

Homeostatic plasticity and emergence of functional networks in a whole-brain model at criticality

(Supporting Figures)

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References

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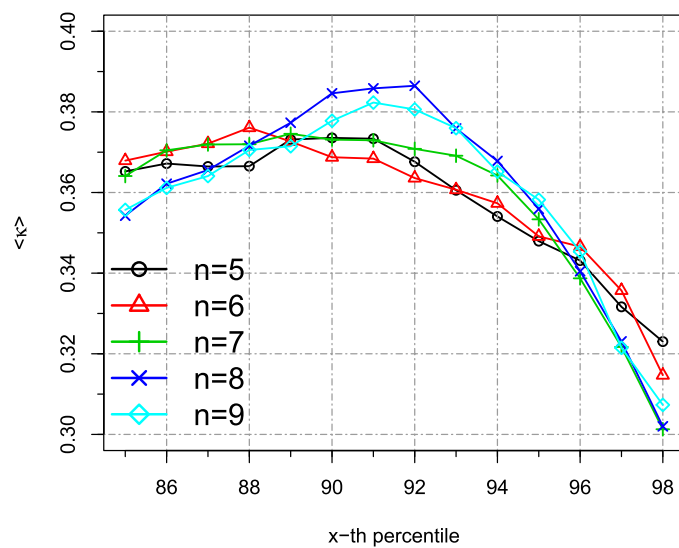


Figure 1: Spatial ICA (sICA) applied to empirical resting state BOLD time-series from the Corbetta et. al. dataset¹. Overall match $\langle \kappa \rangle$ (Cohen's Kappa) between simulated RSNs and a template of well-established human RSNs as a function of the x-th percentile used to threshold and binarize the simulated RSNs. We considered different values of n , i.e., the number of independent components used to decompose the data, in order to find the dyad of parameters that maximizes $\langle \kappa \rangle$. We found a maximum ($\langle \kappa \rangle \approx 0.39$) at $n = 8$ and the 92-th percentile. We then fixed these values when extracting the RSNs from the simulated dynamics.

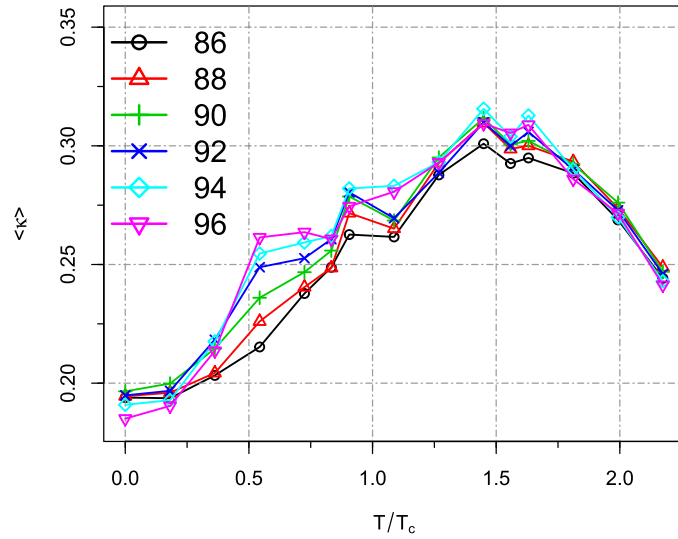


Figure 2: Simulated RSNs using sICA for the not-normalized input matrix W with $n = 8$ components. Overall match $\langle \kappa \rangle$ as a function of T/T_c for different values of the x -th percentile. The highest match is achieved close to the 92-th percentile, in agreement with the previous figure. As discussed in the main text, finite size effects prevent the highest match to coincide with the peak of $\langle S_2 \rangle$.

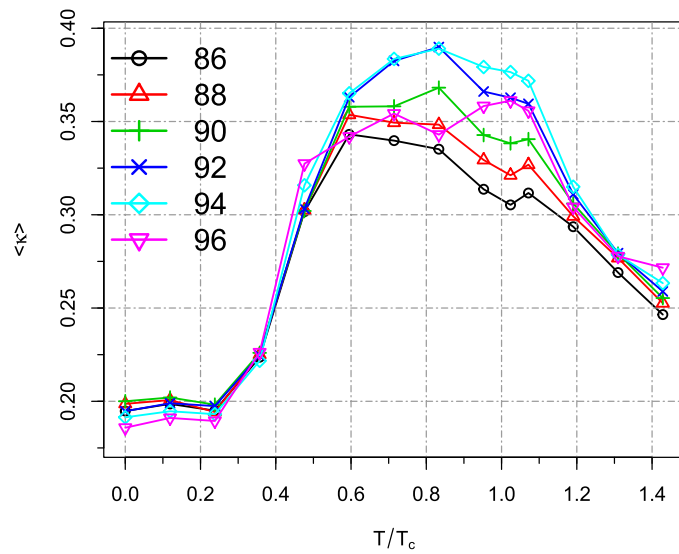


Figure 3: The same as in the previous figure but with the normalized input matrix \widetilde{W} . Normalization of the nodes excitatory input causes a substantial improvement of the simulated RSNs maps as compared with the not-normalized input matrix W . The highest match is now more close to the critical point and again it happens in proximity of the 92-th percentile.