Monte Carlo EM With Hidden Markov Models To Detect Functional Networks In Resting-State fMRI

Wei Liu, Suyash P. Awate, Jeffrey S. Anderson, Deborah Yurgelun-Todd, and P. Thomas Fletcher
Scientific Computing and Imaging Institute, University of Utah, USA
www.sci.utah.edu

Contribution

- Resting State functional MRI can be used to detect intrinsic activity of human brain, and helps the study of functional network connectivity.
- We use a Bayesian framework with Markov random field as prior, and mixture of von Mises-Fisher distribution as likelihood, for partitioning the brain cortex into distinct functional networks .
- Use Monte Carlo EM algorithm to approximate intractable expectation over all possible labelings. MCEM solutions are superior to mode approximation.
- Able to identify visual, motor, salience, and default mode networks with consistency between subjects.

Likelihood

- Normalization $x \leftarrow (x - \overline{x})/\sigma_x$. The sample correlation between normalized time courses is equal to their inner product.
- Model the likelihood function $P(\boldsymbol{x}_i|z_i)$ using the von Mises-Fisher distribution

$$f(\boldsymbol{x}_i; \boldsymbol{\mu}_l, \kappa_l | z_i = l) = C_p(\kappa_l) \exp\left(\kappa_l \boldsymbol{\mu}_l^T \boldsymbol{x}_i\right).$$

- Also define distributions on parameters. We assume that $\forall l \in \mathcal{L}$, $\kappa_l \sim \mathcal{N}(\mu_\kappa, \sigma_\kappa^2)$. This prior enforces constraints that the clusters should not have extremely high or low concentration parameters.

Priors

- Functional network spatial smoothness assumption is model by Markov Random Field

$$P(\mathbf{z}) = \frac{1}{C} \exp\left(-\beta \sum_{i \in \mathcal{S}} \sum_{j \in \mathcal{N}_i} T(z_i \neq z_j)\right).$$

- Spatially smooth functional map has higher probability.
- The Markov-Gibbs equivalence implies that the conditional distribution of z_i at site i is:

$$P(z_i|\mathbf{z}_{-i}) = P(z_i|z_{\mathcal{N}_i}) = \frac{\exp\left(-\beta \sum_{j \in \mathcal{N}_i} T(z_i \neq z_j)\right)}{\sum_{l \in \mathcal{L}} \exp\left(-\beta \sum_{j \in \mathcal{N}_i} T(l \neq z_j)\right)}.$$

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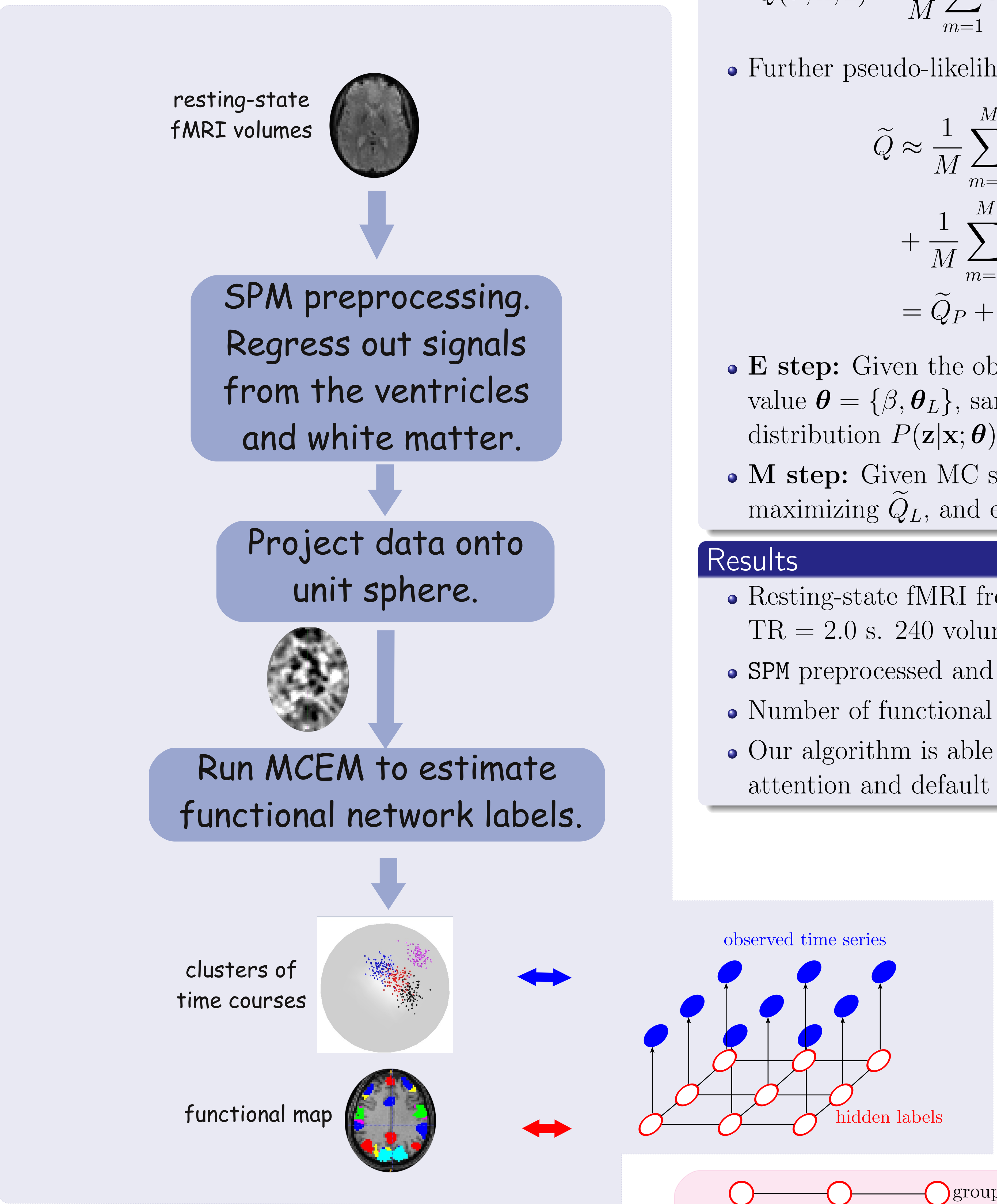
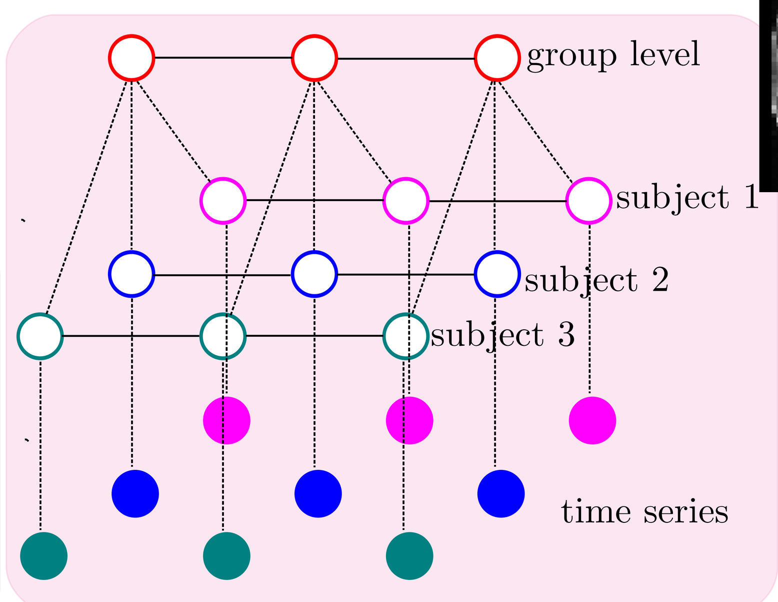
Generative Model

- We assume spatial configuration $\mathbf{z}$ of functional networks is Gibbs distribution.
- Assume each voxel's fMRI time course $\boldsymbol{x}$ is generated conditioned on its network membership.
- Finding the functional connectivity network is equivalent to maximize the posterior probability of functional labels given data.





Future Work

- Hierarchical MRF model with additional group level.
- Build a functional atlas which is the 'mean' of all subjects.
- Still allowing individual's flexibility.

Monte Carlo EM

- Use expectation maximization (EM) to estimate the model parameters and the hidden labels.
- The combinatorial number of configurations for $\mathbf{z}$ makes the expectation $\mathbb{E}_{P(\mathbf{z}|\mathbf{x})}[\log P(\mathbf{x}, \mathbf{z}; \boldsymbol{\theta})]$ intractable, hence a variant of EM called Monte Carlo EM (MCEM).

$$\widetilde{Q}(\boldsymbol{\theta}; \mathbf{x}, \mathbf{z}) \approx \frac{1}{M} \sum_{m=1}^{M} \log P(\mathbf{z}^m; \beta) + \log P(\mathbf{x}|\mathbf{z}^m; \boldsymbol{\theta}_L).$$

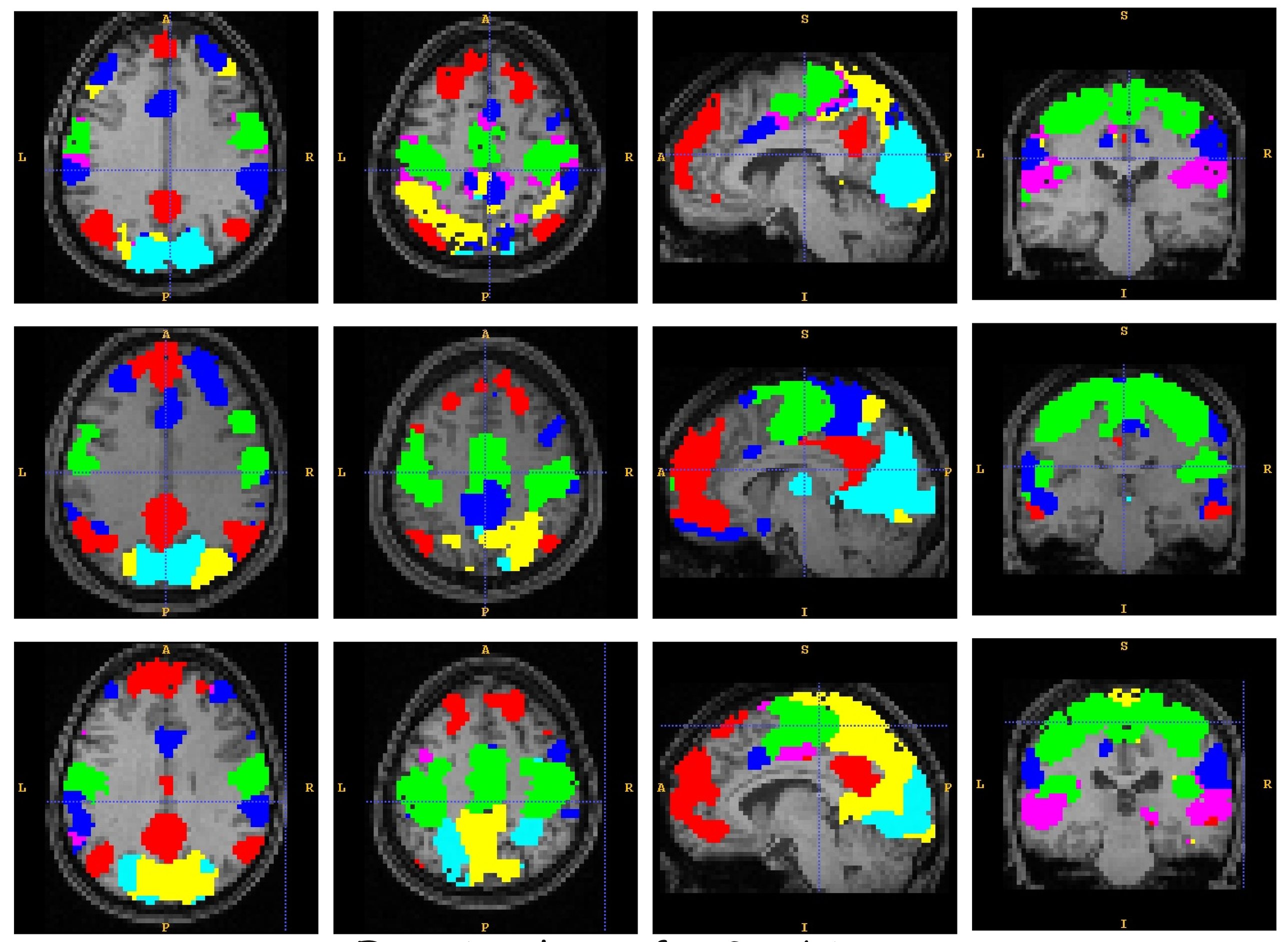
- Further pseudo-likelihood approximation gives

$$\widetilde{Q} \approx \frac{1}{M} \sum_{m=1}^{M} \sum_{i \in \mathcal{S}} \log P(z_i | z_{\mathcal{N}_i}; \beta) + \frac{1}{M} \sum_{m=1}^{M} \sum_{i \in \mathcal{S}} \log P(\boldsymbol{x}_i | z_i; \boldsymbol{\theta}_L) = \widetilde{Q}_P + \widetilde{Q}_L.$$

- **E step:** Given the observed data $\mathbf{x}$ and parameter value $\boldsymbol{\theta} = \{\beta, \boldsymbol{\theta}_L\}$, sample from the posterior distribution $P(\mathbf{z}|\mathbf{x}; \boldsymbol{\theta})$ using Metropolis sampling.
- **M step:** Given MC samples, estimate $\boldsymbol{\mu}$ and $\boldsymbol{\sigma}$ by maximizing $\widetilde{Q}_L$, and estimate β by maximizing $\widetilde{Q}_P$.

Results

- Resting-state fMRI from 16 healthy control subjects. TR = 2.0 s. 240 volumes.
- SPM preprocessed and conn processed.
- Number of functional regions set to 8.
- Our algorithm is able to find visual, motor dorsal attention and default mode network robustly.



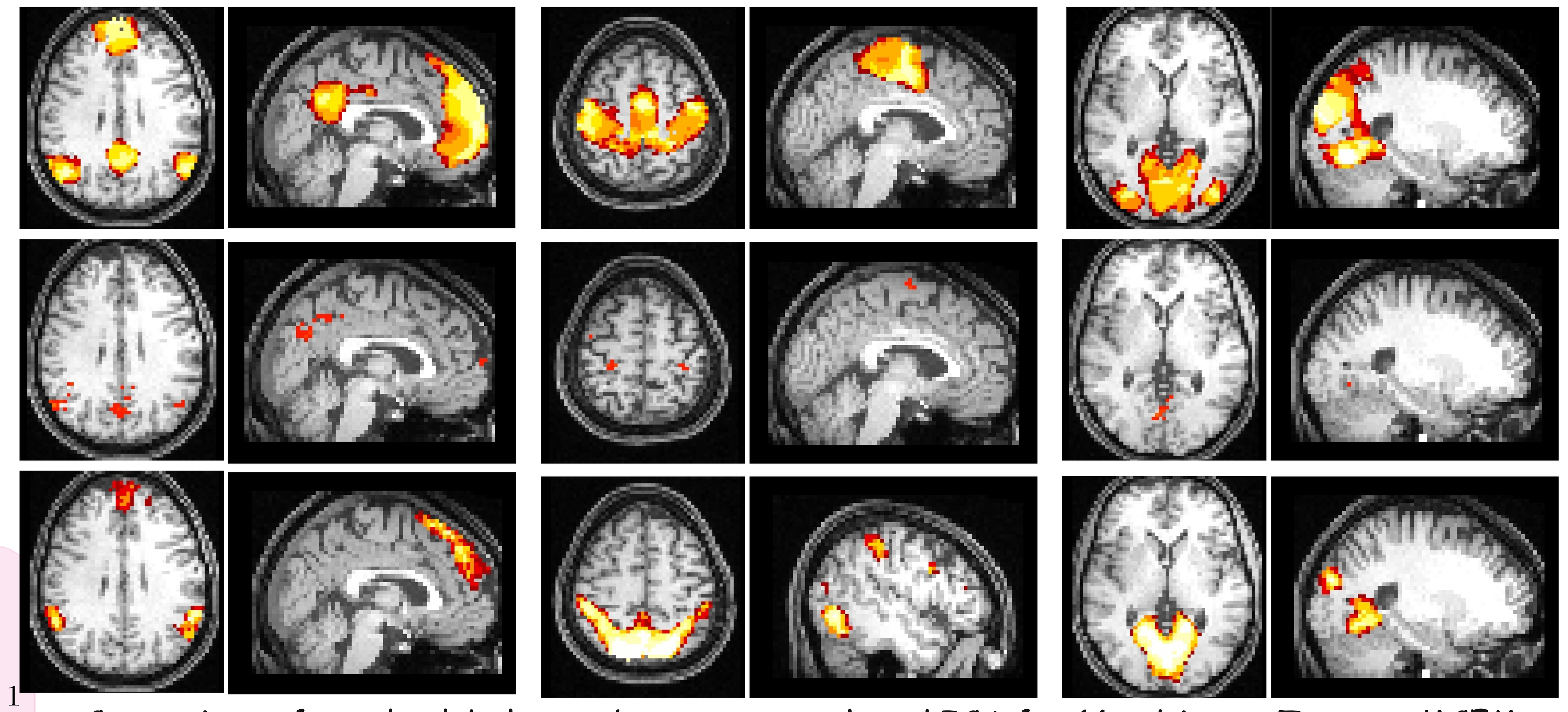
Functional map for 3 subjects.

Comparison with ICA

- Individual ICA and group ICA applied to 3 subjects. Number of components = 16. component map converted to z score and thresholded at 1.
- Compute an overlap map for each functional network by adding the corresponding binary label maps of all 16 subjects.
- Look at each method's overlapped label map and count the number of voxels whose value are greater than 8 as shown in the table.

Table: The number of voxels with value greater than 8 in the overlapped label map.

	DMN	Motor	Attention	Visual
MCEM	5043	7003	3731	5844
Individual ICA	114	167	228	134
Group ICA	3075	5314	3901	3509



Comparison of overlap label maps by our approach and ICA for 16 subjects. Top: our MCEM approach, middle: Individual ICA, bottom: Group ICA. Color ranges from 8 (red) to 16 (yellow).

References

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