Hierarchical model of human brain oscillations

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Abstract

Whole-brain computational modelling of emergent brain dynamics has become an increasingly important tool for understanding the systems-level mechanisms that govern large-scale brain activity in health and disease. Neuronal synchronization and brain criticality are key candidates of such mechanisms both for healthy cognitive functions and in constituting mechanistic biomarkers for several brain disorders. Despite significant advances, there is not an abundance of modeling approaches that yield both *in-vivo*-like critical synchronization dynamics and observables that directly match those obtainable with multi-modal neuroimaging. Here, we advance a framework for hierarchical Kuramoto models where the simplest two-layer model comprises a network of pairwise coupled nodes which each contain a large number of oscillators. Already at two levels of hierarchy, this enables explicit representation of local and inter-areal coupling and observations of emergent multi-scale synchronization dynamics. We show here that the model produces observables of meso- and macro-scale synchronization dynamics that are physiologically plausible when compared to, e.g., magneto- and electroencephalographic (M/EEG) data. We also present here a novel approach for fitting this model with individual experimental data that uses not only functional connectivity but also critical dynamics to converge model parameters that are personalized with individual M/EEG and structural-connectivity data. We posit that brain-dynamics matched personalized models yield a basis for 'digital twins' that may support both clinical applications and basic research on the systems-level mechanisms of cognitive functions. The model and model fitting approach advanced here support both new mechanistic understanding of experimental observations and derivation of predictions for future research.

Introduction

Healthy brain dynamics are characterised by moderate levels of long-range phase synchronization ***Pusil et al.*** (***2019a***), which is fundamental for neuronal communication in brain networks ***Fries*** (***2015***). Changes in the level and pattern of synchronisation are often associated with cognitive workloads such as perception ***Palva et al.*** (***2005***); ***Haque et al.*** (***2020***); ***Hirvonen and Palva*** (***2015***). Abnormal synchronization characterizes also neuropsychiatric diseases such as depression, where abnormalities in synchrony are correlated with the severity of depression symptoms ***Zhang et al.*** (***2016***); ***Kaiser et al.*** (***2015***), and neurological disorders such as epilepsy ***Wang et al.*** (***2023***) and Parkinson's disease ***Boon et al.*** (***2019***).

Neuronal oscillations exhibit considerable variability in characteristics such as frequency, power, or synchronisation, and the variability therein is associated with differences in cognitive performance ***Palva et al.*** (***2010***); ***Pusil et al.*** (***2019b***); ***Simola et al.*** (***2022***), learning ***Micou and O'Leary*** (***2023***) or physiological disorders such as epilepsy ***Wang et al.*** (***2023***). The framework of criticality applied to neural data provides an approach to understanding such variability, the "critical brain" hypothesis proposes that neural systems *in vivo* have an operating point at or near the critical transition between subcritical and supercritical phases in the system's state space. Such activity around the critical point gives rise to observable scale-free long-range temporal correlations and has several functional advantages: information capacity, dynamic range and transmission rate ***Shew and Plenz*** (***2012***); ***Zimmern*** (***2020***); ***Heiney et al.*** (***2021***). In this study we focused on critical-like synchronization dynamics as the biological phenomenon-of-interest.

A system's operating point in defined as its position of a system in control parameter space. Operating at a specific point gives rises to specific emergent dynamics which can be operationalized by specific observables such as phase synchronization and long-range temporal correlations (LRTCs). ***Fuscà et al.*** (***2023***). Despite progress in this area, the exact relationships between the operating point and these observables are not clear, and computational models can provide further insight.

In prior art, several approaches have been used to study phase synchrony dynamics, such as the Wilson-Cowan model, Neural Mass model, or Hopf model ***Cowan et al.*** (***2016***); ***David and Friston*** (***2003***); ***Cabral et al.*** (***2022***). There also exists a wide range of computational models in the field of criticality: simple branching process models ***Hobbs et al.*** (***2010***), statistical-physics inspired Ising models ***Nishimori and Ortiz*** (***2010***), and neurophysiology-based models ***Aburn et al.*** (***2012***).

The Kuramoto model is an example of an oscillator model and represents a self-synchronous system of several basic units - oscillators. The model explicitly simulated the synchronization dynamics and the transition between subcritical and critical states is characterised by a steep change from low local synchronisation to a perfectly synchronised oscillators. In the classical definition of the Kuramoto Model, its dynamics is controlled by a single parameter – a coupling strength between oscillators. The control parameter has a sigmoid-like functional relationship with phase-synchrony between oscillators which opens an easy gradient-descent-like way to fit the Kuramoto model to an experimental data ***Schirner et al.*** (***2023***).

At the same time, criticality emerges from the dynamic interactions between individual elements of a system, where the collective activity reaches a balanced state poised between order and disorder. In context of the critical synchronization dynamics, a true synchronization phase transition is not possible in homogeneous networks with low topological dimension ***Hong et al.*** (***2005***). However, critical dynamics may be observed in systems with lower topological dimension ***Ódor and Kelling*** (***2019***) and even with thousands of interacting elements ***Villegas et al.*** (***2014***). Additionally, in prior studies, the activity of a brain zone or a neuronal population was represented by a single oscillator, making it impossible to apply a criticality framework to its activity and essentially leaving out all the local observables of neural dynamics. Therefore, a model that aims to reproduce the full width of aspects of critical-like behaviour should contain a large number of units with non-linear interactions and heterogeneous structure.

Oscillatory models have been shown to be valuable in studying the computational architecture. However, for clinical applications and for localizing the mechanisms of cognitive functions, models should be personalized. Some studies have tried to create models with biologically realistic synchronization dynamic and derived parameters from a-priori-known human data, such as the adjacency weight matrix between Kuramoto model nodes ***Schmidt et al.*** (***2015***), connectivity structure ***Ódor and Kelling*** (***2019***) or interaction delays estimated from the tract lengths ***Ziaeemehr and Valizadeh*** (***2021***) using the human structural connectome. However, the observed brain recordings are derivatives of underlying parameters and the exact relations between them in each subject are unknown and thus it is not possible to make personalized models without fitting - an inverse process that tunes parameters for better agreement between model and real data.

Typically, oscillatory models are fitted to a functional connectome derived from fMRI time-series such as cross-correlation of BOLD signals ***Deco et al.*** (***2013***); ***Wang et al.*** (***2019***); ***Schirner et al.*** (***2023***) while only a few works on MEG/EEG source signals ***Heggli et al.*** (***2019***); ***Castaldo et al.*** (***2023***) and phase synchrony profiles in particular ***Williams et al.*** (***2023***). Model fitting can be done from different angles, and the process of Bayesian optimization has shown a promise in recent studies ***Hashemi et al.*** (***2020***); ***Lintusaari et al.*** (***2016***); ***Gutmann et al.*** (***2016***), particularly using Dynamic Causal Modeling (DCM, ***Wang et al.*** (***2019***)). In other studies, an evolutionary algorithm was used to investigate the influence of excitation-inhibition balance on neuronal dynamics ***Avramiea et al.*** (***2022***). These approaches are universal and can be used applied to almost any modelling scheme, but adapting these to whole brain modeling is not trivial due to a huge number of learnable parameters which make the optimization convergence impossible or impractically slow.

Another way of fitting a model is to rely on a-priori knowledge about the relations between a model parameters and observables.

In the Kuramoto-based model in particular, the fitting process relies on the observation that phase synchrony generally increases monotonically as a function of a control parameter, often represented by an edge weight between two nodes, and the gradient for parameters can be computed as a difference between an actual and predicted values.

In contrast, fitting to criticality properties poses a more challenging task and has been done only using an evolutionary method in application to LRTCs in spiking models ***Avramiea et al.*** (***2022***). To the best of our knowledge, no existing work has explored how to perform this fitting process for oscillations, particularly the co-fitting of criticality and the functional connectome, although, both theoretical and in-vivo evidence show they are intertwined ***Fuscà et al.*** (***2023***).

Considering these limitations, development of truly personalized oscillatory models requires solving two problems. The first is to create a model that yields signals that are sufficiently similar to real data, allowing for direct comparison between simulated and real brain recordings. This includes also the notion that the model ideally produces the targeted phenomena (synchronization dynamics in the present context) with a minimal amount of parameters and model details. The second is to develop an algorithm that fits a model to multiple observables of brain dynamics, including both the functional connectome and properties of long-range temporal correlations.

To overcome the first limitation, we developed a hierarchical extension of the classical Kuramoto model with two levels of hierarchy. On the first level, basic functional units – oscillators – are grouped into a single node, on the second level those nodes are organized into a network. Following this architecture, the dynamics of a single oscillator has three parts: the natural dynamics or the oscillation frequency, internal dynamics dictated by phase difference between oscillators in the same same node and external dynamics based on the phase difference with other nodes.

The hierarchical architecture has several advantages: each model node can be directly mapped to a brain zone one-by-one thus makes it simple to compare it to a real data. It also increases the heterogeneity in the model and gives rise to the extended critical regime even on node level. From the computational side it encapsulates individual oscillator interactions inside each node and allows to improve performance.

To address the second issue, we expanded on the concept of gradient descent. As demonstrated in previous research, the difference between actual and predicted phase synchronization can be used as a gradient to adjust inter-nodal coupling strength ***Schirner et al.*** (***2023***). To address this issue, we also consider critical characteristics of a model, as are estimated via Long Range Temporal Correlations (LRTCs) and operationalized by the Detrended Functional Analysis (DFA, ***Linkenkaer-Hansen et al.*** (***2001***)). The criticality peaks in systems undergoing phase transitions and the peak point could be stretched in an extended Griffiths phase. Thus, the DFA function can be approximated with a quadratic function, although it can be optimized as a function of the local control parameter.

We demonstrate that by combining these two approaches, the model can simulate an oscillatory signal that exhibits a phase transition between order and disorder and we show the emergence of Long Range Temporal Correlations (LRTCs) in the model during this transition and the extended Griffiths Phase regime. We compared the simulated timeseries with real data and demonstrated that the models from the subcritical slope of the Griffiths Phase yield the most physiologically plausible and similar to the MEG-derived observables. Finally, we show that model fitting algorithm can learn both critical and synchrony properties simultaneously, successfully restores artificially generated phenotypes with known parameters and a fitted model can reproduce critical and phase synchrony profiles of real brain neuronal dynamics.

Results

Whole-brain model of critical oscillations

Oscillations, i.e. rhythmic excitability fluctuations which occur in the brain across a wide frequency range, are a fundamental element of neural brain dynamics arising from the complex interaction of within neuronal populations ***Buzsáki et al.*** (***2012***) and can be measured with electroencephalography (EEG), stereoelectroencephalography (SEEG) and magnetoencephalography (MEG) (Figure 1A, ***Brookes et al.*** (***2011***)). Typically, the original sensor-level recordings are collapsed into a cortical parcellation, the parcellation time series are then filtered to obtain a narrow-band analytical time series (See Figure 1B), from which then observables such as power spectrum (See Figure 1C) or amplitude correlation (See Figure 1D,F) or phase synchrony (See Figure 1E,G) are estimated.

The local field potentials are generated by collective activity of multiple neuronal cells ***Buzsáki et al.*** (***2012***) and oscillations emerge

from time-aligned – rhythmical – neuronal activity which may be approximated using periodic functions. Analogous to a cortical area containing many small sub-populations of neurons, a single model node contains many Kuramoto oscillators ***Kuramoto*** (***1975***); ***Siebenhühner et al.*** (***2020a***), which are uniformly directionally coupled within a node weighted by local control parameter (K , See Figure 1H). Similar to amplitude, which operationalizes local firing rates within a population, we operationalize node order as an average complex value across oscillators, resulting in an complex time series with high absolute value when oscillators are synchronized and low when their phases are distributed across the unit circle (See Figure 1H).

On the next level of hierarchy, model nodes, the coupling is based on directional phase-difference weighted by node order and a structural edge weight between two nodes (See Figure 1I, see Methods for details). This approach encapsulates interaction between different levels of hierarchy, induces an additional level of heterogeneity in the model, and allows to reduce computational costs. It also gives a rise to naturalistically-looking model time series with observables such as amplitude and phase that are easily comparable to narrow band real data (See Figure 1 I) as well as uni- and bivariate statistics such as Power Spectrum (See Figure 1 J), Amplitude Correlation (See Figure 1 K,M) and Phase Synchrony (See Figure 1 L,N).

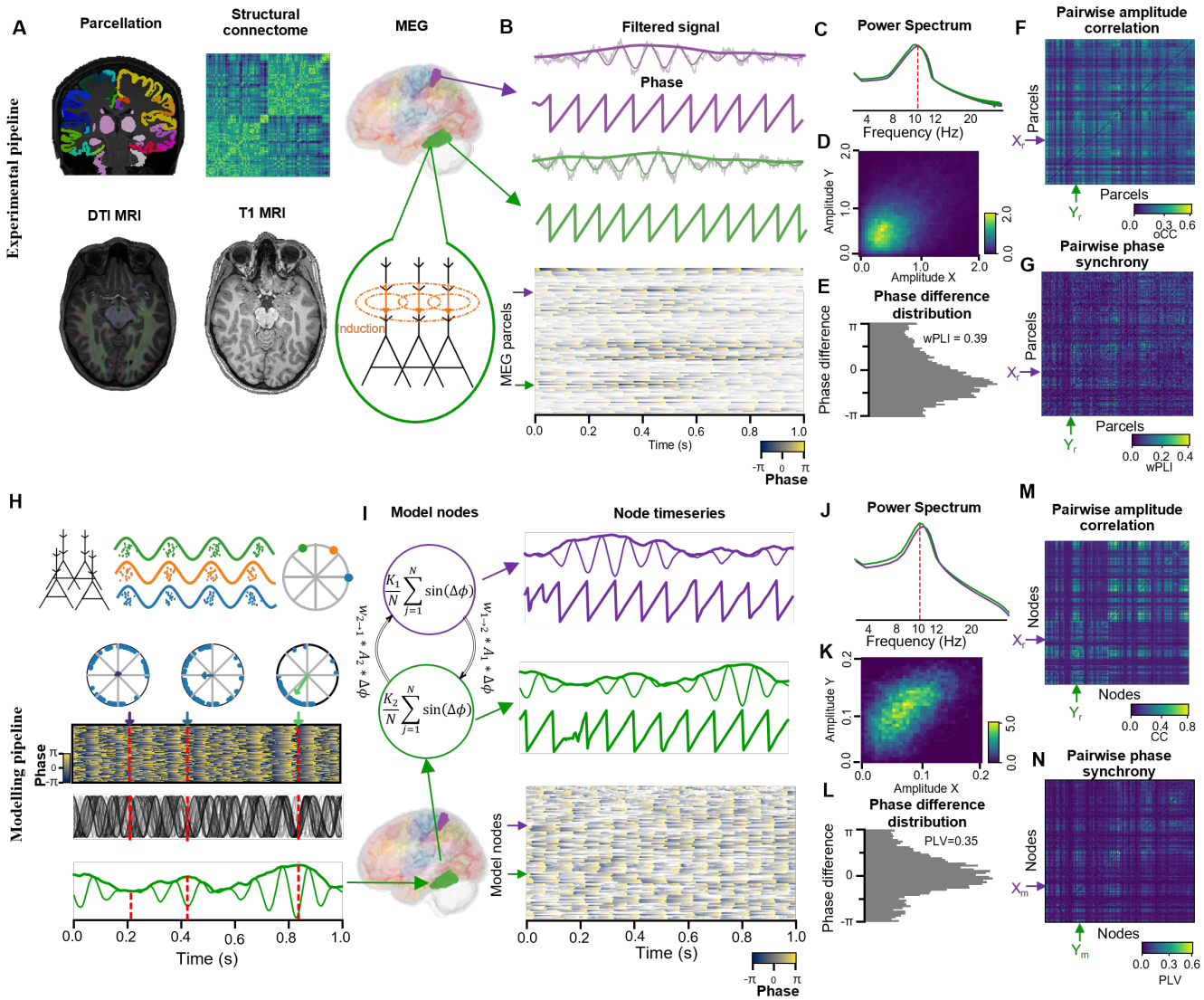

Figure 1. General representation of an experimental pipeline. **A** Examples of the imaging methods (T1 MRI, DWI MRI, MEG) and their derivatives (MRI-based parcellation, structural connectome based on DTI) used in this study. **B** Broadband MEG time series from two parcels (gray) overlaid with the real part of the narrow-band filtered data and its phase. On the bottom, the heatmap of channel phases where samples with low amplitude are transparent. **C** Power Spectrum for two parcels in MEG data. **D** 2D histogram for amplitude of two narrow band MEG signals. **F** Pairwise amplitude correlation heatmap of MEG narrow-band data. **E** Distribution of phase differences for a pair of narrow band MEG signal. **G** Pairwise wPLI of single-subject MEG recording at alpha frequency (10Hz). **Modelling pipeline**. **H** The spiking process of a neuronal population could be approximated using a periodic function in complex space or oscillator. Hundreds of interacting oscillators represent a single model node and their phases are averaged on each time point to obtain a timeseries of a node timeseries. **I** Two-node model scheme with equations for coupling within a node and between them. **J** Power Spectrum obtained from the real part of a simulated timeseries. **K** 2D histogram for amplitude of two simulated timeseries. **M** Pairwise amplitude correlation heatmap of simulated data. **L** Distribution of phase difference for two simulated signals. **N** Pairwise PLV matrix of a simulated timeseries

Local and global control parameters shape the criticality landscape of the model dynamics

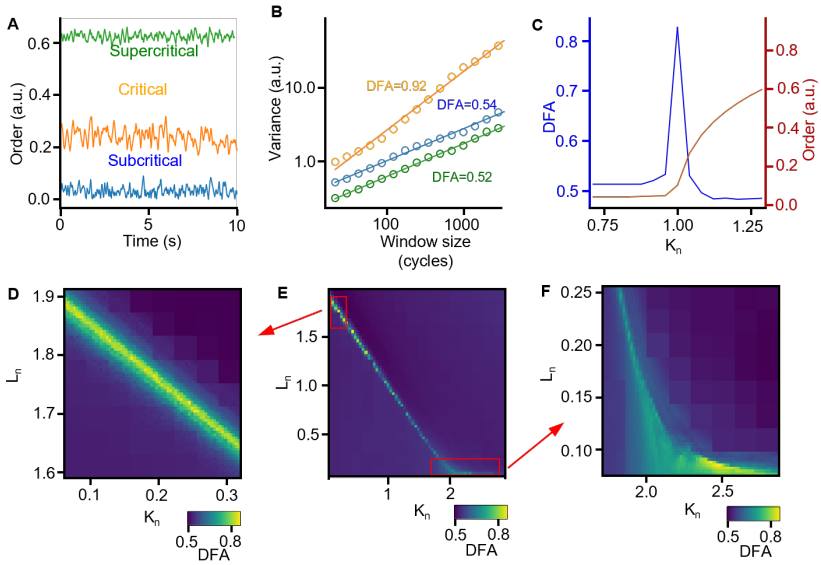

Figure 2. The critical landspace as a function of local and global control parameters. **A** Example simulated time series for the subcritical, critical and supercritical model dynamics. **B** Variance as a function of window size for the example time series shown in **A** and their Detrended Functional Analysis (DFA) fits. **C** An average model DFA and order as a function of a local control parameter normalized by the K with the maximum DFA. **D, E, F** DFA as a function of both local and global control parameters for the region with $K_n \ll L_n$ (**D**), K ~ L (**E**), $K_n \gg L_n$ (**F**).

Brain activity exhibits a $\frac{1}{f}$-like power spectrum and spatiotemporally scale-free dynamics, which have been attributed to brain-criticality. According to the 'critical brain' hypothesis, neuronal systems in vivo operate at the critical transition between subcritical and supercritical states in the system's state space (Figure 2A). In oscillatory network models criticality occurs between desynchronization and complete synchronization on both nodal and inter-node level, operationalized with node order and inter-node phase synchronization, respectively. This critical regime is characterized by Long Range Temporal Correlations (LRTCs).

However, in previous research, oscillatory models of brain activity assigned a single oscillatory unit to an anatomical region, thus they were unable to reproduce critical dynamics of individual brain zone because the order remained constant across time. In our hierarchical Kuramoto model, each node may have thousands of oscillators whose phases are averaged to obtain node time series. Due to differences in natural frequencies of oscillations the node timeseries vary in time and long-range temporal correlations can be measured with detrended fluctuation analysis (DFA, See Figure 2B). We found that this approach makes it possible to capture the critical transition between disorder and complete synchrony and this transition is characterized by a peak in the DFA scaling exponent, indexing high criticality (See Figure 2C).

To assess how model parameters affect the criticality properties of the model, we varied both local and global control parameters, simulated a 5-minutes long time-series for each pair of parameters and computed the DFA exponent. For visualization purposes, to negate the effect of other simulation arguments such as amount of noise or the scaling of control parameters, we selected a K & L pair which were as close as possible, located on the critical ridge and divided the actual the actual values on it to obtain a normalized local (K_n) and global (L_n) coupling weights.

Varying both local and global control parameters, we found that the critical landscape is divided into subcritical and supercritical parts by a critical ridge which has linear shape when K is much lower than L (See Figure 2D) or close to L (See Figure 2E). In contrast, the critical surface becomes non-linear when global connectivity is low while local is high (See Figure 2F), which can be attributed to the decomposition of the whole system into several almost independent nodes.

Correlation between model parameters and observables is modulated by critical properties

In critical-like systems with a second order phase transition, the order as a function of the control parameter follows an S-like shape and the critical observables peak in the phase transition region known as the Griffiths phase. Previous studies have shown that DFA has a negative quadratic correlation with phase synchrony in the critical region and a linear correlation otherwise ***Fuscà et al.***

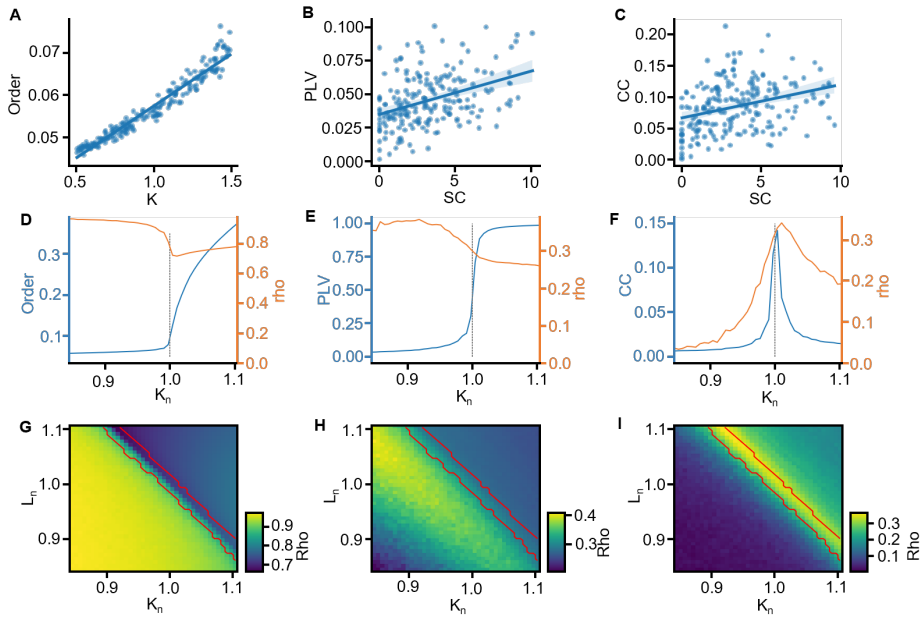

Figure 3. The Griffths phase as a breakpoint for linear correlations in the model. **A, B, C** Examples of model Order , PLV and Order Cross-Correlation as a function of local control parameter (K) and Structural Connectivity (SC). **D,E,F** Pearson Correlation Coefficient between model Order and K, PLV and SC, CC and K as a function of normalized local control parameter (Kn). **G,H,I** The same correlations between model Order and K, PLV and SC, CC and K as a function of both Kn and normalized global control parameter (Ln). The red lines indicate the critical ridge location estimated from the average CC value across nodes (Supplementary Figure 1).).

(***2023***). However, the relationships between the underlying model parameters and the model results are not clear.

To assess the relationships between the model's control parameters and its observables, we sampled K values for each node and L for each edge from the uniform distribution with minimum 0.5 and maximum 1.5, multiplied them by varying the coefficient, calculated the order, the phase locking value (PLV) and the cross-correlation (CC) between the time series envelopes, and assessed the relationships between order and local K (Figure 3A), PLV, CC and local L (See Figure 3B, C) using the Pearson correlation coefficient.

Initially we found that all observables have a non-negative correlation with the control parameters, but the shape of these correlations is different. The order has the highest correlation with K in the subcritical region (Pearson coefficient $\sim 0.9, K_n < 1.0$), decreases in the critical region (Pearson coefficient $\sim 0.6, K_n \sim 1.0$) and starts to increase in the supercritical region, but is still lower compared to the subcritical region (Pearson coefficient $\sim 0.7 - 0.8, K_n > 1.0$) (See Figure 3D).

The correlation of the phase synchrony with the control parameters has a similar behaviour to the order, with maximum values in the subcritical zone (Pearson coefficient $\sim 0.4, K_n < 1.0$), which decreases around the critical zone (Pearson coefficient $\sim 0.25, K_n \sim 1.0$), but then continues to decrease and reaches the minimum values at the end of the K_n range (See Figure 3E).

On the other hand, the correlation between CC and control parameters has a completely different shape from that of order and PLV: it is almost non-existent for the lower part of the subcritical region (Pearson coefficient $\sim 0.0, K_n < 0.9$), starts to increase approaching the critical region (Pearson coefficient $\sim 0.1, 0.9 < K_n < 1.0$), peaks at criticality (Pearson coefficient $\sim 0.3, K_n \sim 1.0$) and begins to slowly decrease in the subcritical region, but remains higher than in the subcritical region (Pearson coefficient $\sim 0.2, K_n > 1.0$, See Figure 3F).

Spectral properties of oscillatory activity are defined by distribution of underlying frequencies

Traditionally, oscillations are operationalized by their magnitude and studied through power spectral techniques, wherein a spectral peak above the "$\frac{1}{f}$" aperiodic component serves as the definitive benchmark indicating the existence of oscillations ***Buzsáki et al.*** (***2012***). In human MEG - EEG recordings power spectrum typically has a peak in alpha (7–14Hz) or beta (14–30Hz) frequencies ***Buzsáki*** (***2006***) and the shape of the power spectrum depends from various factors such as cell firing rate ***Manning et al.*** (***2009***), stimuli representation ***Mazzoni et al.*** (***2008***), cognitive state ***Haegens et al.*** (***2014***) or mental disorders ***Ippolito et al.*** (***2022***). Therefore,

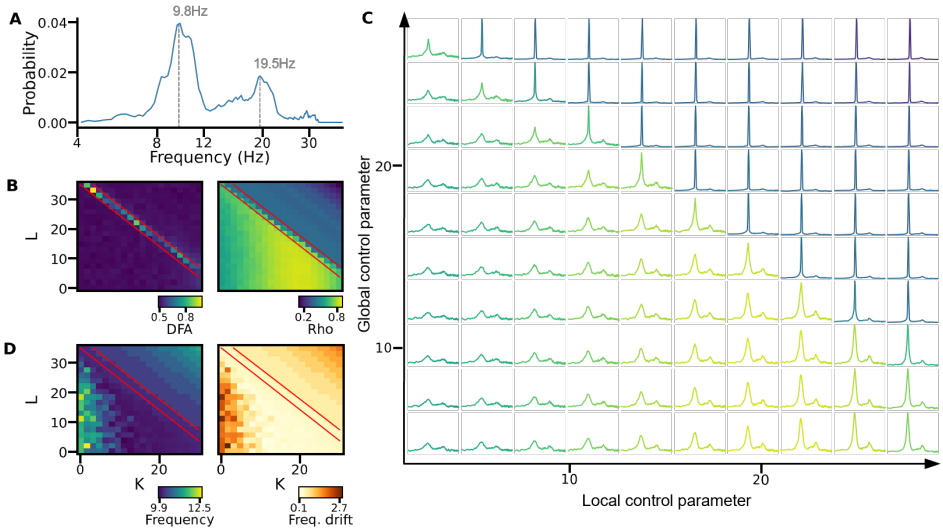

Figure 4. Oscillator frequencies shape the power spectrum. A distribution of oscillator frequencies obtained from individual power spectral density of a real MEG recording with subtracted $\frac{1}{f}$ component. **B** Average detrended fluctuation analysis (DFA) exponent across model nodes (left) and Pearson correlation coefficient between PSD of a real and simulated timeseries (right) as a function of global (L) and local (K) control parameters. The red lines indicate a criticality ridge estimated with DFA exponent ≥ 0.65. **C** PSD of simulated timeseries for different combinations of local and global control parameters colored by their correlation with the PSD of the real data as shown in **B**. **D** A frequency peak derived from power spectrum of simulated timeseries (left) and difference with the peak location in the distribution of oscillator frequencies (right).

plausibly-looking power spectrum is an important aspect of any oscillatory model.

In order to replicate the individual power spectral properties of a subject in a model, we initialized the distribution of oscillator frequencies to match the shape of power spectrum of a recording. To achieve this, we first computed the power spectrum density (PSD) of the MEG recording and transformed it into a frequency probability distribution of oscillator frequencies by subtracting the $\frac{1}{f}$ component and dividing the flat spectra by its cumulative sum (Figure 4A). The local coupling strength was set to the constant value across nodes and the inter-edge weights were sampled from a uniform distribution and divided on the mean value to preserve the mean value of one.

To assess the similarity between real and simulated data, we varied the local (K) and global (L) control parameters, ran a 360-seconds long simulation, cut-off the first 60 seconds to remove the warm-up periods, computed PSD of the simulated data using the Welch method and the Pearson correlation coefficient between the real-data and model power spectrums. We found that the maximum similarity was found in the subcritical slope of the extended critical zone with high local control parameter and low global (See Figure 4B).

The transition from subcritical to critical regime is characterized by emergence of oscillatory peaks which are almost absent for K and L around zero but growing towards the critical ridge and the alpha peak becomes dominant in the critical zone (See Figure 4C). Interestingly, the critical zone and the subcritical regime with high global control parameter (L) exhibits a small drift of the alpha frequency peaks towards the weighted mean (12.85Hz) of alpha (9.8Hz) and beta (19.5Hz) frequency peaks (See Figure 4D), while the high correlation between the simulated and observed power spectrums could be explained by alignment of such peaks.

Brain dynamics is the most correlated with activity in subcritical region

The characterisation of the human brain as a critical oscillatory system is not limited to the power spectrum. Power does not directly measure the construct of rhythmicity, and the phase autocorrelation function (pACF), which measures phase stability, can be used to quantify oscillatory spectra ***Myrov et al.*** (***2024***). Next, as a system with multiple interacting units - nodes - their functional relationship can be quantified by phase synchronisation ***Lachaux et al.*** (***1999***) and moderate levels of phase synchronisation are a signature of healthy brain activity ***Palva et al.*** (***2005***). As a hallmark observable of brain criticality, neural oscillations exhibit scale-free long-range temporal correlations ***Palva et al.*** (***2013***), which are strongest at the critical point and can be operationalised with Detrended Functional Analysis (DFA) ***Linkenkaer-Hansen et al.*** (***2001***).

To assess the similarity of observables of neural dynamics between the real MEG recordings and the simulated data, we initialised

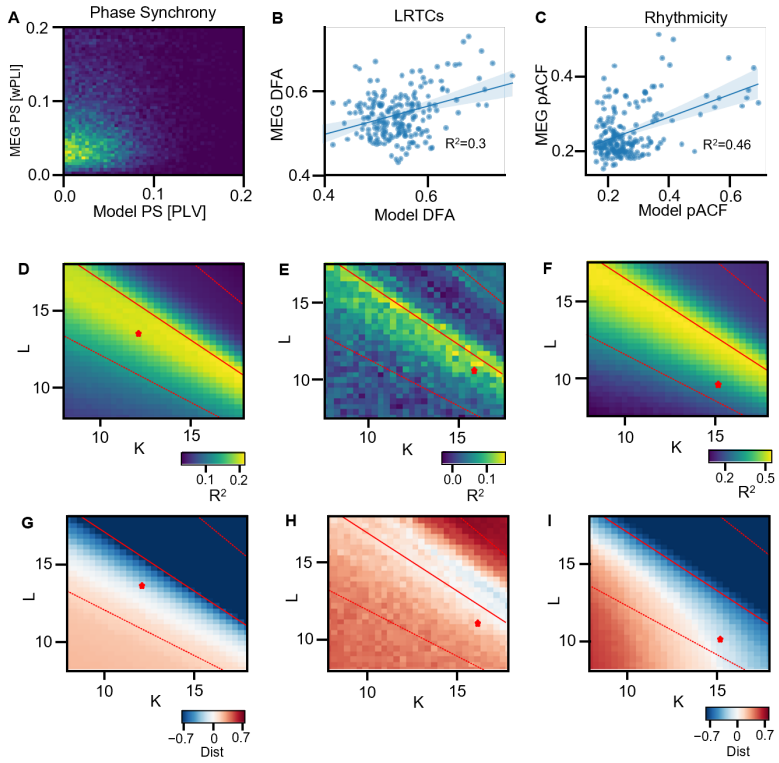

Figure 5. The model observables on the subcritical slope of the Griffiths Phase are the most similar to those found in MEG recordings. A, B, C The primary observables of oscillatory activity compared between real and model timeseries: Phase Synchrony (PS) operationalized with wPLI for MEG data and PLV for the model (**A**), LRTCs operationalized with DFA (**B**), and rhythmicity measured with pACF (**C**). **D, E, F** An average pearson correlation coefficient between the real and simulated PS (**D**), DFA (**E**), and pACF (**F**). **G,H,I** Kolmogorov-Smirnov distance measured between distributions of the real and simulated PS (**G**), DFA (**H**) and rhythmicity (**I**). Positive distance means that the real data observables tend to be higher than in the model and negative means that the model overshoots the physiological values. The red dots indicate location of the model observables and parameters used in **A,B,C**. Solid red lines indicate the median critical ridge, dashed lines indicate 5th and 95th percentiles estimated from an individual node-level positions (Supplementary Figure 2.A).

inter-node weights with a personalised mean-normed structural connectome and simulated time series with varying local and global control parameters. Then, to account for filter-induced artefacts, we filtered the real part of the simulated signal using the Morlet wavelet transform for 41 log-spaced frequencies (from 2 to 99 Hz, number of cycles = 5).

Next, we computed model phase synchrony (PS) using PLV and wPLI in the MEG data (Figure 5A), criticality level using DFA (See Figure 5B), rhythmicity using pACF (See Figure 5C). To assess linear relationships between model simulations and real data, we used Pearson's correlation coefficient between observations from model nodes/edges and MEG parcels belonging to the same anatomical zone. The Kolmogorov-Smirnov test statistic was calculated to test whether the distributions of the values were similar. To account for variability in the location of the critical ridge, we estimated confidence intervals of its position by pooling its slopes and intercepts across all nodes, and calculated the median, 5th, and 95th percentiles and used them as lower and upper bounds.

We found that the anatomical profiles of phase synchronisation are most similar in the subcritical zone, both in terms of correlation and distribution distances (See Figure 5D), and its magnitude in the subcritical zone overshoots, while its magnitude in the critical zone overshoots the values observed in the real data (See Figure 5G). In addition, simulations with the most optimal Kolmogorov-Smirnov statistic (See Figure 5D) belong to a less critical region in contrast to the most optimal correlation.

DFA anatomy is best reconstructed following the critical ridge (See Figure 5E), and values in both subcritical and critical zones are lower than those observed in the MEG recordings (See Figure 5H), which supports the notion that the human brain operates primarily in a subcritical-critical zone. The rhythmicity properties follow a pattern similar to phase synchrony, with the highest correlation observed in a region just below the critical ridge (See Figure 5F), and the distributions of values are closest to those

observed in the less critical region (See Figure 5I). Interestingly, the ridge with the lowest Kolmogorov-Smirnov distance for pACF is not linear as for PS and DFA but rather has a curve-like shape that decreases as the local control parameter K increases (See Figure 5I).

Fitting to predefined phenotypes

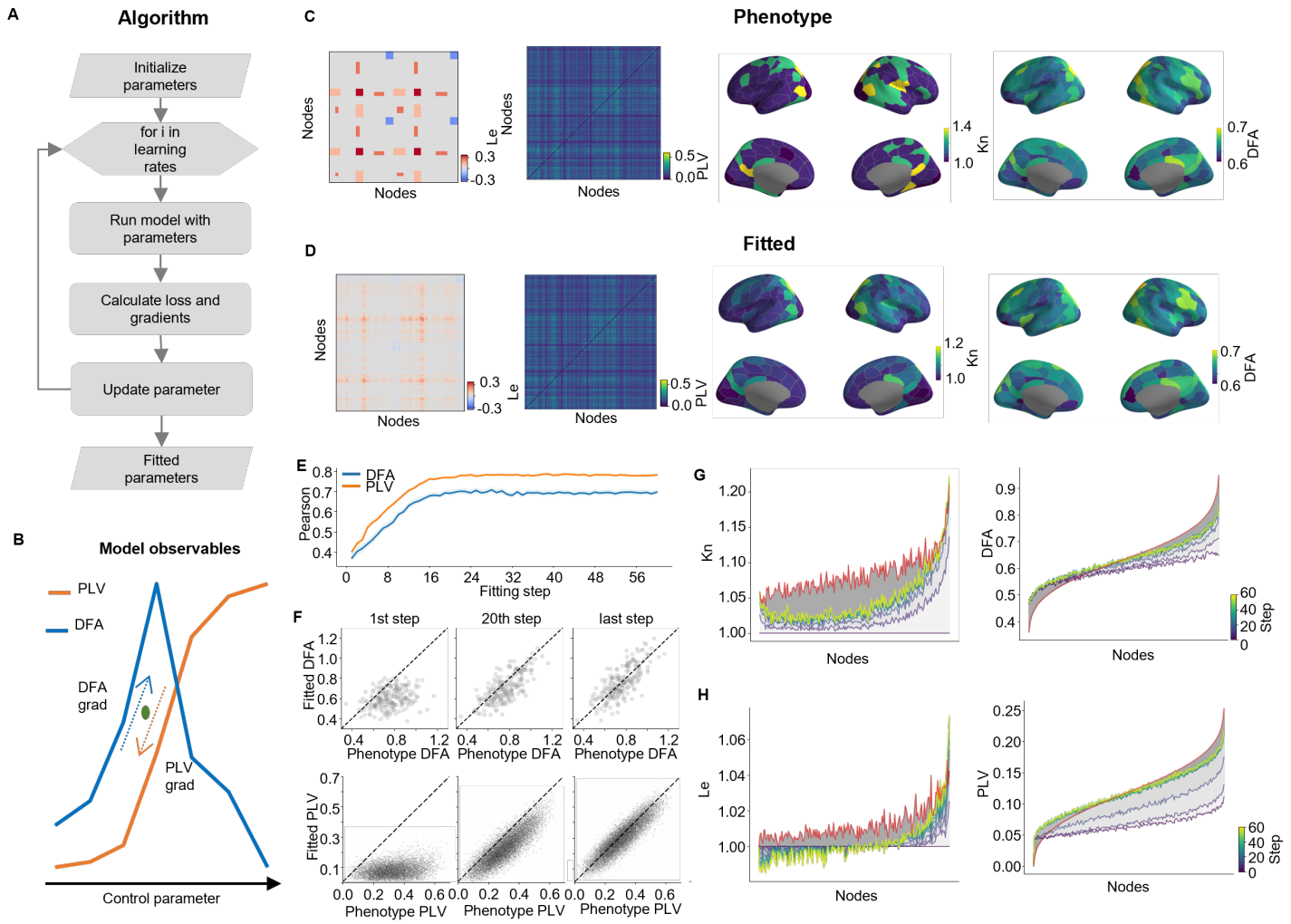

Figure 6. Fitting a model to predefined phenotypes. A A flowchart of the fitting algorithm. **B**. The concept of the gradient direction as a function of a control parameter. **C**. An artificial phenotype created by multiplying edge weights and local control parameters on a multiplier alongside with functional connectome matrix and DFA topography of a phenotype. **D**. Learned parameters of a model fitted to a predefined phenotype and its Functional Connectome and topography of the best-fit model. **E**. Pearson correlation coefficient between a phenotype and a model observables as a function of a fitting step. **F**. Scatterplots of a phenotype and a fitted model observables for different fitting steps. **G**. Learned coefficients for the local control parameter (left) and DFA (right) as a function of the fitting step. **H**. Learned coefficients for the edge weights (left) and PLV (right) as a function of the fitting step.

Although the model with data-driven distribution of inter-node weights was able to reproduce physiologically plausible behaviour, the correlation with individual observables remained quite low, especially for critical properties such as DFA. This can be attributed to the fact that the model behaviour is strongly dictated by its parameters (See Figure 3G-I), such as inter-node weights, while in the real data the correlation between structural and functional connectome remains low (CITE!). This leads to the need for digital twins - personalised models of brain activity designed to reproduce an individual's brain dynamics.

In previous work, models have been fitted to a functional connectome by shifting the weight between nodes according to the difference gradient between an actual and modelled connectome ***Deco et al.*** (***2013***). This approach allows for the accurate reproduction of individual phase synchronisation profiles, but to date there have been no studies of simultaneous fitting to phase

synchronisation and criticality dynamics. To address this issue, we developed an algorithm that works with both functional connectome and DFA to learn model parameters from data (See Figure 5A). We applied the idea of gradient-based learning for the inter-node weights by approximating the DFA as a quadratic function of the local control parameter (Figure 6B, see Methods for details).

To validate the algorithm, we first generated artificial phenotypes with known changes and fitted a model to them. We created phenotype coefficients for local and global control parameters by increasing or decreasing them in functional zones (See Figure 5C) and multiplied them element-wise on the matrix of inter-node weights and the vector of local control values for each node. Then, we ran a phenotype-based simulation, calculated the PLV and DFA observables and used them to fit the model with the pre-phenotyping control parameters (See Figure 5D).

We found that after fitting, the model is able to reproduce the altered dynamics with high similarity (Pearson correlation coefficient for DFA is ~ 0.7 and ~ 0.8 for PLV See Figure 5H) and requires about 15 iterations to converge to optimal parameters (See Figure 5E). The reconstructed profiles are not only close in the distribution of values, but also follow a similar anatomical pattern (See Figure 5G).

Personalized digital-twins of oscillatory neural dynamics

The actual level of neural dynamics observables depend of various individual physiological properties such as genetic polymorphism ***Simola et al.*** (***2022***), cyto-architecture and transmitter density ***Siebenhühner et al.*** (***2024***), excitation and inhibition gradient ***Wang*** (***2020***) and balance ***Abeysuriya et al.*** (***2018***). However, some of those parameters could not be observed directly in the human-based experiments due to being to expensive or ethical limitations. In addition, phenomenological models may not have clear physiological comparison of parameters (such as local coupling in the hierarchical Kuramoto model) to physiological measurements and can only be mapped indirectly. Therefore, it may not be possible to create precise models per-se using only the prior knowledge and any model has to be adjusted to reproduce individual properties.

The idea of computational models tailored to reproduce a personalized model dynamics aka *digital twins* has been a rising research topic in recent years ***San*** (***2021***) especially in application to health studies and medicine ***Laubenbacher et al.*** (***2024***); ***Katsoulakis et al.*** (***2024***), in application to the neuroscience field, a Digital Twin Brain is a system that can reproduce individual neural dynamics. The critical brain hypothesis implies that a critical state-space emerges from the underlying parameters and is a basis for an individual operating point reflected in observables. A Digital Twin Brain shares the same critical space with a real system but the model individual operating point may be different due to non-perfect parameters and model assumptions. To negate this effect a model parameters and thus the position in the critical space may be adjust by following the gradient of different between a model and a target observables (Figure 7C).

The phase synchronization and criticality are fundamental observables in the critical brain hypothesis and their alterations are associated with cognitive states, physiological changes, and mental disorders, so it is natural that a digital twin brain would be able to reproduce such properties of an individual. To create a DTB of a participant, we computed wPLI as a function of frequency and used a wPLI functional connectome at the peak in alpha frequency and DFA values at the same frequency as a fitting target (See Figure 7D).

We discovered that the fitted model successfully replicates individual critical dynamics within both the physiologically plausible range of values and the topographical correlations (See Figure 7E). On the cohort level, we found that the Pearson correlation coefficient between the best-fit model and an individual recordings are higher for DFA that were observed for PS (average 0.63 for DFA and 0.47 for PLV, See Figure 7F). We also found that the fitting quality is positively correlated with the fraction of significant values (Supplementary Figure 3), we assume that the non-significant values are dictated by the noise which is not possible to fit robustly.

As the next step we assessed reconstruction quality for each node and edge individually by computing the correlation between predicted and an real-data DFA exponents (for single nodes) and PS (for edges). While checking the fitted weights of a model we mean-normalized them by dividing all the weights on the average weight for each subject to take into account an individual bias. For DFA exponents, we found that the visual and temporal areas yield the highest correlation simultaneously with the highest weights for local control parameter on average (See Figure 7G), while the default subsystem has the worst predictions and the lowest weights. As for PLV, at first glance, the inter-hemi connections are poorly reconstructed in contrast with intra-hemi (average correlation is 0.51 for connections between hemispheres and 0.64 for connections inside a hemisphere, See Figure 7H). At second

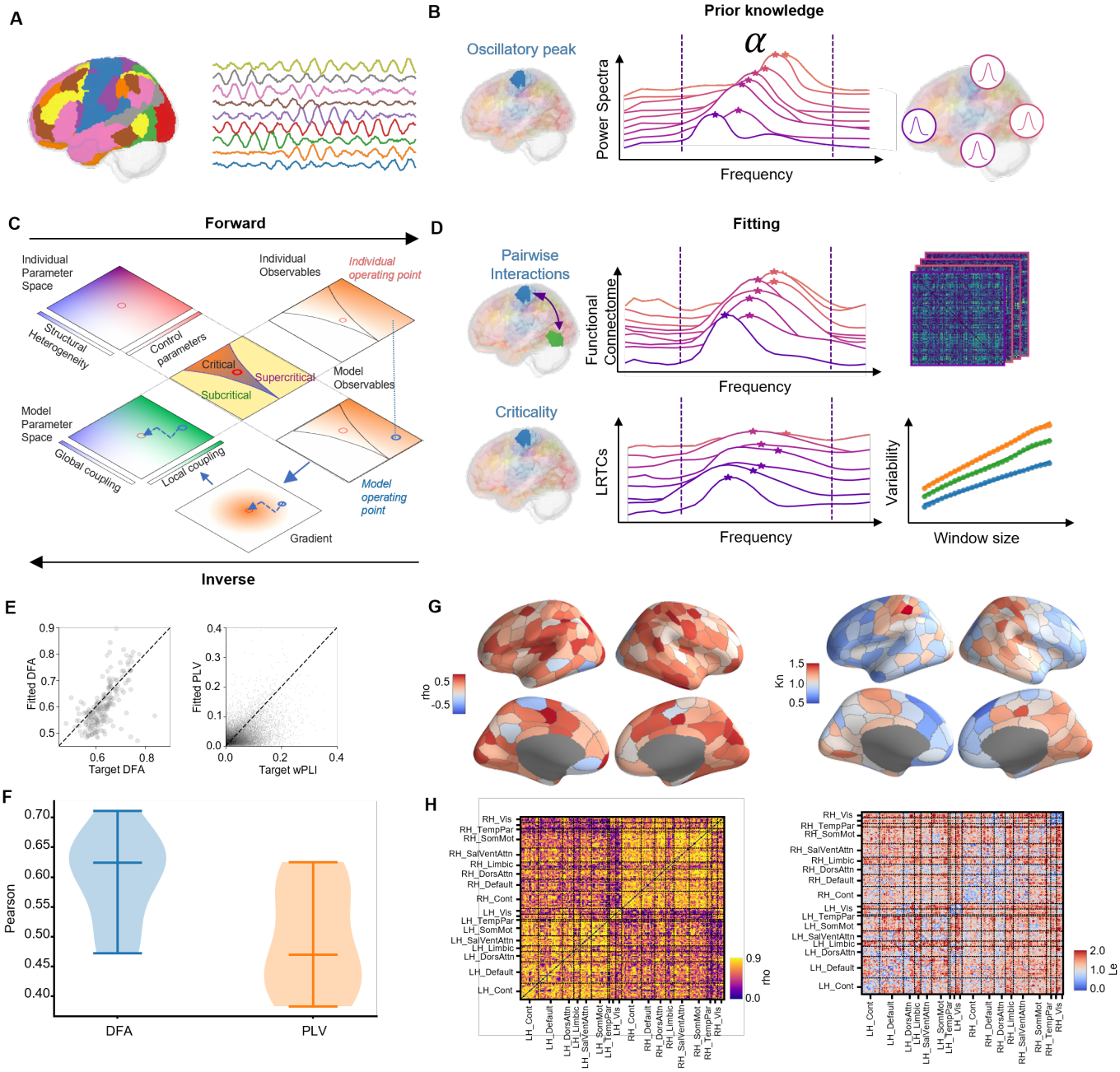

Figure 7. The concept of a Digital Twin Brain. A given Resting-State MEG recordings of a single subject (**A**) are used to extract the oscillatory peaks in the alpha frequency and set central frequencies of each node (**B**). The critical brain hypothesis implies that a critical state-space emerges from the underlying parameters and is a basis for an individual operating point reflected in observables. A Digital Twin Brain shares the same critical space with a real system and the gradient of differences between the model and the target observables can be used to adjust the model parameters (**C**). **D** The metric of pairwise interactions measured with phase synchrony and the DFA exponent are extracted from the MEG recordings and are used to fit the model. **E** Scatterplots of DFA exponents and phase synchrony for a single-subject best fit model. **F** Violinplots for distributions of the Pearson correlation coefficient for best-fit models across the MEG cohort. **G** Topography of correlation coefficients between the best-fit model and target DFA (left) and an average learned local control parameter (Kn, right). **H** Correlation coefficient between the best-fit model and target PS (left) and an average learned global control parameter (right, Le)

glance, we found that the visual subsystem remains an outlier where PS between it and other subsystems was fit with low quality but within it nodes the correlation remains high. Interestingly, the edge weights between nodes that belong to the same subsystem tend to be lower in contrast to the edges connecting different subsystem (0.93 for intra-nodal connectivity and 1.23 for inter-nodal,

See Figure 7H).

Discussion

Neuronal oscillations in the human brain exhibit variation in multiple observables of neural dynamics such as power, synchronization, and rhythmicity. Notably, they also display Long-Range Temporal Correlations (LRTCs) which are a signature of critical-like behaviour. The hypothesis of the 'critical brain' suggests the brain operates near a phase transition between order and disorder. However, up to this day, there have existed no large-scale computational oscillatory models with the ability to reproduce critical behaviour.

In this study, we introduced a nested hierarchical version of the Kuramoto model, featuring multiple interconnected nodes with a large population of basic oscillator units within each node (See Figure 1H). This approach yields realistic oscillatory dynamics with critical properties that are governed by model control parameters. Thus, we were able to map our model to real brains, matching each parcel to a single node and reproducing various aspects of critical brain dynamics such as LRTCs, power spectrum, phase synchrony, and rhythmicity.

The critical regime has several functional benefits, such as increased information capacity or transfer rate, which may be related to behavioral and cognitive correlates of criticality, such as increased cognitive load in working memory task ***Altamura et al.*** (***2012***), error rate in Go/NoGo task ***Simola et al.*** (***2017***) or performance in the Continuous Temporal Expectancy Task ***Irrmischer et al.*** (***2017***). It has also been shown that proximity to criticality may alter the relationships between observables, such as the order and sign of correlations between phase synchrony and LRTCs ***Fuscà et al.*** (***2023***). Analyzing our model, we found that observables of model dynamics are primarily dictated by model parameters, but in individual manners. While node order has the highest correlation with the local control parameter (K) and PLV has the highest correlation with the global control parameter (L) in the subcritical region (See Figure 3D,E), the correlation drops at the critical peak. Meanwhile, the cross-amplitude correlation peaks at criticality and vanish in both sub- and super-critical phases (See Figure 3F).

We then went beyond the phenomenological aspect of the model and compared it to real MEG data. Examining the power spectrum is one of the first steps in analyzing any electrophysiological data, the shape of which may reflect the oscillatory frequencies of the underlying neuronal populations. Thus, to reproduce the power spectrum of a recording, we initialized the distribution of oscillator frequencies to match the shape of the flat FOOOF'ed power spectrum of each node (See Figure 4A). We found that the model is able to reproduce the spectral characteristics with the highest reliability around the critical zone with high values of K and low values of L (See Figure 4B). Varying these parameters changes the rhythmic properties from almost complete absence of oscillations in the subcritical region to strong oscillations being dominated by the most common frequency.

We also investigated similarity between model and real data for bivariate interactions assessed by phase synchrony, for LRTCs assessed with the Detrended Fluctuation Analysis (DFA) exponent, and for rhythmicity assessed by the phase autocorrelation function. We created a model with an inter-node weight matrix obtained from individual diffusion tensor imaging (DTI) to match the physiological nature of the structural connectome. Comparing the model derivatives with the real data, we found that the more physiologically plausible results belong to the subcritical zone, outside a supposed Griffiths phase (See Figure 5). We also found that the shape of the most physiologically plausible region for PLV and DFA follows linear shape as a function of control parameters (See Figure 5 D,E,G,H), but rhythmcity, while having the same linear correlation ridge, has a curved shape for similarity of distributions (See Figure 5 I), where the lifetime of oscillations becomes less physiological with increasing local control parameter and higher than observed in the real data.

Although the distributions of modelled properties of oscillatory activity were similar to those in real data (See Figure 5 G,H,I), the linear correlations between them remained low, especially for DFA exponents. This might result from low correlations between structural and functional connectivity in real data which contradicts the observed model behaviour, implying that precise models require a highly personalized approach to restore the unknown underlying parameters.

In prior-art, the process of fitting was typically implemented using the Bayesian approach (***Williams et al.*** (***2023***); ***Oesterle et al.*** (***2020***)) which is a computationally intensive process and is not really applicable when the number of parameters may reach thousands of values. However, when a model is known, one can apply model-specific methods such as fitting to time-resolved connectome (***Kringelbach et al.*** (***2020***)) or adaptation of the gradient descent by approximating functional connectivity with a sigmoid as a function of the control parameter – the edge weight between two model nodes (***Deco et al.*** (***2019***)). This approach allows to avoid exhaustive search through the model parameter space and converges just in in several dozen iterations.

In this work, we extended the traditional way of fitting oscillatory models to take into account critical properties by approximating DFA as a negative quadratic function of the local coupling parameter (See Figure 6B). We validated the approach on simulated data by creating an artificial phenotype via increasing or decreasing model control parameters on predefined value (See Figure 5C,D) and found that this method allows to reconstruct the phenotype with both high correlation of observables such as DFA exponent and PLV (See Figure 6E) and the restored control parameters are similar and follow the same anatomical pattern as phenotype (See Figure 6G).

Methods and Materials

Hierachical kuramoto model

In the classical Kuramoto model, a population is defined as multiple oscillators with all-to-all coupling mediated by a sinusoidal interaction function with a given frequency for each oscillator

$$\theta_i = \omega_i + \frac{1}{N}\sum_{j=1}^{N} K_{ij} sin(\theta_j - \theta_i)$$

where N is a total number of oscillators, θ_i is a phase, ω_i is the frequency of i-th oscillator and K_{ij} is the coupling parameter between i-th and j-th oscillators.

However, the model represents basic dynamics and for the final analysis, data is often aggregated across all oscillators e.g. by computing a model order defined as the absolute value of the average oscillator phase. This approach makes comparison with real brain imaging data a challenging task. To overcome this we introduce a Myrov-Palva model – a hierarchical extension of the Kuramoto model with multiple nodes where each node may correspond to a recording from a single brain area or electrode.

Each node consists of multiple oscillators and the behavior of each oscillator could be explained in three components:

$$\theta_i = Natural + Internal + External + Noise$$

Where $Natural = w_i$ or the center frequency of an oscillator,

$Internal = \frac{K}{N}\sum_{j=1}^{N} sin(\phi i - \phi j)$ where the phase of each oscillator is shifted towards an average phase diff with oscillators if the same node,

$$External = L_{ij} * \sum_{j=1}^{k} Wi,j * sin(\phi i - \Phi \mathrm{j})$$

where the phase of each oscillator is compared to the average phase of other nodes. Thus K_i is an internal coupling coefficient (local control parameter) between i-th node and L_{ij} is a coupling coefficient between i-th and j-th nodes (global control parameter) and noise which is a random Gaussian phase distortion with mean of 0 and given scale.

Later, we aggregated the signal for each node by averaging the phases of all oscillators from the same node. Thus, one is able to match a model's node to a single brain area or any other source of LFP recordings.

Observables of oscillatory dynamics

One of the fundamental observables of the Kuramoto model is its order – indexing the oscillators' synchrony inside each node – defined as an absolute value of an average complex-valued phase across oscillators that belong to the same node

$$R = |\frac{1}{N}\sum_{i=1}^{N} e^{i*\theta_i}|$$

Where N is the number of oscillators and θ_i is the phase of the i-th oscillator.

To estimate inter-areal phase interactions we computed Phase Synchrony metrics for each pair of nodes (model data) or parcels (MEG). For the model, we used the phase locking value (PLV) defined as absolute value of complex PLV

$$CPLV = E[CS_{x,y}]$$

Where E[.] denotes the expected value and $CS_{x,y}$ denotes the cross-spectrum between a complex signals X and Y. In practice, cPLV is estimated using limited data and sample cPLV is defined as

$$\overline{cPLV}_{sample} = \frac{1}{N}\sum_{i=1}^{N} CS_{x,y}$$

where N is the total number of samples.

For MEG data we used the weighted Phase Lag Index (wPLI) which is insensitive to spurious zero-lag interactions and defined as:

$$wPLI = \frac{|\sum_{i=0}^{N} imag(CS_{x,y})|}{\sum_{i=0}^{N} |imag(CS_{x,y})|}$$

where $imag(CS_{x,y})$ is the imaginary part of the cross-spectrum of the complex time series x and y ***Wang et al.*** (***2018***); ***Vinck et al.*** (***2011***).

To measure long-range temporal correlations (LRTCs) in a model and MEG recordings, we used the Detrended Fluctuations analysis (DFA, ***Hardstone et al.*** (***2012***)), which in order to speed up the estimation we computed in the Fourier domain ***Nolte et al.*** (***2019***). To obtain the DFA exponents from model or MEG data, the fluctuations as a function of window sizes were fitted with a robust linear regression (***Huber*** (***1973***)) with a bisquare weight function.

To estimate rhythmicity of oscillations we applied the Phase Autocorrelation Function (pACF, ***Myrov et al.*** (***2024***)). Typically, pACF assesses the lifetime of oscillations by checking whether the time-lagged PLV crosses a threshold. However, super-critical models yield stable oscillations with lifetime $\rightarrow \infty$. Therefore, we estimated rhythmicity as an average pACF across lags of $1...5$ cycles which ensures that the value is bound in $[0; 1]$.

Data acquisition

Fifteen minutes eyes-open resting-state data were recorded from 20 healthy controls with 306-channel MEG (TRIUX, MEGIN Oy, Helsinki, Finland; 204 planar gradiometers and 102 magnetometers) at BioMag Laboratory, HUS Medical Imaging Center, Helsinki, Finland and 306-channel MEG (TRIUX neo, MEGIN Oy, Helsinki, Finland; 204 planar gradiometers and 102 magnetometers) at MEG Core, Aalto University, Espoo, Finland. Bipolar horizontal and vertical electrooculography (EOG) and electrocardiography (ECG) were also recorded. Participants were instructed to seat in a dimly lit room and keep their eyes open to focus on a cross displayed at the center of a screen in front.

T1-weighted anatomical magnetic resonance imaging (MRI) and diffusion weighted imaging (DWI) scans were obtained with a 3 Tesla whole-body MRI scanner (Magnetom Skyra, Siemens, Munich, Germany) at AMI Centre, Aalto University using a 32-channel head coil. T1-weighted MRI data were recorded with a resolution of 0.8×0.8×0.8 mm, repetition time of 2530 ms, and echo time of 3.42 ms. DWI data were recorded with a resolution of 3.0×3.0×3.0 mm, repetition time of 4100 ms, and echo time of 105 ms.

The study protocol for MEG, MRI, and DWI data was approved by (**HUS/3043/2021**, 27.4.2022), written informed consent was obtained from each participant prior to the experiment, and all research was carried out according to the Declaration of Helsinki.

MEG data preprocessing and source modeling

The MNE software (https://mne.tools/stable/index.html) was used for data preprocessing and source modeling. Temporal signal space separation (tSSS) in the Maxfilter software (Elekta Neuromag Ltd., Finland) was used to suppress extracranial noise from MEG sensors, interpolate bad channels, and compensate for head motions. Independent components analysis was used to identify and remove components that were correlated with ocular (using the EOG signal), heart-beat (using the magnetometer signal as reference), or muscle artefacts.

We used the FreeSurfer 7.3.2 software (https://surfer.nmr.mgh.harvard.edu/) for volumetric segmentation of MRI data, surface reconstruction, flattening, and cortical parcellation. Source reconstruction was performed with minimum norm estimation (MNE) using dynamic statistical parametric maps (dSPM). A surface-based source space with 5 mm spacing and 1 layer (inner skull) symmetric boundary element method (BEM) was used in computing the forward operator, and noise covariance matrices was obtained from preprocessed data filted to 151-249 Hz. We then estimated vertex fidelity to obtain fidelity-weighted inverse operators to reduce the effects of spurious connections resulting from source leakage and collapsed the inverse-transformed source time series into parcel time series in a manner that maximizes the source-reconstruction accuracy (***Korhonen et al.*** (***2014***); ***Siebenhühner et al.*** (***2020b***)). Source time series were collapsed to the 200 parcels of the Schaefer atlas (***Schaefer et al.*** (***2018***)).

In this study, we used complex Morlet wavelets to obtain a narrow-band representation of a MEG signal (***Cohen*** (***2019***)). 50 Hz line-noise and it's harmonics were suppressed with a notch filter with 1 Hz band transition widths. The band-pass (1-249 Hz) filtered data were then separated into narrow frequency bands with 41 equally log-spaced Morlet wavelets with frequencies ranging from 1 Hz to 100 Hz (number of cycles in a Morlet Wavelet = 5.0).

DWI data preprocessing

The DWI data preprocessing, including denoising and motion correction, was conducted using the MRtrix3 3.0.1 Toolbox (***Tournier et al.*** (***2019***)) and FMRIB Software Library (FSL) 6.0.5 (***Jenkinson et al.*** (***2012***)). To lessen potential biases or artifacts arising during image acquisition or processing, the Advanced Normalization Tools (ANTs) 2.3.5 was used (***Avants et al.*** (***2009***)). For T1-weighted anatomical MRI data preprocessing, creation of head models and cortical surface reconstruction, we used the open-source FreeSurfer 7.3.2 software (available at https://surfer.nmr.mgh.harvard.edu/, ***Fischl*** (***2012***)). T1-weighted anatomical MRI and DTI coregistration was performed using the Spm 12 package within MATLAB R2022a software. To refine the quality of the diffusion image and minimize tractogram reconstruction biases, we applied the Spherical informed filtering of tractograms approach (SIFT2, ***Smith et al.*** (***2013***)). All preprocessing steps were executed on the CentOS Linux operating system, operating on the Triton high-performance computing cluster at Aalto University.

Following preprocessing, structural connectomes (SCs) were constructed as edge-adjacency matrices representing the count of white matter connections between parcelled cortical and subcortical brain regions. The resulting matrices are symmetric, reflecting undirected pairwise connections between brain regions (nodes). The nodes correspond to the 200 parcels of the Schaefer atlas (***Schaefer et al.*** (***2018***)), matched with Yeo 17 networks (***Yeo et al.*** (***2011***)).

Model fitting

The dependency of PLV over parameters was defined as a sigmoid function ($S(P)$) since PLV shows monotonically increasing behavior. This, the gradient of edge weights matrix is equal to the difference between simulated and a target functional connectome matrix, while the sign of difference shows the direction of the gradient as well (See Figure 6B).

$$grad = [S(P) * (1 - S(P))] * loss \tag{1}$$

Where S is a sigmoid function, P its parameter (e.g. global or local control parameter) and loss is the difference between target and model FC.

The critical state is characterized by peak in the DFA as a function of control parameter (K, See Figure 6B), therefore it is possible to approximate this dependency using the inverted parabola function and use its derivative for a gradient decent-based fitting as shown in the equation 2.

$$grad = -2 * loss * P \tag{2}$$

We applied the multiobjective steepest descent method (***Liu and Reynolds*** (***2016***)) to integrate gradients from various objective functions and we used sum of normalized gradients if they have same direction. Following the approach from ***Liu and Reynolds*** (***2016***), we determined the Pareto optimal solution in case where gradients exhibited divergent directions:

$$G = (\frac{||g_2||^2 - g_1^T g_2}{||g_1||^2 - g_1^T g_2} * -g_1) - g_2 \tag{3}$$

Local control parameter affects both criticality and phase synchrony properties and following this observation, we computed the gradients for K fitting as a sum of DFA and PLV gradients. Because DFA function is not a monotonically growing, we used a sign of the PLV gradient:

$$G_K \leftarrow sign(grad_{kPLV}) * abs(\frac{grad_{kDFA}}{||g_1||^2||grad_{kDFA}||} + \frac{grad_{kPLV}}{||g_1||^2||grad_{kPLV}||}) \tag{4}$$

Regularization was applied to avoid overfitting and improve performance.

We incorporated the Root Mean Square Propagation (RMSprop) strategy for the adaptive learning rate:

$$grad_i = \beta * grad_{i-1} + (1 - \beta) * grad_i^2 \tag{5}$$

Where $\beta = 0.9$ and represents the default value for the moving average coefficient, $grad_i$ is a gradient value at step i.

And control parameters were updated following the next equation 6:

$$P = P - \frac{lr * grad}{\sqrt{grad^2}} \tag{6}$$

where P is either a local or global control parameter, lr is a learning rate, $grad$ is a gradient for the parameter.

Combining all of these steps, the final fitting follows the next algorithm:

Algorithm 1 Fitting algorithm

Require: $target_{DFA}, targetl_{wPLI}$
Ensure: $weights, K_n$

function fitting(target)
  $G_{Ksquared} \leftarrow 0$
  $G_{wsquared} \leftarrow 0$
  $weights \leftarrow 1$
  $K_n \leftarrow 1$
  for $lr \leftarrow 1$ to N **do**
    $loss_{PLV} \leftarrow model_{PLV} - target_{wPLI}$
    $loss_{DFA} \leftarrow model_{DFA} - target_{DFA}$
    $grad_{kPLV} \leftarrow [S(K) * (1 - S(K))] * loss_{PLV}$
    $grad_{kDFA} \leftarrow -2 * loss_{DFA} * K_n$
    $grad_{wPLV} \leftarrow [S(weights) * (1 - S(weights))] * loss_{PLV}$
    $grad_{wDFA} \leftarrow -2 * loss_{DFA} * weights$
    if $grad^T_{wPLV} * (grad_{wPLV} - grad_{wDFA})) > 0$ **then**
      $G_w \leftarrow (\frac{||grad_{wDFA}||^2 - grad^T_{wPLV} * grad_{wDFA}}{||grad_{wPLV}||^2 - grad^T_{wPLV} * grad_{wDFA}} * -grad_{wPLV}) - grad_{wDFA}$
      $G_w \leftarrow -G_w / ||G_w||$
    else
      $G_w \leftarrow grad_{wPLV} / ||grad_{wPLV}|| + grad_{wDFA} / ||grad_{wDFA}||$
    end if
    $G_K \leftarrow sign(grad_{kPLV}) * abs(grad_{kDFA} / ||grad_{kDFA}|| + grad_{kPLV} / ||grad_{kPLV}||)$
    $G_{Ksquared} \leftarrow 0.9 * G_{Ksquared} + 0.1 * G_K^2$
    $G_{wsquared} \leftarrow 0.9 * G_{wsquared} + 0.1 * G_w^2$
    $weights = weights - lr * G_w / \sqrt{G_{wsquared}}$
    $K_n = K_n - lr * G_K / \sqrt{G_{Ksquared}}$
  end for
  return $weights, K_n$
end function

Data availability

Raw data cannot be made available due to data privacy regulations set by the ethical committees. The data underlying results to reproduce the main findings will be deposited in a suitable repository prior to the publication. Other types of data can be shared upon reasonable request.

Code availability

The model code will be open-sourced prior to the publication. There are also several tutorials to guideline the basic usage of the model.

The code to reproduce this study results will also be published in a suitable repository prior to the publication.

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Contributions

V.M. and J.M.P. conceived the study; V.M. wrote the model code; A.S. implemented the fitting algorithm; V.M. and A.S. wrote ehe analysis code; W.L. provided preprocessed MEG data; S.K. provided preprocessed DWI data; P.P. and M.V. recorded MRI and MEG data; All authors contributed to the writing of the manuscript. All authors read and approved the manuscript.

Citations

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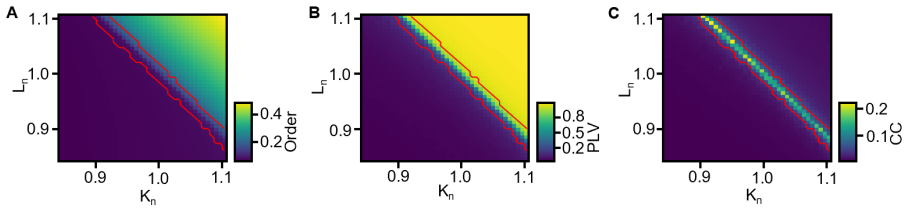

Figure S1. A,B,C An average model order (**A**), PLV (**B**) and CC (**C**).

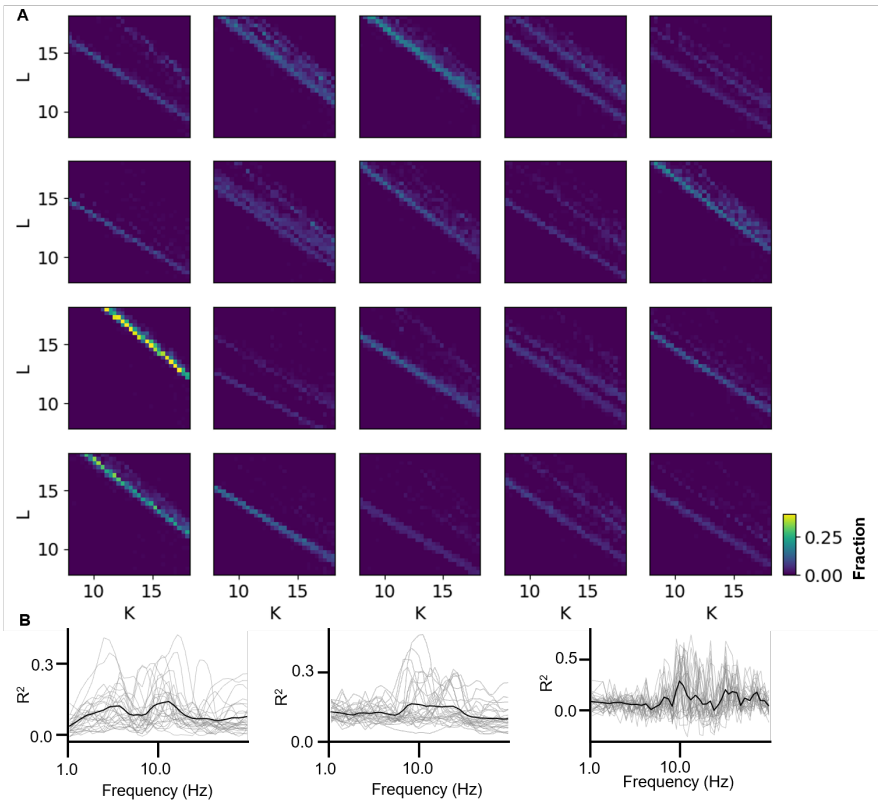

Figure S2. A A fraction of nodes with DFA $>= 0.7$ for models based on individual structural connectome. **B** R^2 between predicted and actual PS matrices (left), DFA (middle) and pACF (right) as a function of frequency.

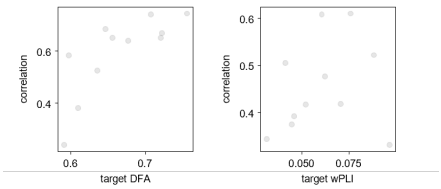

Figure S3. A correlation between predicted and target phase synchrony (left) and DFA (right) as a function of the target metric value.