Conserved Ising Model on the Human Connectome

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Ising models on structural brain networks, with a dynamics conserving the magnetization, may be seen as a model of neural activity subject to an homeostatic principle. Using a recently proposed network measure, cross-modularity, and the mean square error between the spin correlations and the empirical functional correlations of the resting brain, we show that conserved Ising models provide better prediction of the empirical correlations than Ising with Glauber dynamics; we show that at the peak of the specific heat (the most critical state) the spin correlations are minimally shaped by the underlying structural network, hence it is not surprising that the best match is obtained at the onset of criticality. Moreover, the fit is better in anesthesia conditions than in wakefulness, in agreement with recent experiments suggesting that under anesthesia the structure-function interplay is enhanced.

Possible interpretation of the conservation law of spin dynamics is that it approximates the coupling from metabolic resources to neural activity.

One of the key challenges in the study of complex networks is understanding the relation between the structure and the collective dynamics stemming from it. This issue is of special relevance in neuroscience, where the question is how statistical dependencies between brain regions relate to the brain structural architecture, both in healthy and pathological conditions. Recent advances in diffusion imaging and tractography methods allow the noninvasive mapping of white matter cortico-cortical projections at high spatial resolution, yielding a connection matrix of interregional connectivity. A comparison of diffusion imaging and resting state functional MRI (fMRI) data reveals a close relationship between structural and functional connections. In recent studies the structure-function interplay has been studied by simulating spontaneous brain activity through the implementation of models of dynamical oscillators with different levels of complexity and biological foundation on the connectome structure, retrieving in some cases correlation-based networks similar to those observed from the analysis of neuroimaging data (mainly fMRI at rest), even with models less biologically realistic such as the Ising one. In these studies it has been shown that functional correlations may be predicted to some extent on the basis of the anatomic connectivity for pairs of brain regions. In the large scale pattern of empirical brain correlations was compared with those from a large two-dimensional Ising model, showing that the match is optimal when the statistical system is close to the critical temperature. However, there are two fundamental classes of spin dynamics: one in which magnetization is preserved and one in which magnetization is not preserved. The former class describes for example alloy systems, where the two different spin states naturally correspond to the two component atoms that comprise the alloy. If we consider the Ising model on the human connectome as a dynamical system for neural activity, the conservation of magnetization may be seen as the conservation of the total neural activity, a sort of homeostatic principle for the overall activity of the brain.

The question we address in this work is whether the introduction of a conserved dynamics on the human connectome might improve the prediction of functional connectivity based on the structural connectivity between two brain regions. We show that the answer is positive, at least at the spatial scale that is considered here. We consider pair exchange update rules for the Ising model defined on the real structural brain network, and we get a better match with empirical functional correlations w.r.t. non-conserved Ising model, on a data set of awake healthy subjects and anesthetized subjects, a condition in which the structure-function relation is modified. The improved prediction of the empirical correlations from model correlations suggests that the conservation law of the Kawasaki dynamics might admit a physiological basis: a possible interpretation is seeing it as an effective implementation of the coupling from metabolic resources to neural activity, a key ingredient that is missing in neural models on the connectome. We believe therefore that our findings will be relevant for the construction of brain models to better reproduce the phenomenological behavior of the brain.

First of all we describe the behavior of conserved Ising model on the well known anatomical connectivity matrix of, which has been already considered w.r.t. non-conserved Ising model in. The couplings are given by \( J_{ij} = \beta A_{ij} \).
where $A$ is the $998 \times 998$ symmetrical structural matrix and the parameter $\beta$ plays the role of an inverse temperature. Considering the configurations $\{\sigma_i(t)\}_{i=1,\ldots,n}$ of the Ising system of $n$ spins, the energy of a given configuration is:

$$E = - \sum_{ij} J_{ij} s_i s_j,$$

the magnetic field is supposed to be zero. The lagged spin vectors are denoted $\Sigma_i(t) = \sigma_i(t - 1)$. The non-conserved Glauber dynamics, corresponds to set $s_i = 1$ with probability $p_i$, where

$$p_i = \frac{1}{1 + \exp(-2 \sum_j J_{ij} \sigma_j)}.$$  

In the conserved dynamics, the Kawasaki algorithms swaps two spins randomly chosen with probability $\exp(-\Delta E)$,

where $\Delta E$ is the variation of the energy corresponding to exchanging the two spins. A full iteration consists in tentatively update of all the spins (pairs of spins) for Glauber (Kawasaki) dynamics.

In both dynamics the pairwise transfer entropy $TE$, measuring the information flow from spin $i$ to spin $j$ in each pair connected by a link in the underlying network is computed as follows:

$$TE_{ij} = \sum_{\sigma_j = \pm 1} \sum_{\sigma_i = \pm 1} \sum_{\Sigma_j, \Sigma_i} p(\sigma_j, \Sigma_j, \Sigma_i) \log \frac{p(\sigma_j, \Sigma_j) p(\Sigma_j, \Sigma_i)}{p(\sigma_j, \Sigma_j, \Sigma_i)}$$  \hspace{1cm} (1)

where $p(\Sigma_j, \Sigma_i)$ is the fraction of times that the configuration $(\Sigma_j, \Sigma_i)$ is observed in the data set, and similar definitions hold for the other probabilities. Spin correlations are evaluated using the classical linear Pearson correlation. In figure (1) top left we depict the specific heat $C$ for the conserved Ising model implemented on the 998-nodes connectome of [9] as well as separately on the two subnetworks of it corresponding to the left and right hemispheres respectively. We observe that the models on the hemispheres display a peak at two different temperatures, in other words if considered isolated, the two hemispheres would became critical at slightly different temperatures. On the other hand, the whole brain exhibits a wide range of temperatures where $C$ is maximal, with two peaks; the whole range corresponds to the critical brain when its dynamics is approximated by the conserved Ising model. In figure (1) top right we depict the average correlation among all pairs of spins in the three cases as a function of the inverse temperature $\beta$: since for conserved dynamics both positive and negative values of correlations are present, the average correlation is always very small. Therefore in figure (1) bottom left we report the average absolute value of correlations: the Ising models on the hemispheres show a single peak, whilst the model on the whole connectome exhibits two maxima. The average transfer entropy $TE$ over anatomically connected pairs of spins also shows peaks located at the same temperatures as the specific heat and the correlations. This means that also for conserved dynamics, as already shown in [8] for Glauber dynamics, the critical state can be characterized as the one with maximal circulation of information. This is different from what is observed in the regular 2D lattice Ising model, where the information flow peaks in the disordered phase [17], thus suggesting that information dynamics may be able to predict an imminent transition in some complex systems. Our results suggest that this is not the case for human brain topology.

In figure (2) we consider the following problem: to which extent are the functional patterns of the Ising systems shaped by the underlying topology? We compare the anatomical network with the functional networks provided by the dynamical system, as a function of the inverse temperature. The following quantities are depicted: the correlation between $TE$ and $J$ over all the anatomically connected pairs and the correlation between $c$ and $J$ over all the anatomically connected pairs. The plots of the average absolute value of the correlation and the average transfer entropy are also displayed, for comparison. The four panels in figure (2) refer to the Ising model with conserved dynamics, on the full connectome and on the two subnetworks corresponding to the two hemispheres; we have also plotted the corresponding panel for the Ising model with Glauber dynamics, already studied in [8]. In all the four cases we find that the critical states are also the ones with the minimal correlation of $TE$ and $c$ with $J$. These results confirm that there is an intrinsic limitation of reconstruction of anatomical connections in the underlying structural network, from the observed directed and undirected functional connectivities. In other words the critical states appear to be the ones such that the functional networks is minimally shaped by the underlying structural network. For completeness we show that this behavior is found also for the Ising model with non-conserved dynamics.

In order to elucidate how the structure-function relationship is modulated by the level of consciousness we now turn to consider fMRI data recorded from healthy subjects in awake conditions and during propofol anesthesia. The motivation for the study, the underlying physiological issues, and the protocol are extensively described in [19]. The
functional MRI (fMRI) data was preprocessed with FSL (FMRIB Software Library v5.0). The first 10 volumes were discarded for correction of the magnetic saturation effect and for the remaining volumes, first movement is corrected and then, the slice-time is also corrected for temporal alignment. All voxels were spatially smoothed with a 6mm FWHM isotropic Gaussian kernel and after intensity normalization, a band pass filter was applied between 0.01 and 0.08 Hz. Finally, linear and quadratic trends were removed. We next regressed out the motion time courses, the average CSF signal, the average white matter signal and the average global signal. Data was transformed to the MNI152 template, such that a given voxel had a volume of 3mm x 3 mm x 3mm. Finally we obtained 116 time series, each corresponding to an anatomical region of interest (ROI), by averaging the voxel signals according to an anatomical template [20]. We selected this partition for being the most used in fMRI connectivity analysis, and for including subcortical structures.

In order to obtain the structural connectome corresponding to the same parcellation we used the public diffusion imaging (dMRI) data contained in the Nathan Kline Institute- Rockland sample described and downloadable at http://fcon_1000.projects.nitrc.org/indi/pro/enKI_RS_TRT/FrontPage.html.

To analyze this data, the eddy current correction was applied to overcome artifacts produced by changes in the gradient field directions of the MR scanner and subject head movement. In particular, the eddy-correct tool from FSL was used to correct both eddy current distortions, and simple head motion, using affine registration to a reference volume. After this, DTIFIT was used to perform the fitting of the diffusion tensor for each voxel, using as an input the eddy-correct output. Two computations were performed to transform the atlas to each individual space: (1) the transformation between the MNI template to the subject structural image (T1), and (2) the transformation between the T1 to the diffusion image space. Combining both transformations, each atlas region is transformed to the diffusion space, allowing to count the number of fibers connecting all ROIs pairs. Using the corrected data, a local fitting of the diffusion tensor was applied to compute the diffusion tensor model at each voxel. Then, a deterministic tractography algorithm (FACT) [21] was applied using TrackVis [22], an interactive software for fiber tracking.

It is worth to note that for group level analyses at the scales considered in this study it’s not relevant that the structural connectivity used for the simulations is not the one obtained from the same subjects for which the functional connectivity was computed and compared. Indeed the spatial correlation between real and simulated functional connectivity for the same subjects from which the structural connectivity was extracted overlaps to the results reported here (results not shown).

We are then able to obtain the functional connectome across 116 ROIs from 14 healthy subjects in wakefulness and propofol anesthesia. These functional connectomes were averaged across subjects. Varying the temperature we implemented the Ising model with both Glauber and Kawasaki dynamics on the structural architecture connecting the same ROIs. According to the specific heat we can locate the critical range of \( \beta \) for both models; for Kawasaki dynamics the peak is at \( \beta = 2 \) and broadens in the interval \([1.5, 2.5]\). For Glauber dynamics the interval corresponding to the peak of the specific heat is \([0.8, 0.11]\) and the maximum is at \( \beta = 0.95 \). We compare the corresponding spin correlations with the empirical functional correlations. As depicted in figure 4, when the link-wise correlation between model and empirical functional patterns is considered, the match between model and empirical correlations has not a clear dependency on the temperature, although it is clear that best match is obtained by the Kawasaki dynamics, and a better fit is obtained in the anesthesia case w.r.t. wake conditions. In order to better describe the relation between functional patterns (empirical and from models), at the modular level, we have evaluated the cross-modularity (CM) [18] as a function of the number of modules and \( \beta \). In [18] hierarchical clustering, to integrate SC and rsFC datasets gathered independently from healthy human subjects, was applied within an approach that resulted in a common skeleton shared by brain structure and function; the optimal brain partition was extracted by maximizing CM, a figure of merit for partition which takes into account the modularity of the structure network, the modularity of the functional network and the similarity between the subnetworks, in the two networks, corresponding to the partition under consideration. Here we use CM to quantify the relation between empirical functional correlations and spin correlations from the model, while performing hierarchical clustering of the empirical functional connectivity for wake subjects and subjects under anesthesia. In figure 4 CM is plotted for Kawasaki dynamics and Glauber dynamics. On one side it is confirmed that Kawasaki performs better than Glauber dynamics in predicting the empirical correlations, and we see that under anesthesia the structure-function interplay corresponds to higher values of CM w.r.t. awake conditions. On the other hand the highest values of CM are obtained at the onset of criticality, whilst the maxima of CM provide the optimal number of clusters, as a function of the temperature. In figure 4 the match between empirical and spin correlations is measured in terms of the mean square error between the two patterns, i.e. the average of \( (c_{ij}^{\text{spin}} - c_{ij}^{\text{empirical}})^2 \) over all the pairs of brain regions, \( c_{ij}^{\text{spin}} \) being the spin correlation of the Ising models and \( c_{ij}^{\text{empirical}} \) the empirical functional connectivity; the best match is obtained in the critical range but, as already shown using CM, the minima of MSE correspond to the two temperatures delimiting the critical range, for Kawasaki dynamics. At the peak of the specific heat, instead, MSE has a maximum, as a consequence of the (already mentioned) fact that at the peak of criticality the pattern of functional correlations are minimally shaped by
the structural underlying network. Therefore, also the analysis of MSE confirms that Kawasaki dynamics provides a better fit with empirical correlations, and that, remarkably, the fit is better for anesthesia than for wakefulness. This evidence is in accordance with recent results [23] showing that the structure-function correspondence is enhanced under anesthesia. Applying the cross-modularity described above to the real data (structural and functional) considered here, we see that this quantity is always much greater for anesthesia, for any number of modules (6(a)). Furthermore, CM between model functional connectivity and real structural connectivity is maximized at the same value of the temperature for which the similarity with real functional connectome is highest (6(b)).

In order to visualize our results, in figure 7 we depict the $116 \times 116$ structural connectivity, the empirical functional connectivity for wake and anesthesia conditions and the pattern of correlations of the Kawasaki model tuned at the temperature providing the best similarity with the empirical anesthesia patterns.

Summarizing, we have considered the conserved Ising model on the human connectome, and, in agreement with recent theoretical frameworks [15], our results suggest that a wide range of temperatures corresponds to criticality of the dynamical Ising system on the connectome, rather than a narrow interval centered in a critical state; in critical conditions the correlational pattern is minimally shaped by the underlying structural network. It follows that, assuming that human brain corresponds to critical [16], there is an intrinsic limitation in the relationship between structure and function that can be observed on data. We have shown that empirical correlations among brain areas are better reproduced using a model which conserves the global magnetization, and that this match can be described in terms of a network measure like cross-modularity or in terms of the MSE between the simulated and empirical patterns. The fit is better in anesthesia conditions than in wakefulness.

![Figure 1](image_url)

**FIG. 1:** The conserved Ising model is implemented on the 998-nodes connectome (red line), and on the left (green line) and right (blue line) hemispheres separately. The following quantities are depicted versus the inverse temperature $\beta$: (top left) the heat capacity $C$; (top right) the average correlation, over all the pairs of spins; (bottom left) the average absolute value of the correlation, over all the pairs of spins; the average transfer entropy $TE$, over all the anatomically connected pairs of spins.

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FIG. 2: The panels refer to the conserved Ising model on the 998 nodes connectome (top left), on the left hemisphere (top right), on the right hemisphere (bottom left) and non conserved Ising model with Glauber dynamics on the 998-nodes connectome. The following quantities are depicted in these cases as a function of $\beta$: the correlation between the value of $TE$ and $J$ over all the anatomically connected pairs (red line); the correlation between the value of $c$ and $J$ over all the anatomically connected pairs (cyan line); the average absolute value of the correlation (blue line); the average transfer entropy (green line).

FIG. 3: The link-wise correlation between the model spin correlations and the empirical functional connectivities is depicted as a function of the temperature $\beta$ for Kawasaki and Glauber dynamics, and for wake and anesthesia conditions.

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FIG. 4: (Top) The cross-modularity between empirical and model functional networks, as a function of the number of modules and $\beta$ is depicted for Kawasaki and Glauber dynamics, and for wake and anesthesia conditions. The modular decomposition is obtained by hierarchical clustering of the empirical functional network.

FIG. 5: The mean square error between the model spin correlations and the empirical functional connectivities is depicted as a function of the temperature $\beta$ for Kawasaki and Glauber dynamics, and for wake and anesthesia conditions.

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FIG. 6: (a) Cross-modularity between structural connectome and averaged empirical functional connectivity for wakefulness and anesthesia as a function of the number of modules. (b) Cross-modularity between structural connectome and simulated functional connectivity as a function of the number of modules and of $\beta$.

FIG. 7: Top left: the structural connectivity of the 116 regions. Top right: the empirical functional connectivity for wake conditions. Bottom left: the empirical functional connectivity for anesthesia conditions. Bottom right: the spin correlation of the Ising Kawasaki model with the temperature tuned to minimize the MSE with the anesthesia empirical correlations.