Poster #1195

Seed-based Correlation Analysis on Isolated Perfusion Lag Structure in the Resting-state fMRI Signal

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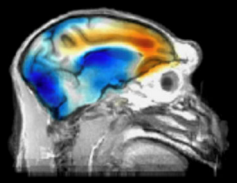
There is a lag structure in fMRI data

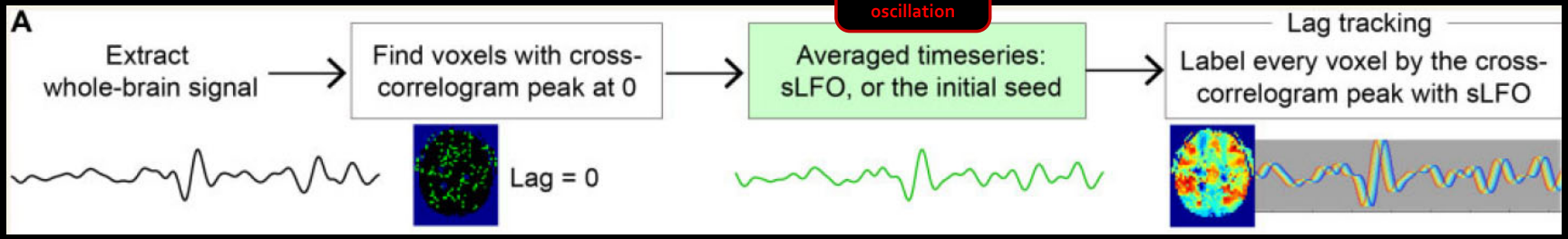
- Propagation of spontaneous low-frequency oscillation of systemic origin (Tong & Frederick 2010)

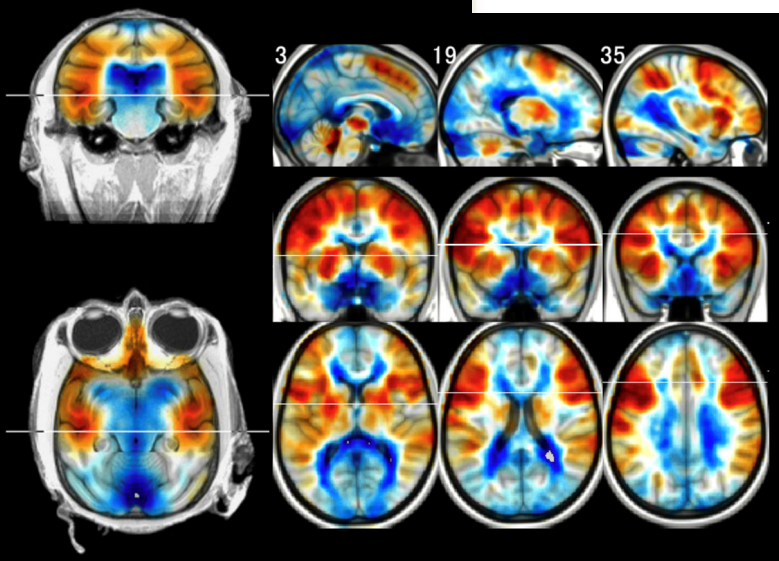
sLFO
Spontaneous low-frequency oscillation

"Narrower" than the global signal

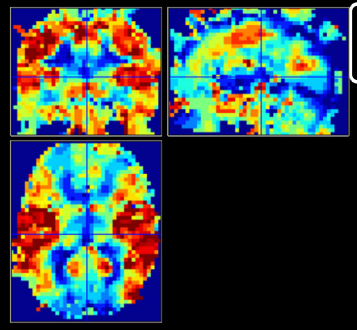


Aso, HBM2020

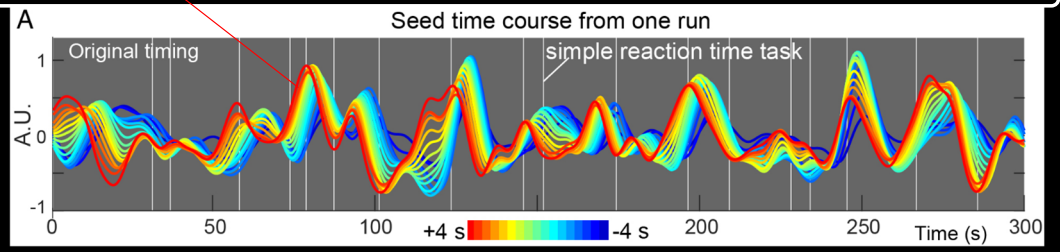




"Lag Map"

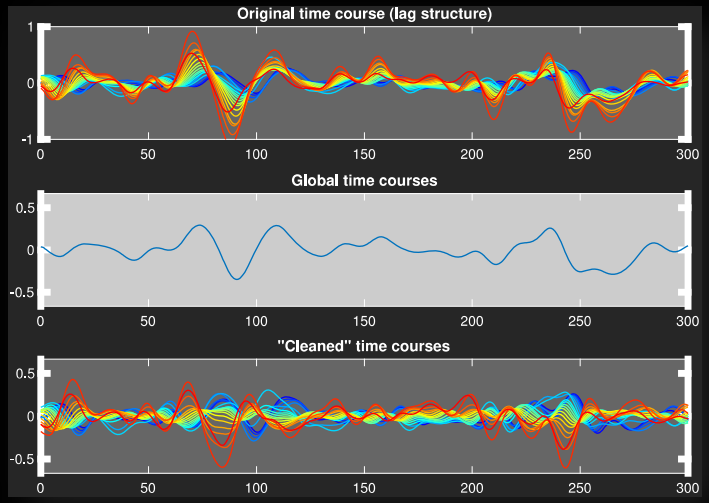


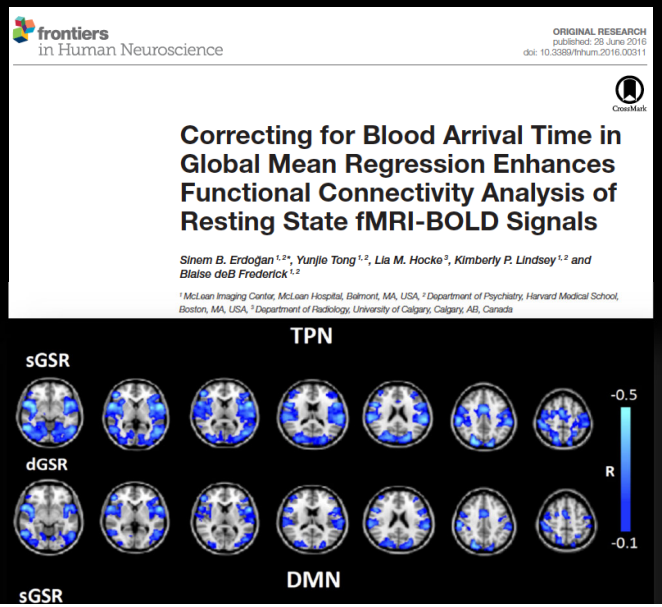
Red curve≒average timeseries from red voxels



Lag structure is a global noise for fMRI

- >30% of total variance (in the low-frequency range)
- Not eliminated by global signal regression

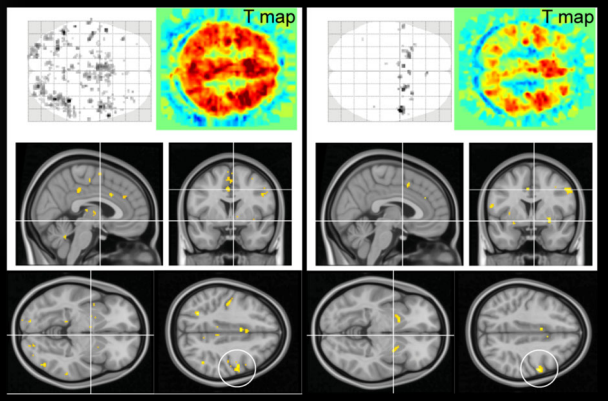




Erdoğan, 2016

"Dynamic GSR" for resting-state fMRI

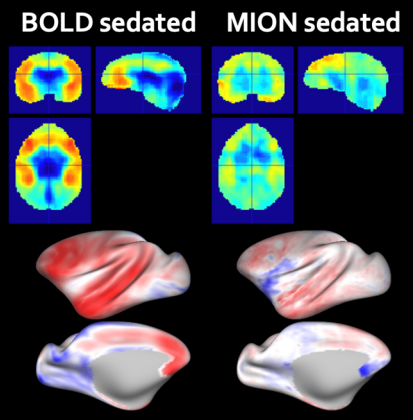
Aso, 2019



Denoising of task fMRI

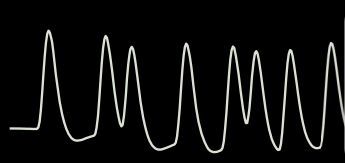
sLFO = variation of deoxy-Hgb density

- Hypothesis: sLFO is largely a non-vascular phenomenon
- Deoxy-Hgb fluctuates with oxygen saturation, hematocrit, CO2, etc.
- It's in the blood! (at least partly)



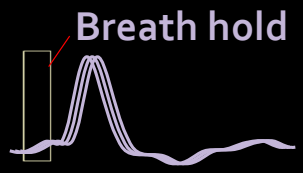
No sLFO / lag stgructure in CBV-fMRI (USPIO)
Aso, ISMRM2020

Neuro-vascular coupling



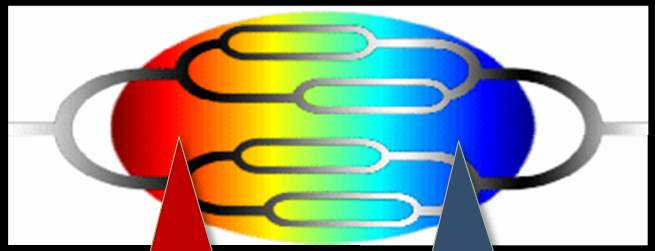
CBF↑CBV↑

Auto-regulatory response



CBF↑CBV↑

sLFO
Spontaneous low-frequency oscillation



Parenchyma near arterial trunks

Parenchyma near major veins

How does it affect fcMRI?

- By creating non-neural correlation

frontiers in Human Neuroscience

ORIGINAL RESEARCH
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Can apparent resting state connectivity arise from systemic fluctuations?

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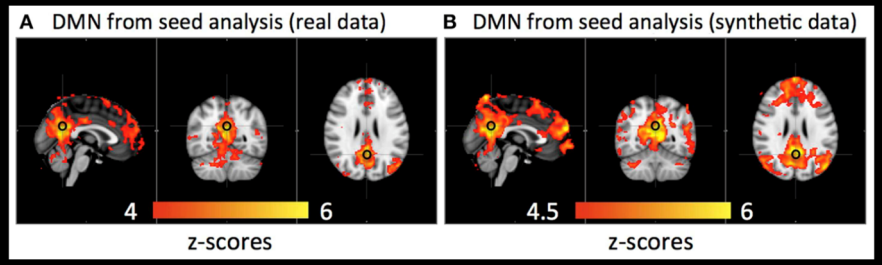
Default mode network



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Resting-state "physiological networks"

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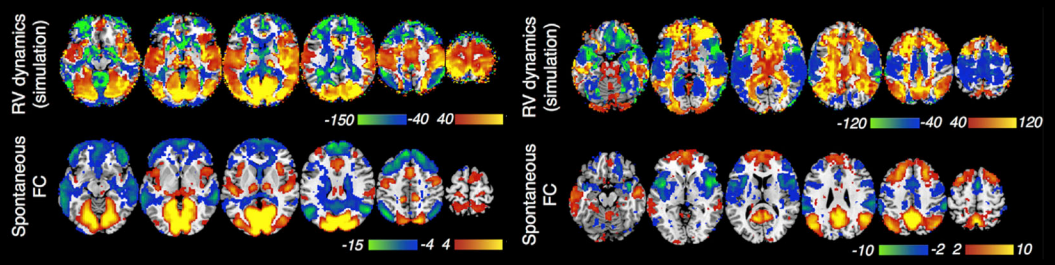
Primary visual

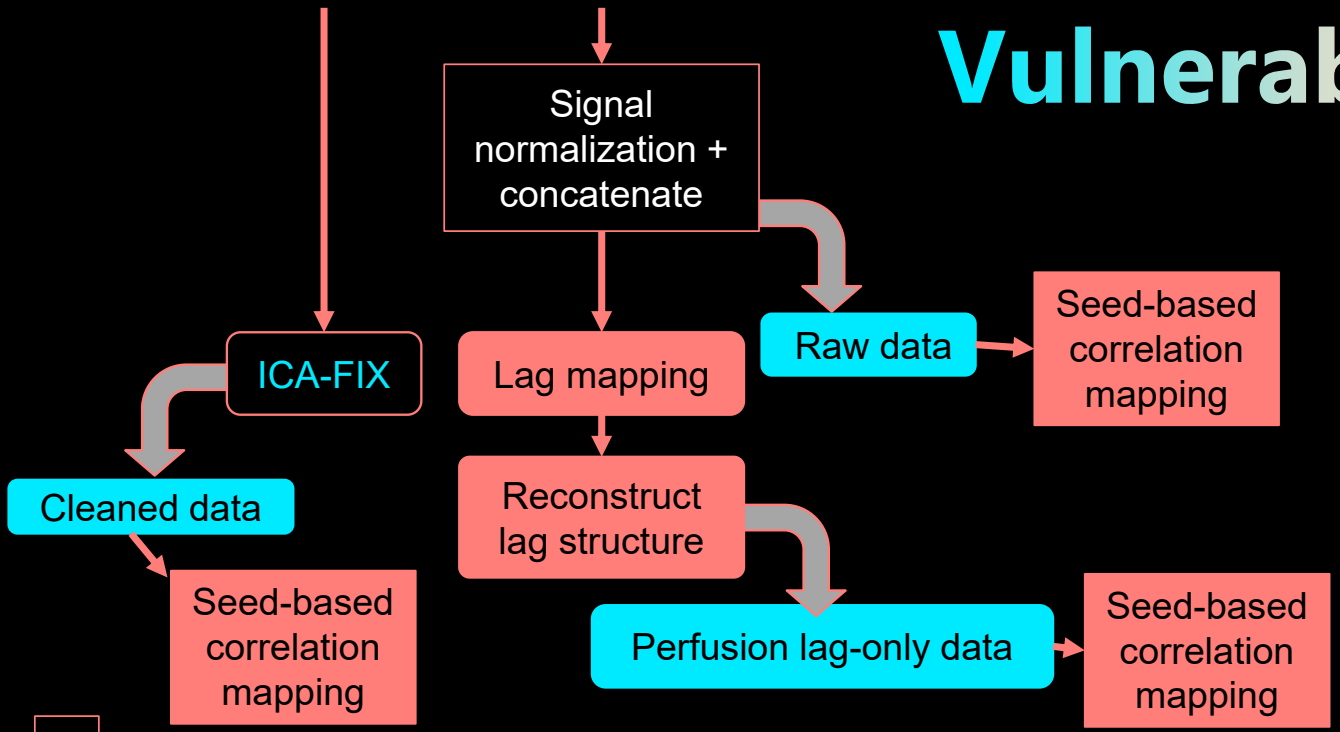
Default mode network



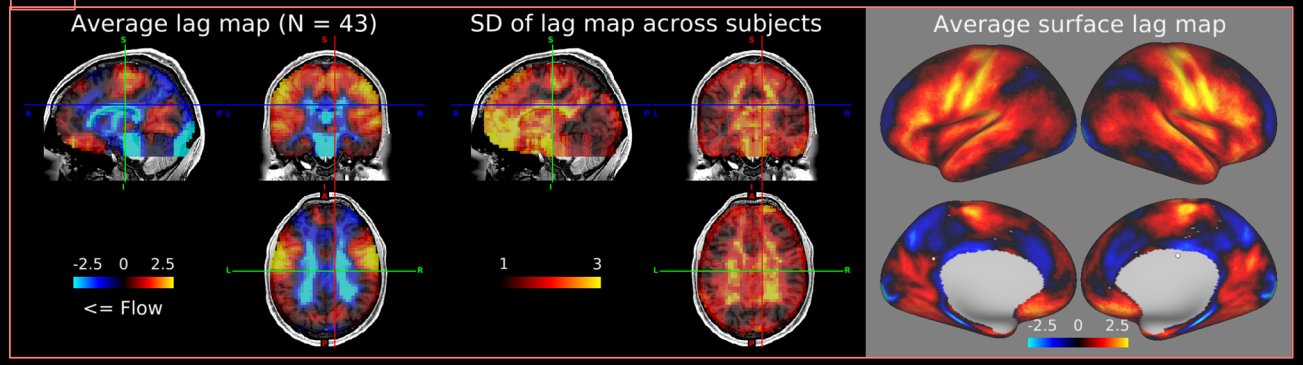
Vulnerable connectivity?

A

HCP test-retest (N=43), multi-run rs-fmri data



B



Evaluation in HCP-style surface parcellation

Methods

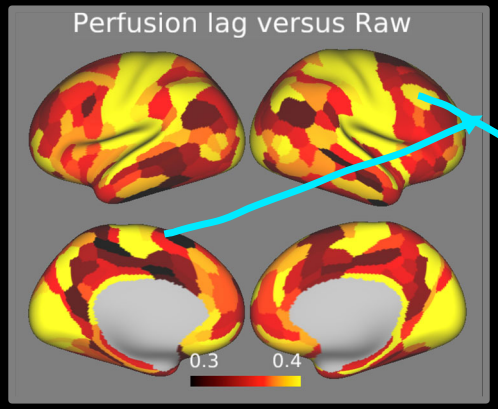
A, Analysis workflow

B, Mean and standard deviation of the lag map across individuals. Warm colors indicate earlier arrival in the proximities of large arteries such as the middle cerebral artery. Cool colors are in the vicinities of major veins.

The surface version was created by pooling individual surface lag maps based on MSMAll alignment.

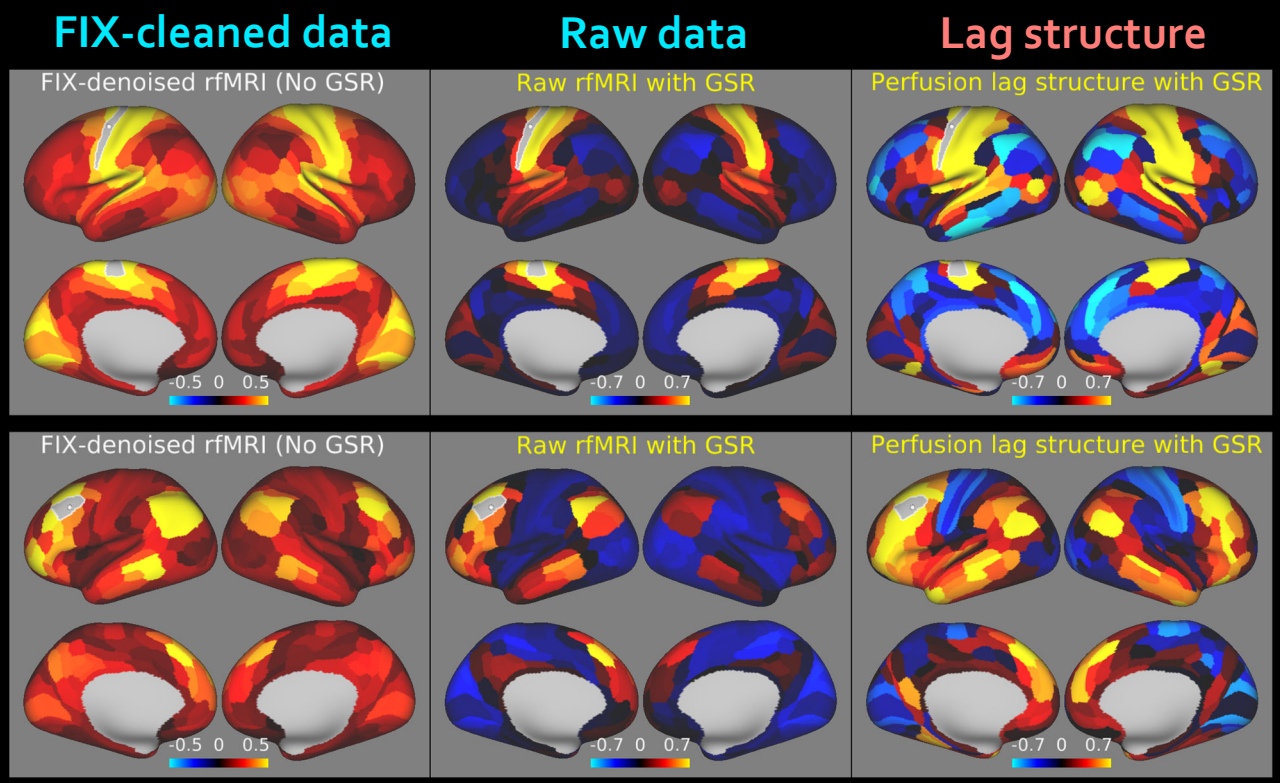
Correlations likely to be contaminated

Similarity of correlation map for each seed (Z) (Lag versus Raw)



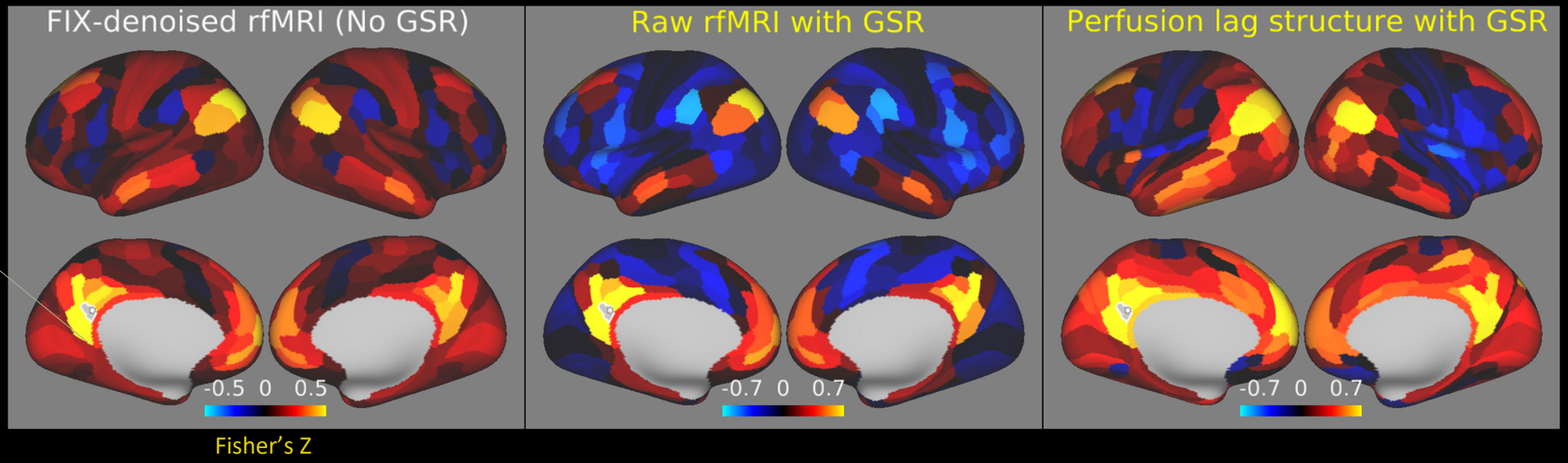
Primary-motor area seed

BA8c seed - frontoparietal network

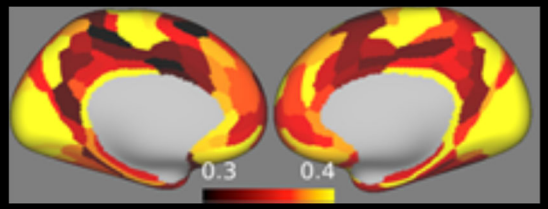


- **Be careful with symmetric connectivities!**

DMN: moderate contamination

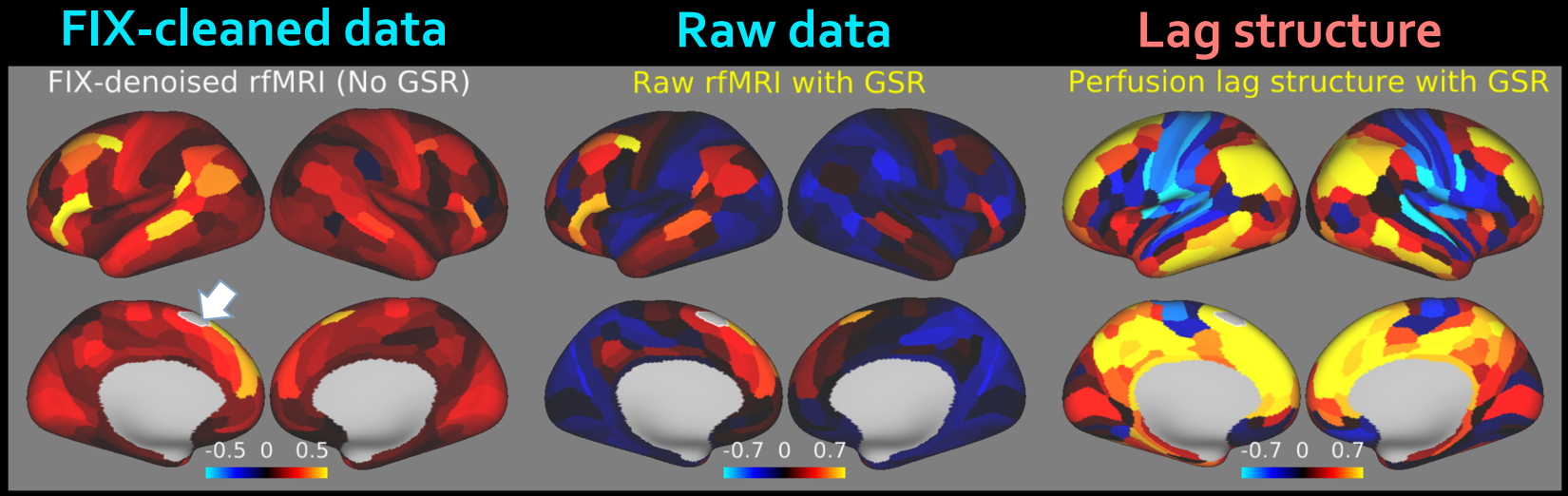


- **Also depends on the seed selection**



(Seemingly) less affected correlation

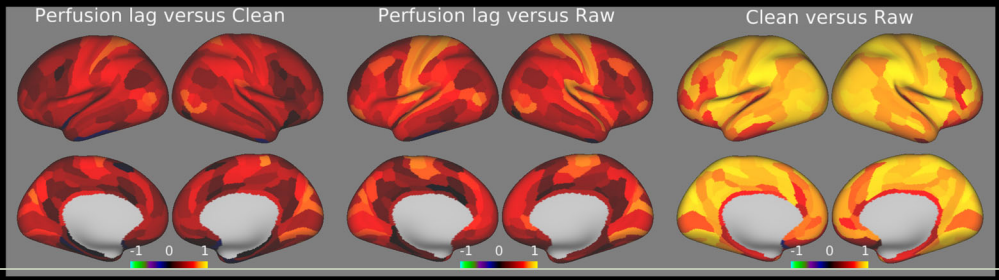
Superior frontal language-area seed (Glasser, 2016)



- **Bias from the lag structure may still affect the connectivity**

Summary

- Correlations within the pure perfusion component (lag structure) can show similar patterns with the known FC
- The similarity varied across seeds
  - Relationship with the gross vascular structure seemed important
  - Underlying neuro-BOLD coupling may be poor for some networks
- Removal of the lag structure may help
- Evaluation of the subcortical structures is warranted



Similarity of the seed-based correlation map