupled equations (Deco et al., 2017c):

$$\begin{aligned}\frac{dx_n}{dt} &= [a_n - x_n^2 - y_n^2]x_n - \omega_n y_n + G \sum_{p=1}^N C_{np}(x_p - x_n) + \beta \eta_n(t), \\ \frac{dy_n}{dt} &= [a_n - x_n^2 - y_n^2]y_n + \omega_n x_n + G \sum_{p=1}^N C_{np}(y_p - y_n) + \beta \eta_n(t).\end{aligned}\quad (3)$$

286 **Model Fitting: Comparing empirical and simulated probability metastable space  
 287 states**

288 For optimal spatiotemporal fit of whole-brain models to their empirical PMS space, the value  
 289 of  $G$  was ranged from 0 to 0.5 in steps of 0.01, and the model was iterated 200 times. LEiDA  
 290 was computed to the Hilbert-transformed simulated signal using the centroids already defined by  
 291 the empirical substates in order to compute the simulated PMS space. Each model was fitted to  
 292 the empirical data by deciding which value of  $G$  approximated it better (Deco et al., 2019). This  
 293 corresponded to the lowest Kullback-Leibler (KL) distance between the empirical and simulated  
 294 probabilities of each substate (Deco et al., 2019), given by:

$$KL(P_{emp}, P_{sim}) = 0.5 \left( \sum_i P_{emp}(i) \ln \left( \frac{P_{emp}(i)}{P_{sim}(i)} \right) + \sum_i P_{sim}(i) \ln \left( \frac{P_{sim}(i)}{P_{emp}(i)} \right) \right), \quad (4)$$

295 where  $P_{emp}(i)$  and  $P_{sim}(i)$  are the empirical and simulated probabilities respectively of metastable  
 296 substate  $i$ .

297 **Model Optimization: Method for updating Effective Connectivity**

298 After defining the value of  $G$  of each model, the models were optimized separately and the  
 299 SC was updated in order to access potential missing connections. The initial value of  $C$  for each  
 300 of the models was provided by a primer empirical DTI structural connectivity corresponding to  
 301 the average of control subjects (Deco et al., 2015). Specifically,  $C$  was initially normalized to  
 302 a maximum value of 0.2 in order to have the same range of values as in previous works (Deco  
 303 et al., 2019, 2017c). The SC was then transformed to effective connectivity (EC) in an iterative  
 304 manner by calculating the distance between the grand average phase coherence matrices of the  
 305 model  $FC_{ij}^{phases-mod}$  and the empirical matrices  $FC_{ij}^{phases-emp}$ . Each structural connection between  
 306 different nodes  $i$  and  $j$  was adjusted with a gradient descent approach given by:

$$C_{ij} = C_{ij} + \epsilon \left( FC_{ij}^{phases-emp} - FC_{ij}^{phases-mod} \right), \quad (5)$$

307 where  $\epsilon = 0.01$ , and the grand average phase coherence matrices are defined:

$$FC_{ij} = \left\langle \cos \left( \varphi_j(t) - \varphi_i(t) \right) \right\rangle, \quad (6)$$

308 where  $\varphi(t)$  denotes the Hilbert transform BOLD signal phase of the nodes  $j$  and  $i$  at time  $t$ , and  
309 the brackets indicate the average across time. This was repeated until the difference between the  
310 empirical and simulated values was smaller than 0.001 (Deco et al., 2019)

### 311 Unilateral Perturbation of the Whole-Brain Model

312 After obtaining the models, the transitions from the DoC states towards a control state were  
313 studied (**Figure 1c**). The models for DoCs were stimulated *in silico* by moving locally in a  
314 unilateral way the local bifurcation parameter  $a$  of each of the 214 brain areas. Different levels  
315 of intensity were applied area by area under the protocols of synchronization and noise. The  
316 protocols were represented by the sign of the local bifurcation parameter (positive and negative,  
317 respectively), and the stimulation intensities by the absolute value of each step (Deco et al., 2017c).  
318 In the synchronization protocol, the bifurcation parameter was shifted positively from 0 to 0.2 in  
319 steps of 0.01, whereas for the noise modality, it was shifted from 0 to -0.2 in steps of -0.02. Each  
320 simulation was repeated 3 times the results were averaged to minimize random effects from the  
321 Gaussian noise of the model (Deco et al., 2019). The fitting to the target states was measured by  
322 calculating the KL distance (described in the previous section) between the probabilities of each  
323 substate of the simulated DoC models separately, which are the source, and the empirical control  
324 PMS, which is the target. The areas more prone to promote a desired transition after simulation  
325 were detected from the ones presenting the lowest KL distance.

### 326 Statistical Analysis

327 Statistical analysis were performed using MATLAB R2022a software from MathWorks (Natick,  
328 MA, USA). Permutation-based Wilcoxon tests with 1000 iterations were used to test the results of  
329 the LEiDA method, specifically the probability of occurrence of the whole range of explored clus-  
330 tering conditions ( $k$  from 3 to 8). The Wilcoxon test was used to compare each permutation with a  
331 significance threshold of 0.05. We applied the False Discovery Rate (FDR) method (Hochberg and  
332 Benjamini, 1990) to correct for multiple comparisons when testing the differences between groups  
333 (controls, MCS, and UWS) and the number of cluster centers (i.e., substates). All p-values shown  
334 correspond to the differences that remain significant after FDR correction.

## 335 Results

### 336 LEiDA

337 We selected the minimum number of clusters ( $k$ ) that statistically differed between the three  
338 groups. The configuration that best described the empirical data across all participants and distin-  
339 guished between groups was detected at  $k=4$ . The probability of occurrence for the PMS of each  
340 group is visualized in **Figure 2a** and the cluster centroid eigenvectors are rendered onto brain  
341 maps in **Figure 2b**. The leading eigenvectors had positive and negative signs partitioning the  
342 network into communities as red and blue colors, respectively. The strength of the color describes  
343 the strength with which each area belonged to the placed community (Cabral et al., 2017b).

344 The first substate presented the same sign for all eigenvector elements. The probability of  
345 occurrence was higher in controls [ $0.493 \pm 0.030$  (mean  $\pm$  standard error)] compared to MCS  
346 [ $0.351 \pm 0.037$ ,  $P=0.012$ ] and UWS [ $0.232 \pm 0.069$ ,  $P=0.003$ ]. Furthermore, the probability was  
347 lower in UWS than in MCS [ $P=0.035$ ]. The rest of the substates (i.e., substates 2, 3, and 4) were  
348 characterized by subsets of brain areas that disengaged from the whole-brain network aligning with  
349 each other. In substate 2, central areas (motor network) represented a pattern of activation. In this  
350 substate controls had the lowest probability of occurrence [ $0.155 \pm 0.020$ ] compared to MCS [ $0.242$   
351  $\pm 0.029$ ,  $P=0.022$ ] and UWS [ $0.362 \pm 0.050$ ,  $P=0.001$ ]. Moreover, the probability was higher in  
352 UWS than in MCS [ $P=0.033$ ]. Substate 3 exhibited a functional network led by the occipital lobe  
353 (visual network). In controls, the probability of substate 3 was lowest [ $0.129 \pm 0.013$ ] compared  
354 to MCS [ $0.242 \pm 0.022$ ,  $P<0.001$ ] and UWS [ $0.234 \pm 0.024$ ,  $P=0.001$ ]. This substate did not  
355 discriminate significantly between DoC groups. Substate 4 had a coordination between areas of  
356 the medial-frontal network, fronto-parietal network, DMN (i.e., precuneus) and subcortical areas  
357 (i.e., thalamus). This metastable substate only discriminated between controls [ $0.224 \pm 0.018$ ] and  
358 MCS [ $0.165 \pm 0.018$ ,  $P=0.018$ ].

### 359 **Fit whole-brain computational model to the brain states of DoC groups**

360 For the MCS and UWS groups, we fitted the PMS to a causal mechanistic whole-brain model.  
361 We optimized and adjusted the models in order to select the parameters that displayed the most  
362 approximate regime to empirical PMS (see Materials and Methods). The best fit between the  
363 empirical and simulated PMS was found at  $G=0.08$  and  $G=0.05$  for MCS and UWS models,  
364 respectively (**Figure 3**).

### 365 ***In silico* stimulations to force transitions from DoC to a control target 366 state**

367 Following model fitting and optimization, we systematically perturbed the PMS model of each  
368 DoC group and compared it with the empirical PMS of the control group. Each brain node was  
369 shifted by increasing the absolute value of the bifurcation parameter  $a$ , representing the intensity  
370 of stimulation. A synchronization protocol was addressed with positive values, and a noise protocol  
371 with negative values. Optimal perturbation was the one that resulted in the smallest KL distance  
372 between the PMS after perturbing each node individually, and the empirical PMS of the target  
373 (control group).

374 The results of the *in silico* stimulation with different protocols and intensities for MCS and UWS  
375 are shown in **Figures 4a** and **4b**, respectively. The color scale represents the KL distance between  
376 the perturbed PMS and the target PMS after stimulating each individual brain area separately.  
377 The best fit is indicated by a lower KL distance, note that the color scales are different for each  
378 DoC condition, adjusted accordingly for better resolution. For the synchronization protocol, a  
379 successful transition was forced from the source states of MCS and UWS to the control state. We  
380 can observe that for MCS most regions promoted a transition with lower stimulation intensity  
381 compared to UWS. In contrast, in the noise protocol, the KL distance did not decrease for both

382 MCS and UWS (i.e., colors are red and yellow rather than green and blue). This means that as  
383 a result of applying a noise protocol, the transition from DoC to a control target state was not  
384 possible, evidenced by poorer fit.

385 In the synchronization protocol, a transition was likely to occur in many areas if they were  
386 sufficiently stimulated. **Figure 4c** illustrates the rendering of the KL distance between the per-  
387 turbed PMS and the target PMS after stimulating each individual brain area separately, at their  
388 particular optimal stimulation intensity. Areas in the motor network were the most sensitive ones,  
389 including subcortical areas (i.e., thalamus), provoking transitions in both cases (MCS and UWS).  
390 Specifically, the best fit to the control PMS space was obtained when stimulating the left post-  
391 central gyrus with an intensity of 0.2 for MCS and the right postcentral gyrus with an intensity  
392 of 0.16 for UWS. As a result, the perturbed and target probabilities were very similar in all four  
393 metastable substates of the PMS (**Figure 5**).

## 394 Discussion

395 We successfully applied model-free and model-based approaches to find causal evidence for the  
396 brain dynamics in DoC and transitions to a control state, following the methodology of Deco et al.  
397 (2019). Firstly, we significantly distinguished between brain states by characterizing the PMS of  
398 DoC and controls using LEiDA. For each group, we identified metastable substates (i.e., patterns)  
399 with an associated probability of occurrences and alternation profiles (Cabral et al., 2017b). We  
400 then fitted a Hopf model to each empirical PMS for each DoC state. In this way, we were able  
401 to force a transition from the PMS DoC models (MCS and UWS separately) to the target control  
402 state using exhaustive off-line *in silico* unilateral perturbations. Finally, by varying stimulation  
403 intensities, we revealed how changes in local brain areas using a synchronous modality can reshape  
404 whole-brain dynamics in DoC. In this way, we could determine the mechanistic global effects of all  
405 possible local perturbations and the most sensitive areas in terms of their perturbability.

406 In the model-free approach, using LEiDA, we identified substates with network-specific changes  
407 whose probabilities varied in each brain state (**Figure 2**). In particular, we found controls were  
408 more able to access substates 1 and 4. Substate 1, in which all BOLD signals followed the leading  
409 eigenvector, has been shown to exist in previous LEiDA studies (Lord et al., 2019; Figueiroa et al.,  
410 2019; Cabral et al., 2017a). This substate has been associated with a global state (Zhang and  
411 Northoff, 2022), synchronized stability (Farinha et al., 2022), or noise artifacts (Olsen et al., 2022).  
412 Furthermore, we found substate 4 had a coordination of areas overlapping the medial-frontal  
413 network, fronto-parietal network, DMN (i.e., precuneus) and subcortical areas (i.e., thalamus).  
414 The DMN is important for internal self-related and external perceptual awareness, cognition, mind-  
415 wandering, and autobiographical memory, and some studies have shown this network disrupted  
416 in patients with DoC (Panda et al., 2022; Edlow et al., 2020; Bodien et al., 2017; Qin et al.,  
417 2015; Demertzi et al., 2015; Fernández-Espejo et al., 2012; Vanhaudenhuyse et al., 2011, 2009;  
418 Demertzi et al., 2013). On the other hand, our results show DoC patients were more likely to be  
419 in substates 2 and 3, which exhibited a functional network led mainly by areas from the motor  
420 and visual networks, respectively. Notably, Demertzi et al. (2015) found a correlation between rs-

421 fMRI connectivity of the aforementioned networks (DMN, fronto-parietal, sensorimotor, and visual  
422 networks) and CRS-R assessment results, indicating these networks are critical to brain function  
423 in DoC. This is also supported by Cao et al. (2019), which reported changes in brain activity in  
424 the DMN, somatomotor, and visual networks, and by Crone et al. (2014), which measured altered  
425 network properties in the fronto-parietal cortex, both studies in DoC patients.

426 In the model-based approach, we modelled brain activity as a system of non-linear Stuart-  
427 Landau oscillators (also known as Hopf bifurcation) to link the underlying anatomy with local  
428 dynamics (Deco et al., 2017c). Hopf models have allowed simulating several brain states in health  
429 and disease with high fitting accuracy (Escrichs et al., 2021b, 2022; Sanz Perl et al., 2023; Soler-  
430 Toscano et al., 2022; López-González et al., 2021; Deco et al., 2019; Jobst et al., 2017; Deco and  
431 Kringelbach, 2014). These models have been able to capture both local and global brain dynamics  
432 (Deco et al., 2017c,b), while having lower computational costs (Deco et al., 2017a; Deco and Jirsa,  
433 2012) and risks of overfitting (Deco and Kringelbach, 2014) than more detailed models such as  
434 spiking neurons (Deco and Jirsa, 2012; Cabral et al., 2014). Here, during fitting and optimization,  
435 we observed that the MCS group had a higher value of global coupling weight  $G$  than the UWS  
436 (**Figure 3**). This parameter represents the relationship between local and global brain dynamics  
437 and the effects of structural connectivity on brain dynamics. The greater the value of  $G$ , the less  
438 restricted the brain network interaction is to areas with high structural connections. In line with  
439 previous studies, we found that MCS showed more propagation of brain activity and connectivity  
440 between distant brain areas than UWS (Escrichs et al., 2021b; López-González et al., 2021).

441 By combining the model-based approach with *in silico* stimulations, we explored brain trans-  
442 sitions between different states. This strategy allowed us to find the optimal areas to stimulate  
443 and re-balance the underlying brain dynamics in patients with DoC towards more healthy states  
444 (Escrichs et al., 2021b; Sanz Perl et al., 2021). Thus, *in silico* stimulation provided us a way  
445 to test exhaustive trials without the ethical constraints of real-world experiments (Deco et al.,  
446 2017c; Clausen, 2010). We shifted the brain dynamics' landscape rather than the working point  
447 per se. This ensures propagation and facilitates plasticity, targeting a system reorganization with  
448 long-term effects (Deco et al., 2019, 2017a). We evidenced transition from DoC states to control  
449 using the synchronization and not the noise protocol, in line with Deco et al. (2019), since the KL  
450 distance between the perturbed PMS and the control target PMS decreased in the synchronous  
451 modality (**Figure 4**). Bifurcation parameters below the bifurcation edge were, therefore, indicative  
452 of DoC states and could not force systems to a control target. Both MCS and UWS progressively  
453 came closer to the target state with increasing positive intensities for the desired transitions (i.e.,  
454 the synchronization protocol). In this regard, our results are consistent with the notion that syn-  
455 chronous oscillations have a role in neuronal communication and long-range functional connectivity  
456 between brain areas (Cabral et al., 2022; Fries, 2005). A further finding was that overall, MCS  
457 exhibited higher sensitivity to external perturbations than UWS. Metastable substates with the  
458 highest probability of PMS spaces in both DoC groups shifted from substates with subsets of brain  
459 areas aligned within each other in the motor network (substate 2) and visual network (substate  
460 3) to a substate dominated by regions from the medial-frontal network, fronto-parietal network,  
461 DMN and subcortical areas (substate 4), and to a substate with global brain activity (substate

462 1) (**Figure 5**). In terms of brain areas promoting a transition, most were found in the motor  
463 network, relevant to DoC (Panda et al., 2023; López-González et al., 2021; Demertzi et al., 2015;  
464 Piccione et al., 2011). Particularly, the most sensitive area was the postcentral gyrus, which has  
465 been associated with impaired somatosensory functions (Cao et al., 2019) and found to distinguish  
466 DoC patients by its weighted global connectivity (Kotchoubey et al., 2013). Lastly, a specific  
467 subcortical area prone to transition and important in DoC studies was the thalamus (Panda et al.,  
468 2023, 2022; Sanz Perl et al., 2021; Lutkenhoff et al., 2015; Monti et al., 2015; Schiff et al., 2007),  
469 given its key role in information processing and as a sensory relay station (Alnagger et al., 2023;  
470 Zheng et al., 2021).

471 The classification of patients with DoC is an existing debate in neuroscience. Identifying MCS  
472 and UWS can depend on the CRS-R metric's effectiveness, inter-rater variability, and consistency  
473 of caregivers' reports (Opara et al., 2014). It is challenging to distinguish between MCS and  
474 UWS since some patients who are classified as UWS may remain aware even though they do not  
475 demonstrate behavioral signs. They may be classified incorrectly as being awake and unaware  
476 when they are actually conscious (Owen, 2020; Bodien et al., 2015; Tagliazzucchi and Laufs, 2014;  
477 Fingelkurts et al., 2014). The circular nature of brain state definition and assessment could have  
478 compromised the efficacy and validity of our model definitions since they are subjected to the  
479 correct classification and typification of the empirical primary data source (Arsiwalla and Verschure,  
480 2018). It would be helpful to investigate the generalizability of our results with a broader range of  
481 DoC patients (Vohryzek et al., 2022a; López-González et al., 2021).

482 Overall, we were able to characterize and differentiate brain dynamics of DoC and healthy con-  
483 trols. We used a robust quantitative definition of brain states based on spontaneous spatiotemporal  
484 fluctuations (Deco et al., 2015; Constable, 2006). Furthermore, we provide a causal mechanistic  
485 explanation for the differences between brain states in DoC. Crucially, our perturbation approach  
486 could be used as a specific model biomarker relating local activity with global brain dynamics. In  
487 light of the exciting results, future applications could benefit from developing personalized pro-  
488 tocols by constructing individualized patient brain models (Vohryzek et al., 2022a,b; Kringelbach  
489 and Deco, 2020; Luppi et al., 2019; Muldoon et al., 2016; Constable, 2006). In addition, causal  
490 whole-brain modelling can help understand other brain states (e.g., meditation, anesthesia) (Seth  
491 and Bayne, 2022) and elucidate propagation properties (Rossini et al., 2015), network level im-  
492 pact (Kringelbach and Deco, 2020; Muldoon et al., 2016) and sensitive areas (Ipiña et al., 2020;  
493 Kringelbach et al., 2011). Overall, our results may eventually contribute to the field of external  
494 perturbation as a principled way of re-balancing the dynamics of post-coma patients towards more  
495 healthy regimes.

## 496 Data availability statement

497 Due to the restrictions imposed by the approved ethics protocols, neuroimaging datasets cannot  
498 be shared publicly since they contain clinical information from patients. However, the data can be  
499 requested to the authors.

## 500 **Funding**

501 P.D. was supported by the FI-SDUR Grant (no. 2022 FISDU 00229) funded by the Catalan Agency  
502 for Management of University and Research Grants (AGAUR). A.E. and G.D. were supported  
503 by the project eBRAIN-Health - Actionable Multilevel Health Data (id 101058516), funded by  
504 the EU Horizon Europe. G.D. was also supported by the AGAUR research support grant (ref.  
505 2021 SGR 00917) funded by the Department of Research and Universities of the Generalitat of  
506 Catalonia and by the project NEurological MEchanismS of Injury, and the project Sleep-like  
507 cellular dynamics (NEMESIS) (ref. 101071900) funded by the EU ERC Synergy Horizon Europe.  
508 Y.S.P. was supported by the European Union's Horizon 2020 research and innovation program  
509 under the Marie Skłodowska-Curie grant 896354. S.L., and J.A. were supported by the HBP  
510 SGA3 Human Brain Project Specific Grant Agreement 3 (grant agreement no. 945539), funded by  
511 the EU H2020 FET Flagship. The study was supported by the University and University Hospital  
512 of Liège, the Belgian National Funds for Scientific Research (F.R.S-FNRS), the MIS FNRS project  
513 (F.4521.23), the BIAL Foundation, AstraZeneca Foundation, the Generet funds and the King  
514 Baudouin Foundation, the James McDonnell Foundation, and Mind Science Foundation. O.G. is  
515 a research associate and S.L. is a research director at the F.R.S-FNRS.

## 516 **Competing interests**

517 The authors declare no conflict of interest.

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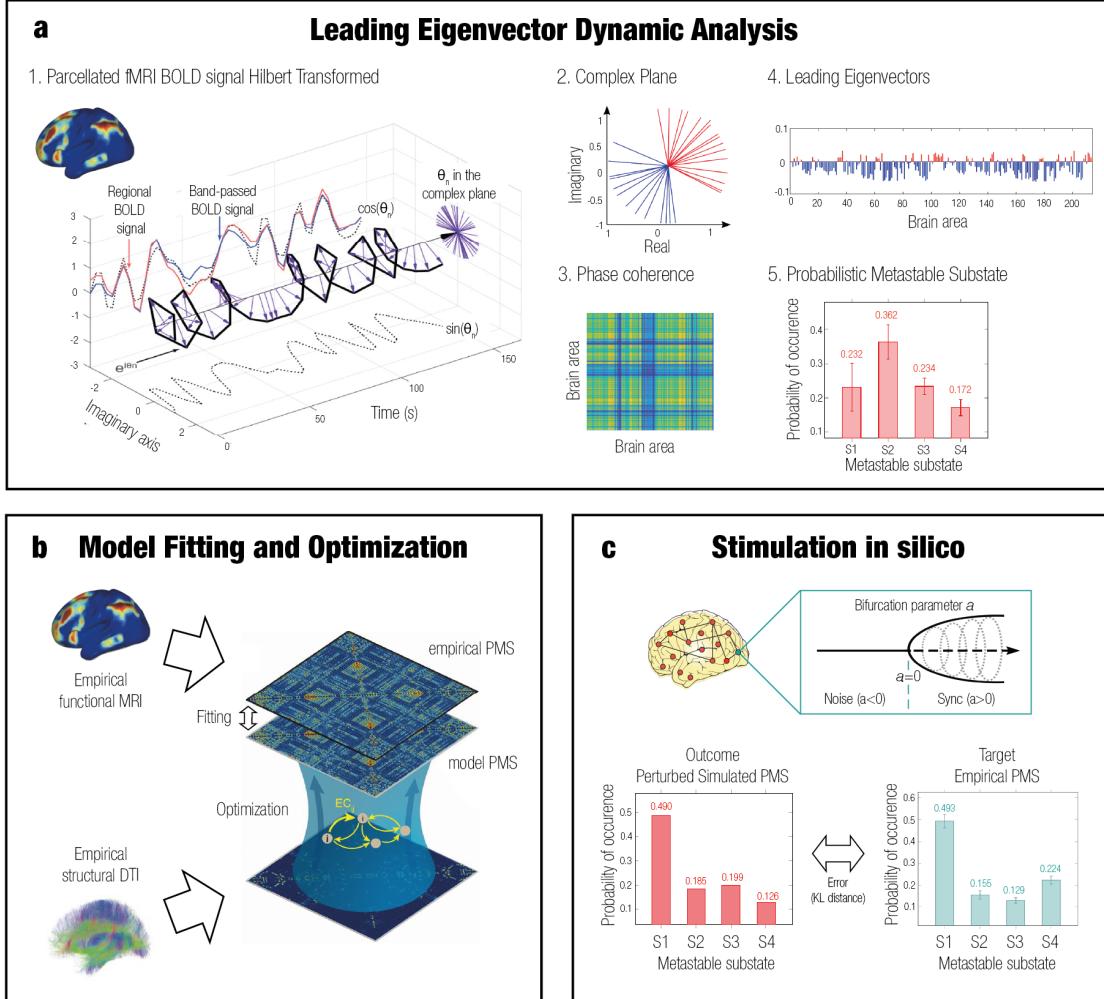
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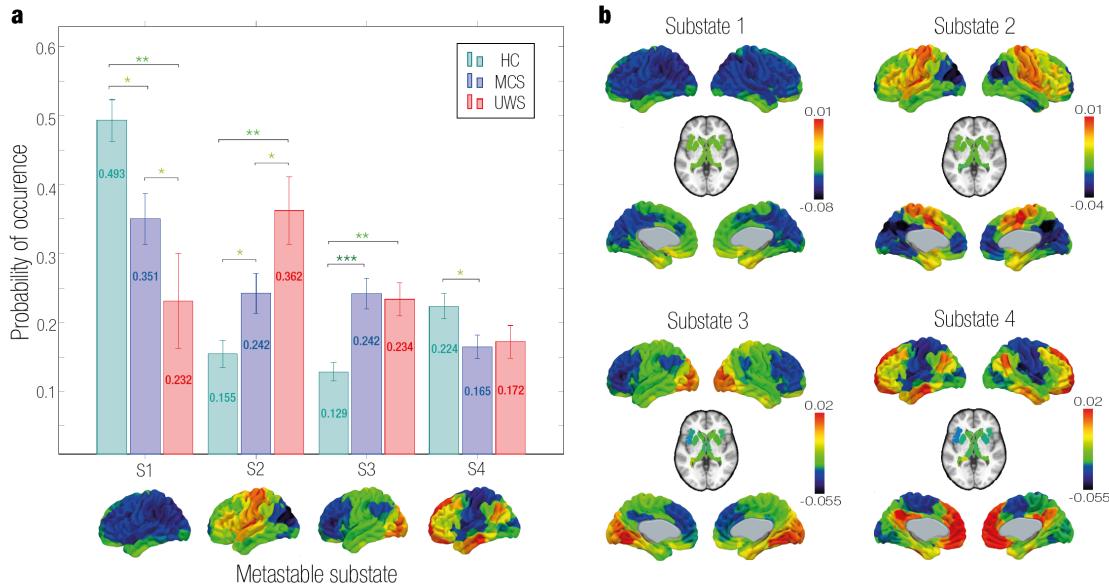
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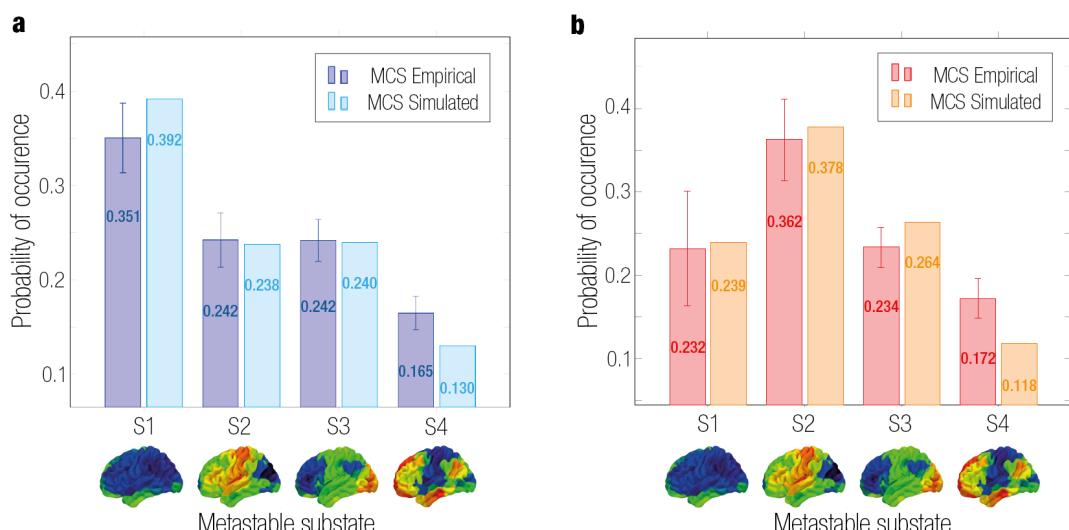
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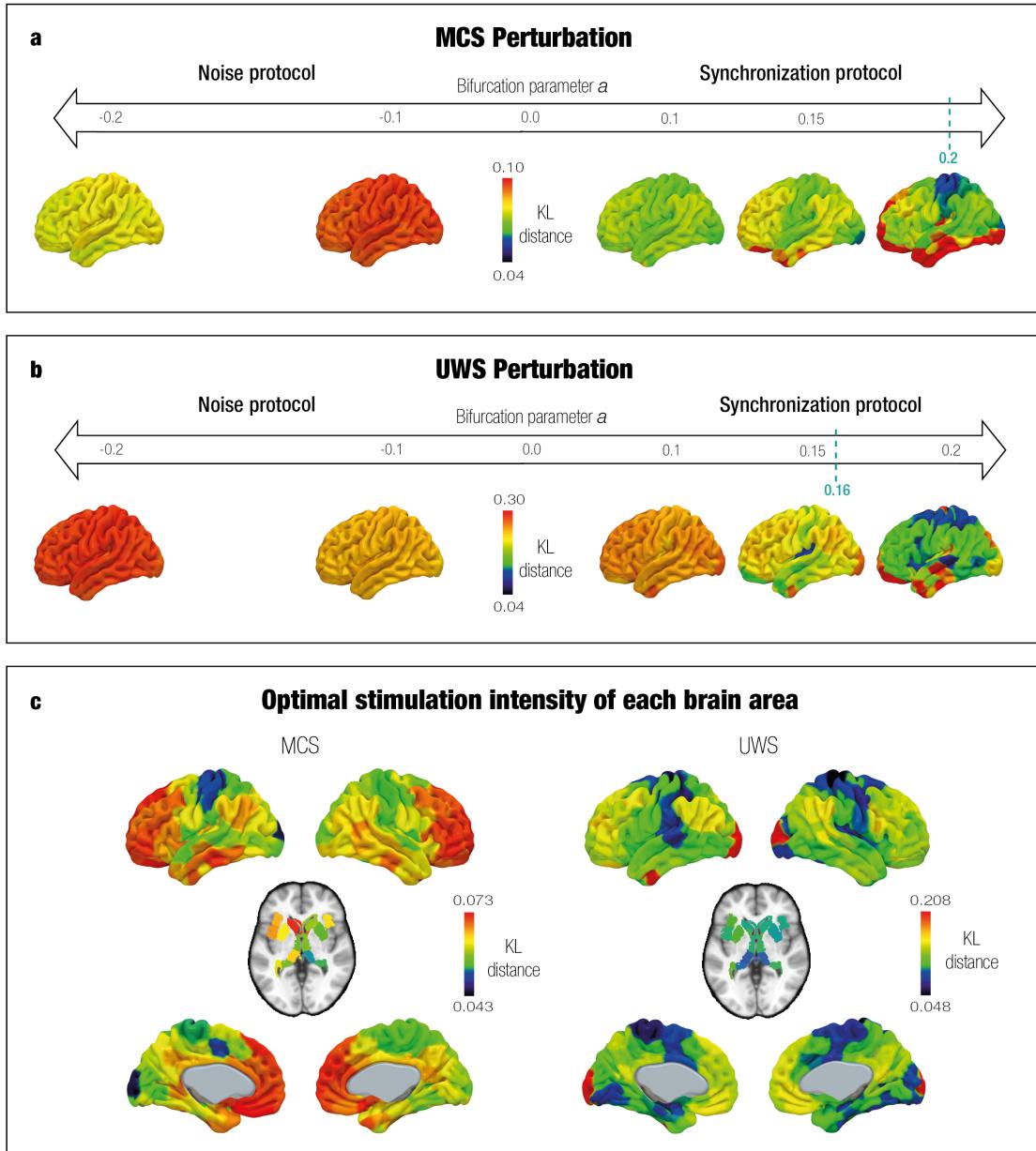
**Figure 1: Overview of model-free and model-based frameworks.** **a** Model-free framework: Leading Eigenvector Dynamic Analysis (LEiDA). The BOLD time signal for each of the 214 brain areas was band-passed filtered and Hilbert transformed. The complex plane shows the positive and negative real and imaginary components at a specific timepoint  $t$ . The phase coherence matrix  $dFC(t)$  between brain areas for each time window was calculated. Then, the leading eigenvector  $V_1(t)$  capturing the principal orientation of the BOLD phase for each of the matrices was calculated for each time  $t$  - positive values in red, negative values in blue. The leading eigenvectors for all time points of all participants were clustered using K-means ( $k=4$ ), and the probability of occurrence of each of the cluster centers is shown in the Probabilistic Metastable Substate (PMS) Space. **b** Model-based framework: whole-brain model. A whole-brain model based on the frequency  $w$  of the empirical fMRI data and DTI was fitted to the empirical PMS space by calculating the value of the global coupling  $G$  that minimized the KL distance between the empirical and the simulated PMS. The model was optimized using the effective connectivity (EC) by adjusting each connection with a gradient descent approach until convergence. **c** Model-based framework: stimulation *in silico*. A transition was forced systematically from a source state to a target state by stimulating each brain area separately. The bifurcation parameter was shifted positively and negatively for synchronization and noise protocols, respectively. The optimal unilateral perturbation was obtained at the minimal KL distance between the stimulated modelled PMS and the target empirical PMS.



**Figure 2: Model-free results: Empirical Probabilistic Metastable Substate (PMS) Space.** **a** Probability of Occurrence. The mean probability of occurrence for each group in each substate was calculated with a 95% confidence interval. The substates 1 and 4 had a higher probability of occurrence for the control group compared to DoC. The substates 2 and 4 had a lower probability of occurrence for the control group compared to DoC. Statistically significant differences are represented with asterisks (\*  $p < 0.05$ , \*\*  $p < 0.01$  and \*\*\*  $p < 0.001$ ). **b** Rendered brains represent the leading eigenvectors of each substate plotted onto the cortex. Substate 1 was characterized by all elements of the eigenvector with the same sign. Substate 2 had a functional community formed by areas in the motor network. Substate 3 presented a local coordination in the occipital lobe (visual network). Substate 4 showed coordination in brain areas from the medial-frontal network, fronto-parietal network, DMN and subcortical areas.



**Figure 3: Model-based results: Whole-brain model fitting and optimization.** Comparison between empirical and simulated PMS of each group. Optimal fit was given by the minimal KL distance value corresponding to a global coupling weight of **a**  $G=0.08$  for MCS and **b**  $G=0.05$  for UWS.



**Figure 4: Model-based results: *In silico* probing to force transition from DoC to control target state.**  
 We used synchronization and noise stimulation protocols to shift the local bifurcation parameter. The strength of the unilateral perturbation corresponds to the absolute value of the bifurcation parameter and the sign to the modality (synchronous with positive values, noise with negative values). The x-axis shows the stimulation intensity (from softer to stronger), and the color scale represents the KL distance. The best effectiveness was found where KL distance was minimal. For both DoC (a and b), the synchronization protocol forced a transition to the control state. This can be observed with the lower KL distance when increasing values of the local bifurcation parameter in a positive manner. The left sides of the x-axis show that the noise protocol presented poor effectiveness given that KL distances were longer than in the synchronization protocol. c contains the KL distance rendered onto brain maps with the optimal stimulation for each brain area in the synchronous protocols. The color scale represents the KL distance given by the best stimulation, with the lowest values corresponding to the motor and some subcortical areas (the best targets).

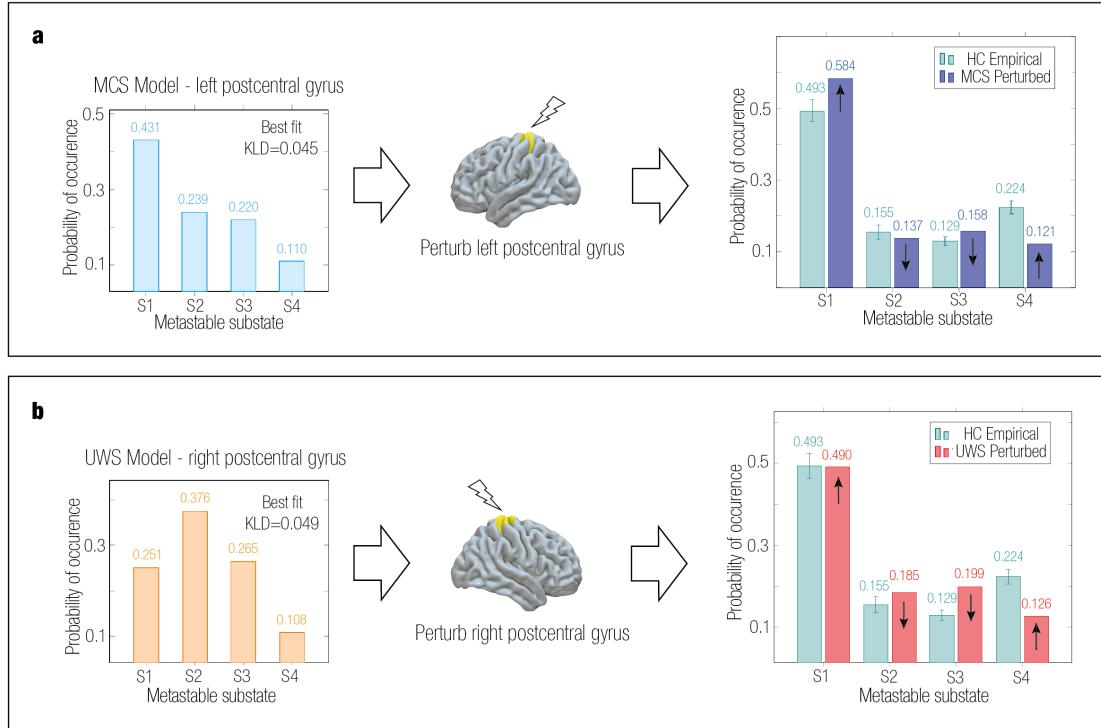


Figure 5: **Comparison between perturbed PMS of MCS and UWS groups to target control PMS.** We show the simulated and perturbed PMS for DoC groups and the empirical target control PMS. For both groups, the synchronization protocol increased the probability of the first and last substates and decreased the probability of the other substates, consistent with the empirical PMS of the control group. **a** Simulated MCS had a best approximation to the PMS of controls by perturbing unilaterally the postcentral gyrus (left) with an intensity of 0.2. **b** Simulated UWS had the best approximation to the PMS of controls by perturbing unilaterally the postcentral gyrus (right) with an intensity of 0.16.

## 848 Supporting information

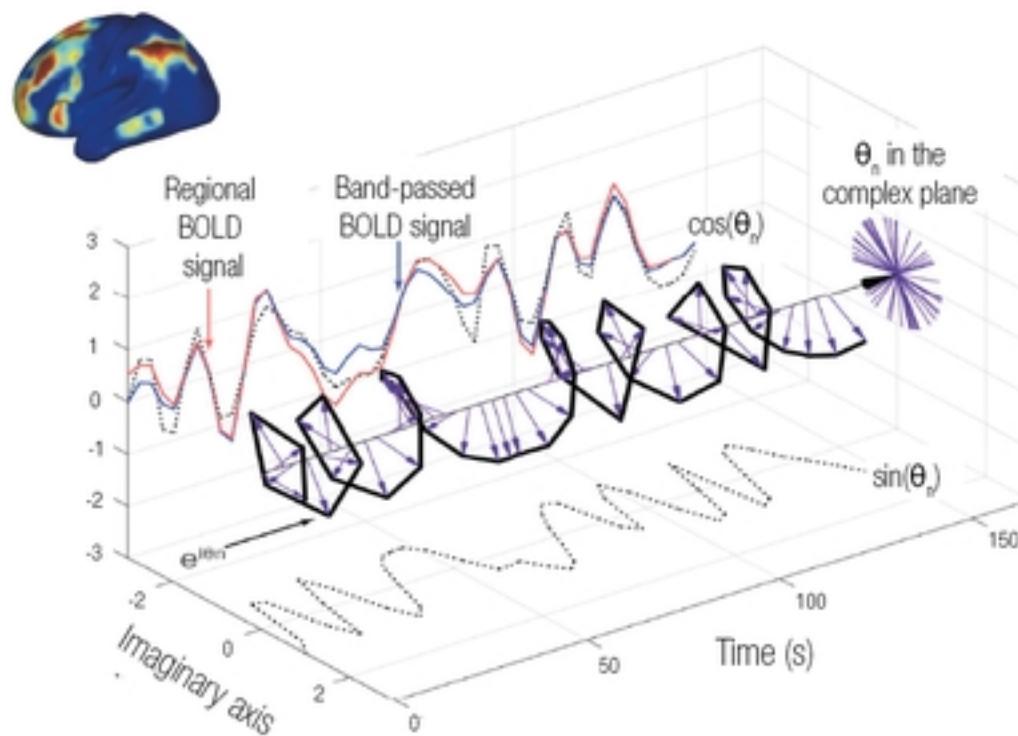
849 **S1 Table. Top 20 most sensitive regions for perturbing MCS model.** The first column  
850 corresponds to the KL distance between the PMS of the perturbed model, and the PMS of the  
851 target control state, after stimulating a given brain area. The second column shows the brain area  
852 in the Shen parcellation (Shen et al., 2013). The third column indicates the overlap between the  
853 brain area and the AAL structural parcellation (Tzourio-Mazoyer et al., 2002).

854 **S2 Table. Top 20 most sensitive regions for perturbing UWS model.** The first column  
855 corresponds to the KL distance between the PMS of the perturbed model, and the PMS of the  
856 target control state, after stimulating a given brain area. The second column shows the brain area  
857 in the Shen parcellation (Shen et al., 2013). The third column indicates the overlap between the  
858 brain area and the AAL structural parcellation (Tzourio-Mazoyer et al., 2002).

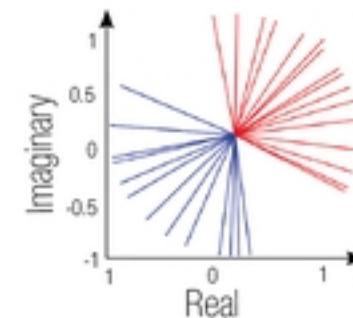
**a**

bioRxiv preprint doi: <https://doi.org/10.1101/2023.07.17.549269>; this version posted July 18, 2023. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

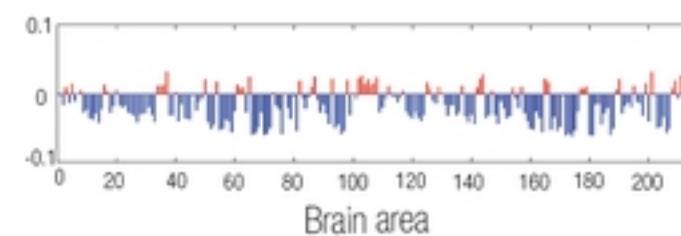
### 1. Parcellated fMRI BOLD signal Hilbert Transformed



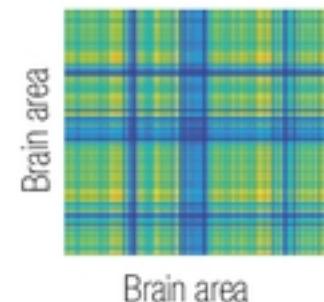
### 2. Complex Plane



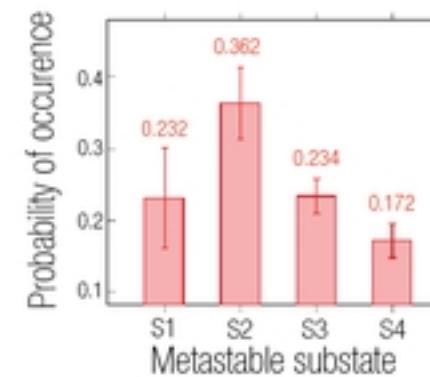
### 4. Leading Eigenvectors



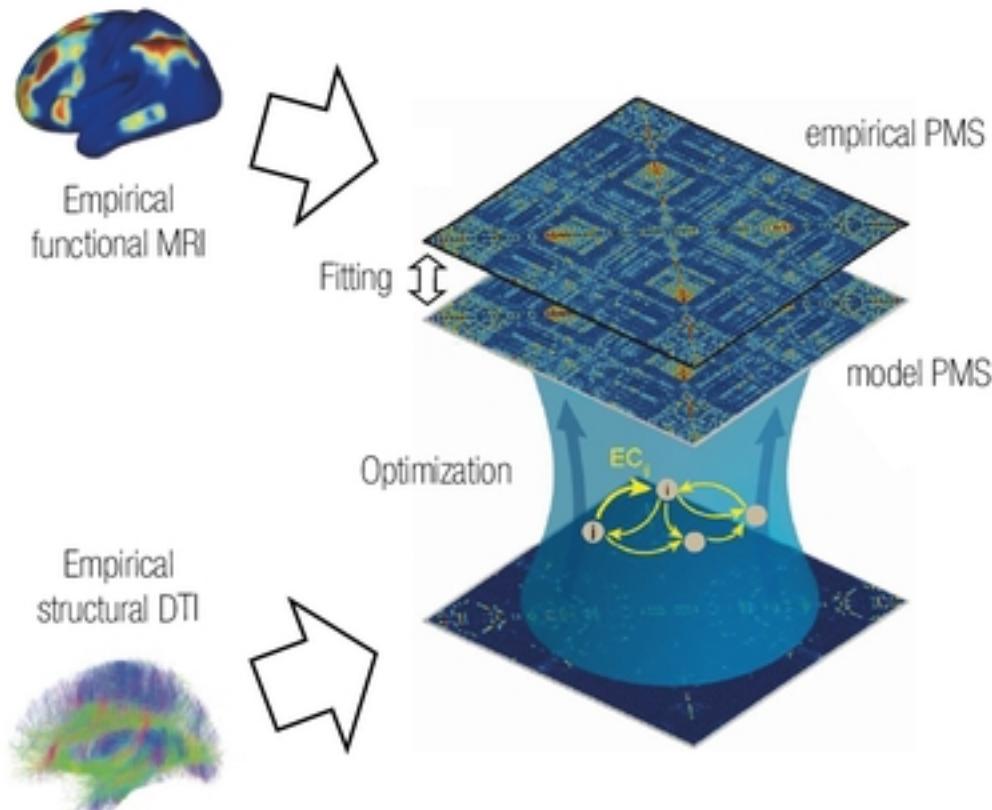
### 3. Phase coherence



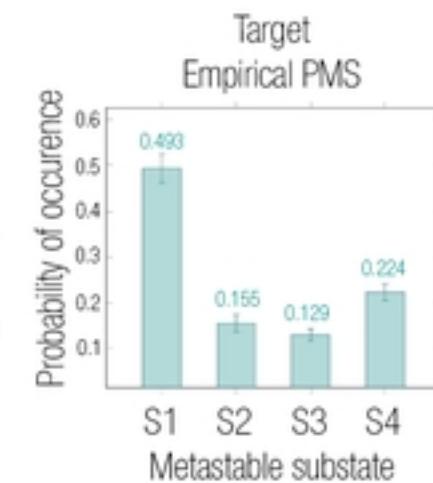
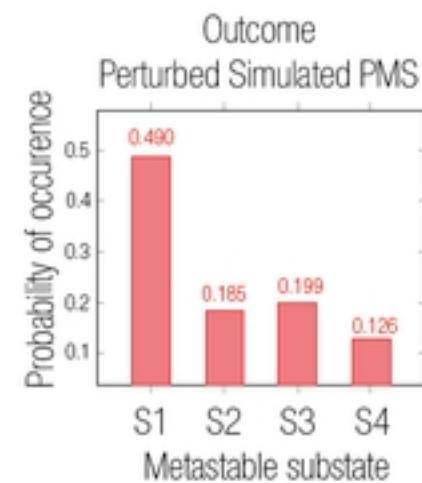
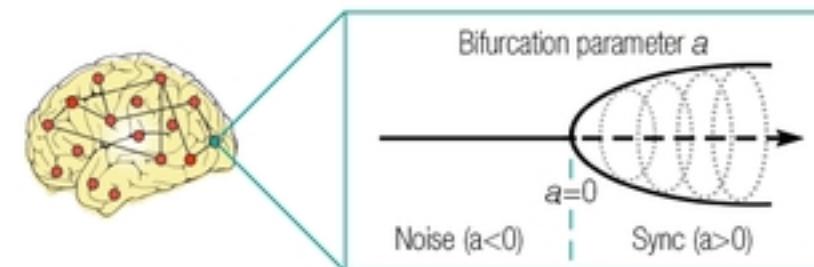
### 5. Probabilistic Metastable Substate

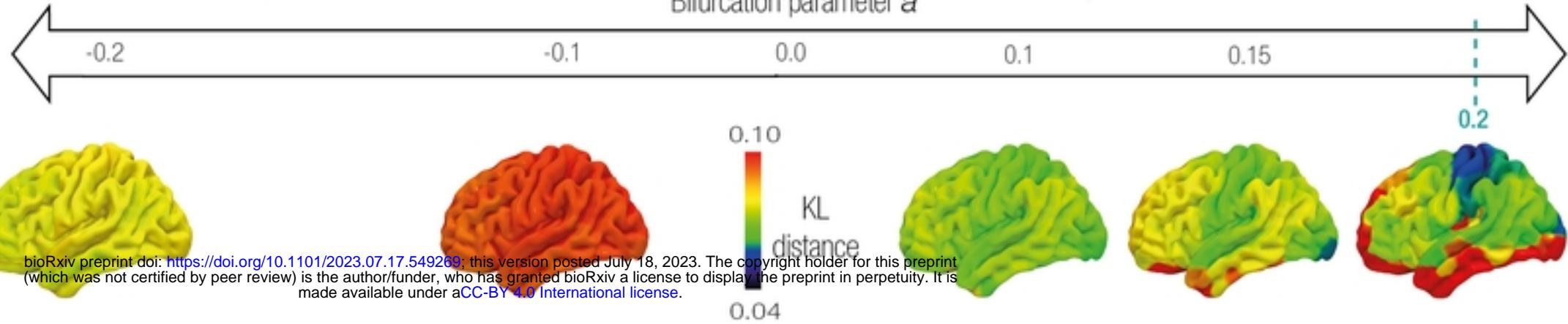
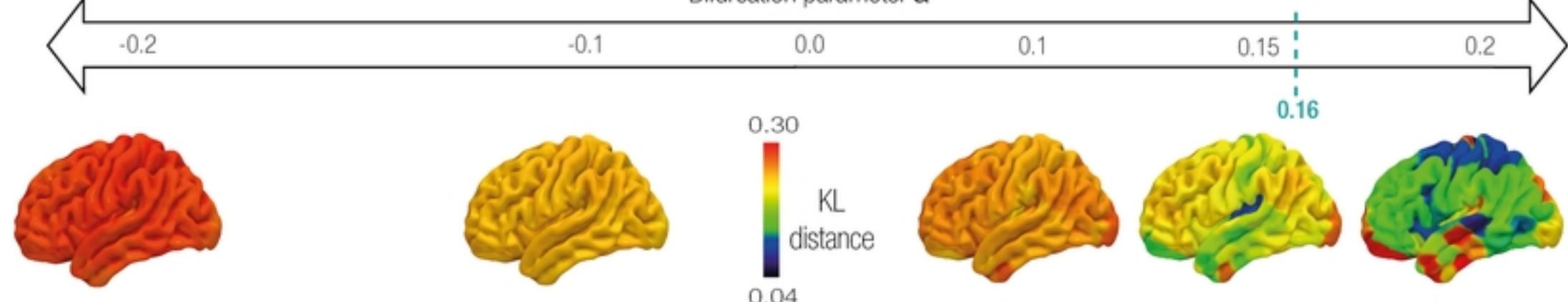
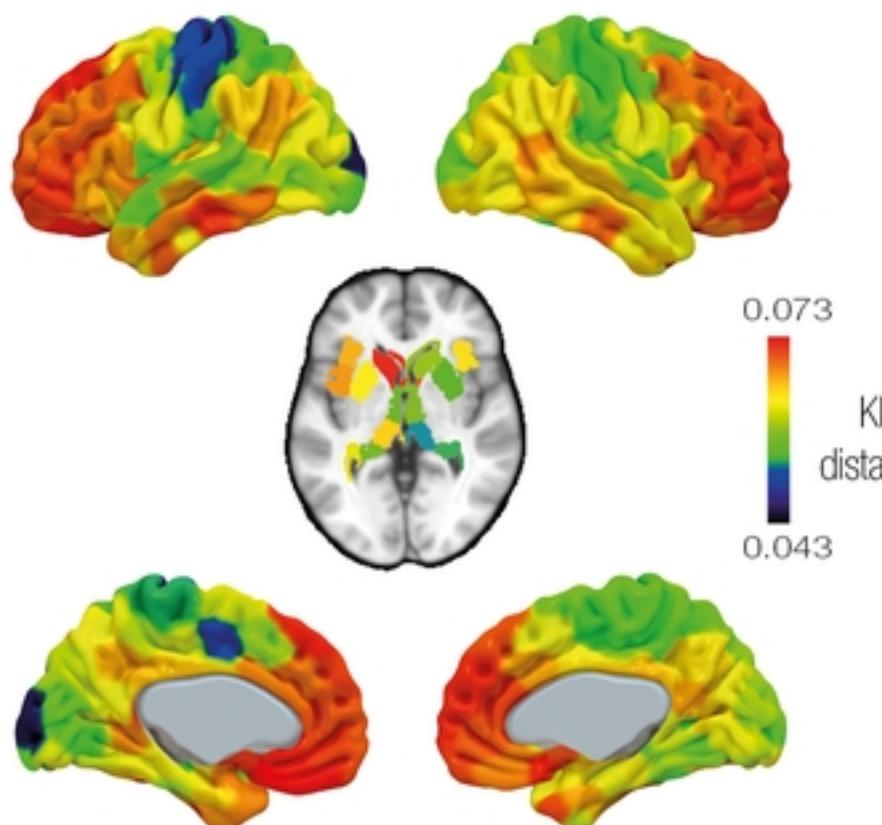
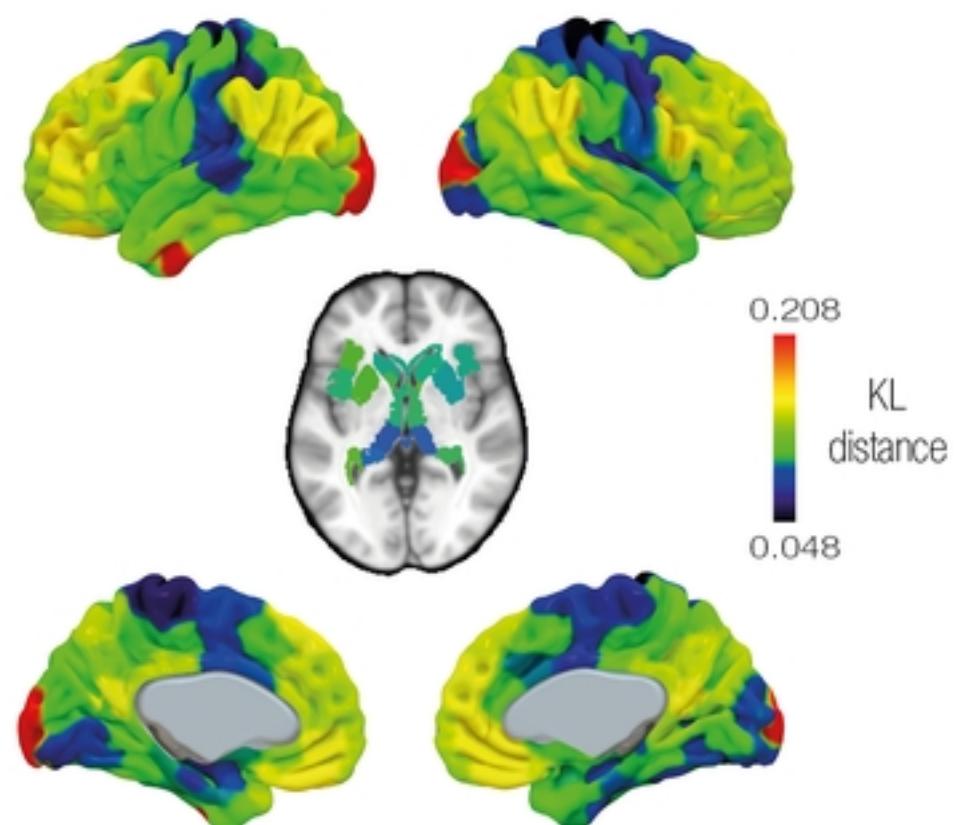


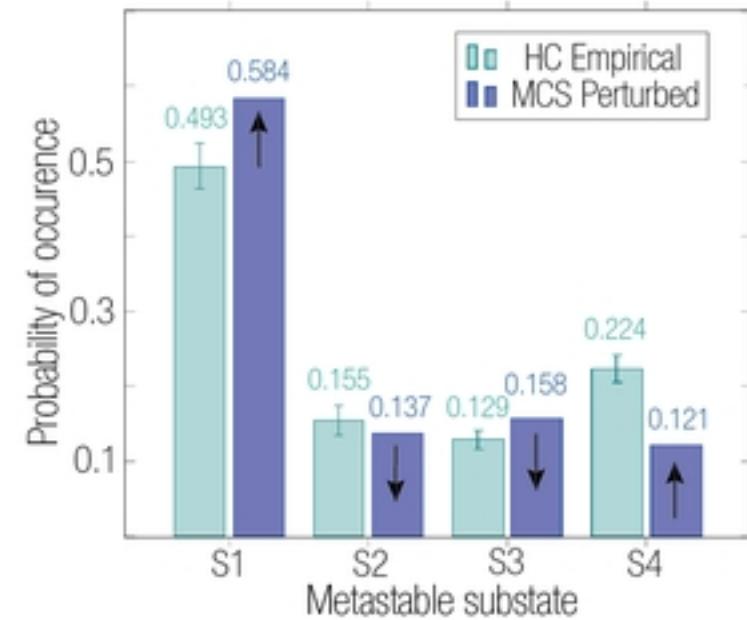
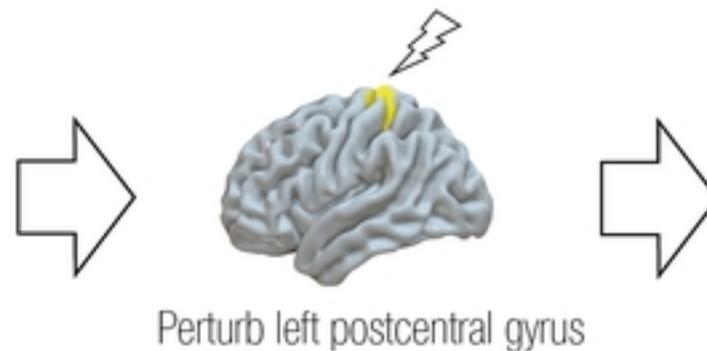
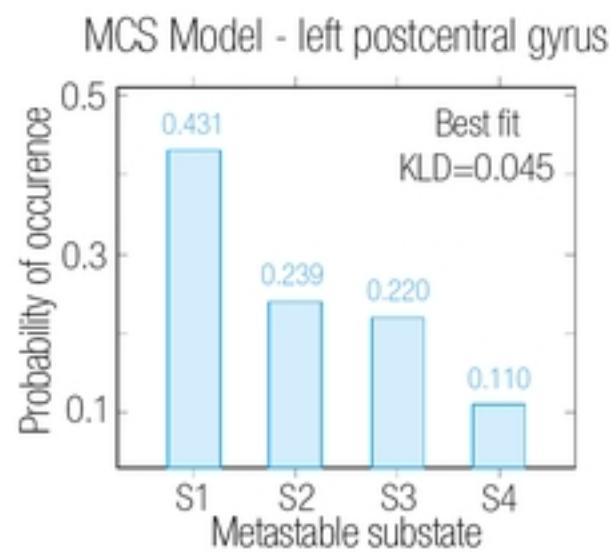
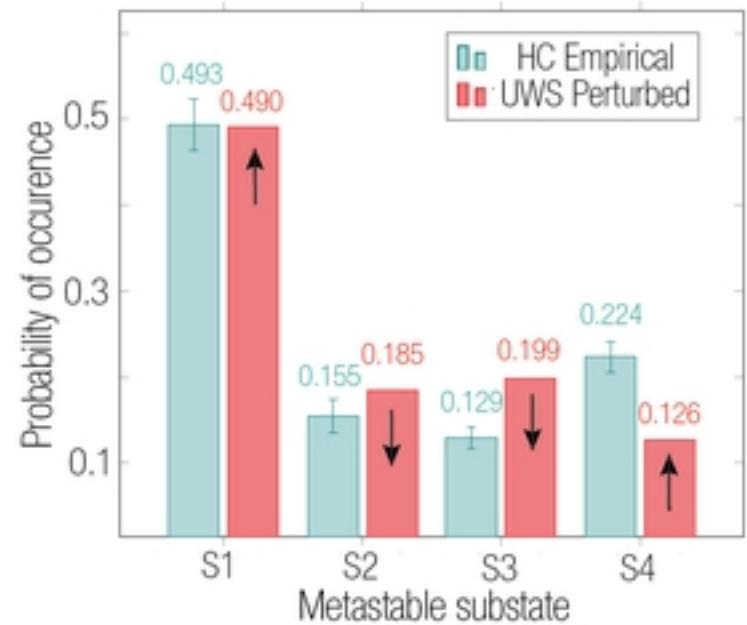
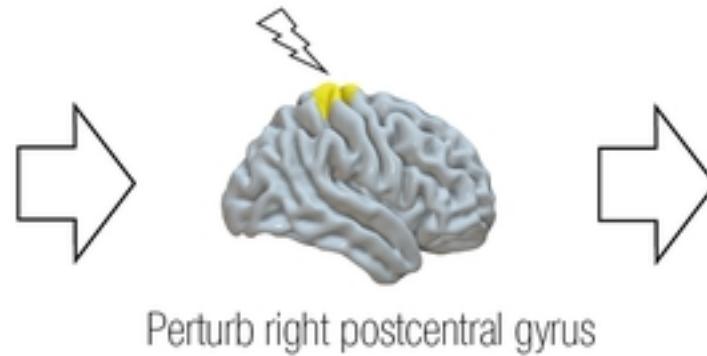
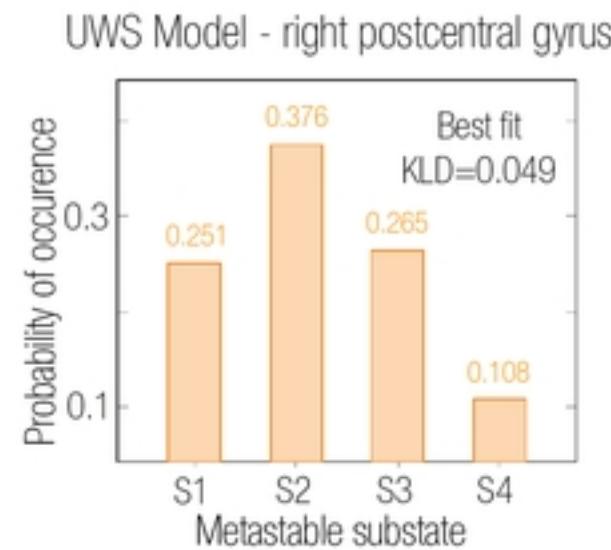
### b Model Fitting and Optimization

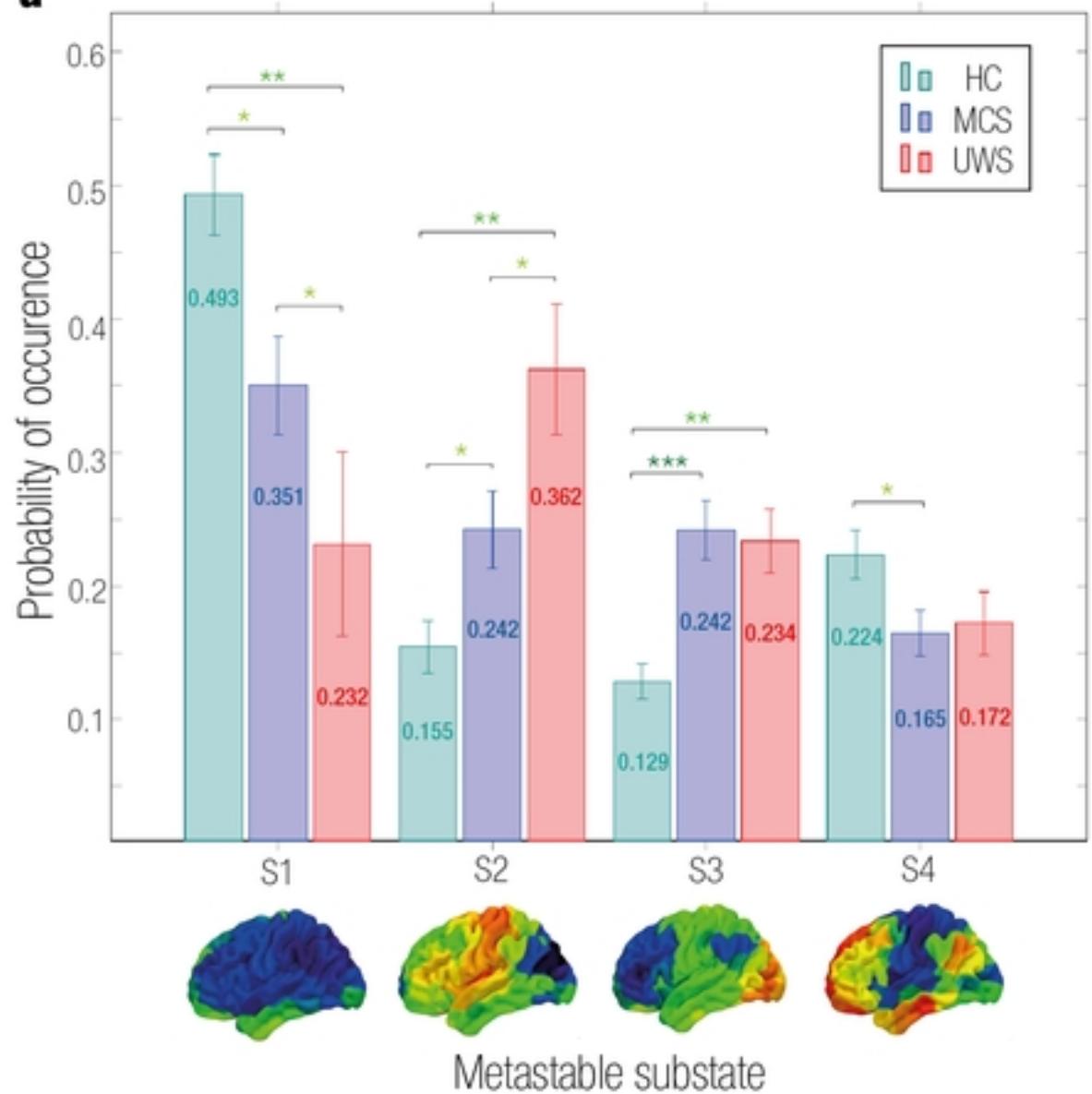
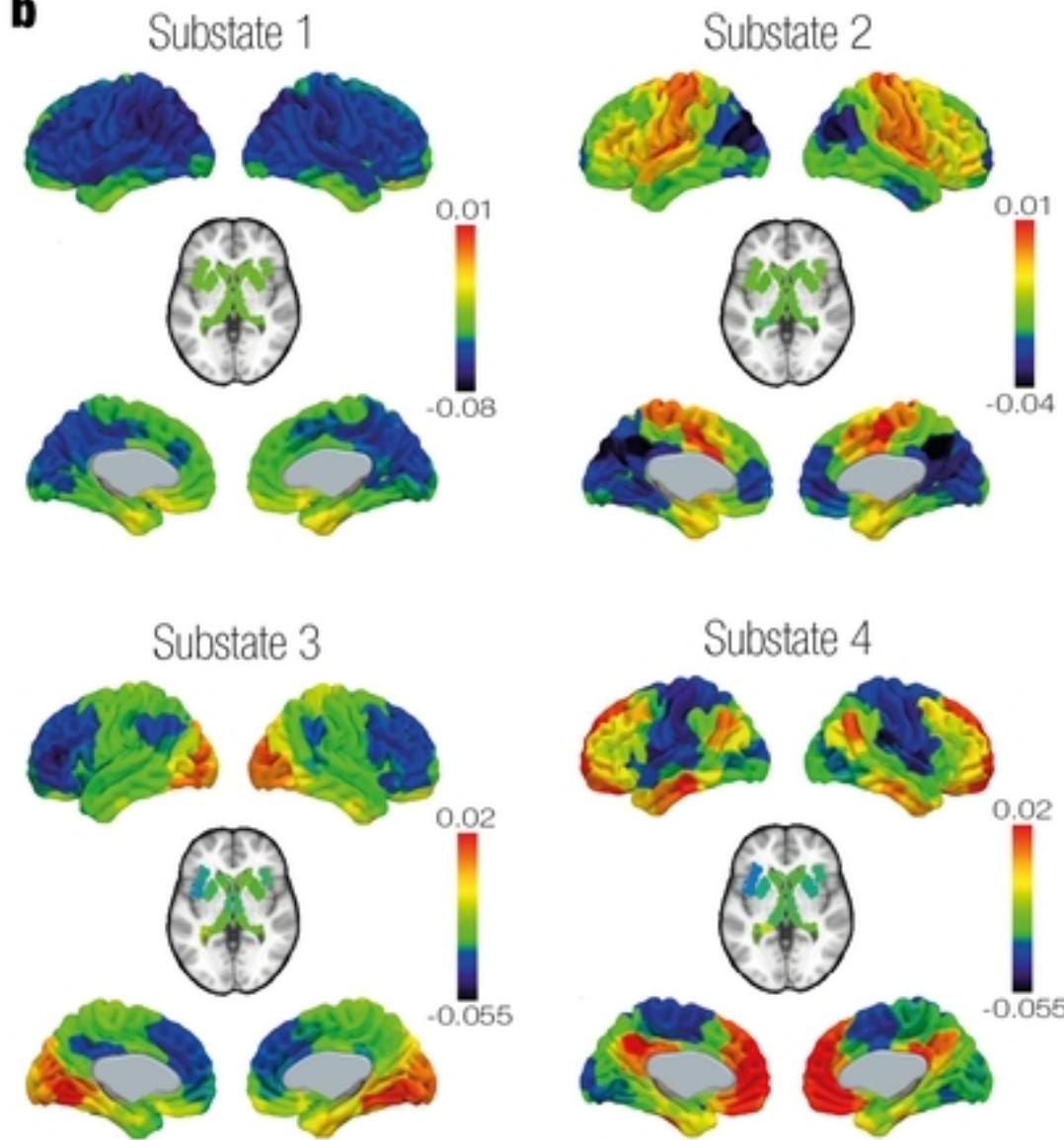


### c Stimulation in silico



**a****MCS Perturbation****Noise protocol**Bifurcation parameter  $a$ **Synchronization protocol****b****UWS Perturbation****Noise protocol**Bifurcation parameter  $a$ **Synchronization protocol****c****Optimal stimulation intensity of each brain area****MCS****UWS**

**a****b****Fig5**

**a****b****Fig2**

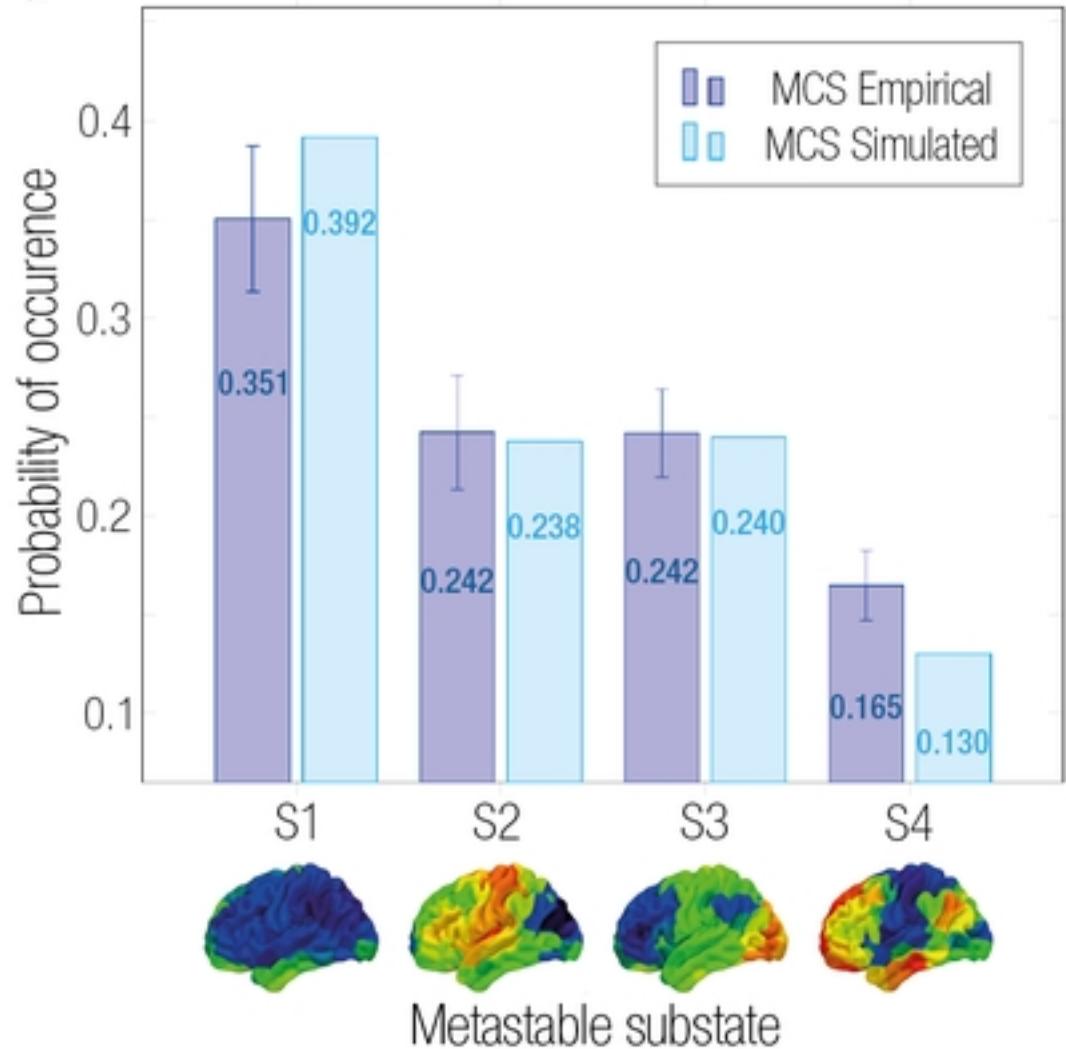
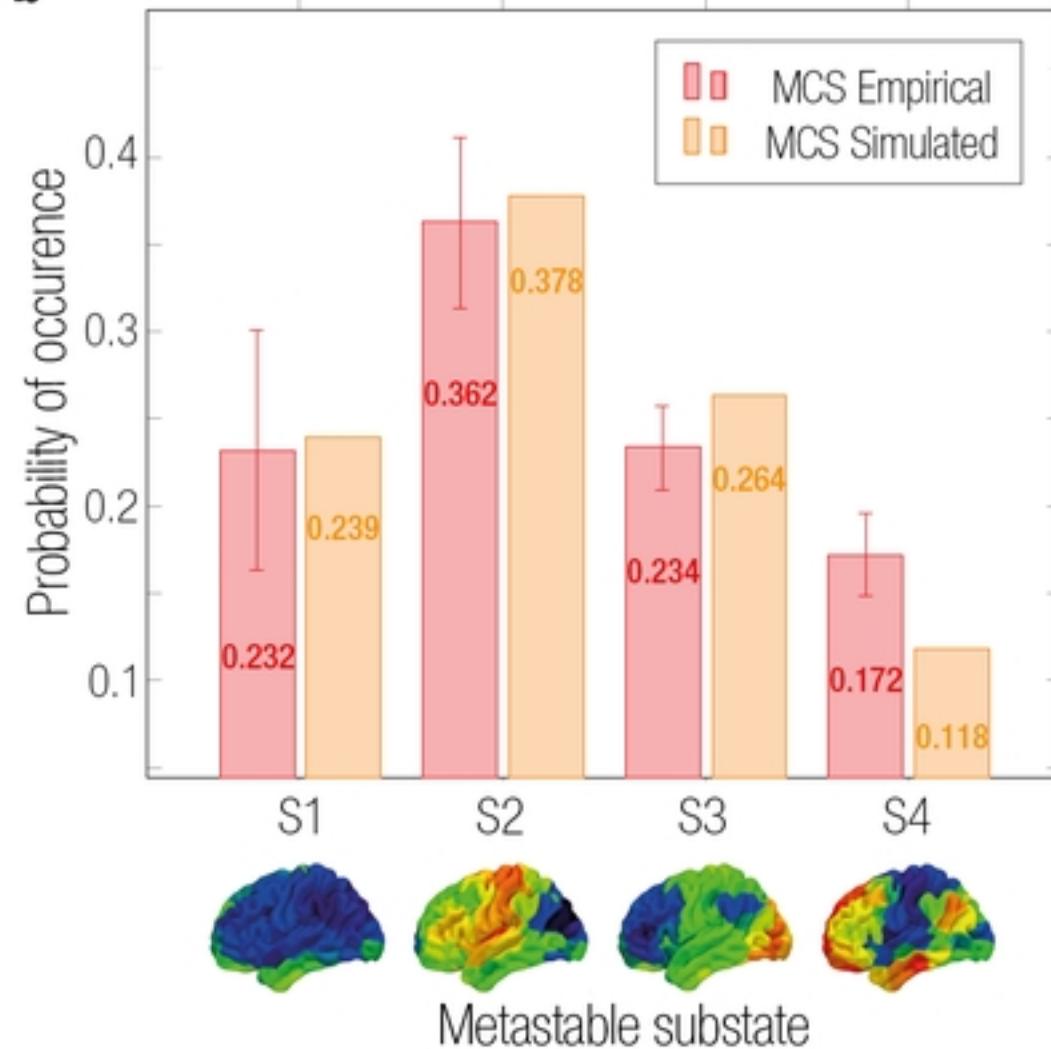
**a****b**

Fig3