From Static to Fast Transient Dynamic Brain Networks

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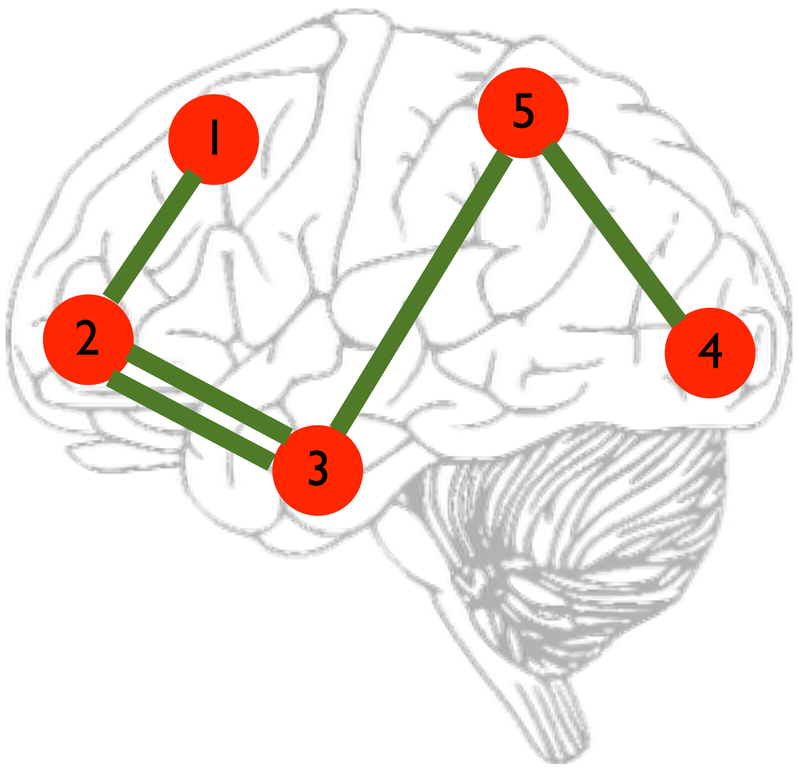
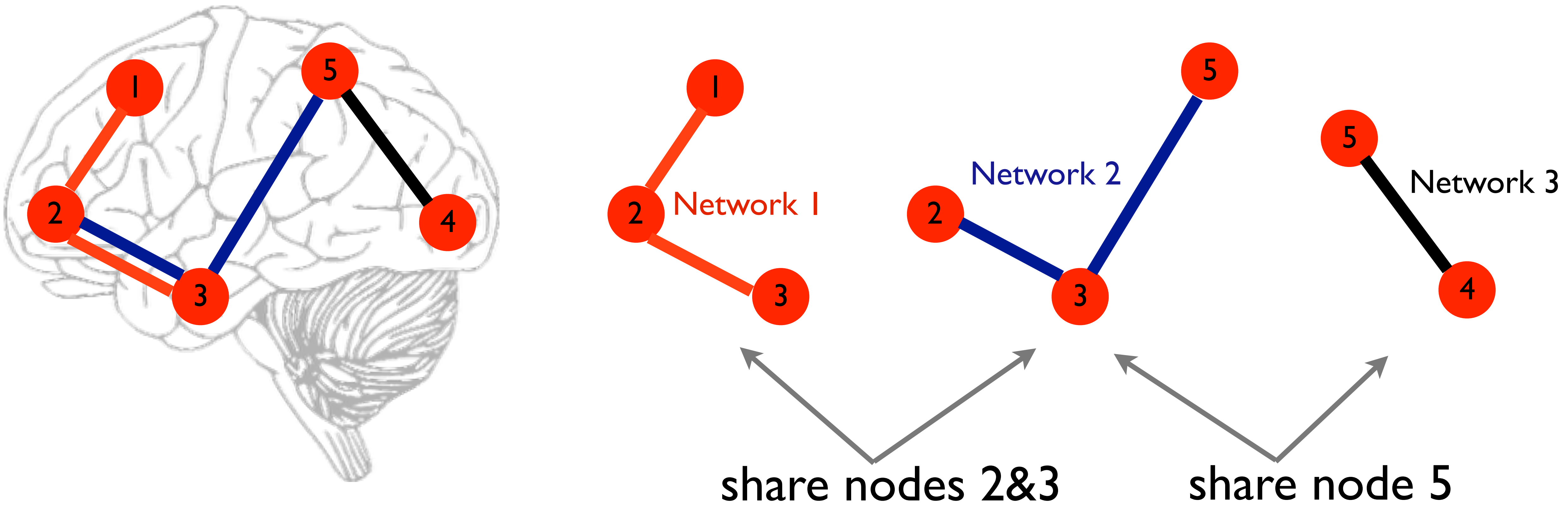
Resting state network



Resting state network



Network 1, 2 and 3 have distinct spatial and temporal characteristics that could not have been found in a static analysis

Goals

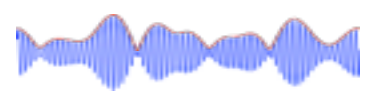
- What is happening at **faster** time-scales?
- What are the specific temporal interactions, or network dynamics?
- How activity organises temporally and spatially in rest, and how connectivity is modulated in task

Can we use MEG to answer these questions?

State-of-the-art methods: ICA

Temporal Independent Component Analysis

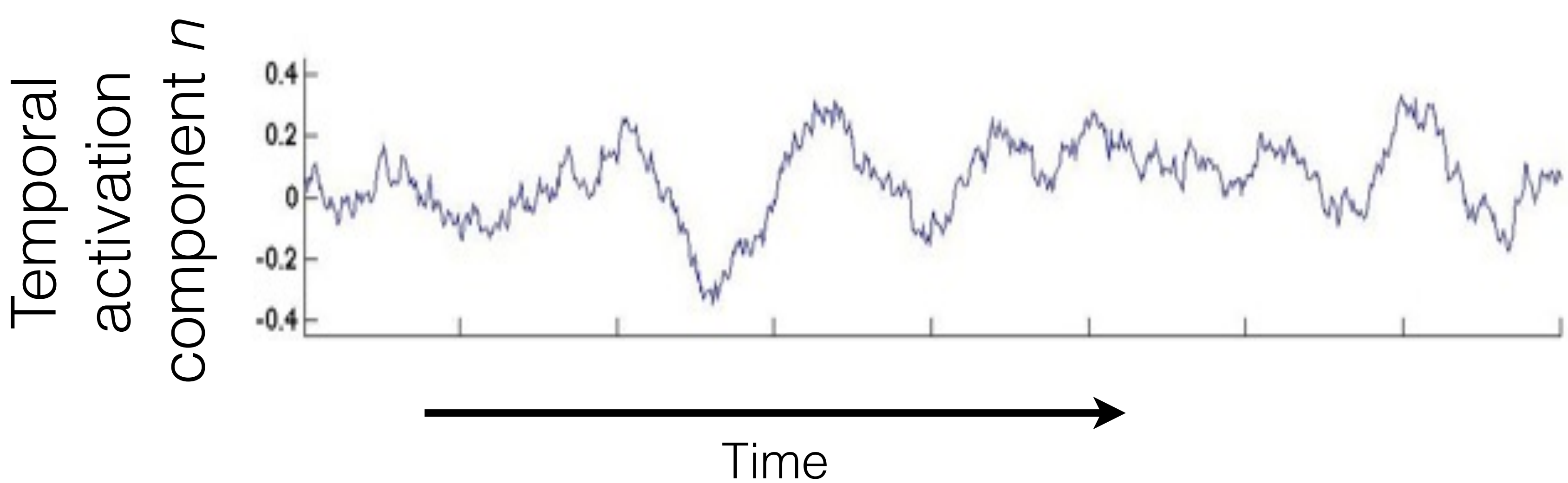
- Activation pattern or components (A)
- Component time courses (S)

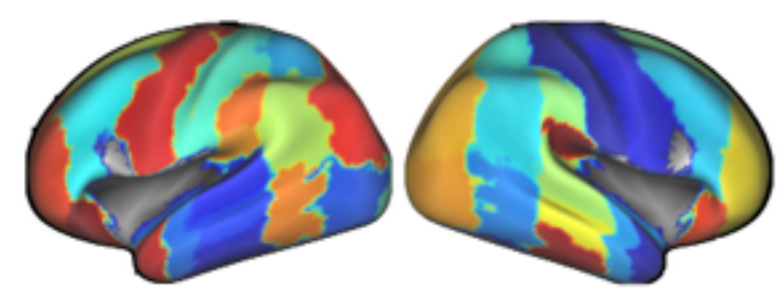
- Specified on power time series 
- Components do not reflect functional connectivity

$$X = S \quad A$$

time × regions; time × components; components × regions

Spatial activation component *n*

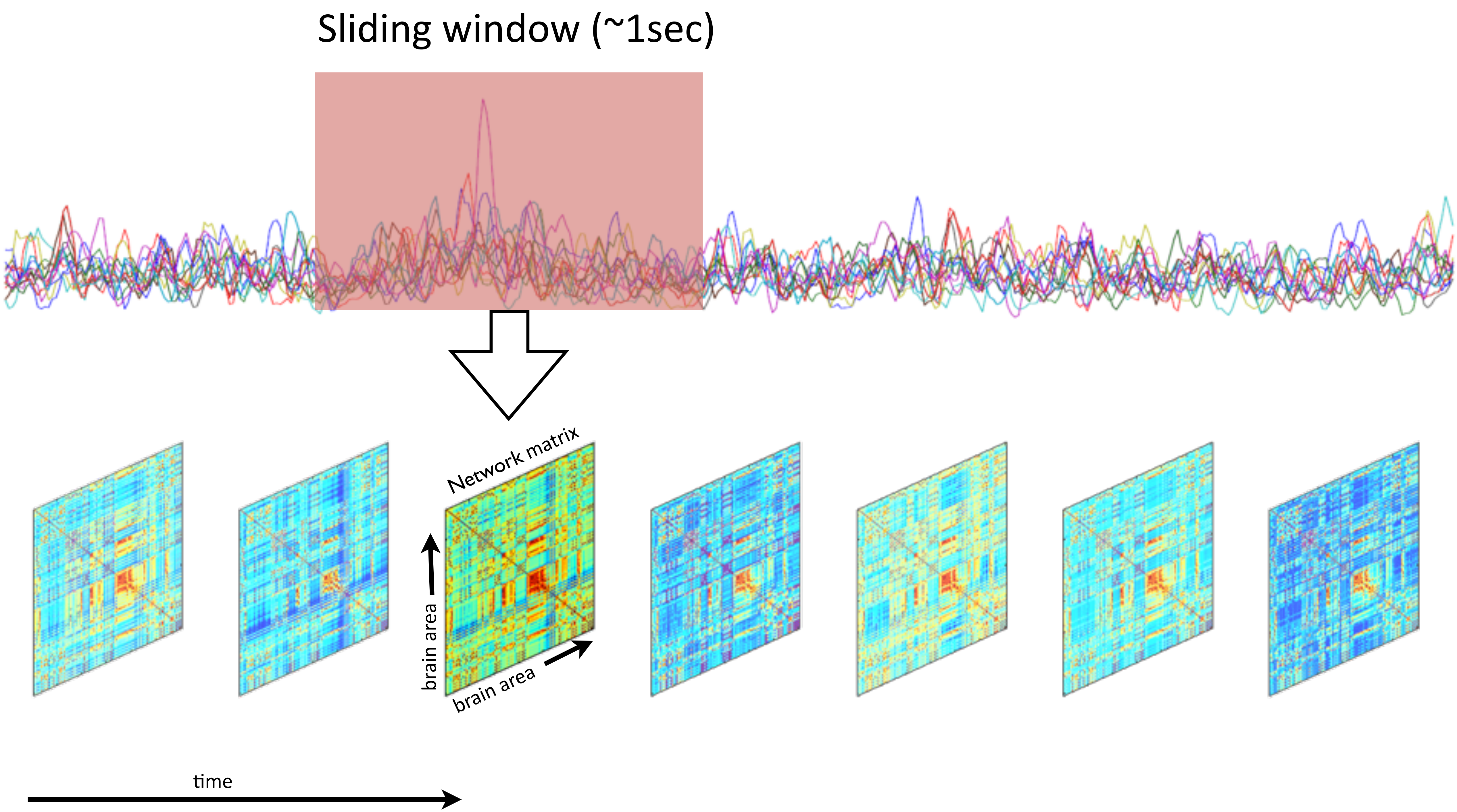




Brookes et al (PNAS 2011)

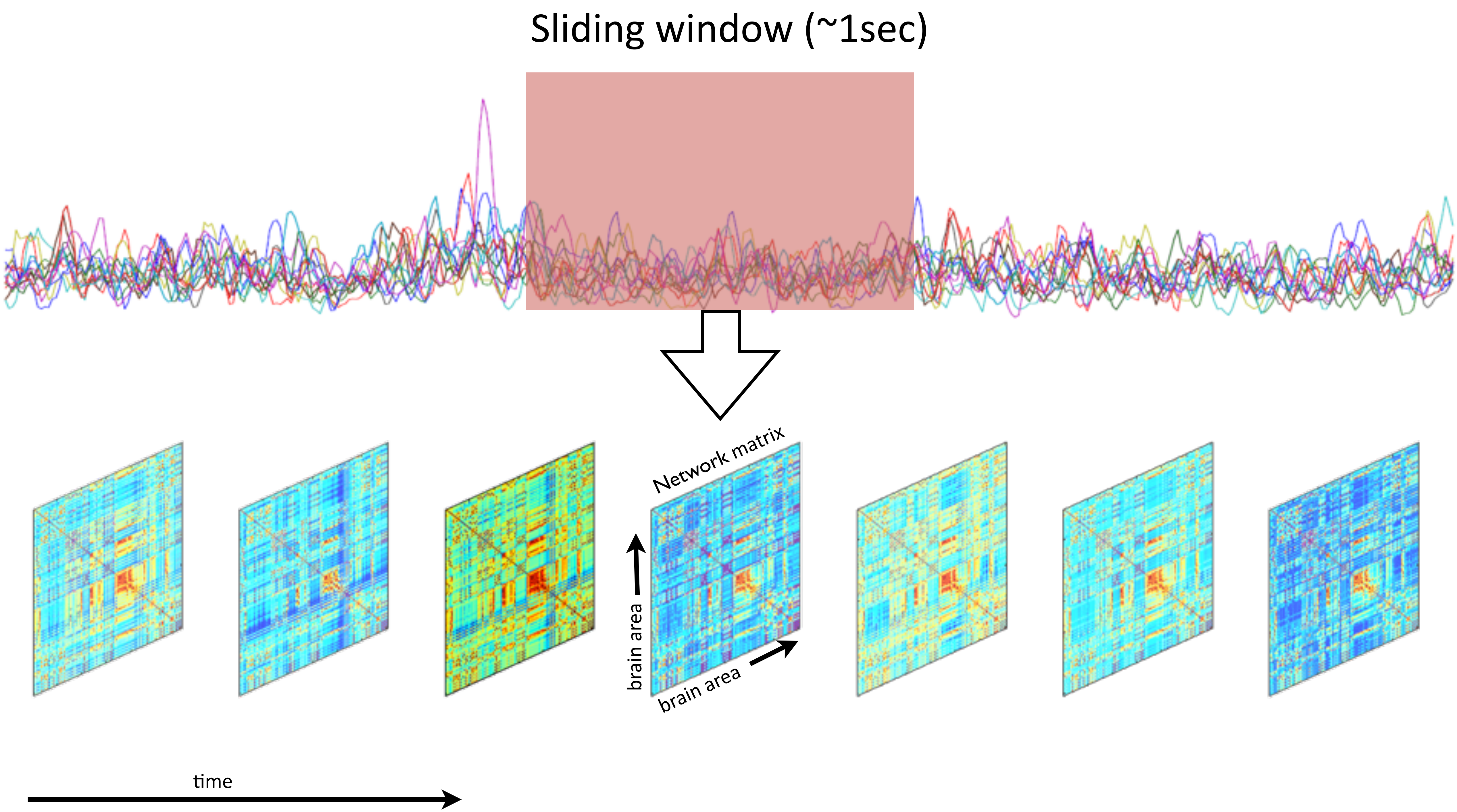
State-of-the-art methods: Sliding Windows

Compute **sliding window** correlation network matrices

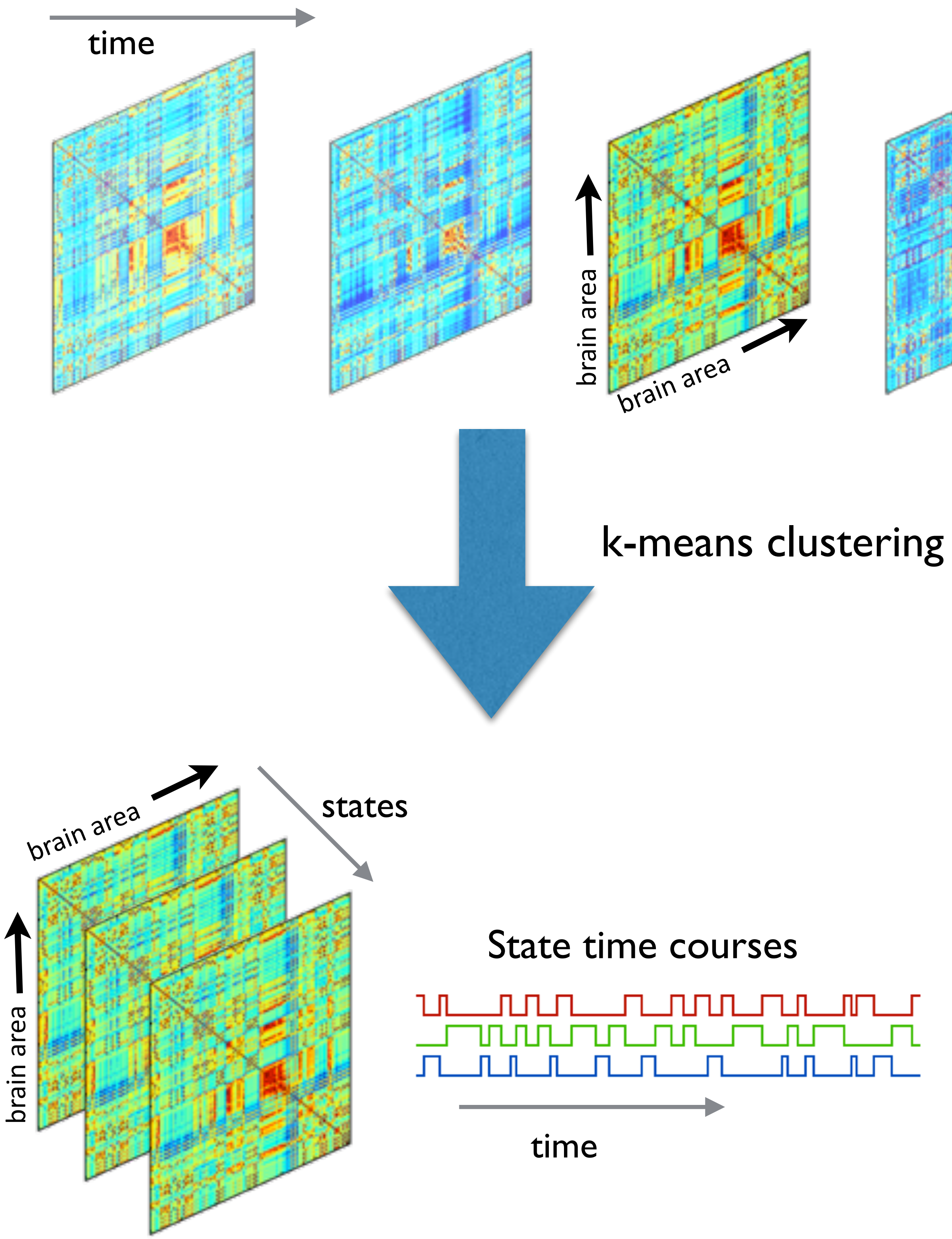


State-of-the-art methods: Sliding Windows

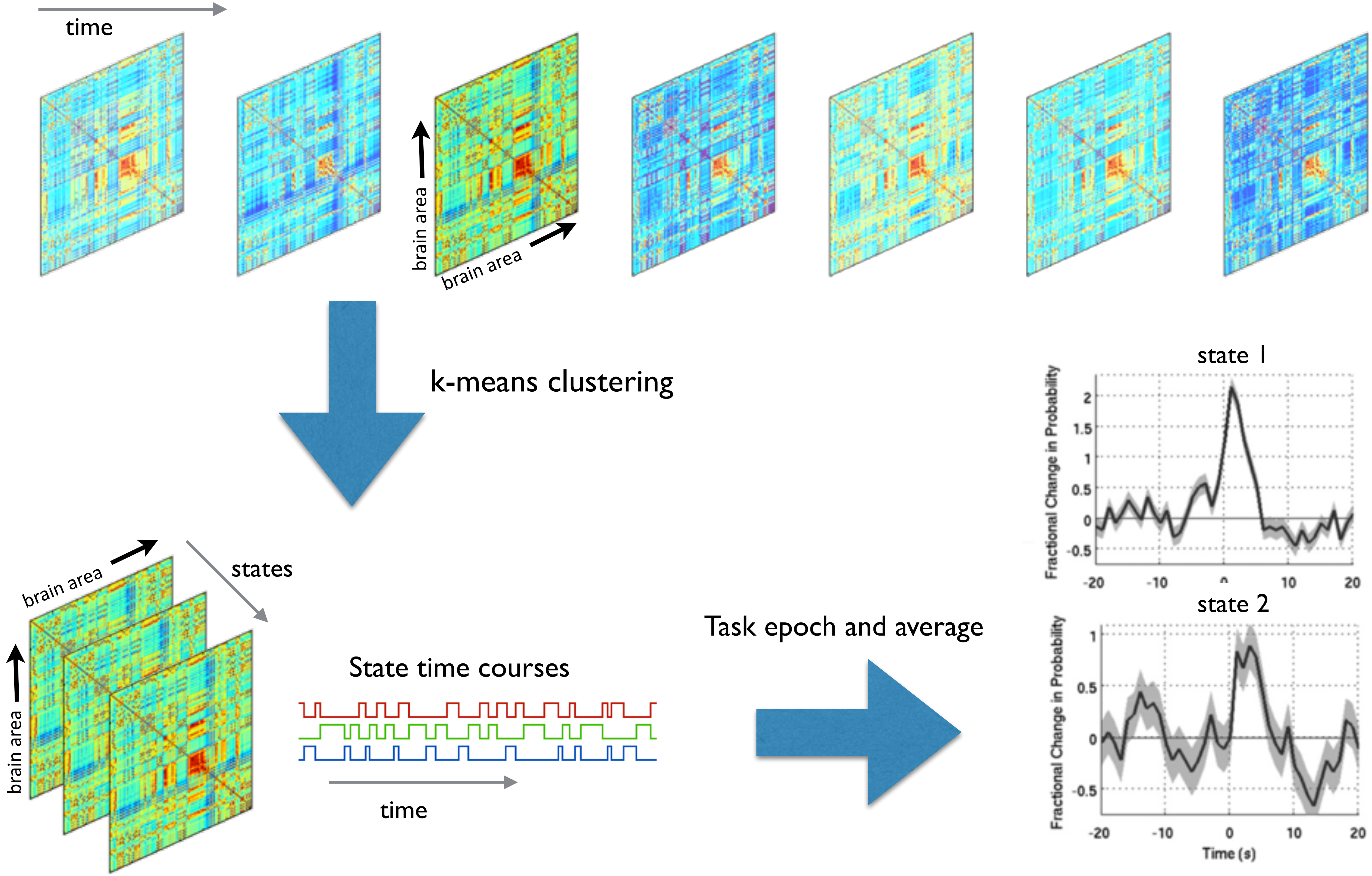
Compute **sliding window** correlation network matrices



State-of-the-art methods: Sliding Windows



State-of-the-art methods: Sliding Windows



O'Neil et al.; Neuroimage (2015)

State-of-the-art methods: Sliding Windows

Issues:

How to choose the width of the window?

- too short - unstable, unreliable estimation
- too long - misses quick changes

Inefficient use of the data

- No matter how much data we have, each estimation is based on a small portion of the data

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Can sliding-window correlations reveal dynamic functional connectivity in resting-state fMRI?

R. Hindriks [a,*], M.H. Adhikari [a], Y. Murayama [d], M. Ganzetti [b,c], D. Mantini [b,c], N.K. Logothetis [d], G. Deco [a,e]
[a] Center for Brain and Cognition, Computational Neuroscience Group, Department of Information and Communication Technologies, Universitat Pompeu Fabra, Barcelona, Spain
[b] Department of Health Sciences and Technology, ETH Zurich, Switzerland
[c] Department of Experimental Psychology, University of Oxford, United Kingdom
[d] Department of Physiology of Cognitive Processes, Max Planck Institute for Biological Cybernetics, Tübingen, Germany
[e] Institució Catalana de la Recerca i Estudis Avançats (ICREA), Universitat Pompeu Fabra, Barcelona, Spain

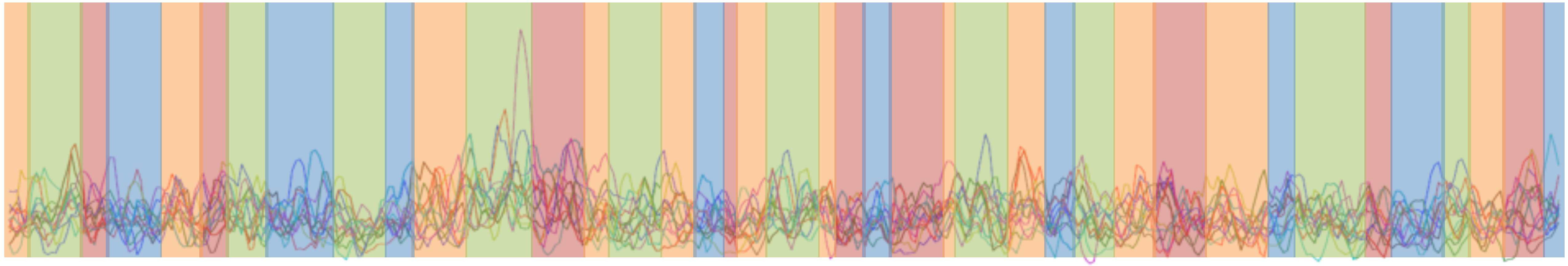
Cerebral CORTEX
ORIGINAL ARTICLE

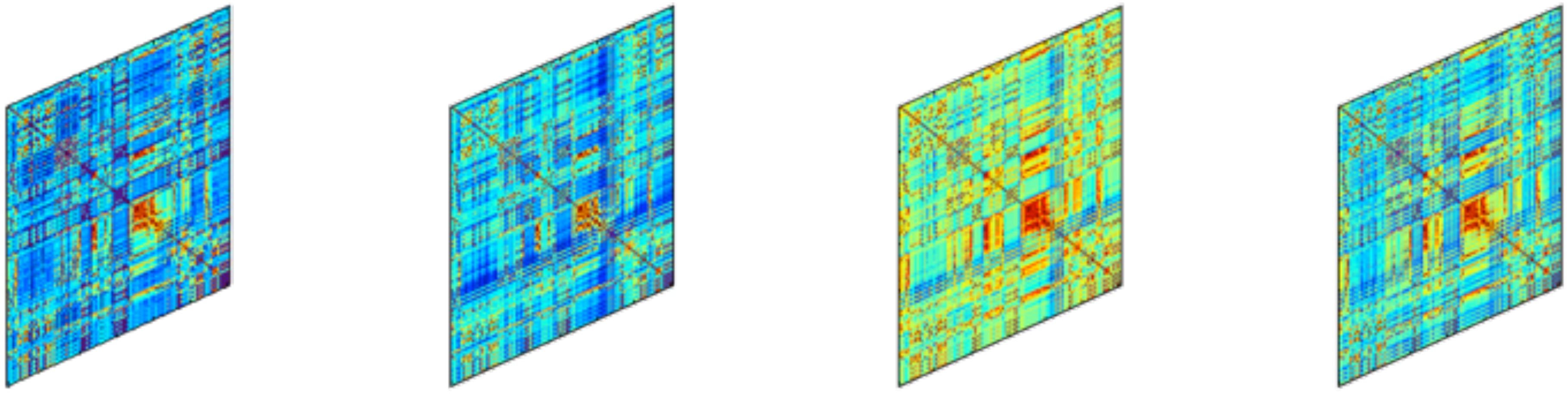
On the Stability of BOLD fMRI Correlations

Timothy O. Laumann[1], Abraham Z. Snyder[1,2], Anish Mitra[2], Evan M. Gordon[3,4], Caterina Gratton[1], Babatunde Adeyemo[1], Adrian W. Gilmore[5], Steven M. Nelson[3,4], Jeff J. Berg[5], Deanna J. Greene[2,6], John E. McCarthy[7], Enzo Tagliazucchi[8,9], Helmut Laufs[9,10], Bradley L. Schlaggar[1,2,6,11,12], Nico U. F. Dosenbach[1], and Steven E. Petersen[1,2,5,12]

Hidden Markov Model

Instead pool data over disjoint time periods:





State 1 State 2 State 3 State 4

Hidden Markov Model

Fundamental assumptions

- One state is assumed at a time

  although a we effectively estimate the probability of each state being active at each time point t

- Which state is active at time *t* depends on which state was active at time point *t-1*

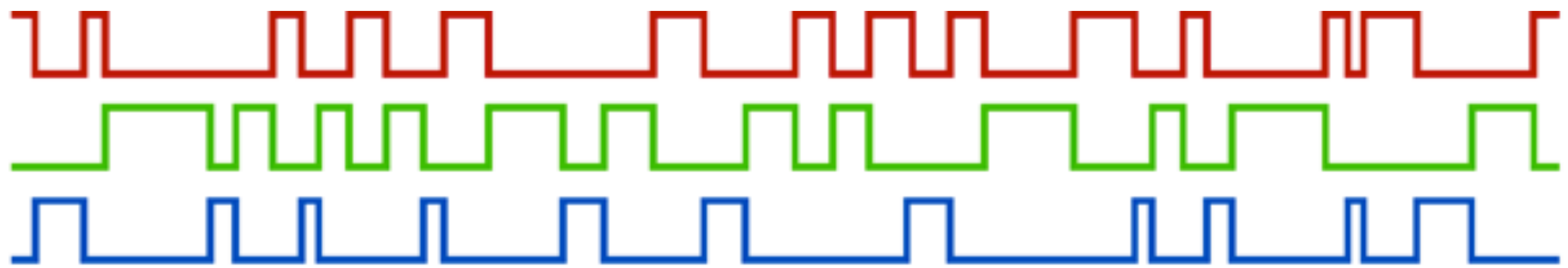
  which means that the influence of the past decreases exponentially

Benefits

- We do not need to specify the window length
- We make an efficient use of the data
- We can access the fastest time scales

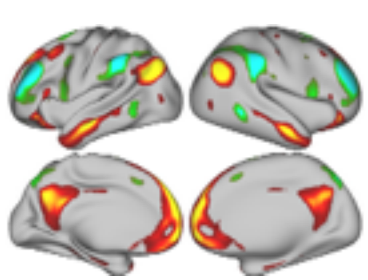
Hidden Markov Model

State time courses:
When

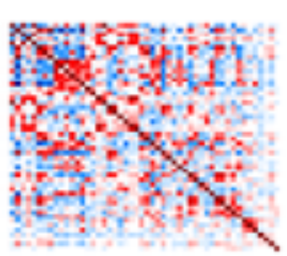


State probability distribution
(one for each state):
What

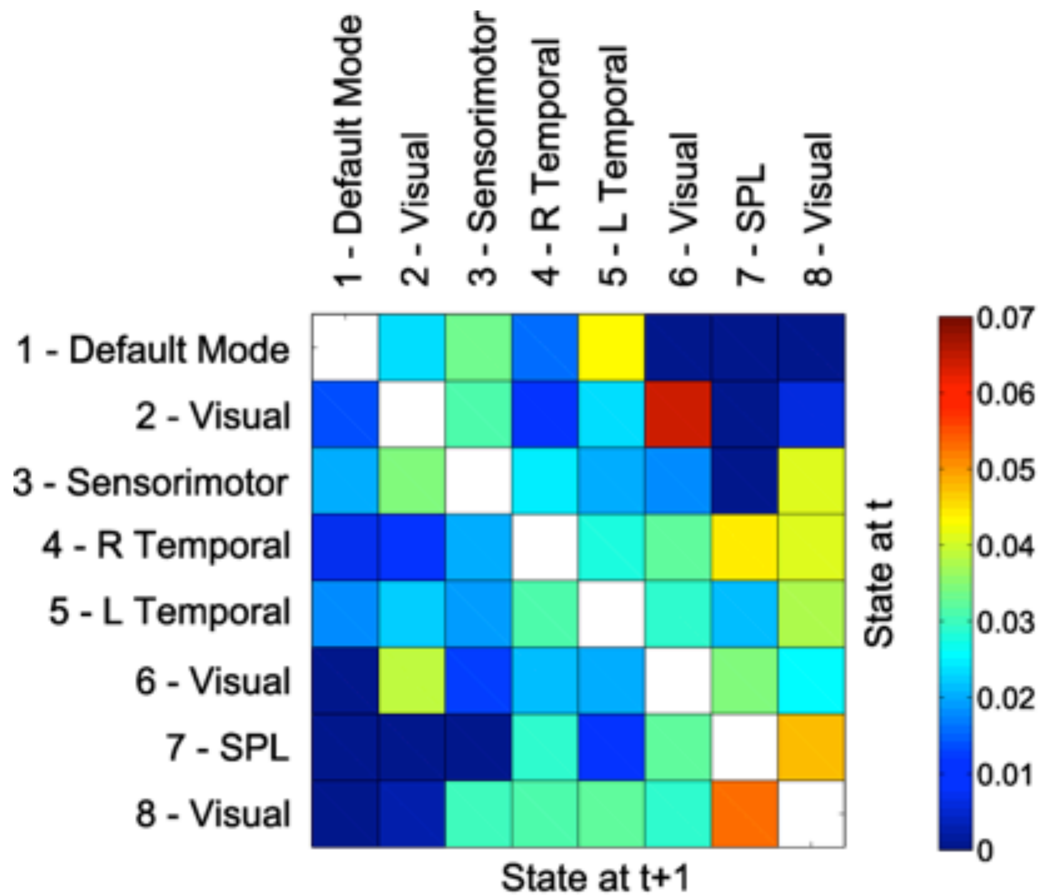
Mean activation



Functional connectivity



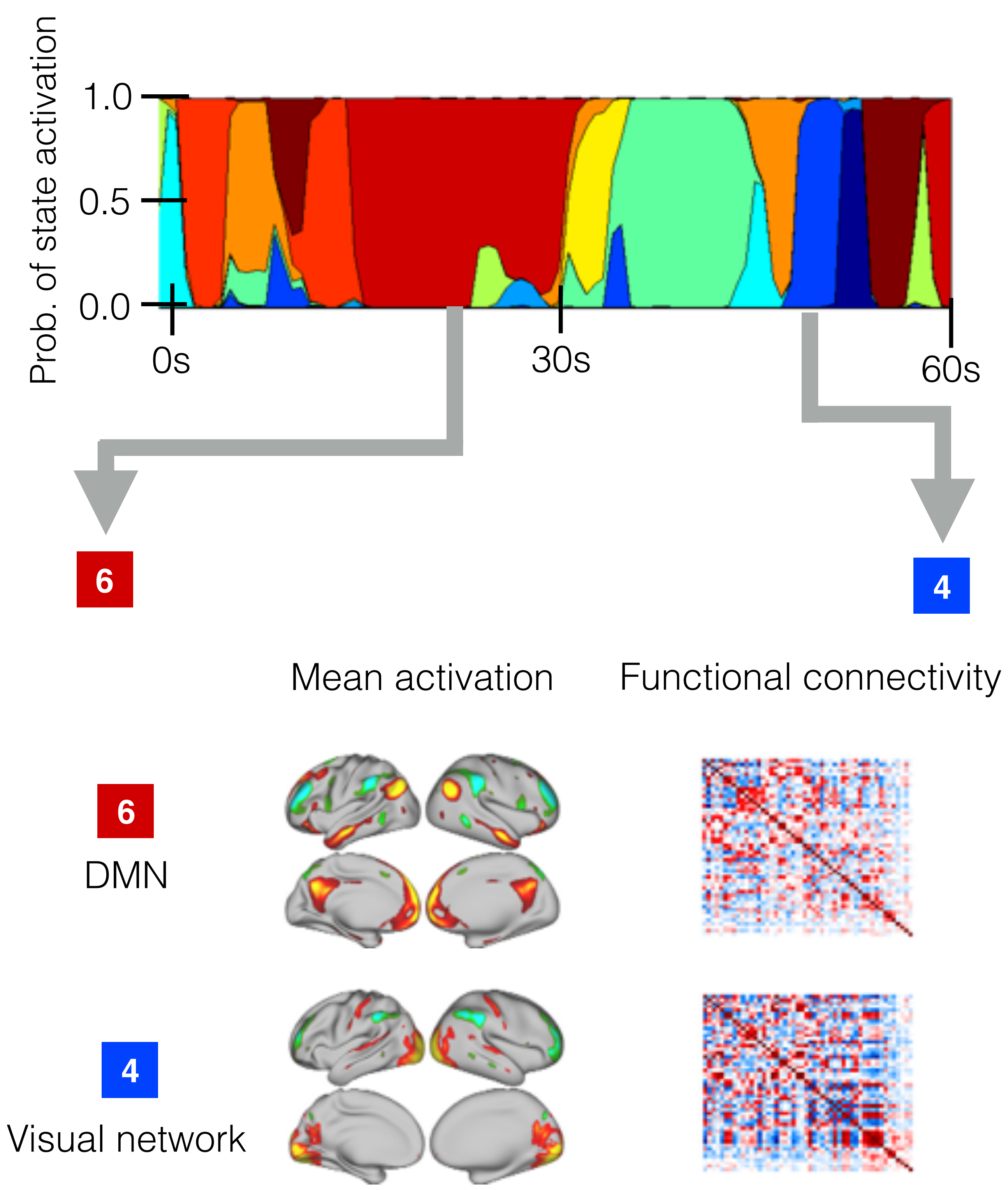
Different classes of probability distributions adapt to different classes of data
this is a user choice



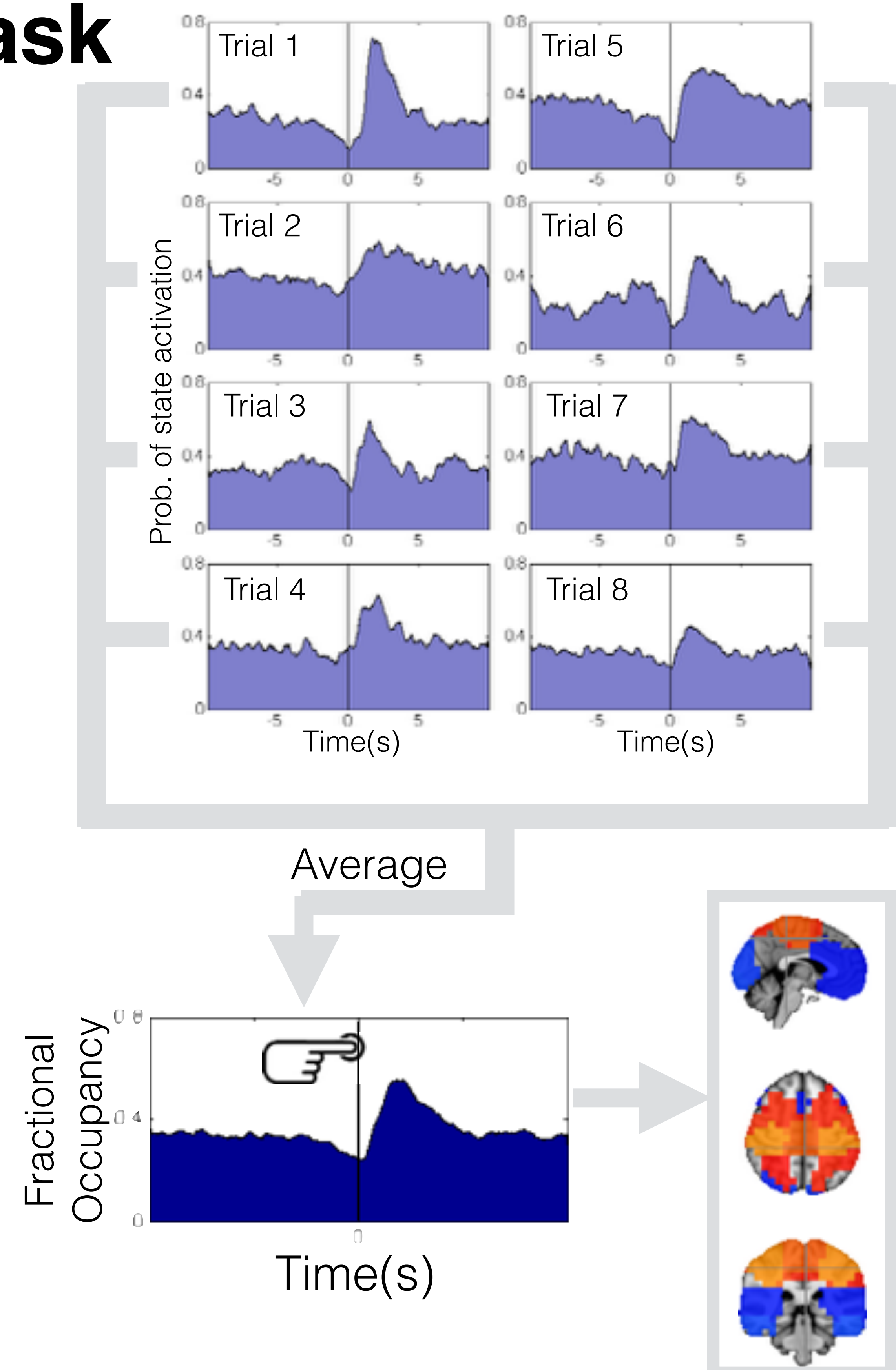
Transition probability matrix

Hidden Markov Model

In rest



In task



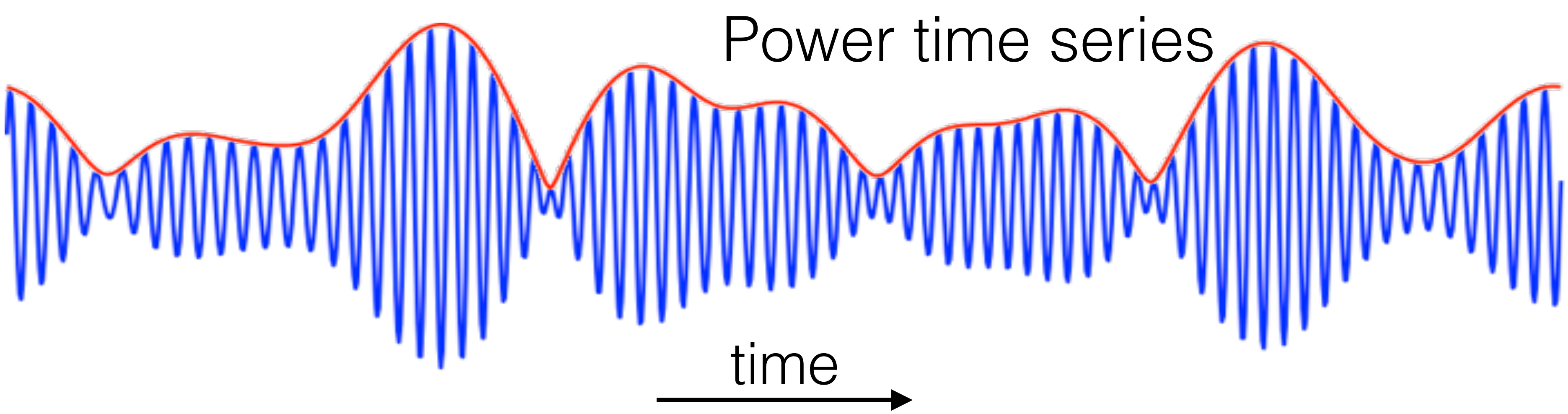
Hidden Markov Model

At the group level

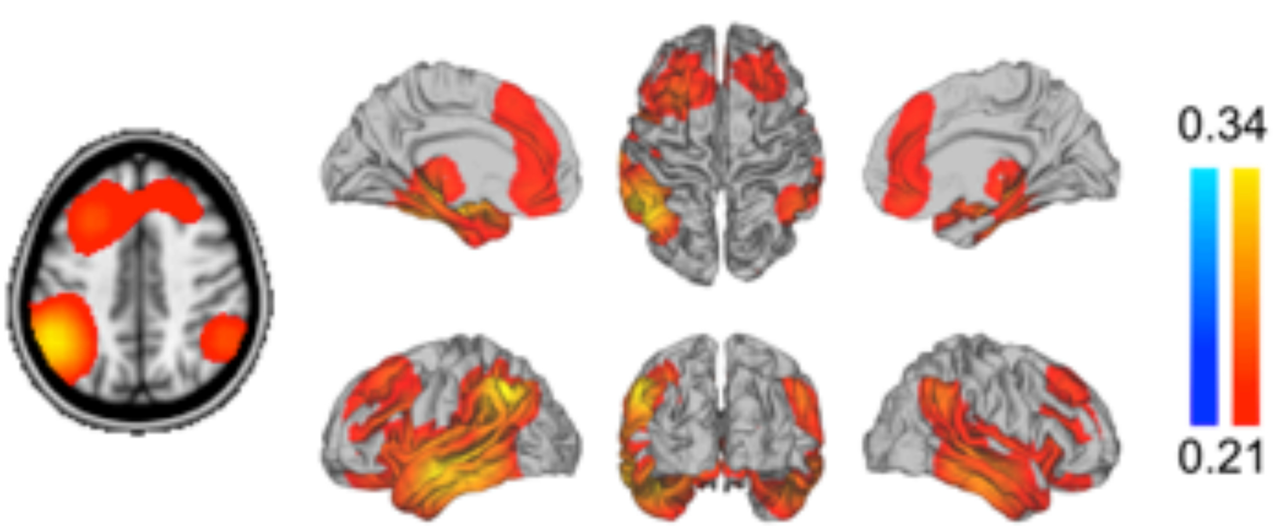
At the subject level

HMM-Gaussian

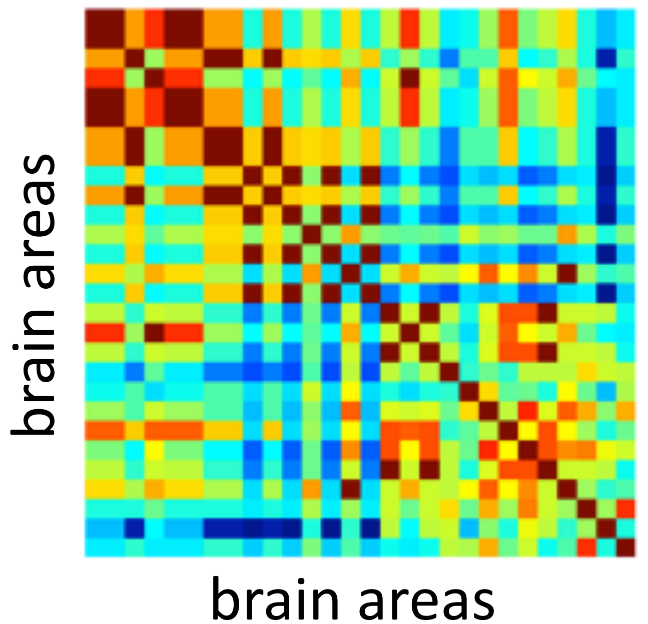
What is a brain state? A Gaussian distribution $\mathcal{N}(\mu,\Sigma)$



Mean activation μ

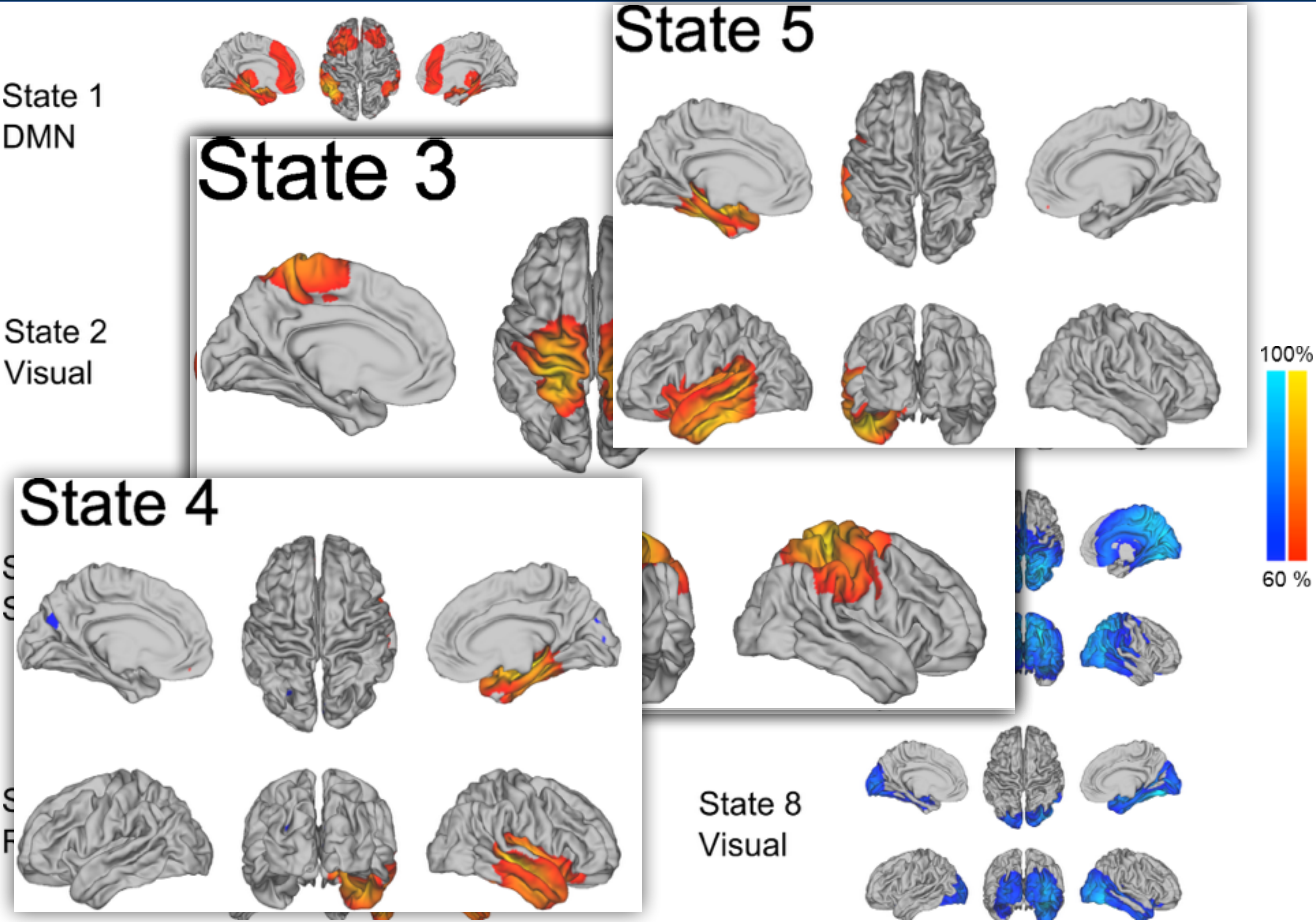


Network matrix Σ
(power correlation)

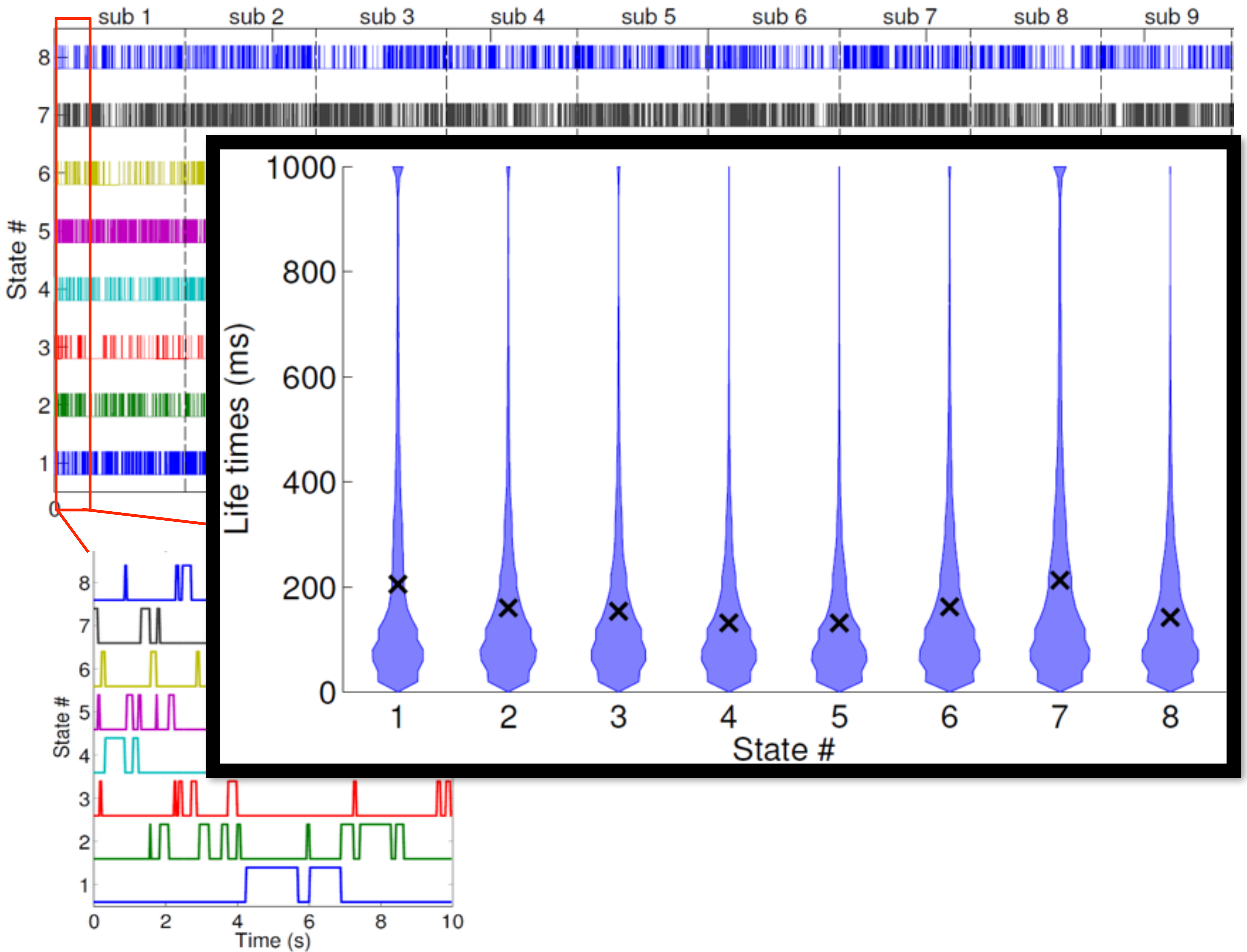


Baker et al (eLife 2014)

HMM-Gaussian



HMM-Gaussian

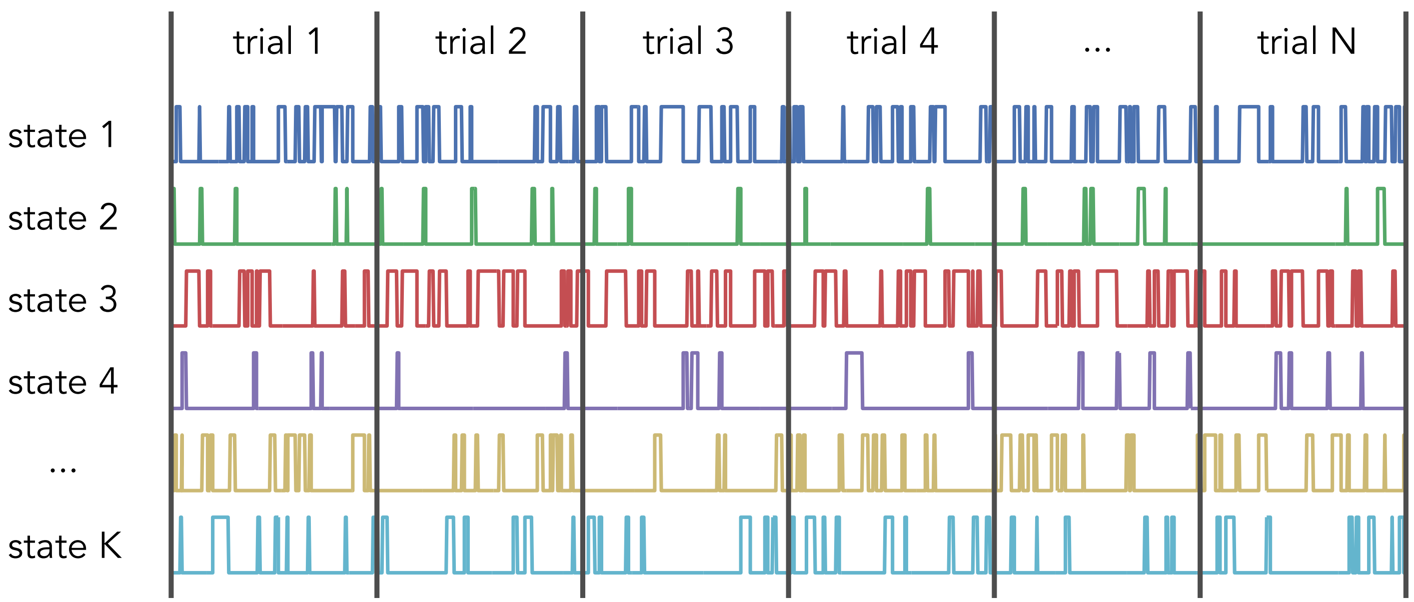


HMM-Gaussian

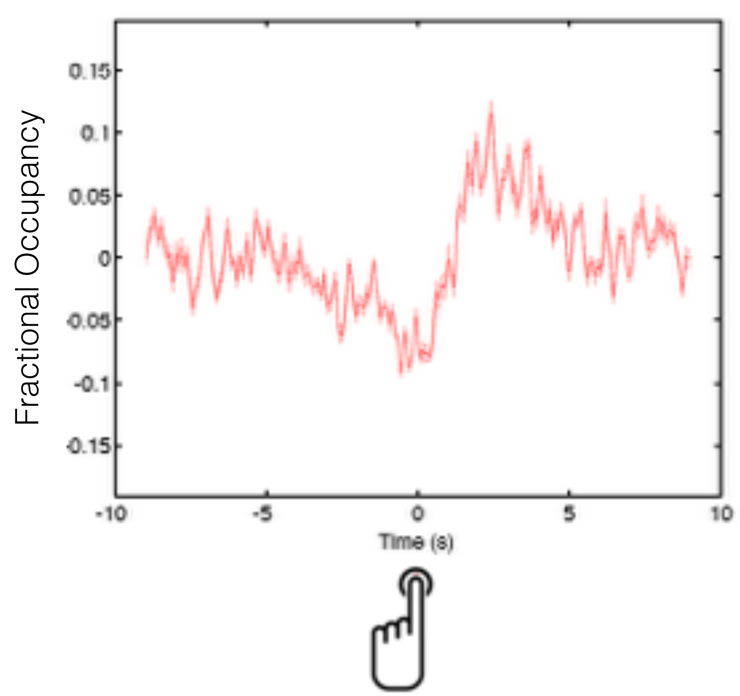
TASK DATA

- Fit HMM to task data, **then** epoch and average the state time courses over trials

HMM state time courses

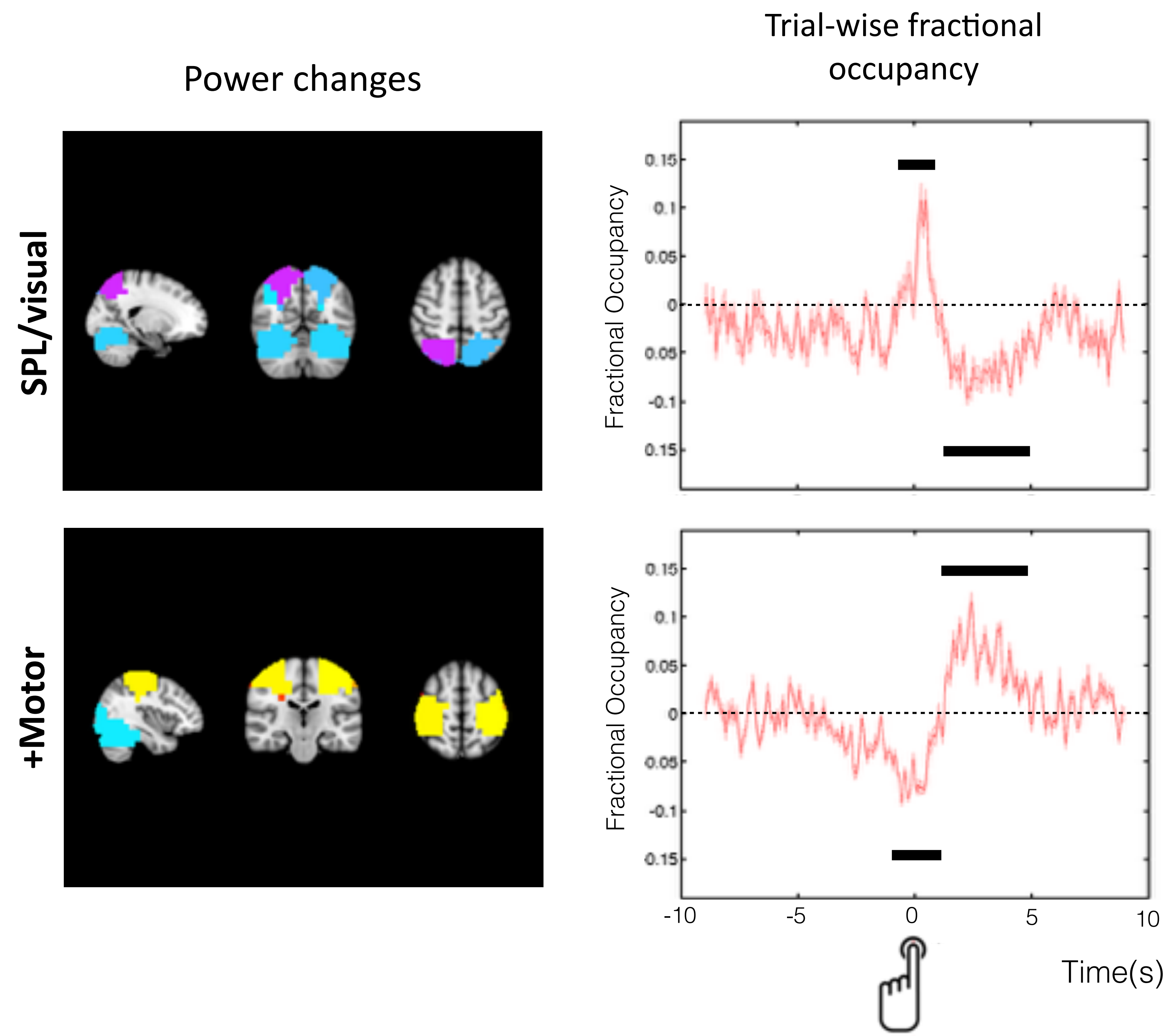


Fractional Occupancy



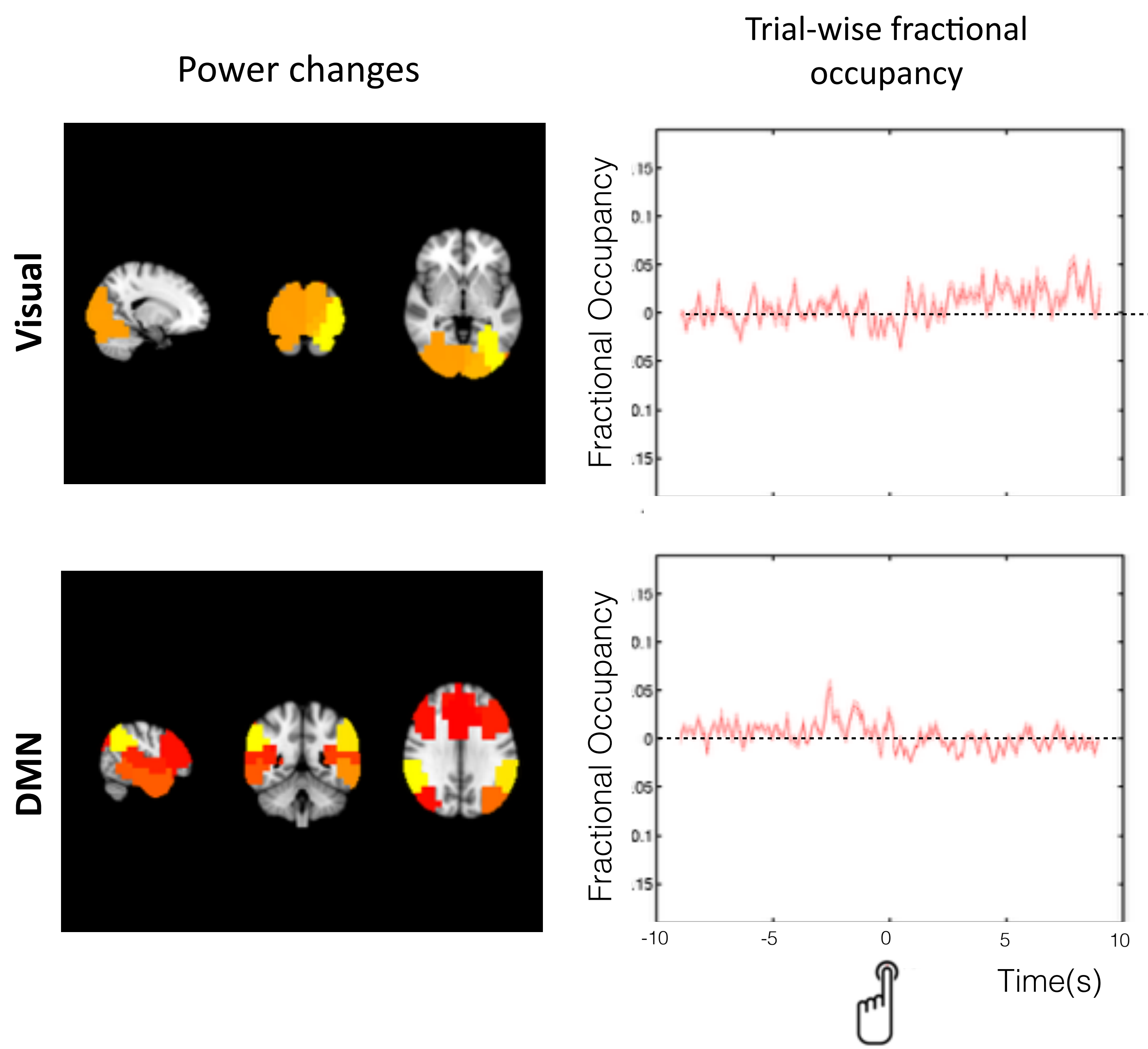
HMM-Gaussian

- **Task-related** HMM states
  - 10 subjects
  - 4-30Hz
  - 8 HMM states



HMM-Gaussian

- **Task-unrelated** HMM states
  - 10 subjects
  - 4-30Hz
  - 8 HMM states



HMM-Gaussian

To set an HMM-Gaussian:

```
> options = struct();
> options.K = 8;
> options.order = 0;
> options.zeromean = 0;
> options.covtype='full';
> [hmm,Gamma] = hmmmar(X,T,options);
```

No. of states

Model the mean

Full connectivity

HMM structure

State time courses

HMM-Gaussian

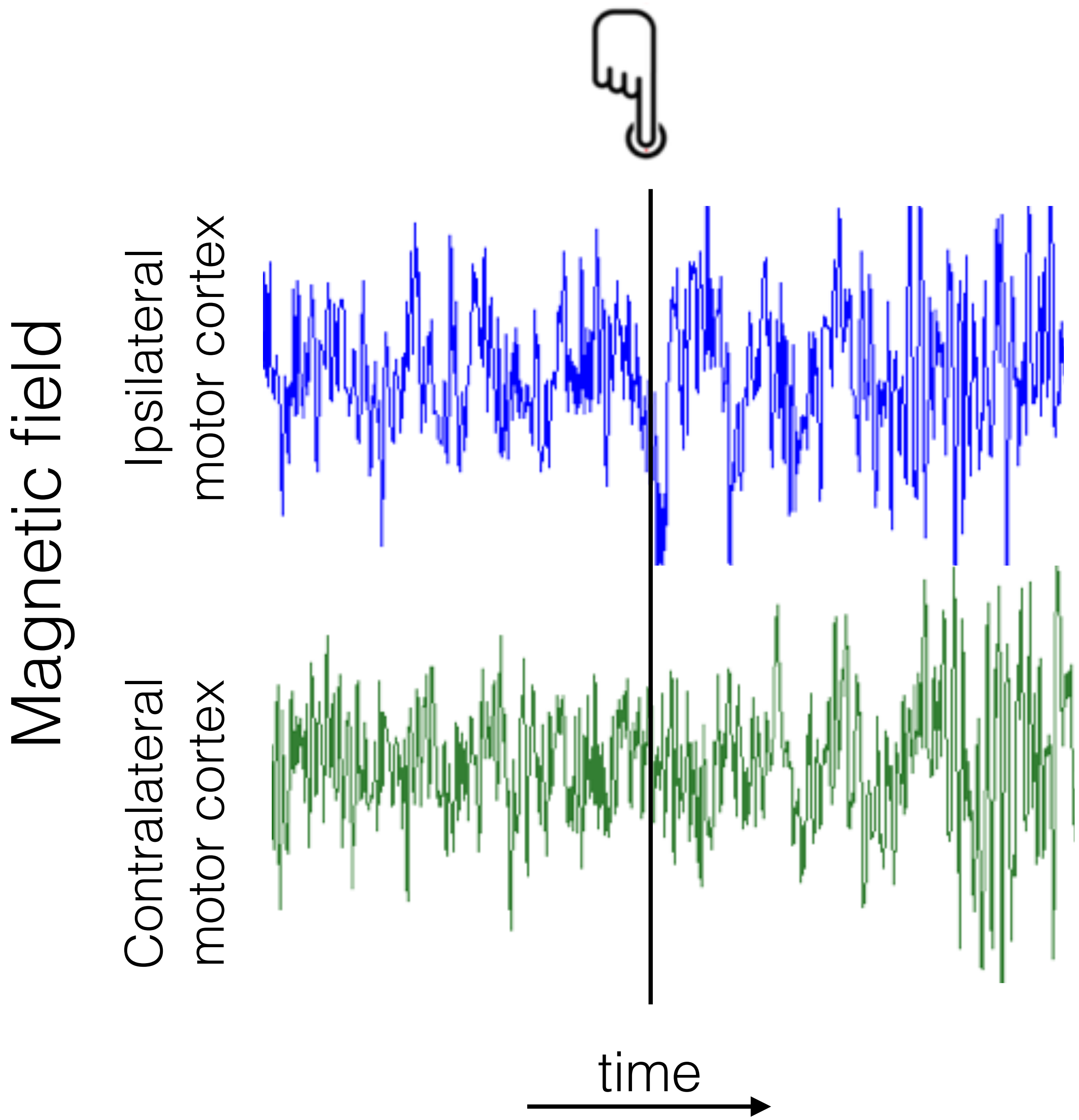
In summary:

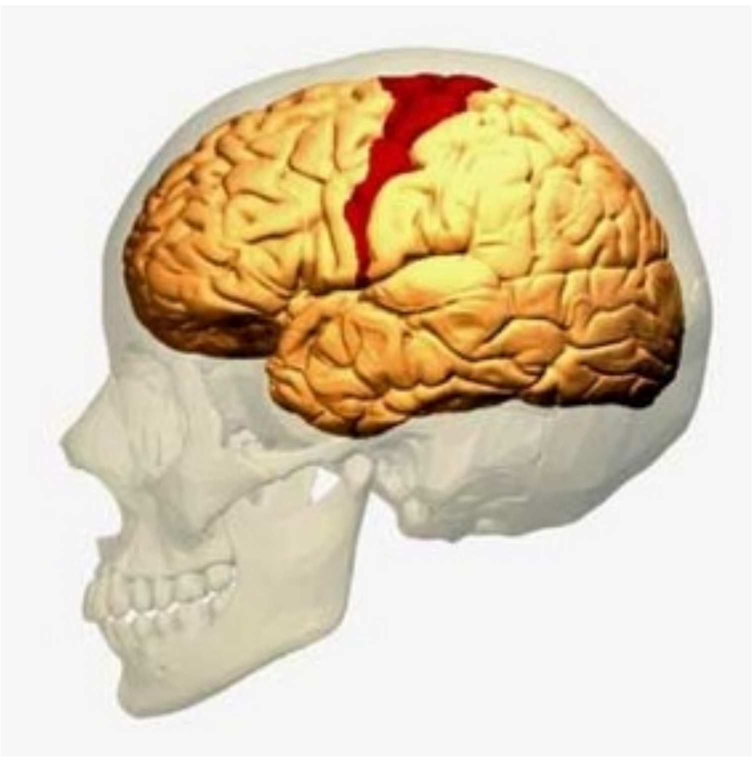
- The *HMM-Gaussian* focuses on **power** and **can be applied to whole brain**

- But: is insensitive to phase and is not frequency-resolved

HMM-MAR

what about working with raw time courses?
e.g. can we then find time-varying phase locking?

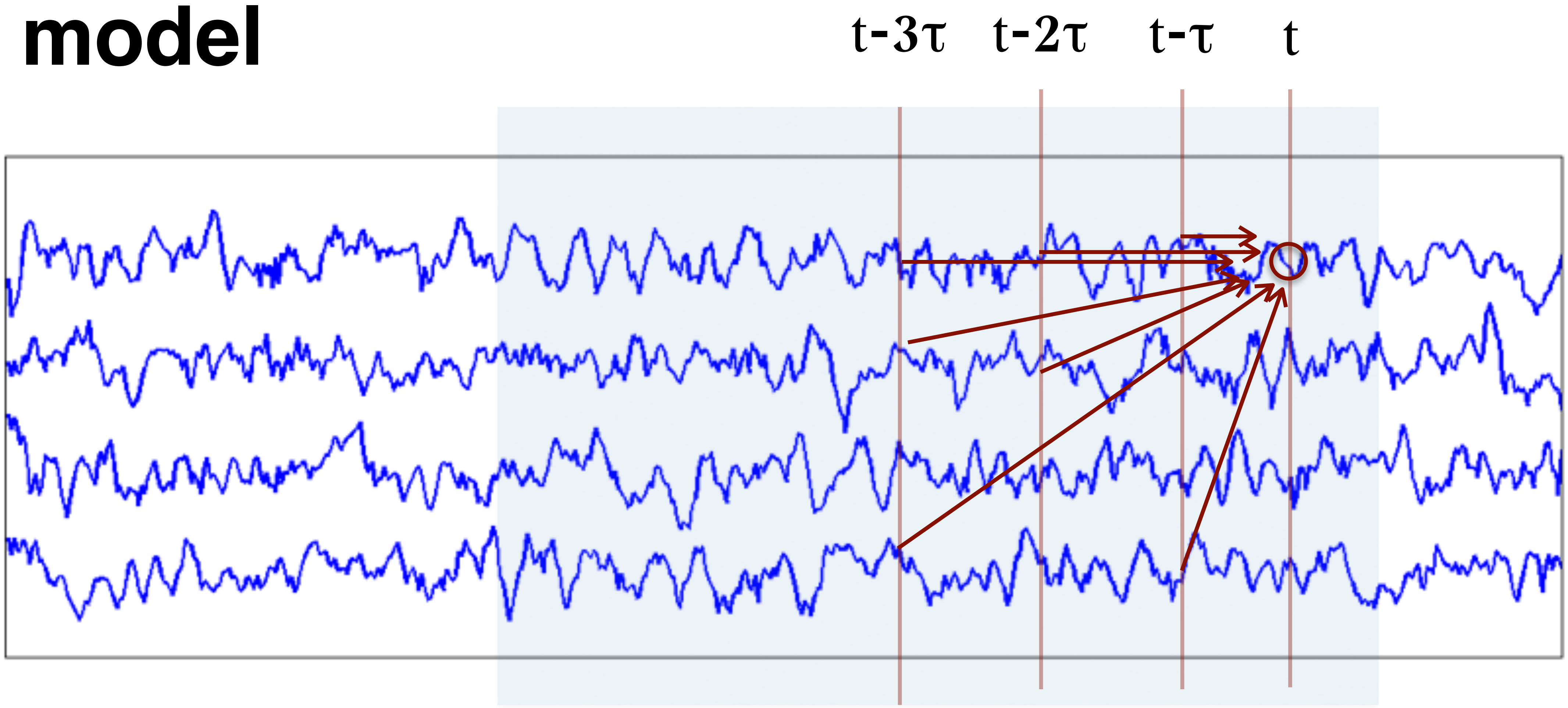




Vidaurre et al (NeuroImage 2016)

HMM-MAR

MAR model



Contains

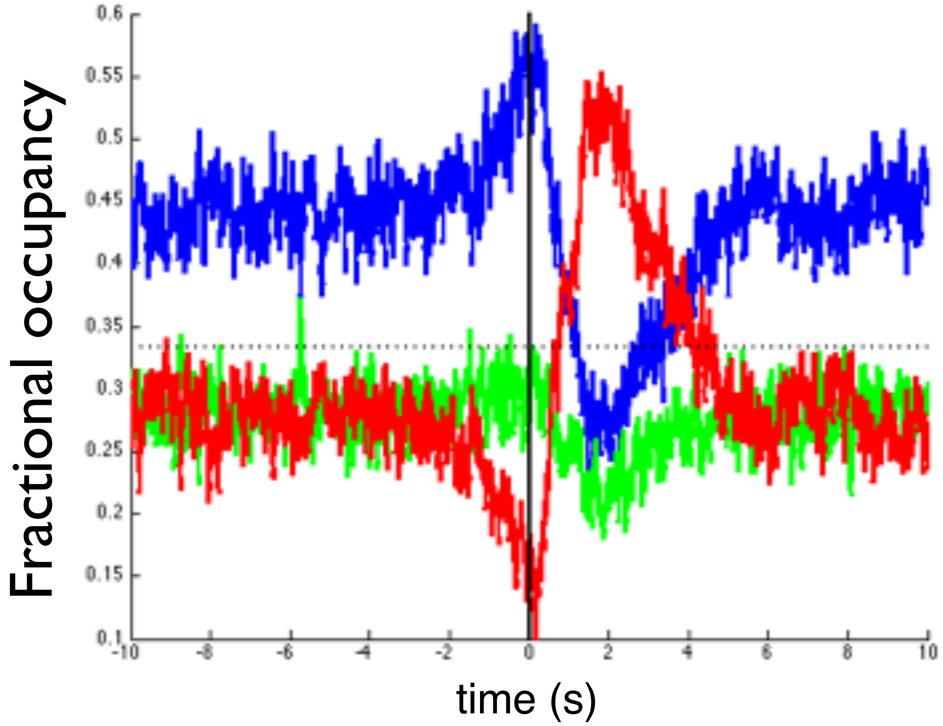
- Power spectral density
- Coherence
- Directed coherence
- Phase

MAR model

- The MAR contains information about **phase**
- It is **spectrally resolved**, i.e. all of these quantities (power, coherence, phase relations) are defined as a function of frequency

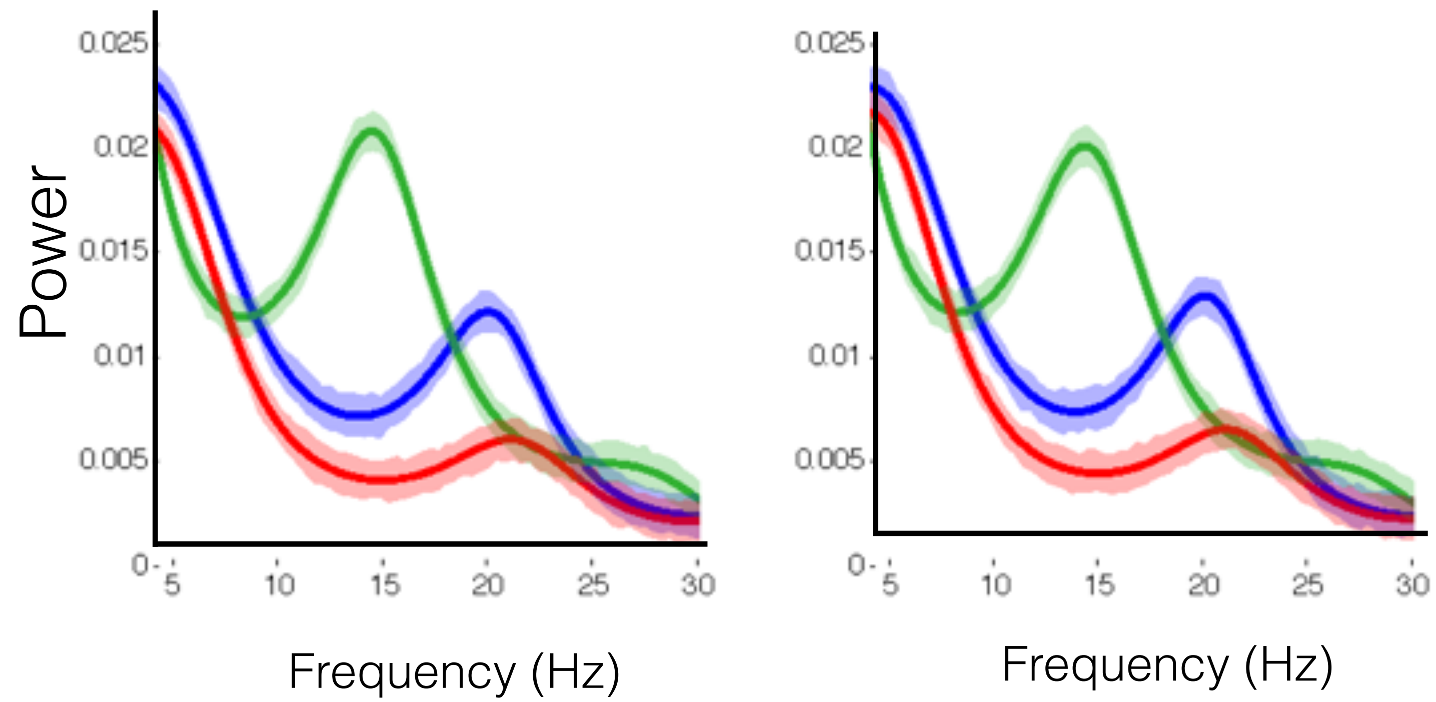
HMM-MAR

HMM state time-courses



Finger-tap (beta suppression)
Post-finger-tap (beta rebound)
Baseline

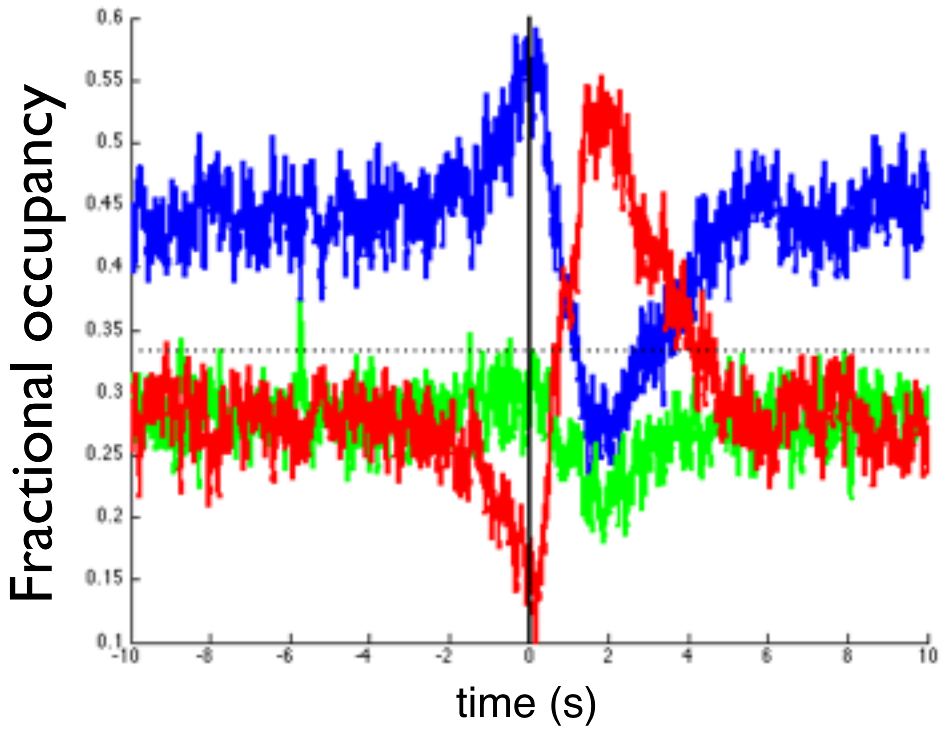
Spectral properties of each HMM state



- significant state-dependent (time-varying) power spectra

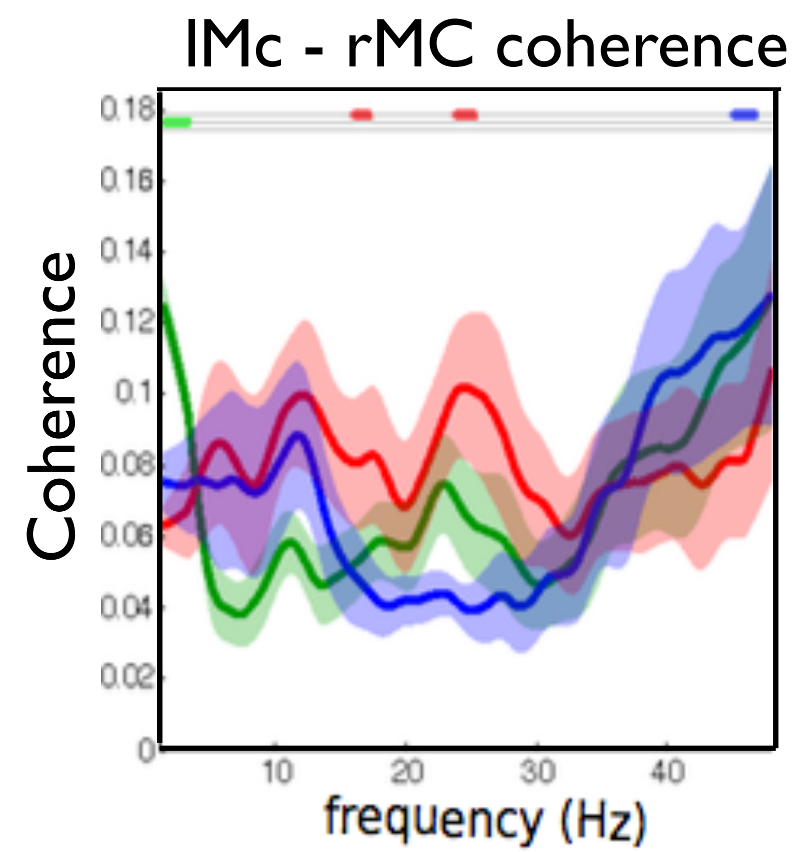
HMM-MAR

HMM state time-courses



Finger-tap (beta suppression)
Post-finger-tap (beta rebound)
Baseline

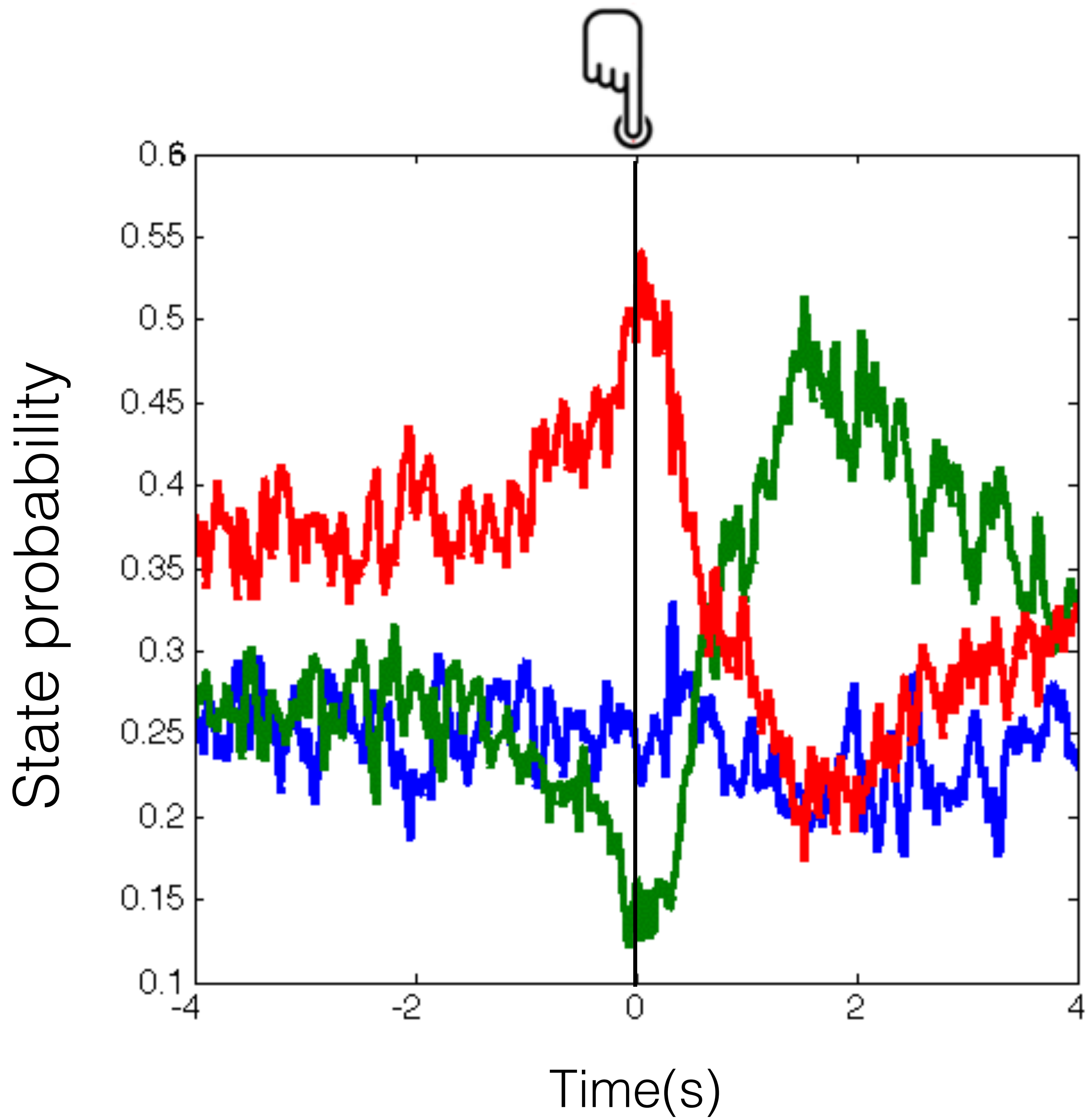
Cross-Spectral properties of each HMM state



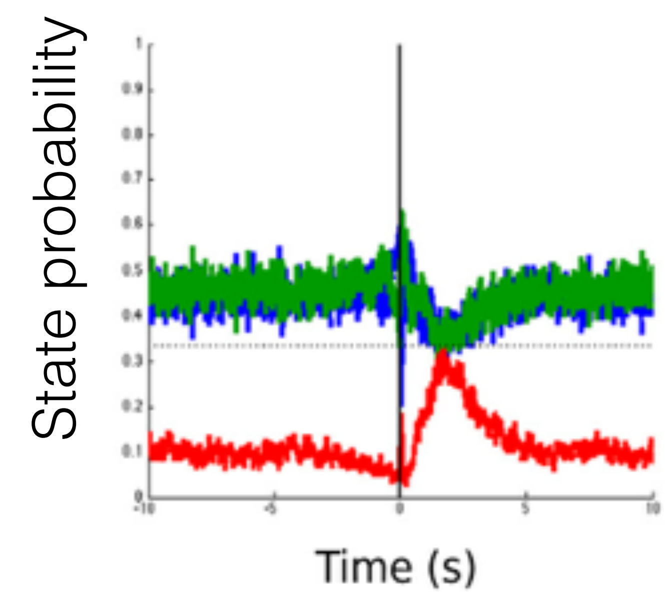
- significant state dependent (time-varying) coherence (phase locking)

HMM-MAR

HMM-MAR

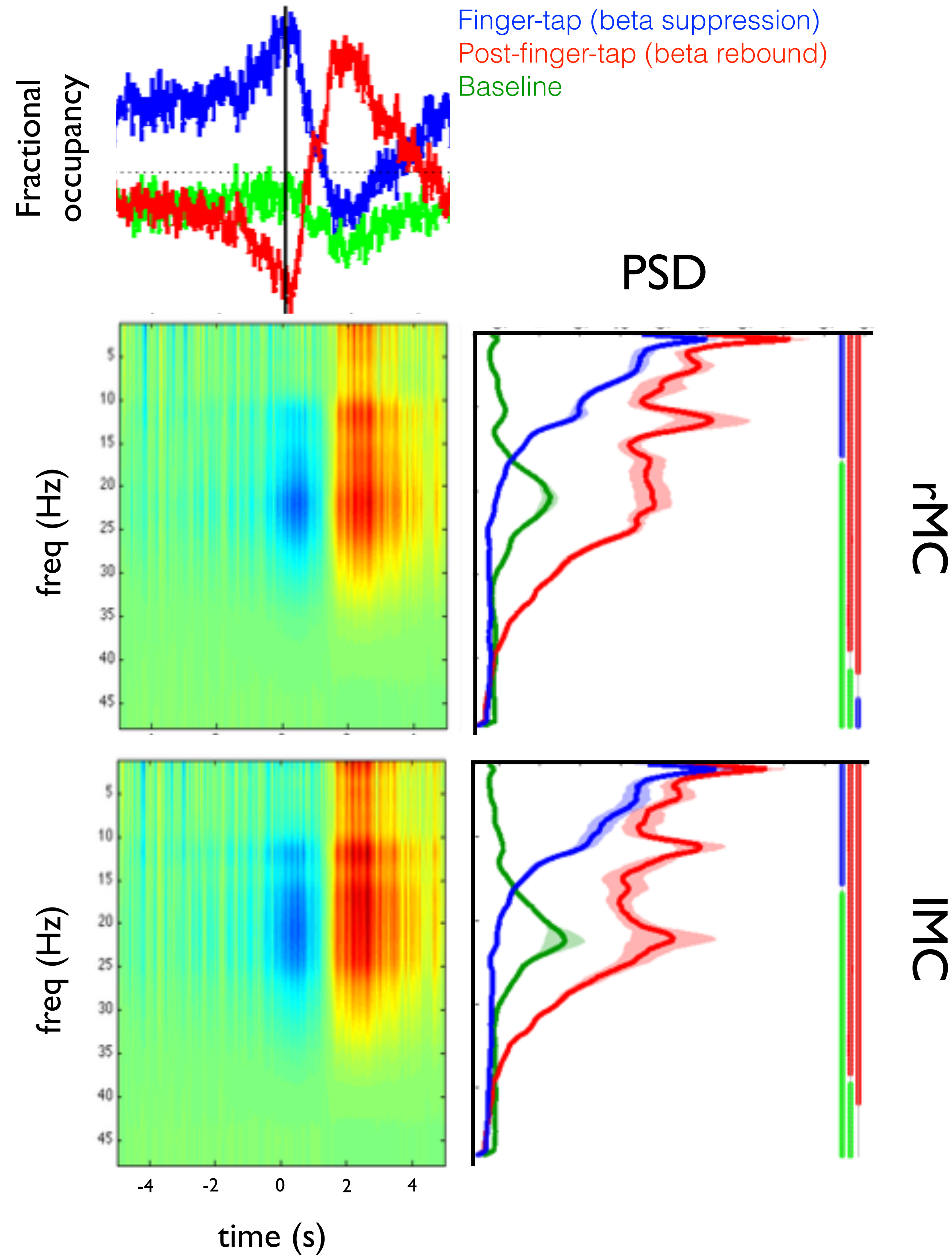


HMM-Gaussian

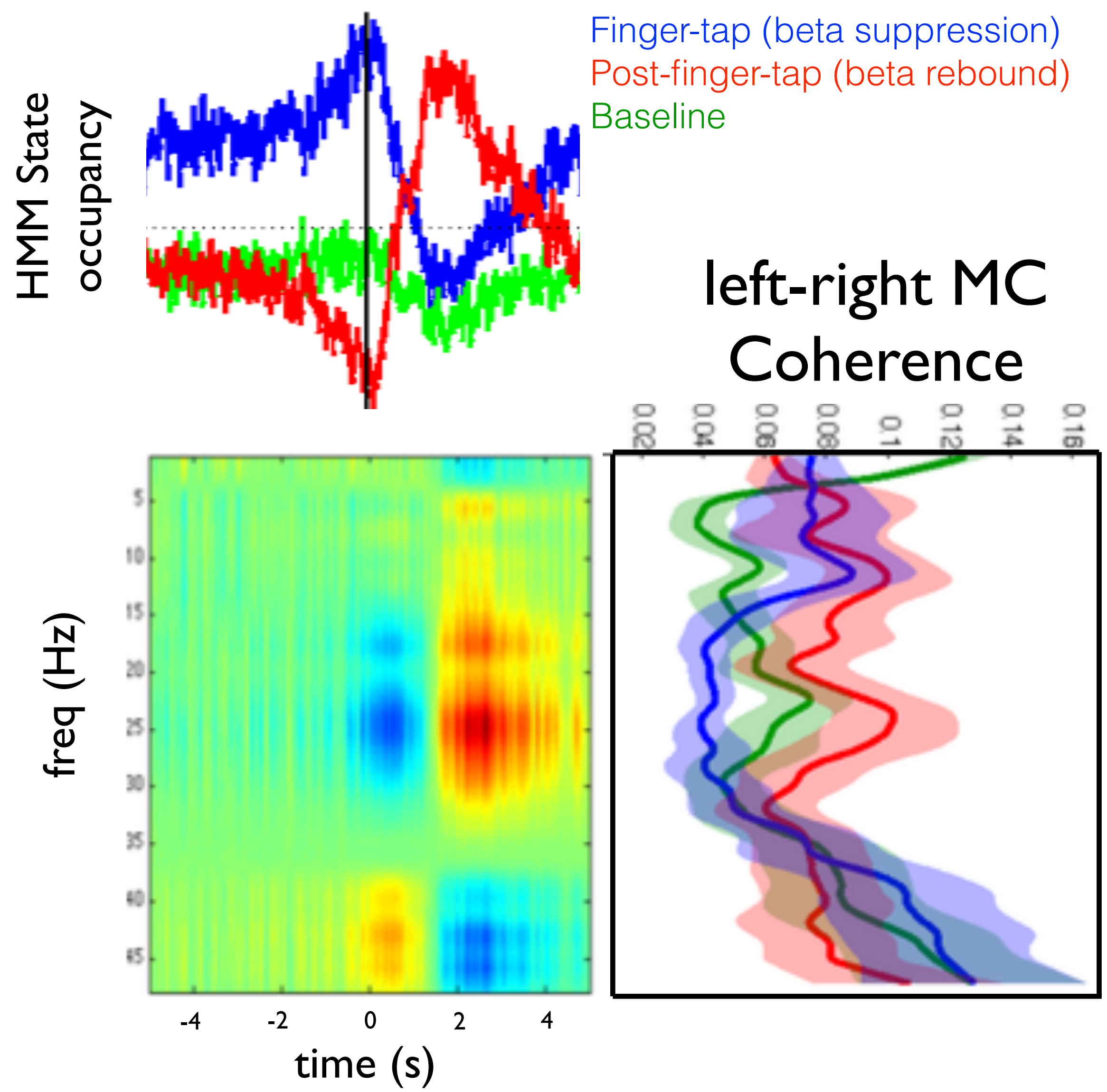


HMM-MAR

Computing T-F Maps from HMM

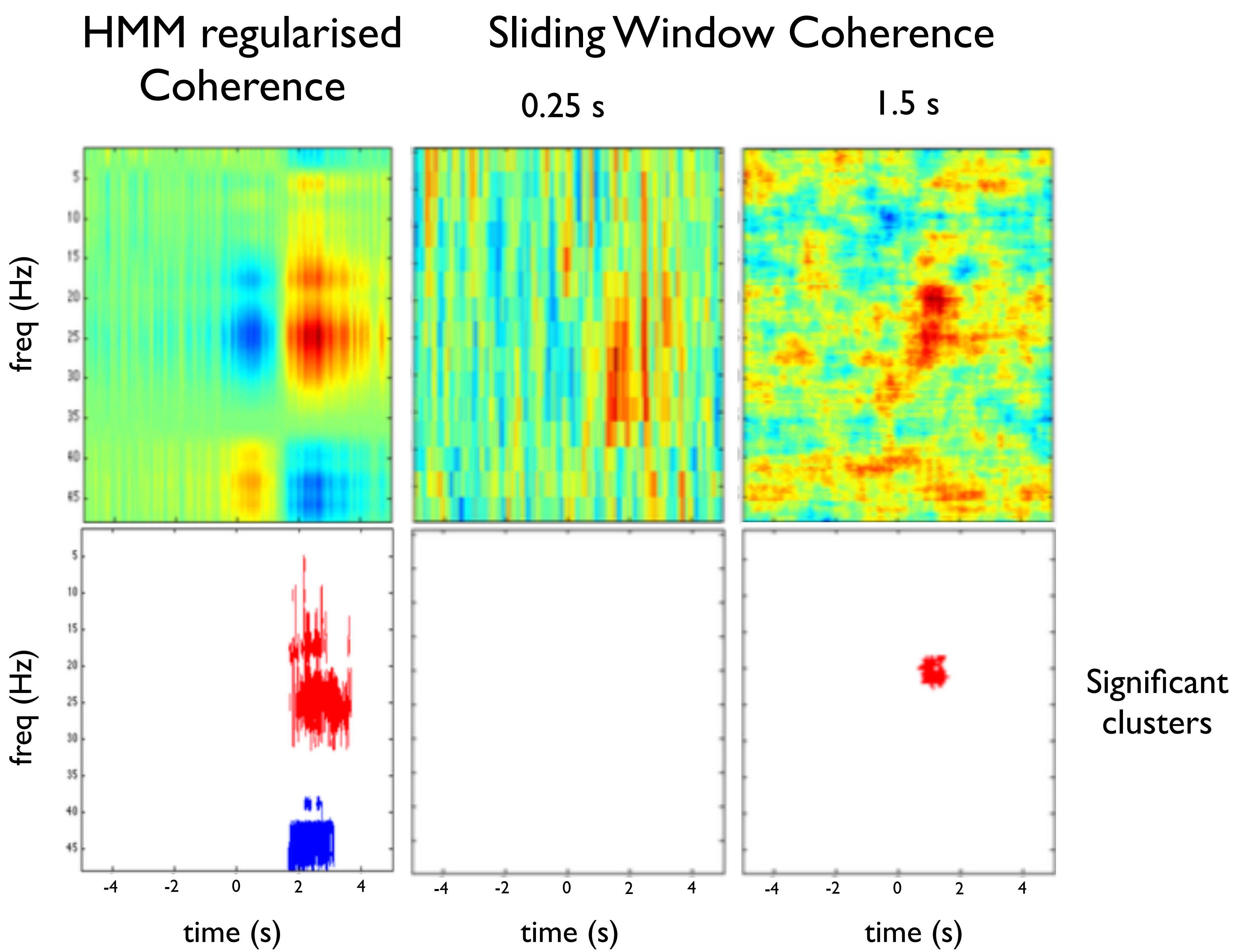


HMM-MAR



HMM regularise
Coherence

HMM-MAR


HMM regularised Coherence
Sliding Window Coherence
0.25 s
1.5 s
freq (Hz)
freq (Hz)
time (s)
time (s)
time (s)
Significant clusters

HMM-MAR

To set an HMM-MAR:

No. of states

MAR order

```
> options = struct();
> options.K = 3;
> options.order = 5;
> options.zeromean = 1;
> options.covtype='diag';
> [hmm,Gamma] = hmmmar(X,T,options);
```

HMM structure

State time courses

Hidden Markov Model

In summary:

- The *HMM-Gaussian* approach focuses on power and **can be applied to whole brain**
- The *HMM-MAR* works on the raw time series and **is sensitive to phase information**, and is applicable to low-to-medium number of regions

More info in : https://github.com/OHBA-analysis/HMM-MAR/wiki

Hidden Markov Model

In the practicals

1. We will apply the *HMM-Gaussian* on resting state whole brain MEG data and find resting state networks that are defined in terms of activation and functional connectivity (power correlation)

2. We will apply the *HMM-MAR* on two motor regions to capture quick changes elicited during a motor task, in terms of power changes and phase coupling