



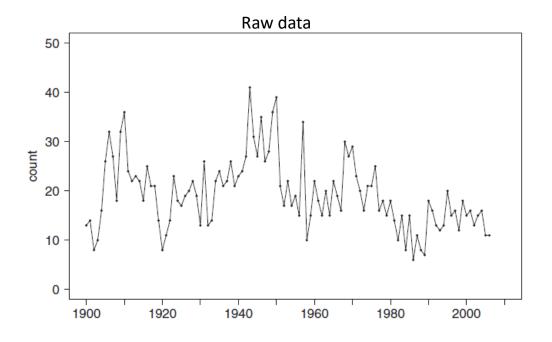
Hidden Markov Models and Sleep

An introduction to the Master's thesis project

Quantification of sleep states using dynamical modeling of functional neuroimaging data

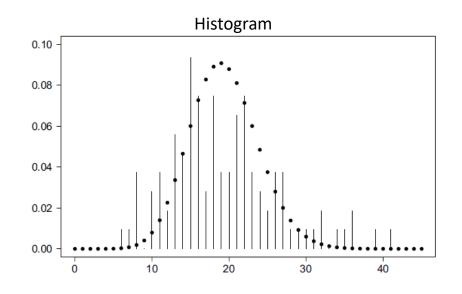
Anders S. Olsen, thesis student

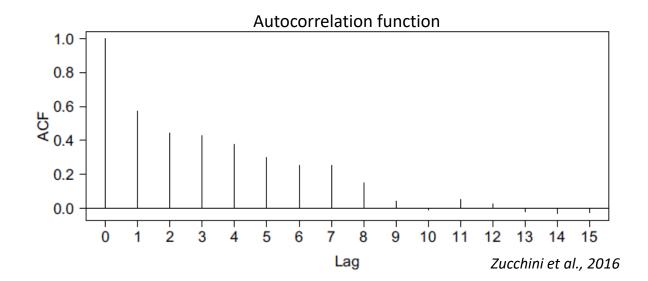




The usual distribution assumption for an unbounded count is the Poisson distribution.

- However, there is considerable overdispersion: $E(X) = 19.36 \neq Var(X) = 51.57$
- Also, there is serial dependence (samples are not IID) Hidden Markov Models can account for this!





- Dealing with overdispersion

In independent mixture models, we have *m* distributions Each distribution is selected by the random variable C:

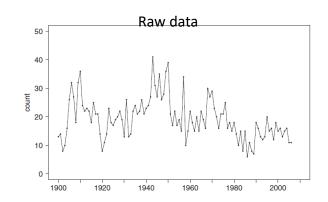
$$C = egin{cases} 1 & ext{with probability } \delta_1 \ dots & dots \ i & dots \ i & dots \ m & ext{with probability } \delta_i \ dots & dots \ m & ext{with probability } \delta_m = 1 - \sum_{i=1}^{m-1} \delta_i \end{cases}$$

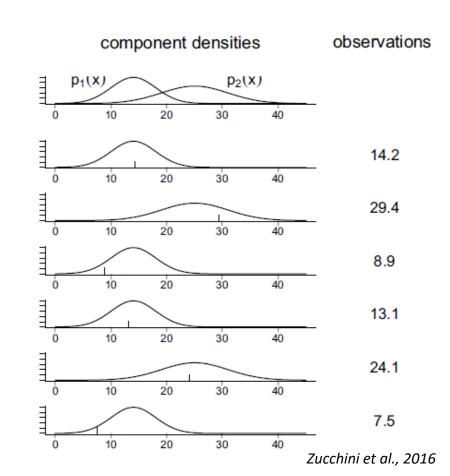
With m=2 and mixing probabilities $\delta_1=0.75, \delta_2=0.25,$ this means that the transition probability matrix is

$$\Gamma = \begin{pmatrix} \gamma_{11} & \gamma_{12} \\ \gamma_{21} & \gamma_{22} \end{pmatrix} = \begin{pmatrix} 0.75 & 0.25 \\ 0.75 & 0.25 \end{pmatrix}$$

Parameter estimation by ML:

$$L(\theta_1, \dots, \theta_m, \delta_1, \dots, \delta_m | x_1, \dots, x_n) = \prod_{j=1}^n \sum_{i=1}^m \delta_i p_i(x_j, \theta_i)$$





active component

compt. 1 compt. 2

 $\delta_1 = 0.75$ $\delta_2 = 0.25$

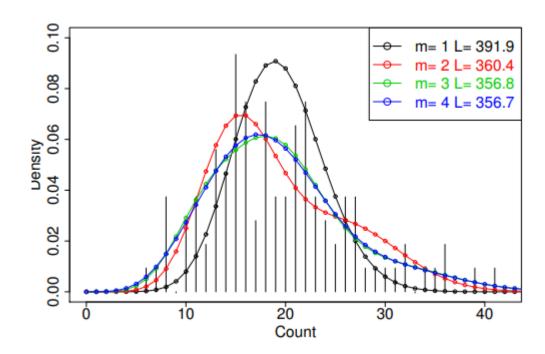
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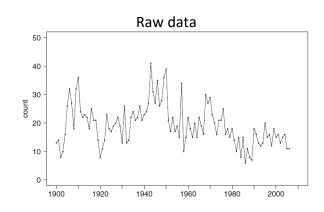
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- Dealing with overdispersion

If we fit independent mixtures of Poisson models to the data:

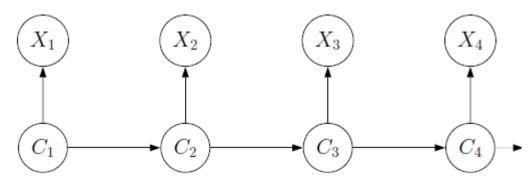




model	i	δ_i	λ_i	$-\log L$	mean	variance
m = 1	1	1.000	19.364	391.9189	19.364	19.364
m = 2	1 2	0.676 0.324	15.777 26.840	360.3690	19.364	46.182
m = 3	1 2 3	0.278 0.593 0.130	12.736 19.785 31.629	356.8489	19.364	51.170
m = 4	1 2 3 4	0.093 0.354 0.437 0.116	10.584 15.528 20.969 32.079	356.7337	19.364	51.638
observations					19.364	51.573

- Dealing with serial dependece

The basic directed graph of an HMM:

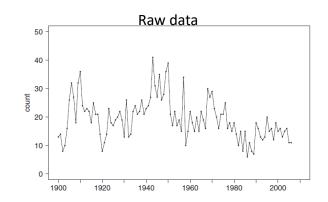


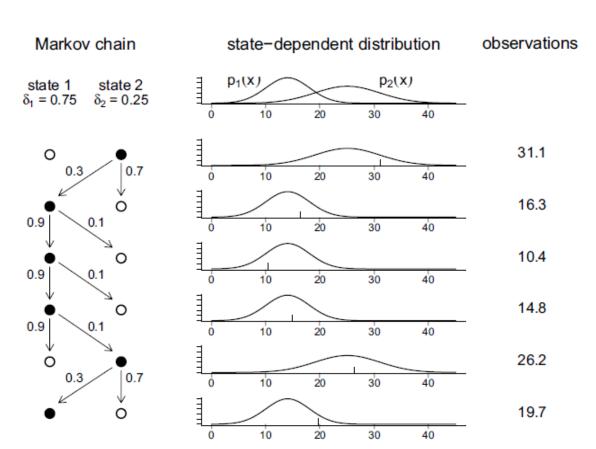
Or,
$$Pr(C_{t+1}|C_t, ..., C_1) = Pr(C_{t+1}|C_t)$$

We still have stationary mixing probabilities $\delta_1 = 0.75$ and $\delta_2 = 0.25$.

The transition probability matrix is now

$$\Gamma = \begin{pmatrix} \gamma_{11} & \gamma_{12} \\ \gamma_{21} & \gamma_{22} \end{pmatrix} = \begin{pmatrix} 0.9 & 0.1 \\ 0.3 & 0.7 \end{pmatrix}$$

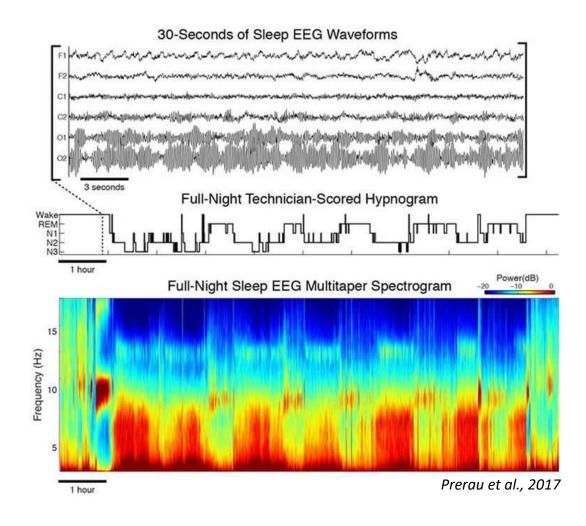




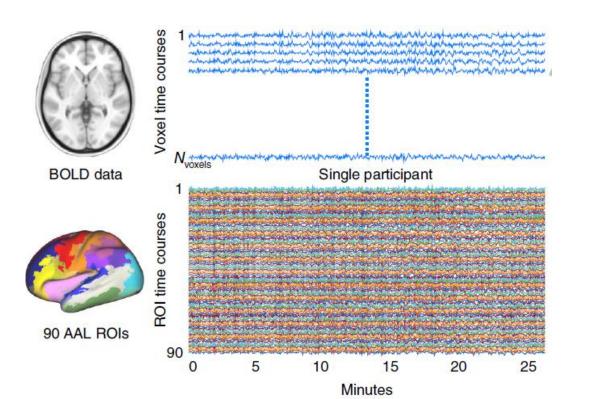
Sleep

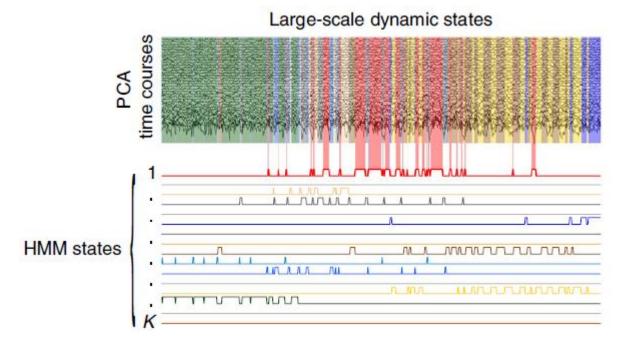
- Historically, sleep has been characterized by polysomnography
- Currently, we work with 5 stages:
 - Wakefulness
 - REM-sleep
 - Non-REM 1-3

 Maybe these stages can be captured by HMM trained on sleep fMRI?

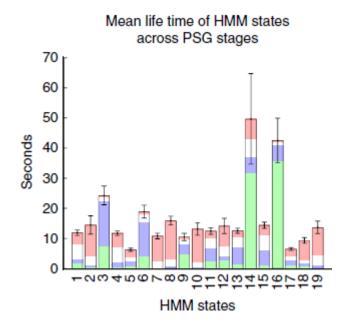


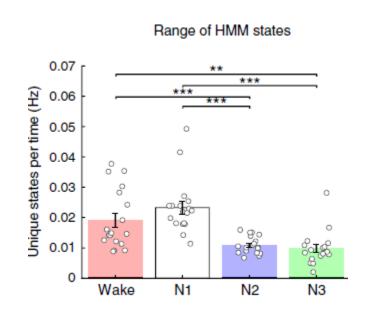
- Stevner and colleagues employed HMM on fMRI-data from 57 participants, of which 18 reached all three non-REM stages.
- The output from HMM may be interpreted from state probabilities or Viterbi decoding

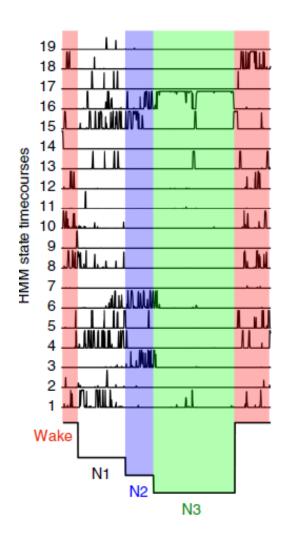




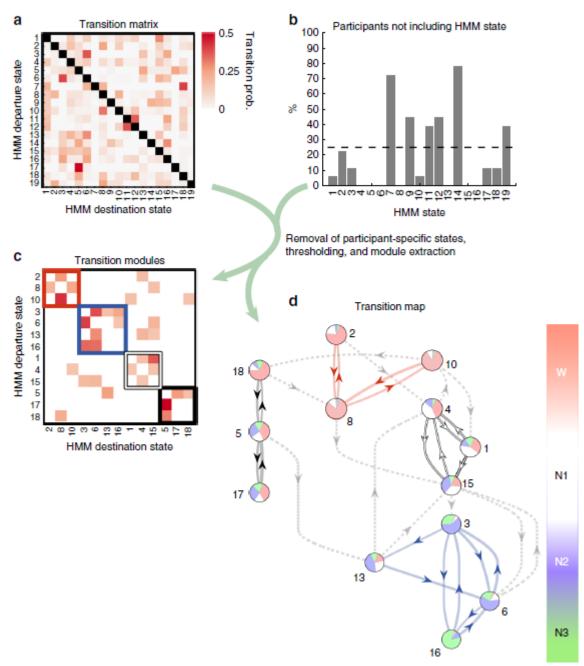
 State probabilities compared with scored PSG-stages may reveal spatial brain characteristics of sleep and wakefulness



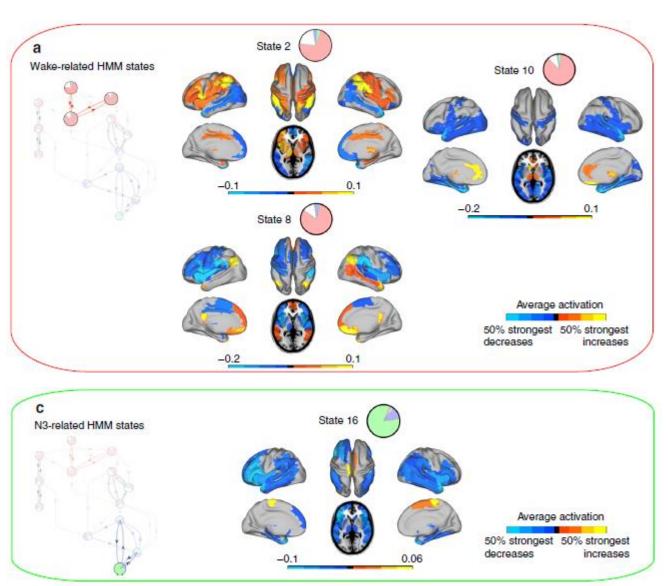




 Investigating modules of transitions between whole-brain network states may reveal a transition map that correlates well with our modern-day understanding of sleep stages.



 Mean activation distributions can be interpreted and potentially lead to new hypotheses

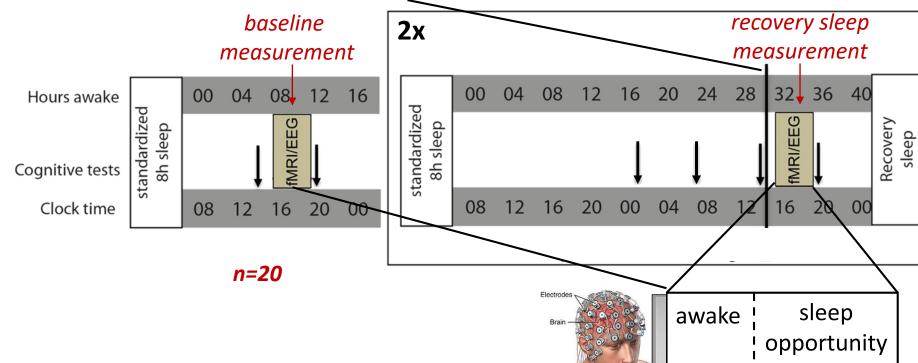


Our data

Administration of placebo or Carvedilol (adrenergic α - & β - antagonist, 25 mg)

10 mins

40 mins



fMRI:

- MREG (10Hz), 434 MREG 5-min scans
- Multiband (4.6Hz) 202 MB 5-min scans

Our data

- Each subject has appeared in three trials: Baseline, sleep deprived with Carvedilol and sleep deprived with placebo.
- For each session we have 40-60 minutes of wake-(sleep)-wake
- Two experts have scored the PSG data as follows:

30s epochs total	BL 2000		Carv 2280		Plac 2210	
Agreement	1521	(76%)	1175	(52%)	1162	(53%)
2-min agreement	1410	(71%)	944	(41%)	943	(43%)
"Artifact"	97	(5%)	167	(7%)	177	(8%)
"Wake"	1286	(64%)	310	(14%)	303	(14%)
"N1"	8	(0.4%)	20	(0.9%)	22	(1%)
"N2"	19	(1%)	242	(11%)	230	(10%)
"N3"	0	(0%)	205	(9%)	211	(9%)

Thesis research questions

- 1. With data from ultra-fast fMRI sequences of wakefulness and sleep, can we reveal vigilance states using dynamical modeling, and what do we gain from having a high temporal resolution?
 - ➤ An approach to Stevner et al,. 2019



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 - > Statistical comparisons of state occupancy, dwell time and transition matrices



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- 1. With data from ultra-fast fMRI sequences of wakefulness and sleep, can we reveal vigilance states using dynamical modeling, and what do we gain from having a high temporal resolution?
 - ➤ An approach to Stevner et al,. 2019
- 2. At the group analysis level, what are differences between the three conditions of which the data originate (Baseline, sleep deprivation + Carvedilol, sleep deprivation + Placebo)
 - > Statistical comparisons of state occupancy, dwell time and transition matrices
- 3. What are the advantages of modeling state transitions, and do Gaussian mixture models provide as much information as HMM?
 - ➤ What do we see when modeling samples as IID?



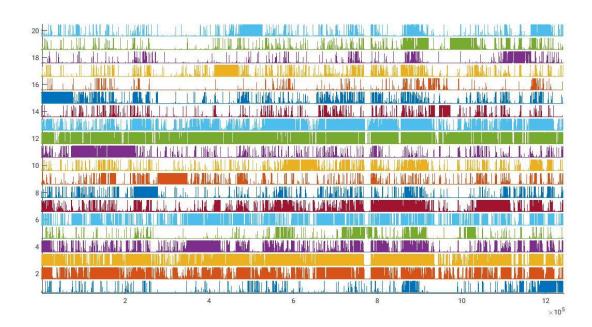
Current stage of project

- fMRI preprocessing completed (awaiting quality check)
- Data extraction completed (using the AAL atlas as in Stevner, 2019)
- Data selection scheme created
- First implementation of HMM-toolbox completed

Immediate next steps:

- Filter physiological artifacts using RETROICOR
- Perform analyses as in Stevner (2019)





Thank you for the attention!

References:

- Damaraju et al., 2020. Connectivity dynamics from wakefulness to sleep. Neuroimage.
- Prerau et al., 2017. Sleep Neurophysiological Dynamics Through the Lens of Multitaper Spectral Analysis. Physiology.
- Stevner et al., 2019. Discovery of key whole-brain transitions and dynamics during human wakefulness and sleep. Nature communications.
- Zucchini et al., 2016. Hidden Markov Models for time series analysis.



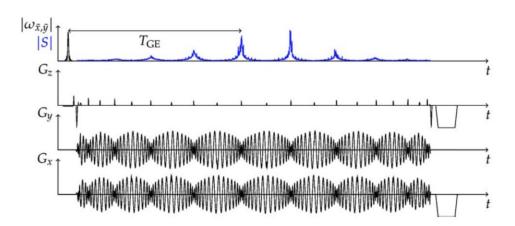
Introduction

Ultra fast MR - Magnetic resonance encephalography (MREG)

- Images represent part "BOLD" and part "soft tissue movements"
- Whole brain imaging with repetition times $T_R \le 100$ ms ($T_E = 36$ ms, 25° flip angle, approx. 10 images per second) with a spatial resolution of ~3x3x3 mm using a >32-channel head coil and "stack of spirals" sampling in K-space.
- Generates a large amount of data : \sim 35 GB data for 10 min recording

• Data is "K-space under sampled", which is associated with complex <u>non-linear</u> image

reconstruction



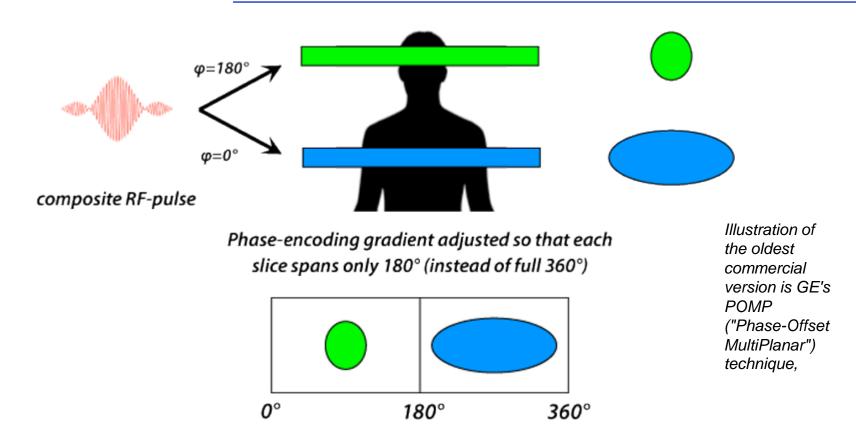
800 a

-800 0 800

k_y [rad/m] -800 k_x [rad/m]

J. Assländer et al., Neurolmage, 2013 Hollingsworth, *Phys Med Biol*, 2015

Multiband method

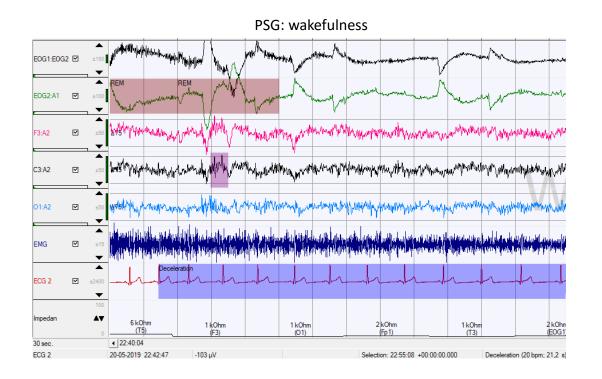


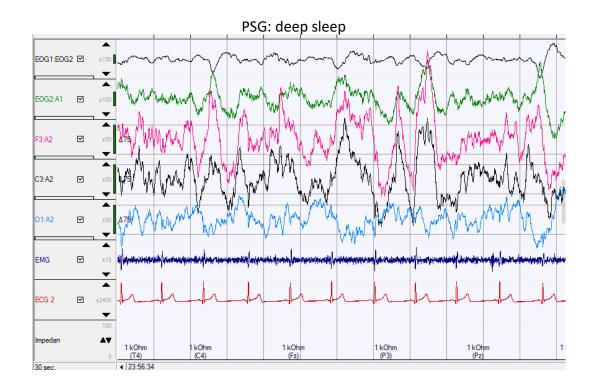
Multiband: An initial complex RF-pulse simultaneously stimulate two or more slices that are encoded using a binary (Hadamard) scheme or view-dependent phase modulatation.

The RF- pulse is a multiplex of the individual RF-pulses needed to stimulate each of the two slices, phase shifted from each other so that the resulting images do not overlap

Sleep 2

• Sleep dynamic function connectivity (dFC) has previously been examined using a sliding windows correlation approach.





Indhold

- Forside: HMM and sleep
- Et par slides om HMM (Markov chains + mixture modeling)
 - Earthwauke example
- Et par slides om Sleep (billede af EEG), AASM inddeling
 - Hvor sejt kunne det ikke være at kunne forudsige søvn fra fMRI
 - Referencer fra BOLD correlates study
- Stevner study mange slides
- Vores data inkludér MREG studies
- Problemstillinger inklusiv deres drawbacks
- I morgen:
 - Billede af EEG + egne resultater
 - referencer