Spatial and temporal patterns of ongoing cortical activity at rest

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Summary

The large-scale ongoing activity of the brain at rest is astonishingly highly structured [1-5]. Most of previous work on resting-state dynamics focused on spatial patterns of correlations. Here we concentrated on spatiotemporal dynamics of resting-state activity. We analyzed resting-state BOLD activity using Hidden Markov Models (HMMs). The HMM clusters the data in a predetermined number of states which represent the multivariate distribution of the BOLD signals. Within this model, the BOLD activity transits through a sequence of states. The states are linked by a state transition probability matrix. Importantly, the distributions and the transition matrix are estimated from the data, via a expectation-maximization (EM) algorithm. HMM has several advantages: i) it detects the moments of transitions between states; ii) it is a probabilistic model that allows to treat noisy systems, possibly emerging from stochastic dynamics; iii) it allows a direct study of dynamic changes in first (mean) and second order statistics (variances and covariances — provided a sufficient amount of data).

Hidden Markov Model (HMM)
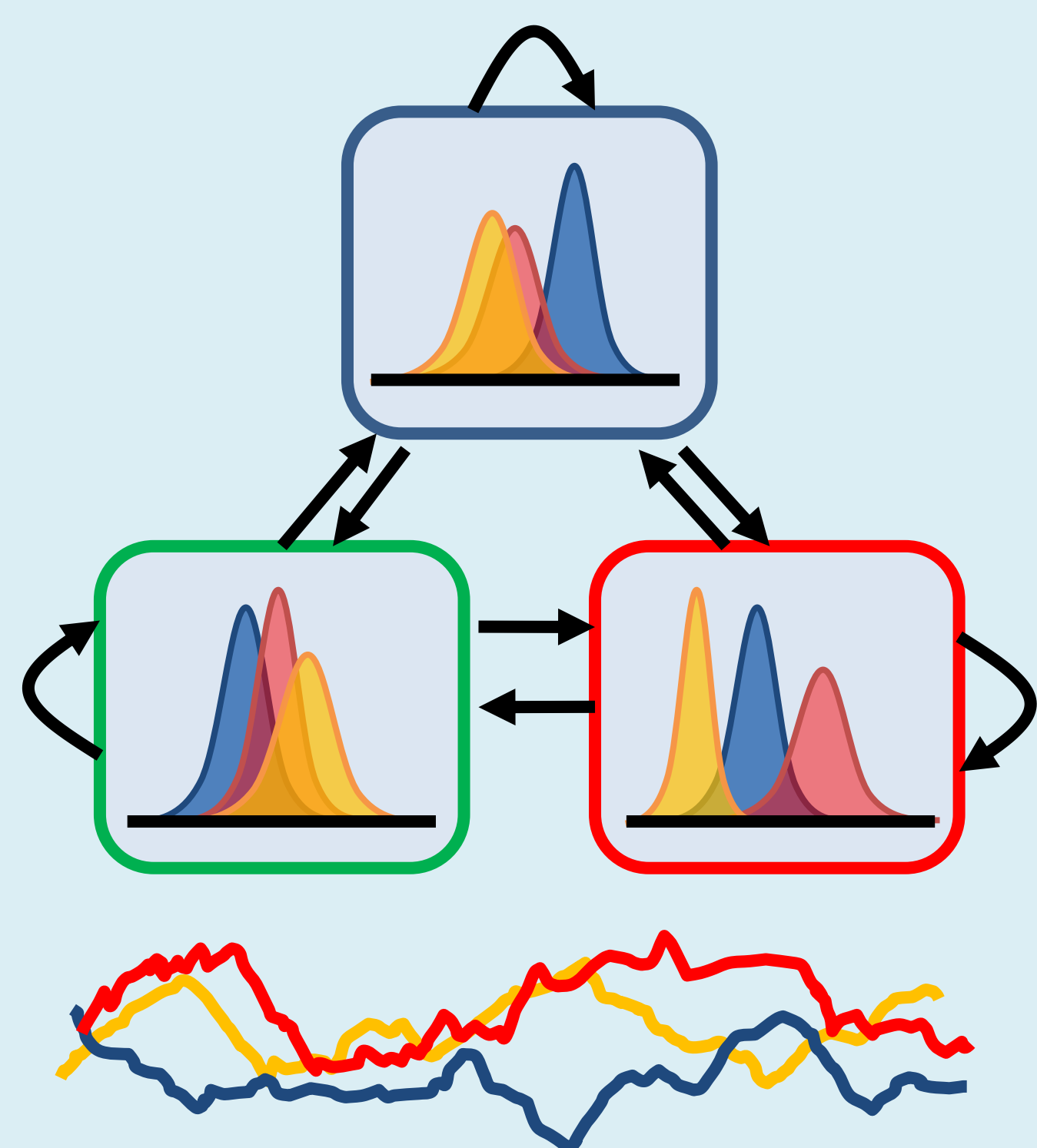
- *N* simultaneously recorded time series (BOLD, MEG, or EEG…)

- In each state, the activity of each channel *i* is determined by a Gaussian distribution with fixed mean, $\mu(i)$, and variance $\gamma(i)$.

- The system of *N* channels transits from state *i* to state *j* with fixed probability: $A_{ij} = P[S(t)=i|S(t-1)=j]$.
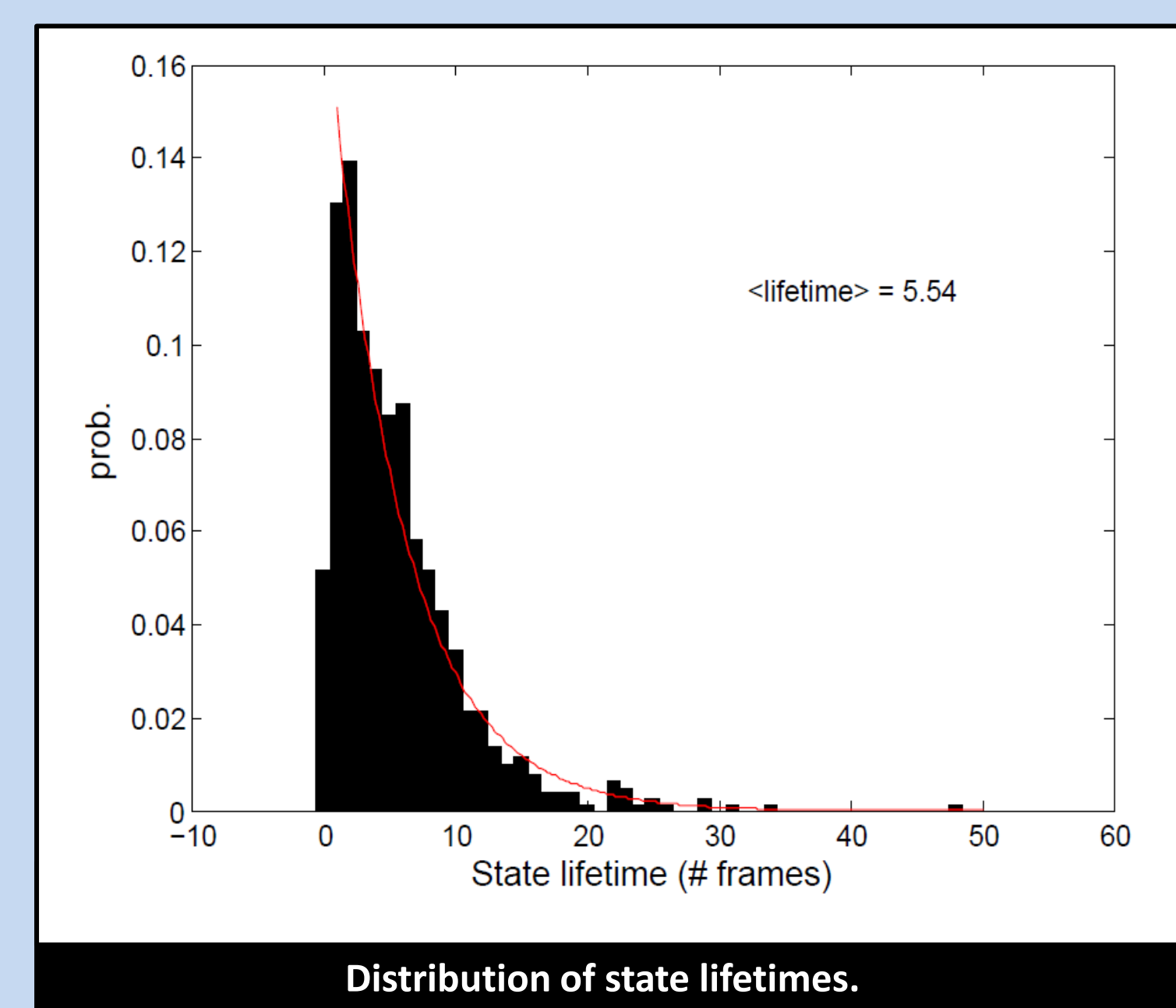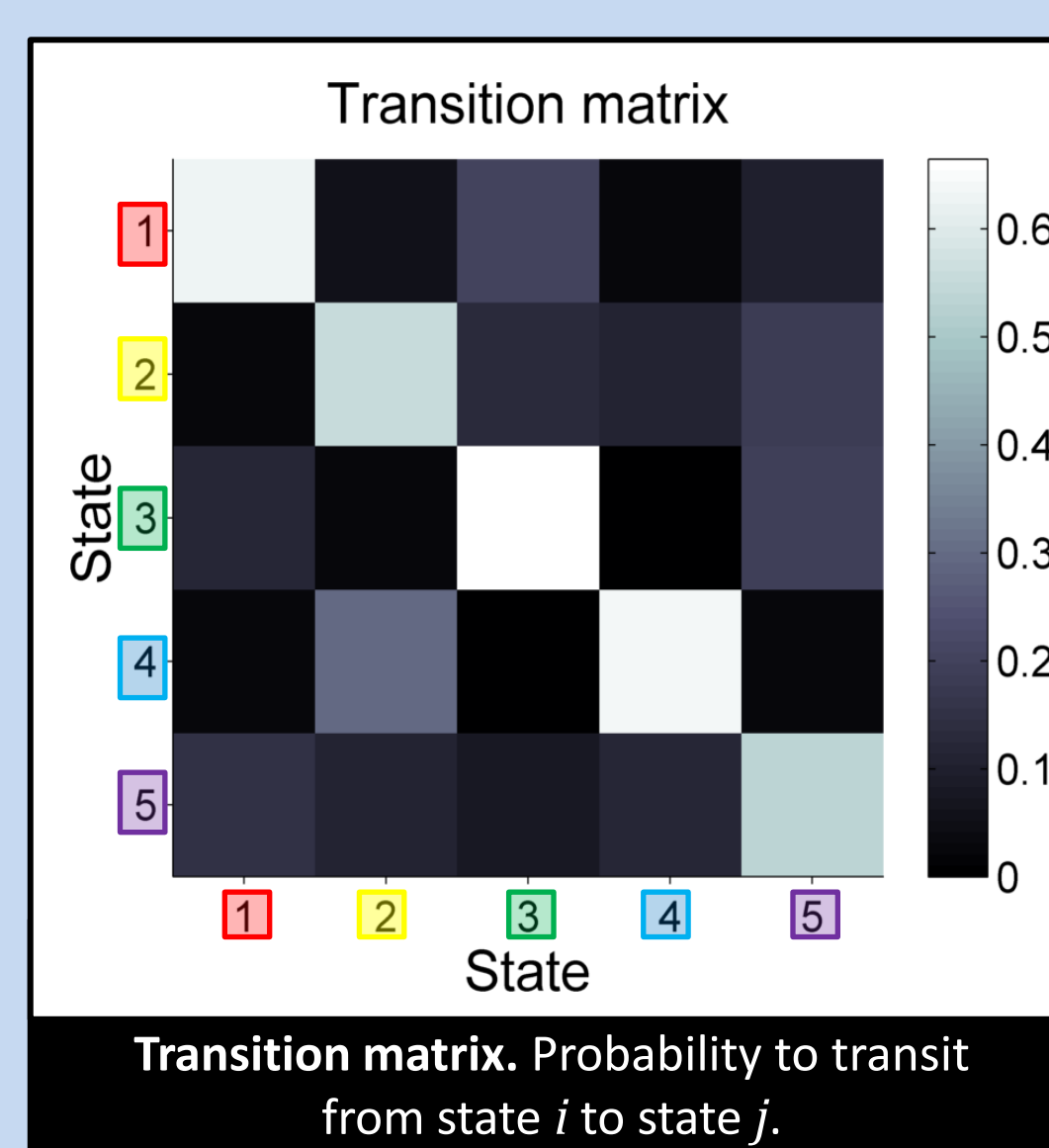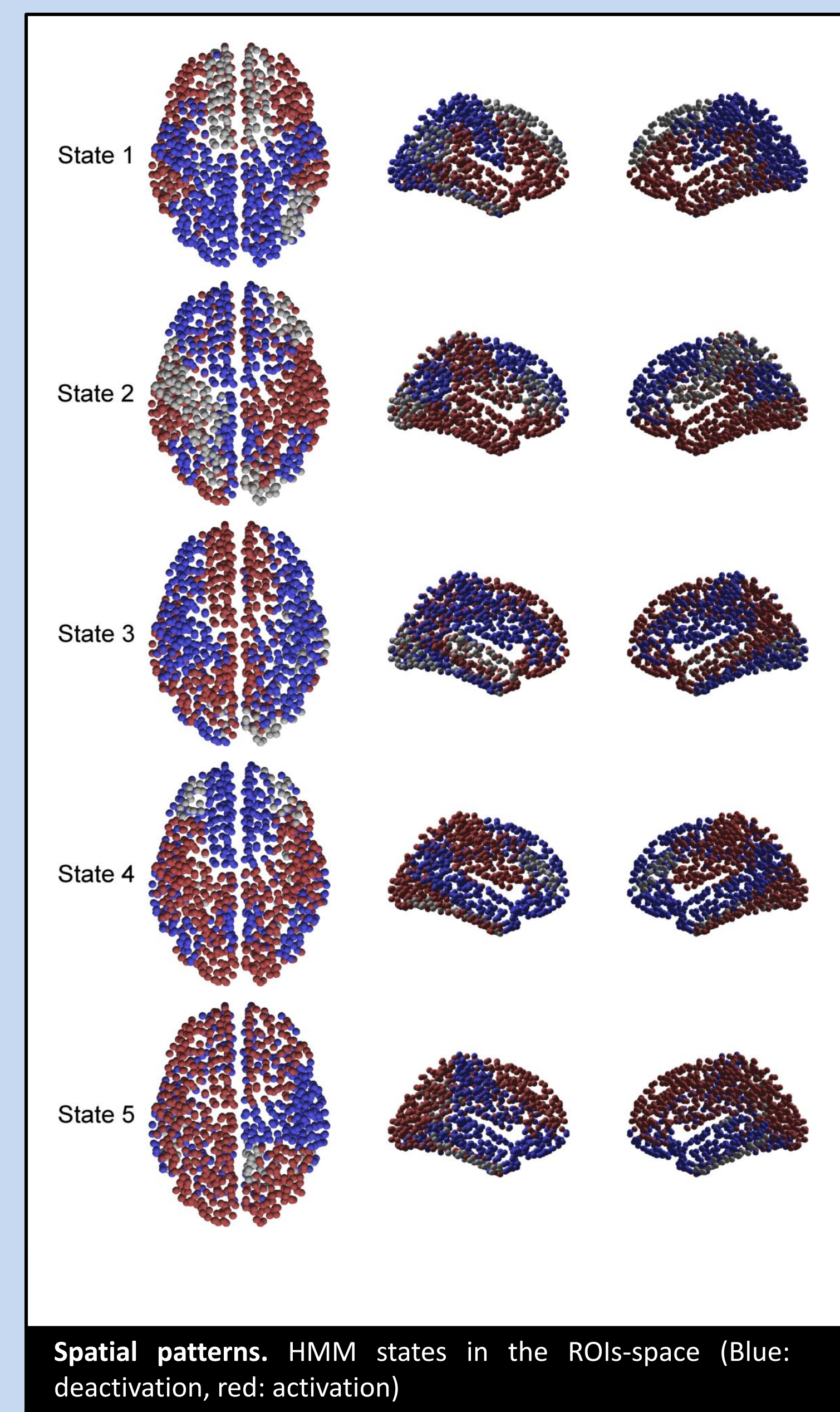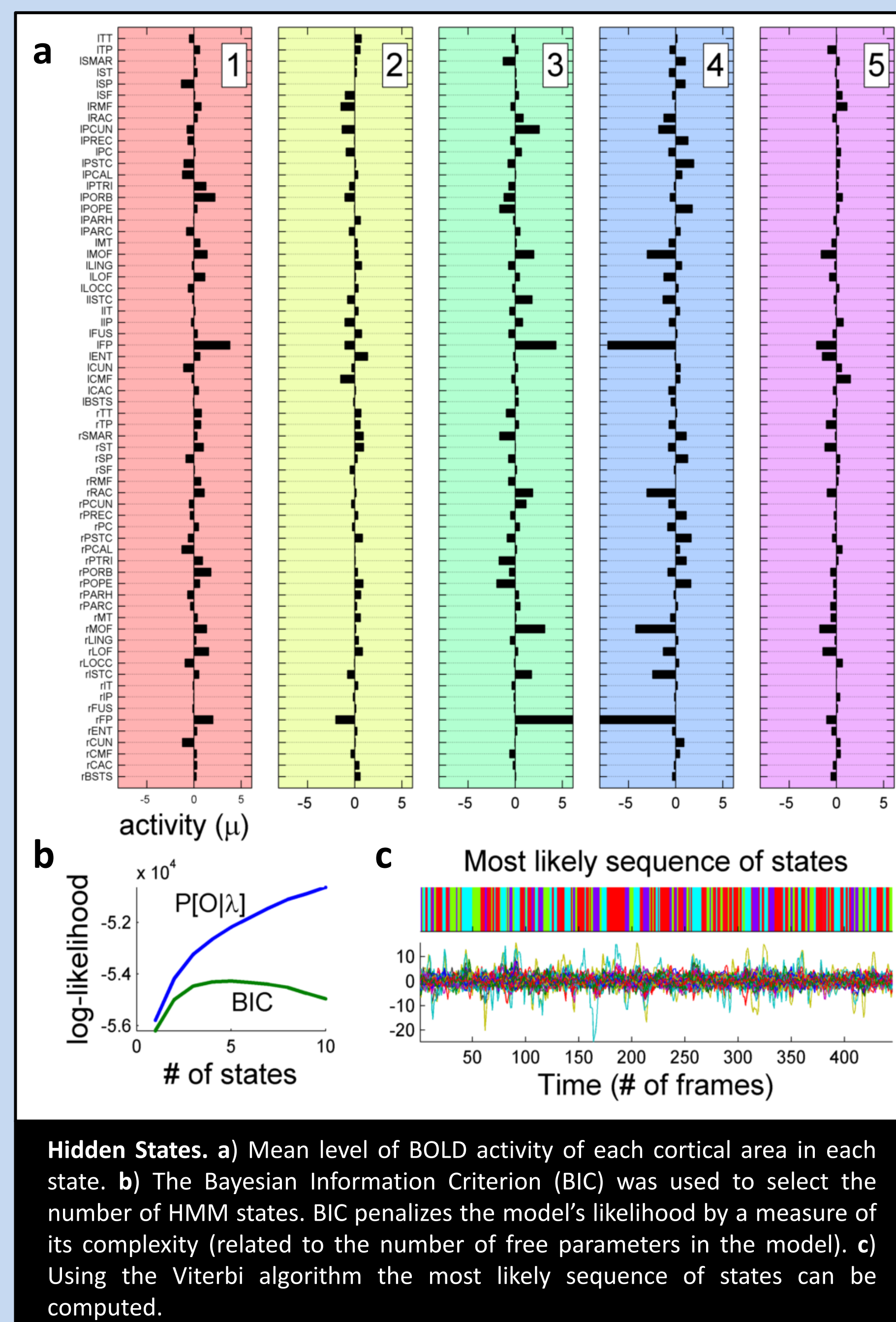
t-2   *t-1*   *t*   *t+1*
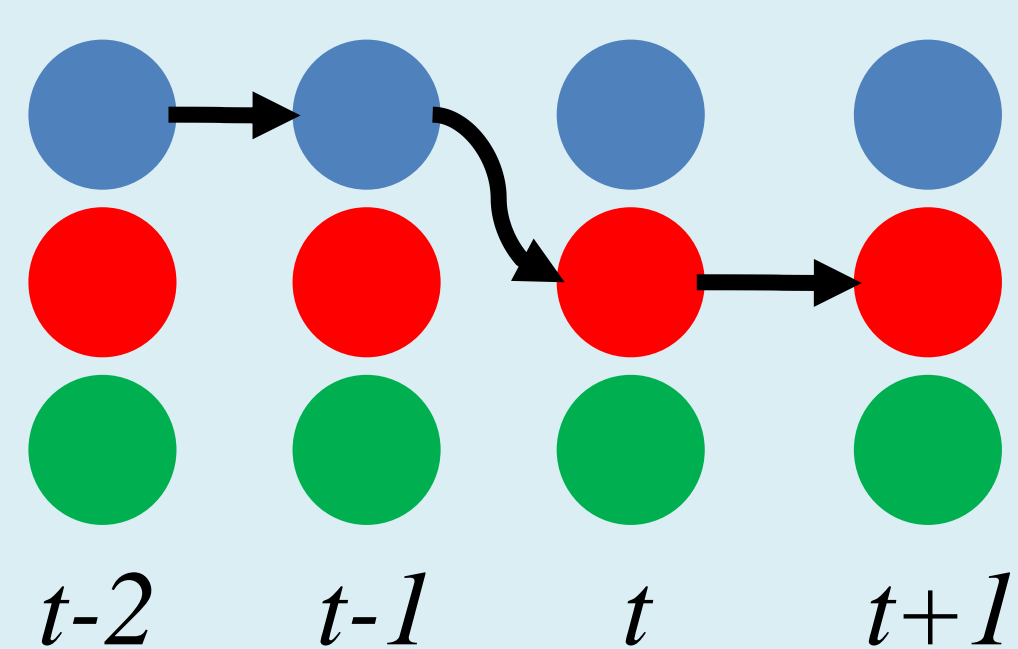
- The transition matrix and the means and variances in each state are estimated from the data (through a likelihood expectation-maximization algorithm [6]) .

- Once the optimal model parameters are estimated, the most likely sequence of states can be computed [6].
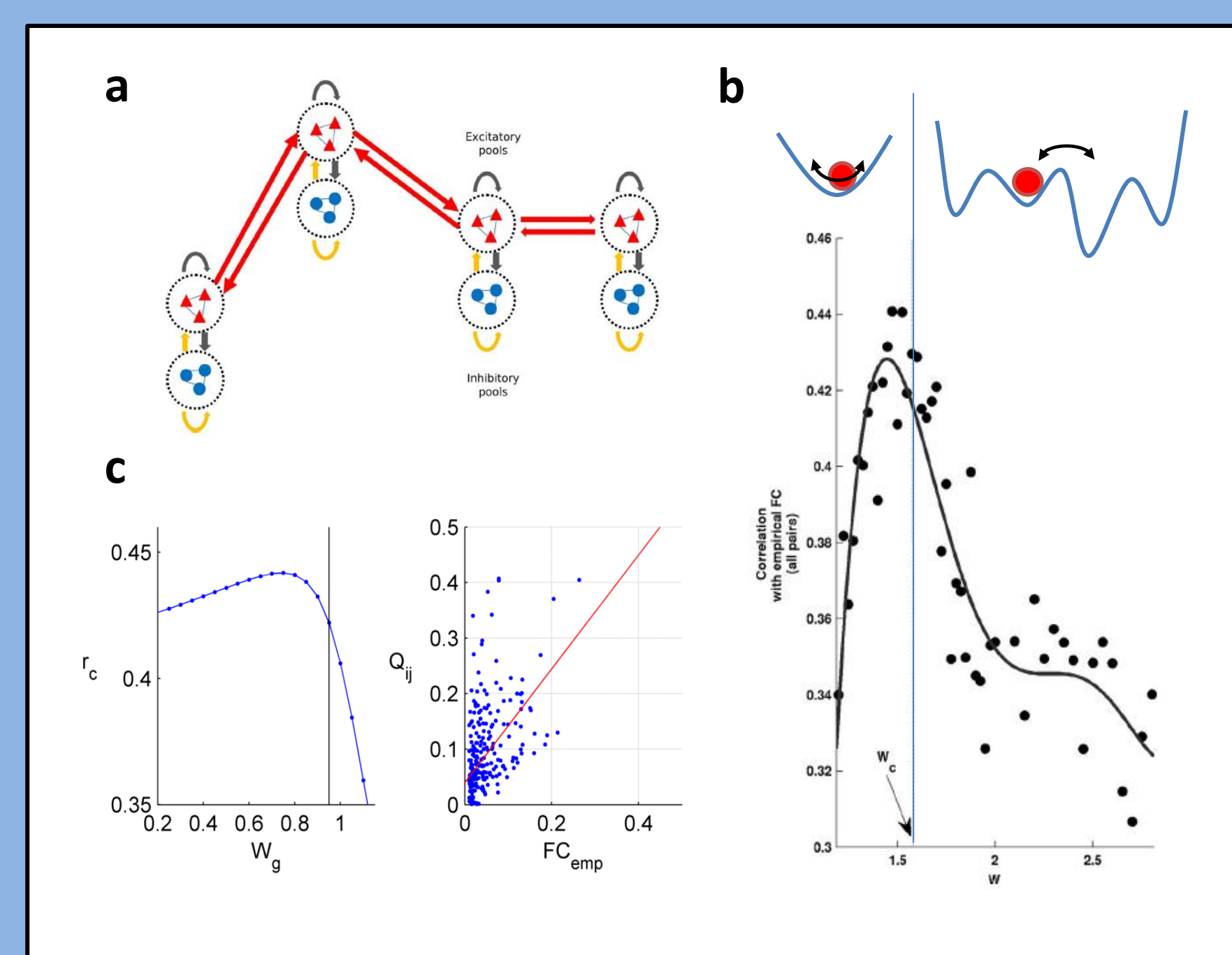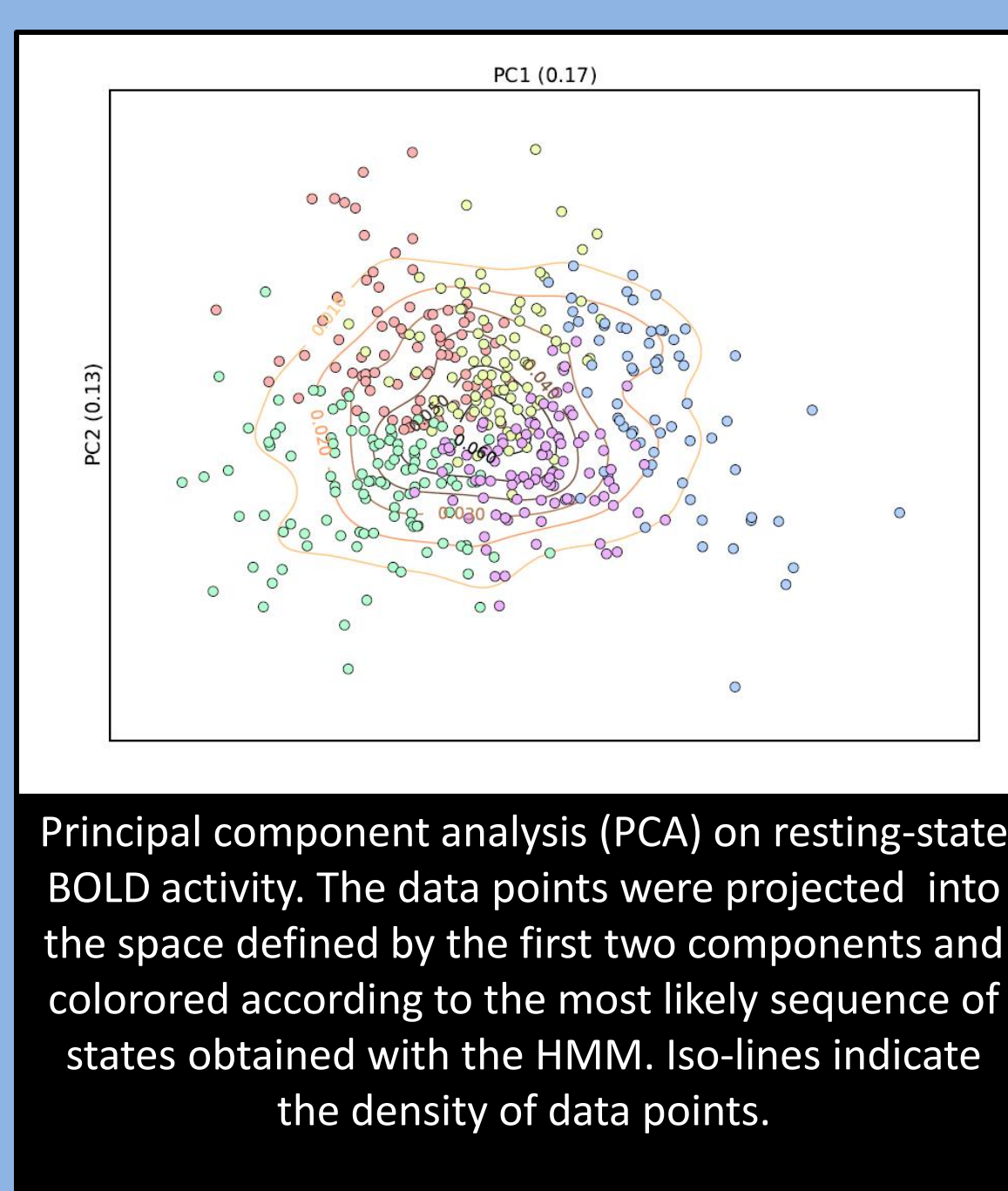
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HMM on fMRI resting-state data

Hidden States. a) Mean level of BOLD activity of each cortical area in each state. **b)** The Bayesian Information Criterion (BIC) was used to select the number of HMM states. BIC penalizes the model's likelihood by a measure of its complexity (related to the number of free parameters in the model). **c)** Using the Viterbi algorithm the most likely sequence of states can be computed.

Spatial patterns. HMM states in the ROIs-space (Blue: deactivation, red: activation)

Transition matrix. Probability to transit from state *i* to state *j*.

Distribution of state lifetimes.

Dynamical regime of spontaneous activity

Principal component analysis (PCA) on resting-state BOLD activity. The data points were projected into the space defined by the first two components and colorored according to the most likely sequence of states obtained with the HMM. Iso-lines indicate the density of data points.

We modeled the resting-state dynamics using a global spiking attractor network of the brain . **a)** The network contains at each node excitatory pyramidal cells and inhibitory interneurons. By integrating the biologically realistic DTI/DSI based neuro-anatomical connectivity into the brain model, the resultant emerging resting state functional connectivity (FC) of the brain network fits quantitatively best the experimentally observed FC in humans when the brain network operates at the edge of a bifurcation separating the spontaneous state and the multi-stability region (**b**). Results published in [7]. **c)** Using perturbation analysis we obtained equations for means, variances and covariances in a reduced version of the model. As result, estimated covariances fit quantitatively best the empirical FC at the edge of the bifurcation.

CONCLUSIONS

The HMM is an effective tool to identify spatial patterns of BOLD resting-state activity and to detect the moments during which these patterns are activated.

We found that state lifetimes follow an exponential distribution, suggesting that state sequences are stochastic.

HMM may be useful to get insight about the dynamical state of spontaneous activity.