Now that I have Multi-echo data, what else can I do with it?

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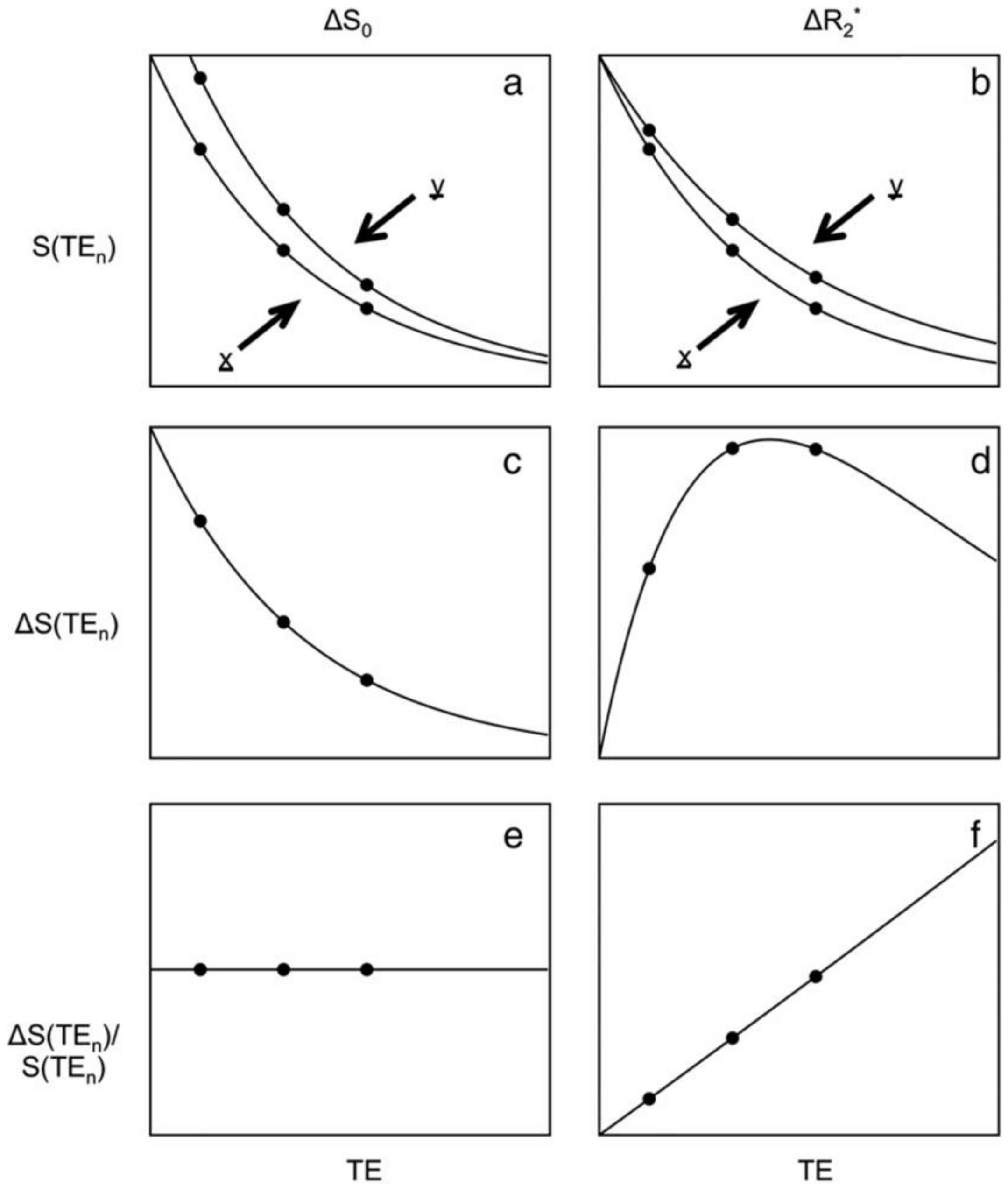
National Institute of Mental Health

OHBM 2026 DISCLOSURES

I have no conflicts of interest in relation to this presentation to disclose.

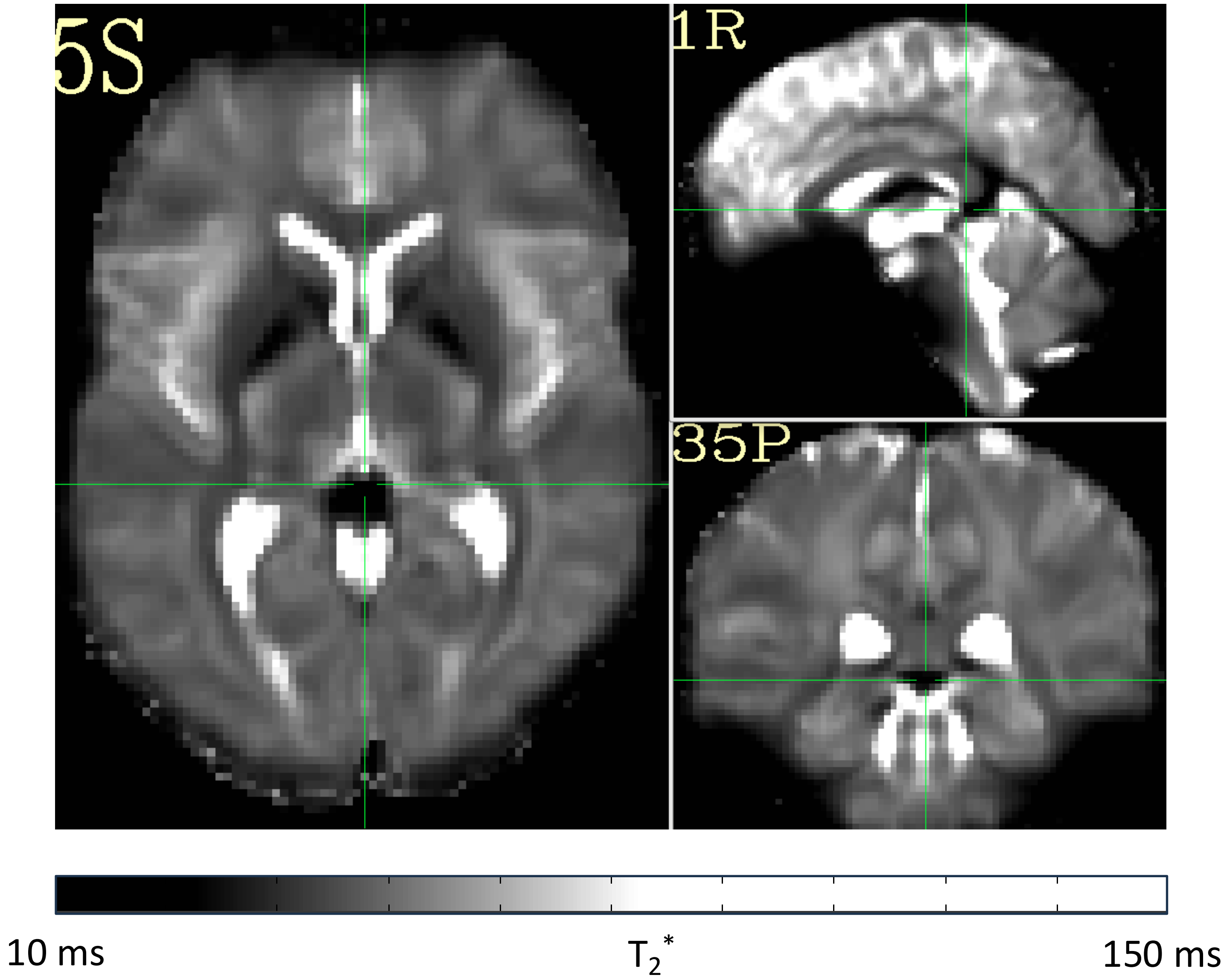
Multi-Echo Information

Differential Behavior for BOLD and non-BOLD Fluctuations



Rho (ρ) Kappa (κ)

Spatial T2* Map



How to take advantage of all this extra info

Automatic Denoising (tedana, ME-ICA, tedana + NN)

ME Hemodynamic Deconvolution

ME Quality Assurance (p_{BOLD})

Study signals from non-GM compartments

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When to use deconvolution analysis?

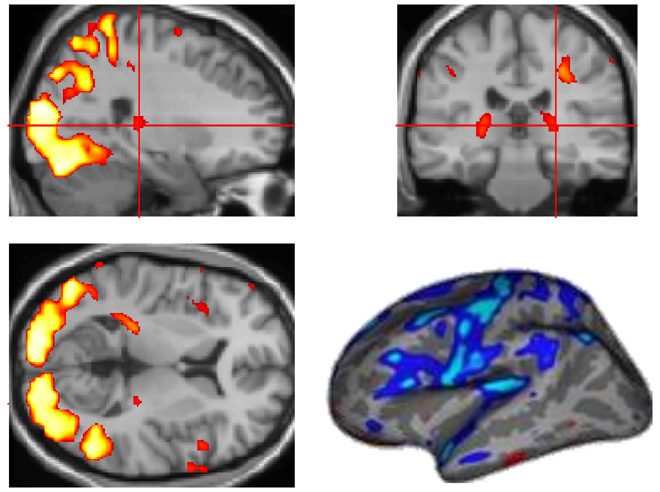
FMRI DATA

Time

DETAILED PARADIGM

Time

DATA PRE-PROCESSING & TRADITIONAL ANALYSIS



There are experimental scenarios where event timing might be missing:

- Naturalistic paradigms
- Clinical studies (e.g., interictal events)
- Resting State

Deconvolution methods are an alternative in such scenarios:

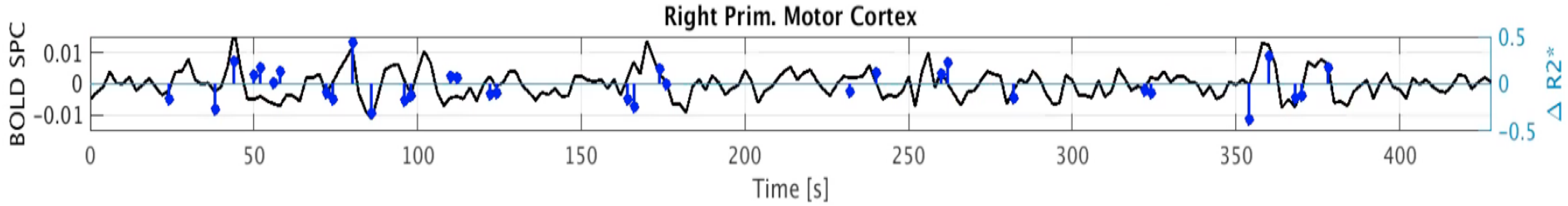
FMRI DATA

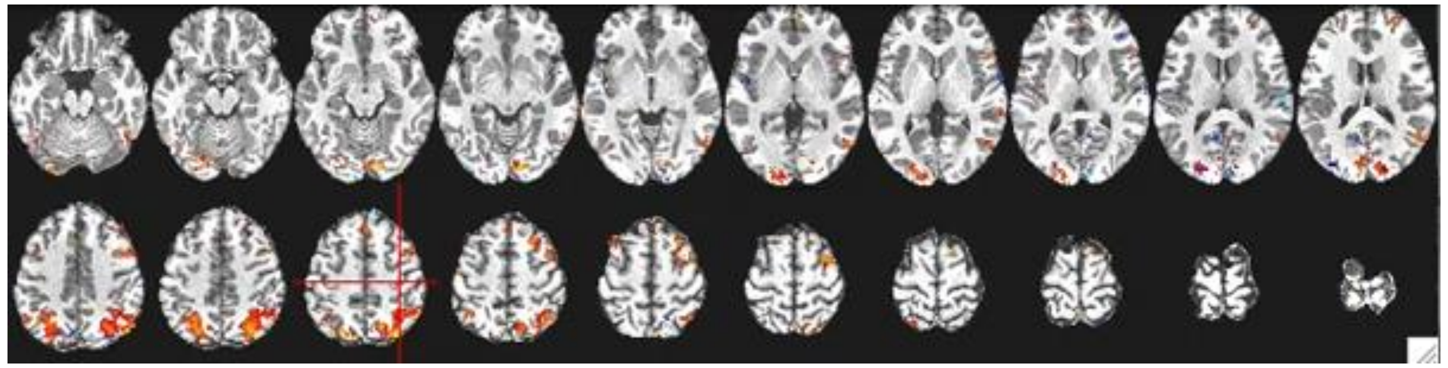
Time

HRF MODEL

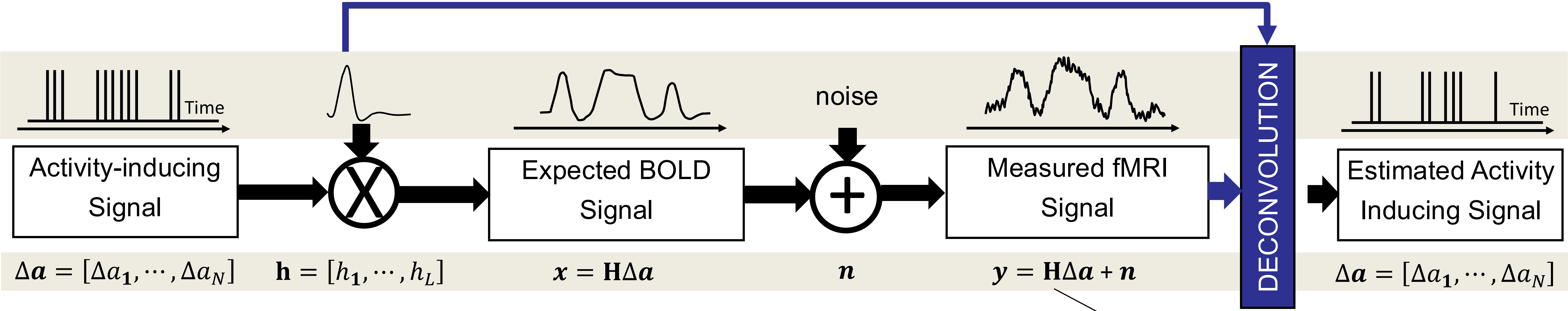
Time

DATA PRE-PROCESSING & DECONVOLUTION





Single-Echo Deconvolution



If one assumes the underlying activity-inducing signal to consist of brief, sparse events, then the formulated deconvolution problem can be solved using LASSO regularization:

$$\Delta\hat{\boldsymbol{a}} = \arg\min_{\Delta\boldsymbol{a}} \frac{1}{2} \overbrace{\|\boldsymbol{y} - \mathbf{H}\Delta\boldsymbol{a}\|_2^2}^{\text{Error Minimization Term}} + \underbrace{\lambda \|\Delta\boldsymbol{a}\|_1}_{\text{L1-Norm Regularization (Sparseness)}}$$

Single-Echo Sparse Free Paradigm Mapping Algorithm

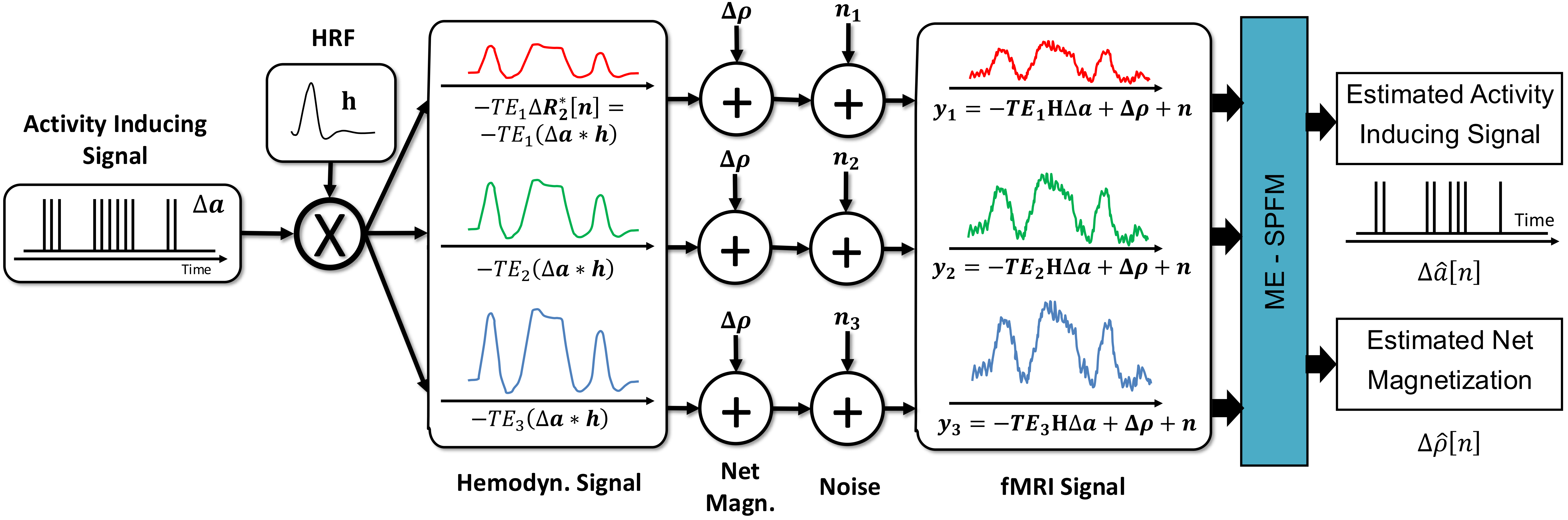
3dPFM

Paper

Code

Caballero-Gaudes et al. HBM (2011)

Multi-Echo Deconvolution



$$\bar{\boldsymbol{y}} \overset{\text{def}}{=} \begin{bmatrix} \boldsymbol{y}_1 \\ \vdots \\ \boldsymbol{y}_K \end{bmatrix} = \underbrace{\begin{bmatrix} \mathbf{I} \\ \vdots \\ \mathbf{I} \end{bmatrix}}_{\bar{\mathbf{I}}} \Delta\boldsymbol{\rho} - \underbrace{\begin{bmatrix} TE_1\mathbf{H} \\ \vdots \\ TE_K\mathbf{H} \end{bmatrix}}_{\bar{\mathbf{H}}} \Delta\boldsymbol{a}$$

Assuming sparsity in both unknowns, we can solve using LASSO regularization

$$\Delta\hat{\boldsymbol{a}}, \Delta\hat{\boldsymbol{\rho}} = \arg\min_{\Delta\boldsymbol{a}, \Delta\boldsymbol{\rho}} \frac{1}{2} \|\bar{\boldsymbol{y}} - \bar{\mathbf{H}}\Delta\boldsymbol{a} - \bar{\mathbf{I}}\Delta\boldsymbol{\rho}\|_2^2 + \lambda_1 \|\Delta\boldsymbol{a}\|_1 + \lambda_2 \|\Delta\boldsymbol{\rho}\|_1$$

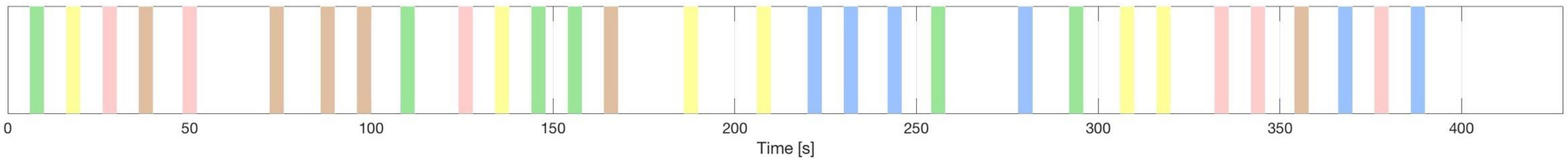
Caballero-Gaudes et al. NeuroImage (2019)

Single-Echo vs. Multi-Echo Deconvolution

- 10 Subjects (5M/5F)
- GRE – EPI @ 3T / 32-Channels Coil
- TE = 16.3/32.2/48.1 ms
- TR = 2 seconds
- Resolution = 3 x 3 x 4 mm^3
- ASSET = 2

Rapid event-related with 5 different tasks / 6 trials per task per run / events are approx. 4 seconds long

SCHEMATIC OF ONE FUNCTIONAL RUN



Listen to an audio clip and select instrument being played from the ones displayed on the screen.

Passive viewing of dot patterns resembling different types of biological motion.

Passive viewing of images of houses

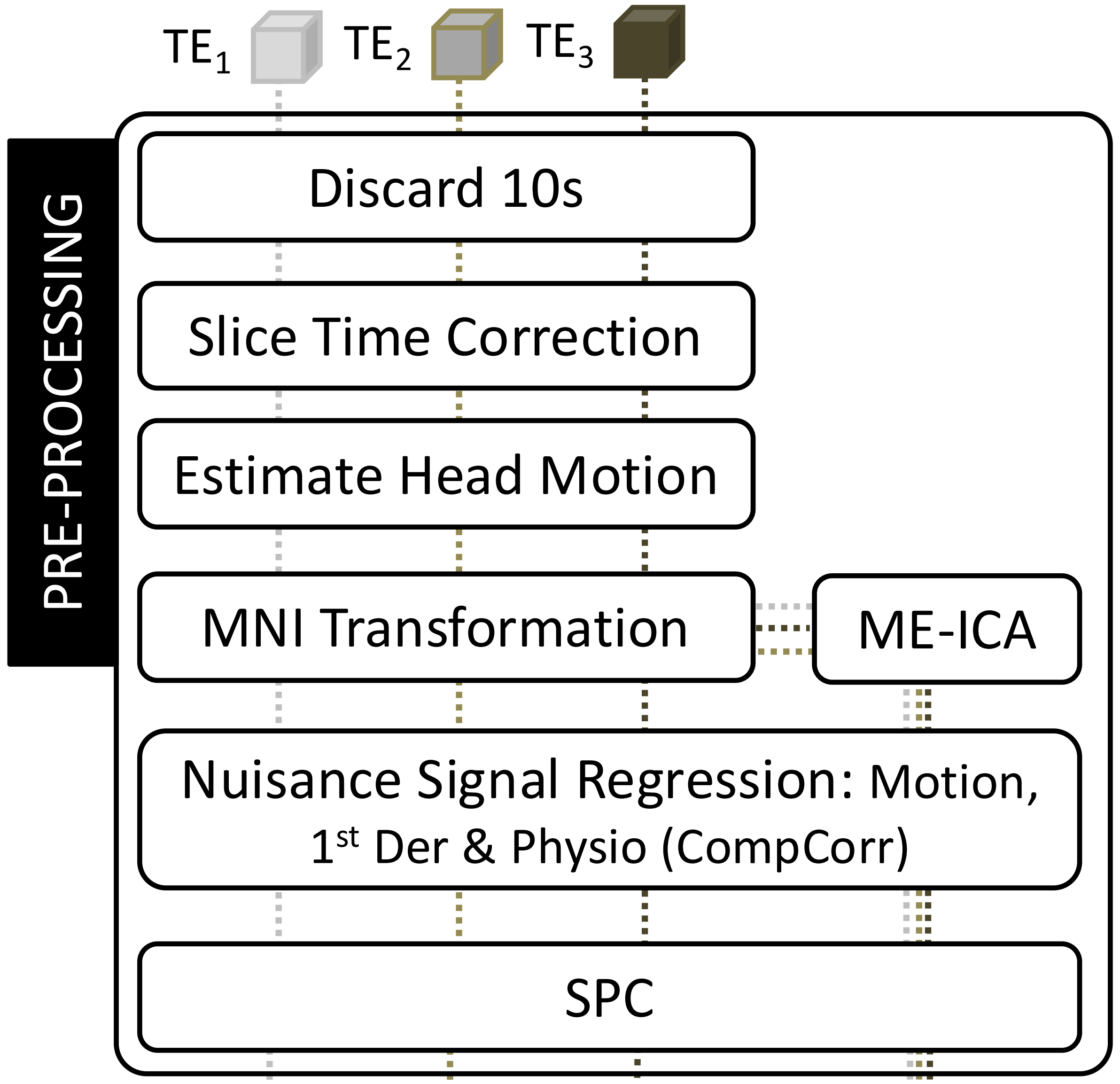
Press a button at an approx. rate of 0.5Hz (following a counter on the screen).

READ THIS

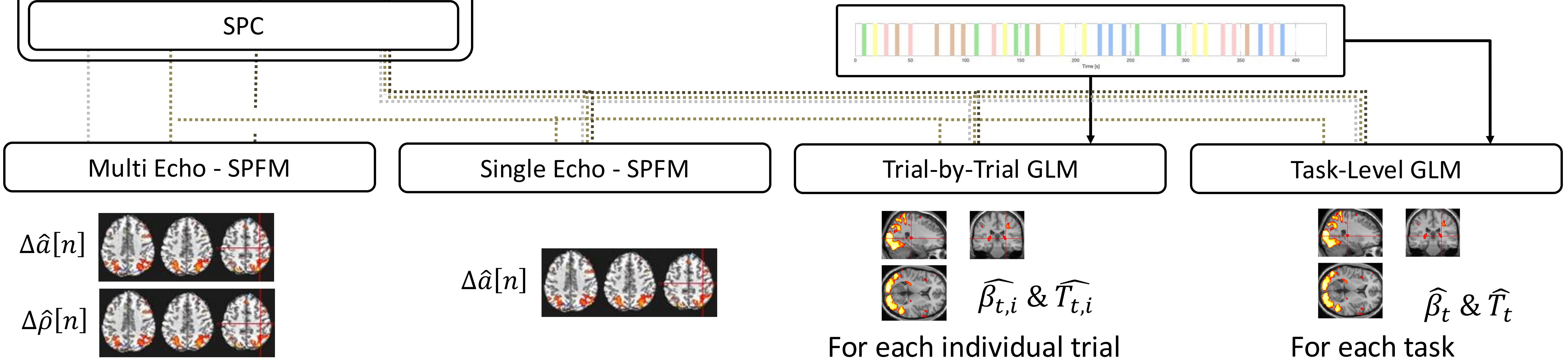
Silently read sentences that appear on the screen one word at a time.

Caballero-Gaudes et al. NeuroImage (2019)

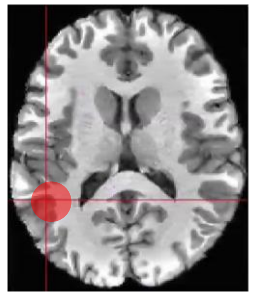
Single-Echo vs. Multi-Echo Deconvolution



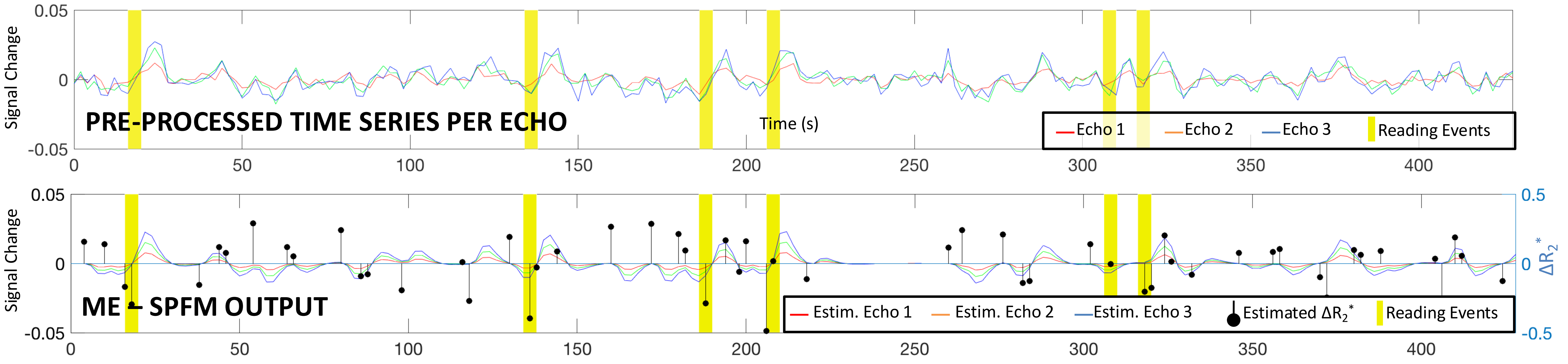
- **<u>ME – SPFM</u>**
  → Newly Proposed Algorithm
- **<u>SE – SPFM</u>**
  → Deconvolution results for original single-echo SPFM algorithm.
- **<u>Trial-by-Trial GLM</u>**
  → ”Best” activation maps for each individual trial
  → Paradigm timing information is available
- **<u>Task – Level Task GLM</u>**
  → GOLD Standard
  → “Best” subject-wise activation map per task type.

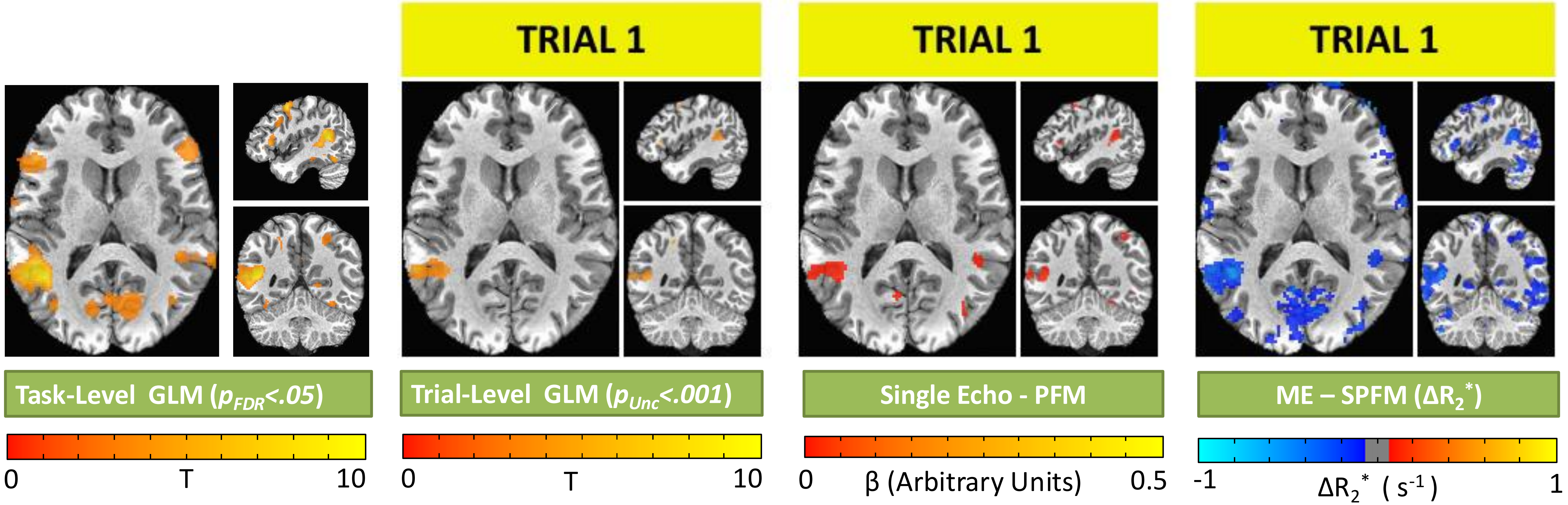


Single-Echo vs. Multi-Echo Deconvolution



READ THIS

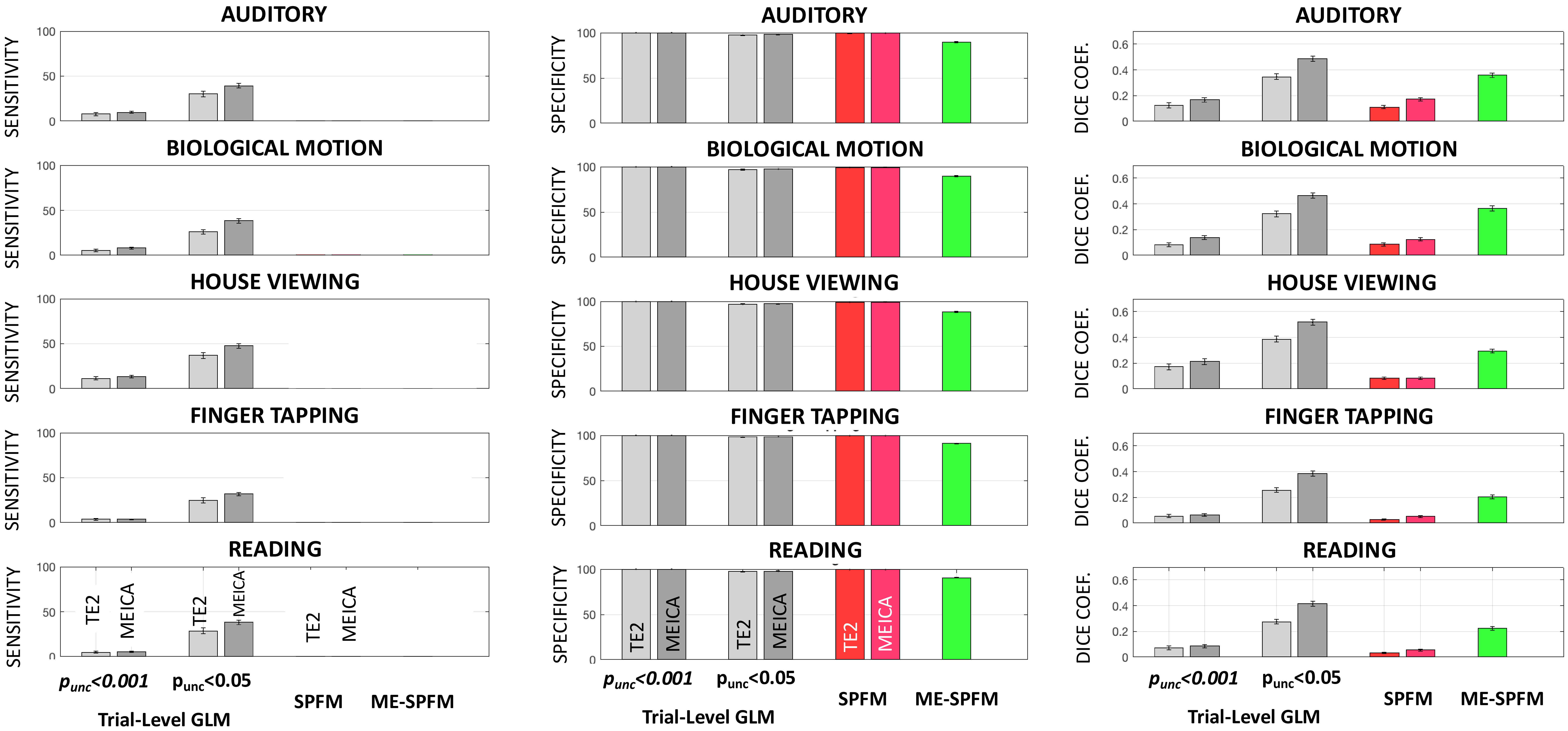




Caballero-Gaudes et al. NeuroImage (2019)

Single-Echo vs. Multi-Echo Deconvolution

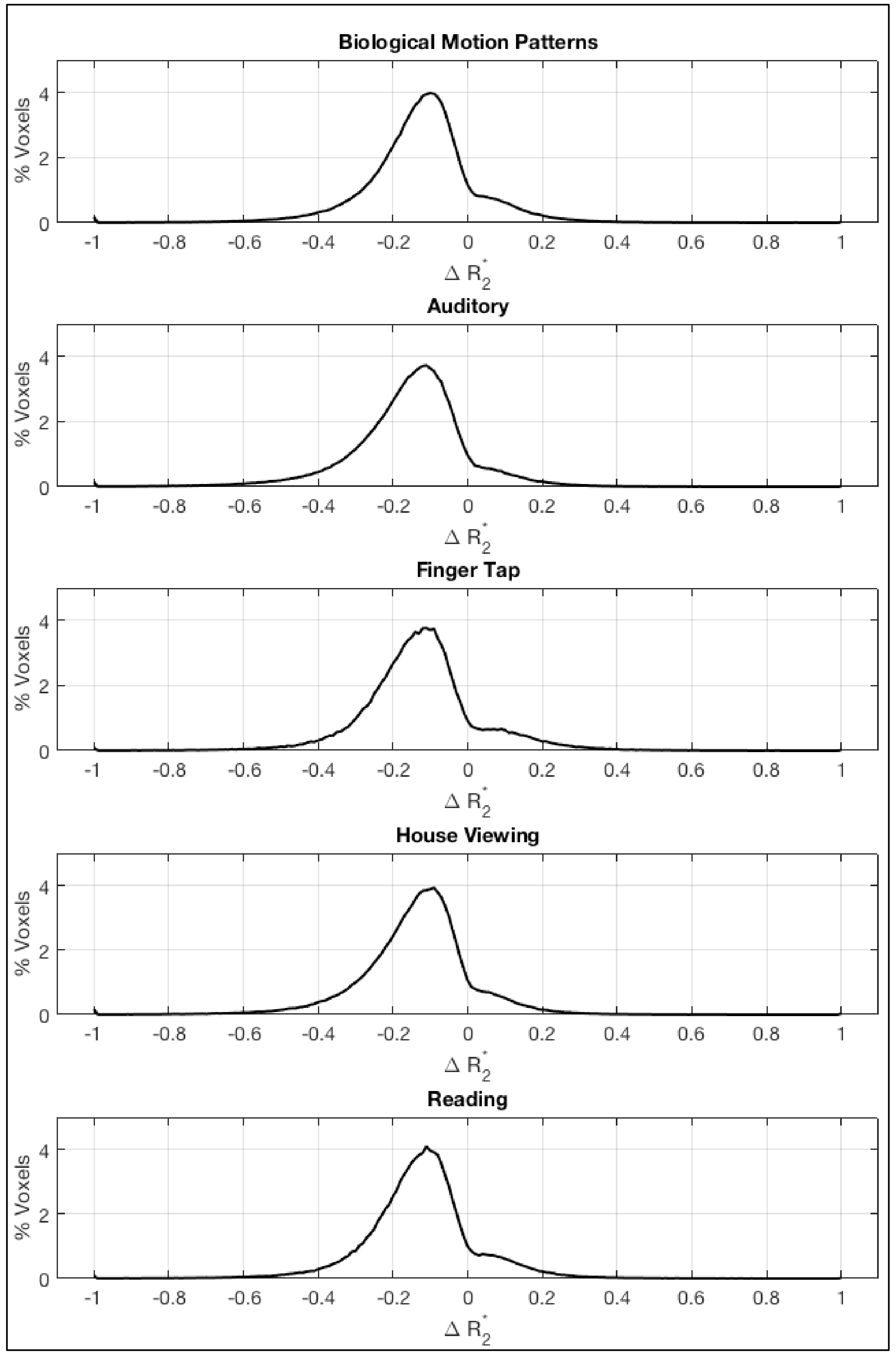
SENSITIVITY vs. TASK-LEVEL GLM | **SPECIFICITY vs. TASK-LEVEL GLM** | **DICE COEFFICIENT**



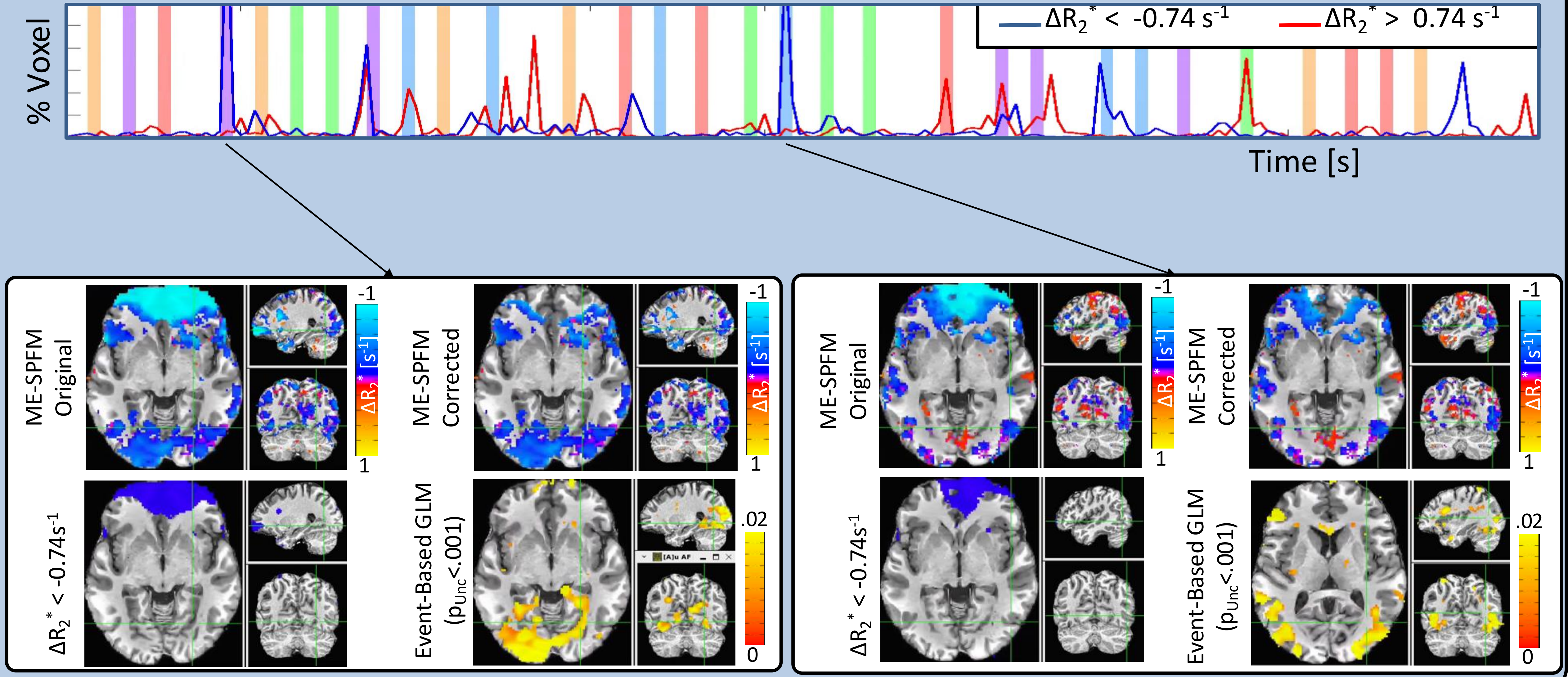
Caballero-Gaudes et al. NeuroImage (2019)

Multi-Echo Deconvolution: Interpretable Units

Distribution of ΔR_2^* in GLM task-level active voxels for each task



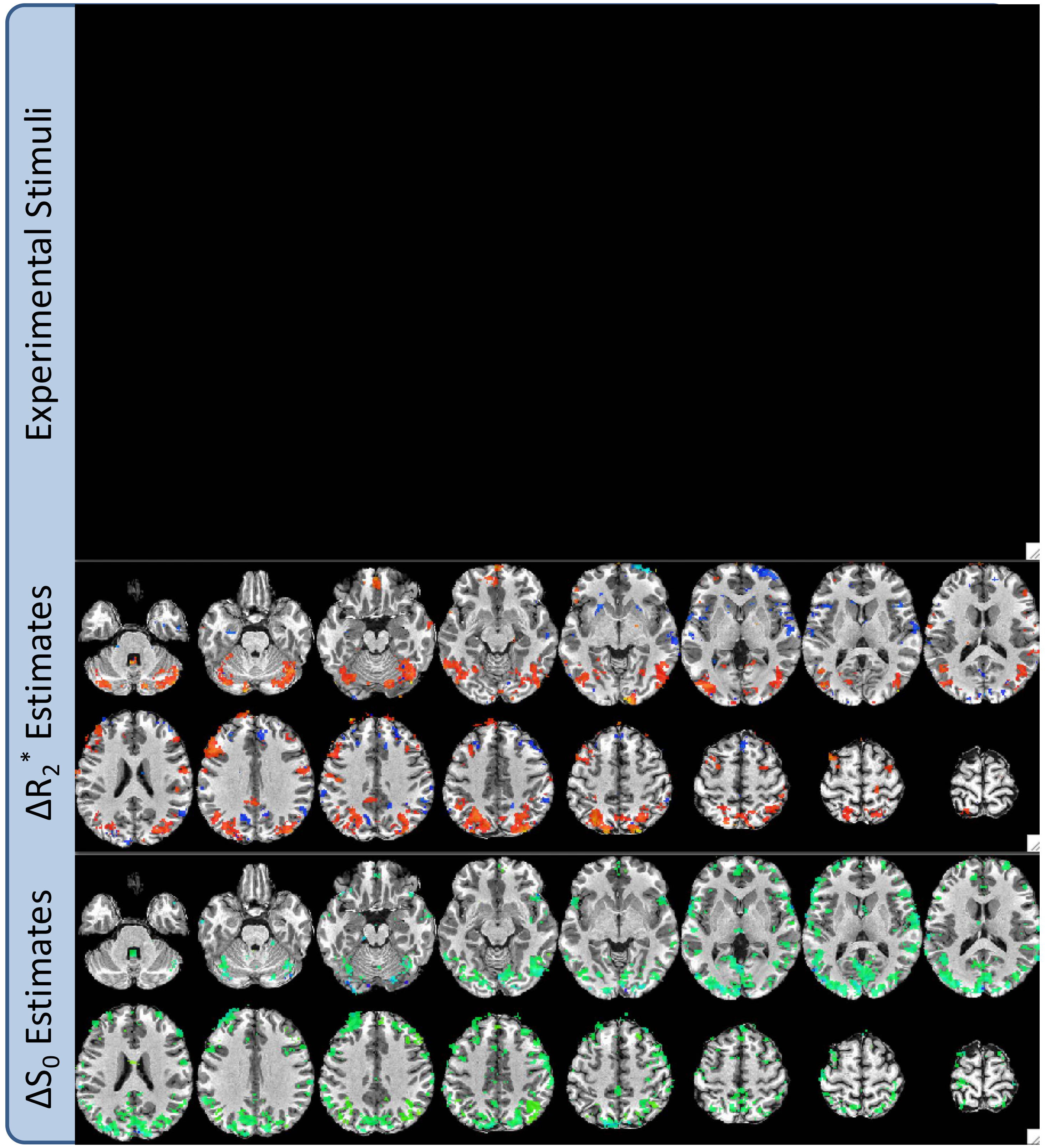
Distribution of ΔR_2^* across all voxels on a volume-by-volume basis



Reference	Region	ROI / Compartment	ΔR_2^* [s^{-1}]
W. Van der Zaag et al, NeuroImage, 2009	Motor Cortex	Voxels active across all echoes	-0.98 ± 0.08
		Voxels active at any echo	-0.54 ± 0.03
Donahue et al, NMR in Biomedicine, 2011	Visual Cortex	Total	-0.74 ± 0.05
		Extravascular	-0.52 ± 0.07

Caballero-Gaudes et al. NeuroImage (2019)

ME-Deconvolution: Conclusions



- ME-SPFM is a deconvolution algorithm specifically formulated for multi-echo data.
- ME-SPFM can reliably detect individual events without a priori information about their timing.
- ME-SPFM outperforms its single-echo counterpart in terms of sensitivity and nearly matches GLM-based results at the single-trial level.
- ME-SPFM estimates ΔR_2^* with interpretable units [s^{-1}], which fell within physiologically plausible limits.
- ME-SPFM can help us decipher the dynamic nature of brain activity in naturalistic paradigms, resting-state or clinical applications with unknown event-timing.

Caballero-Gaudes et al. NeuroImage (2019)

How to take advantage of all this extra info

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ME Hemodynamic Deconvolution

ME Quality Assurance (p_{BOLD})

Study signals from non-GM compartments

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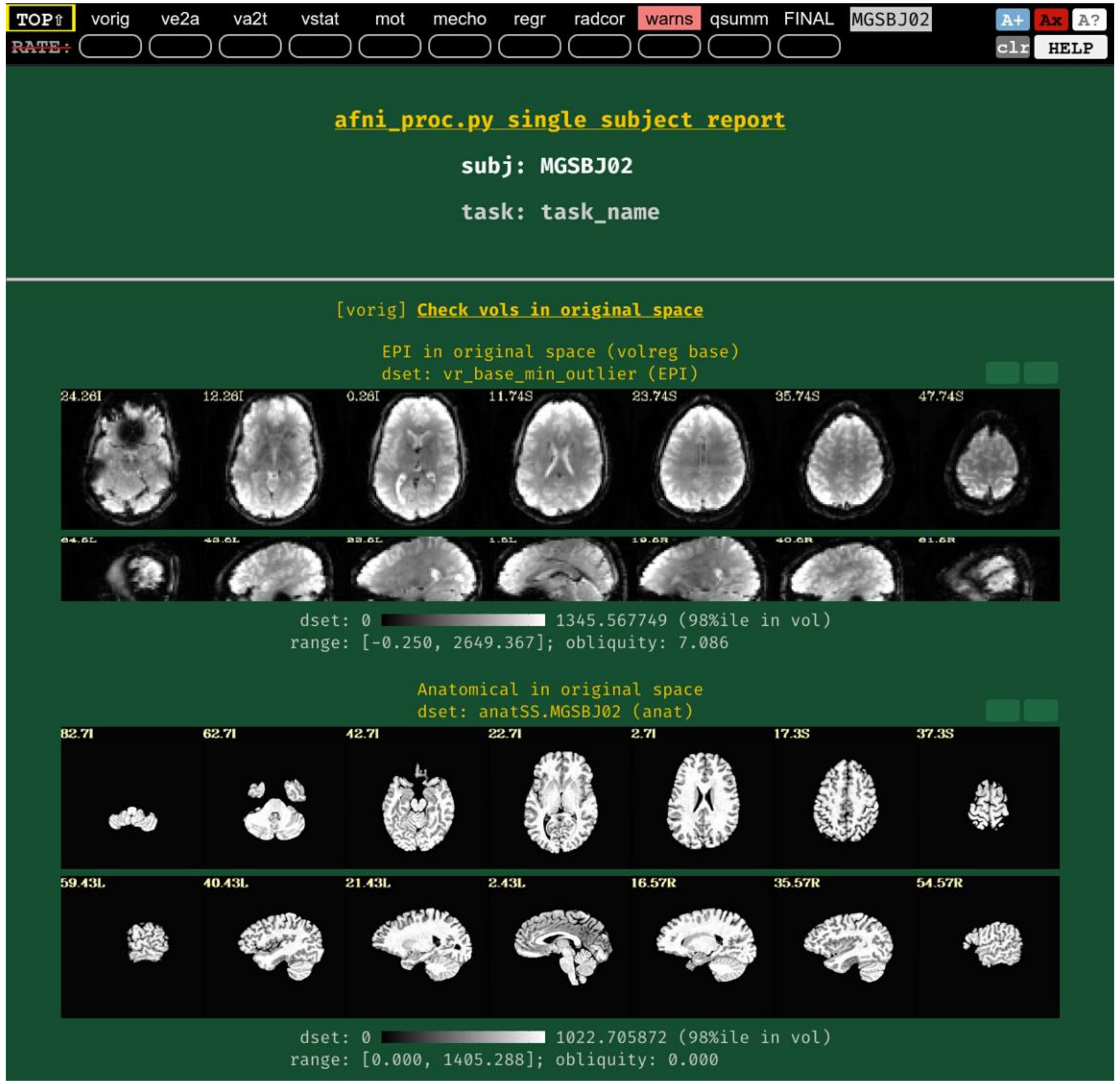
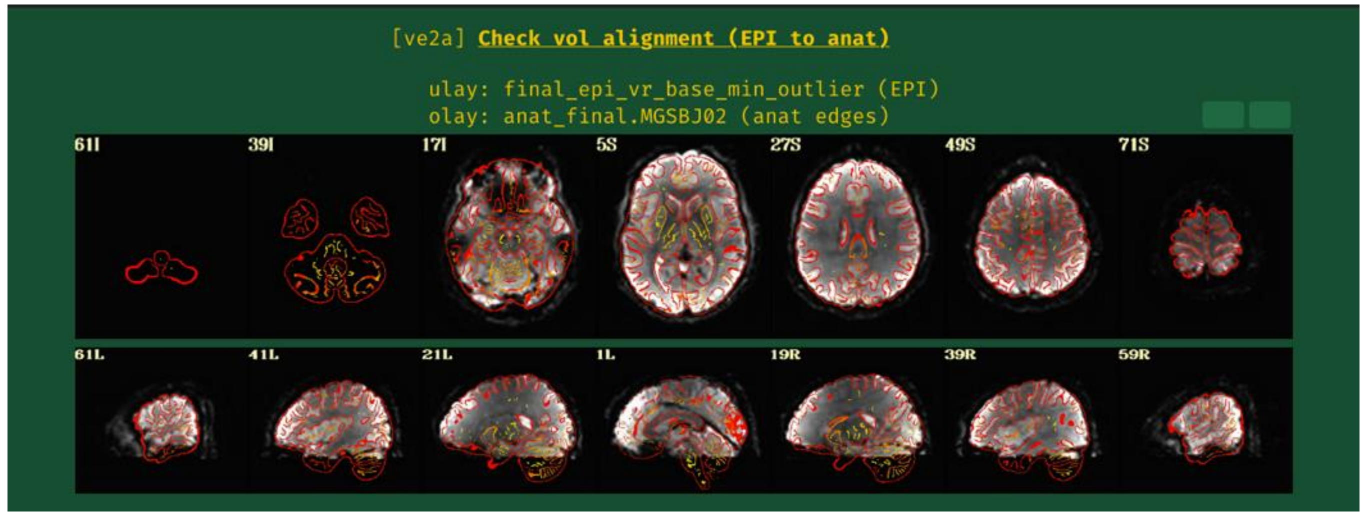
QA for ME-data: Why? (I)

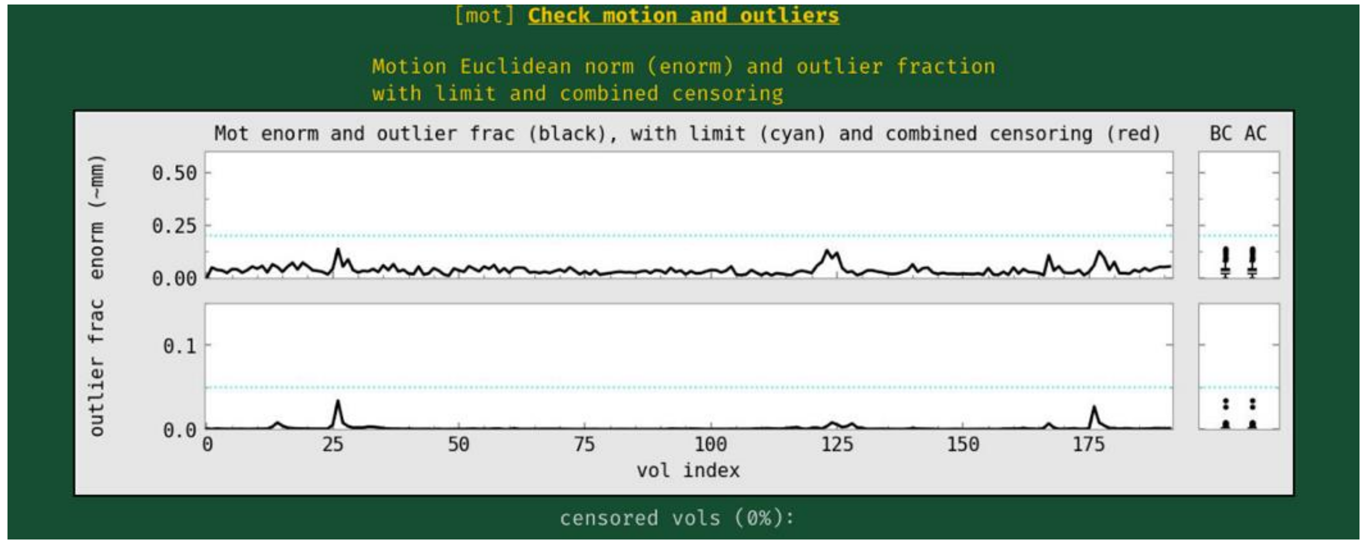
AFNI QC Reports



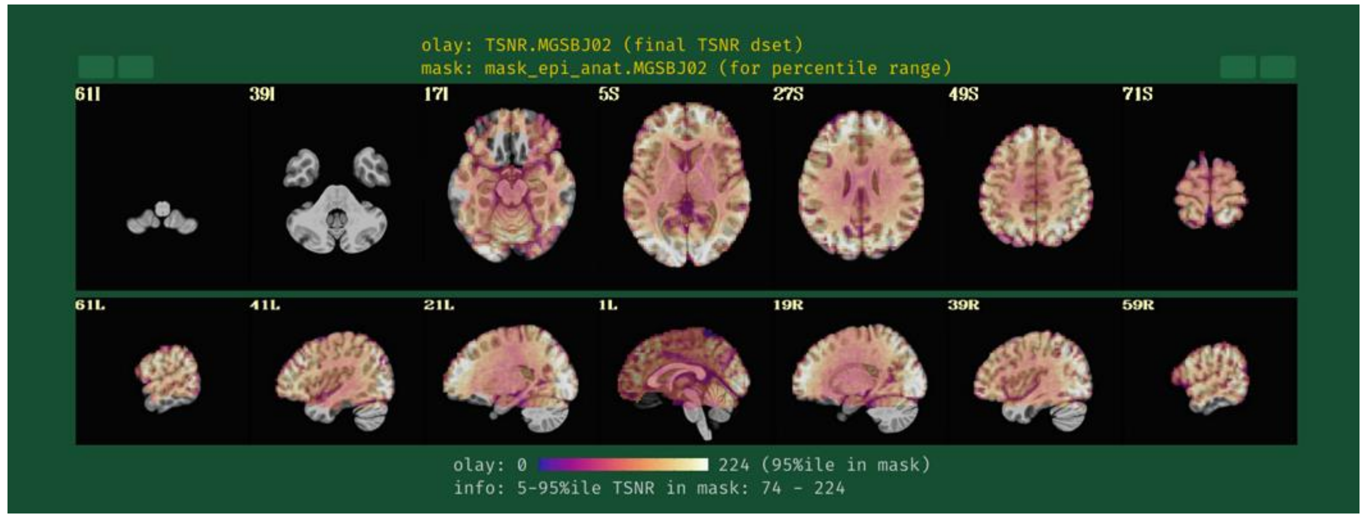
Alignment



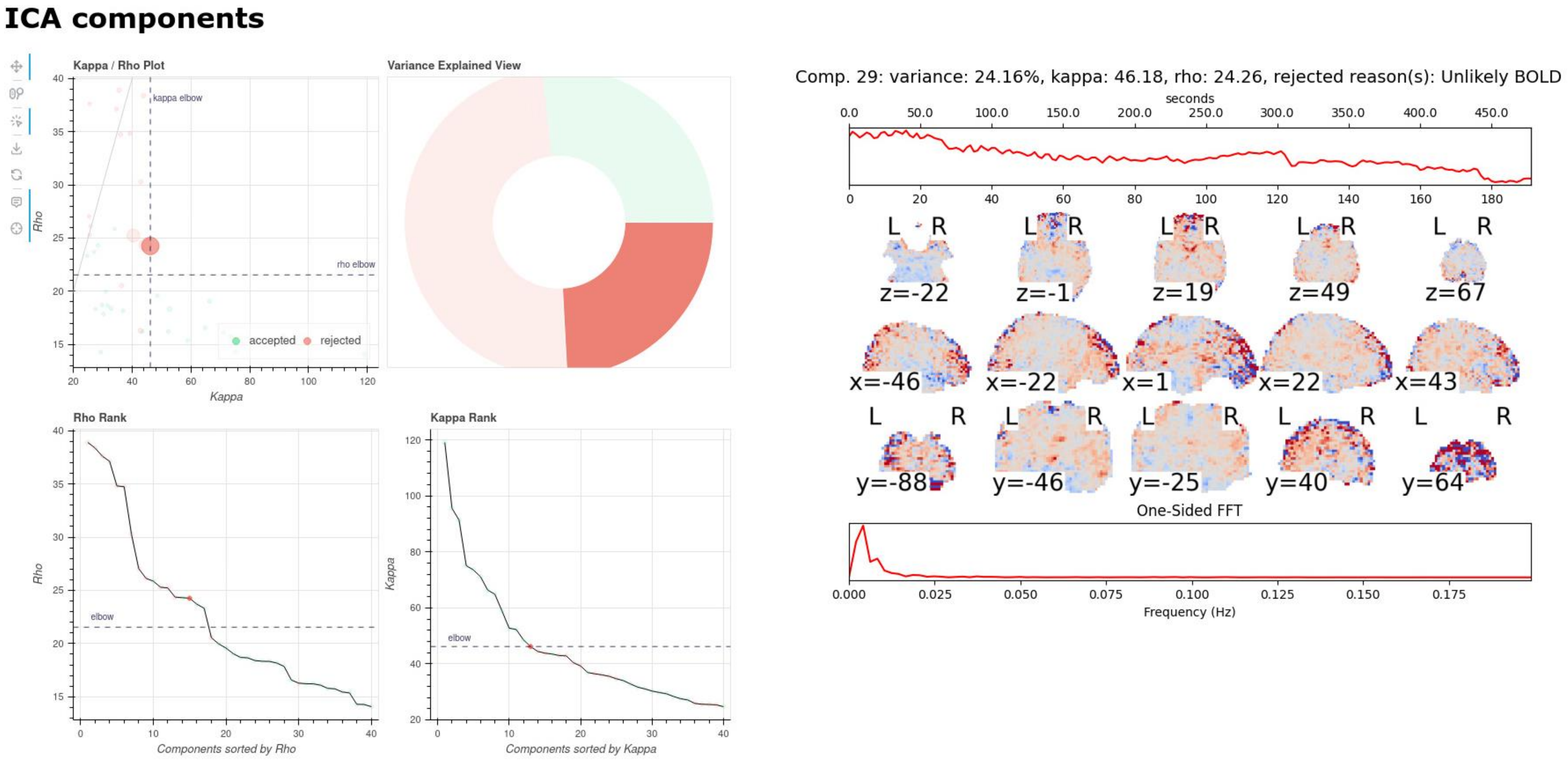
Head Motion



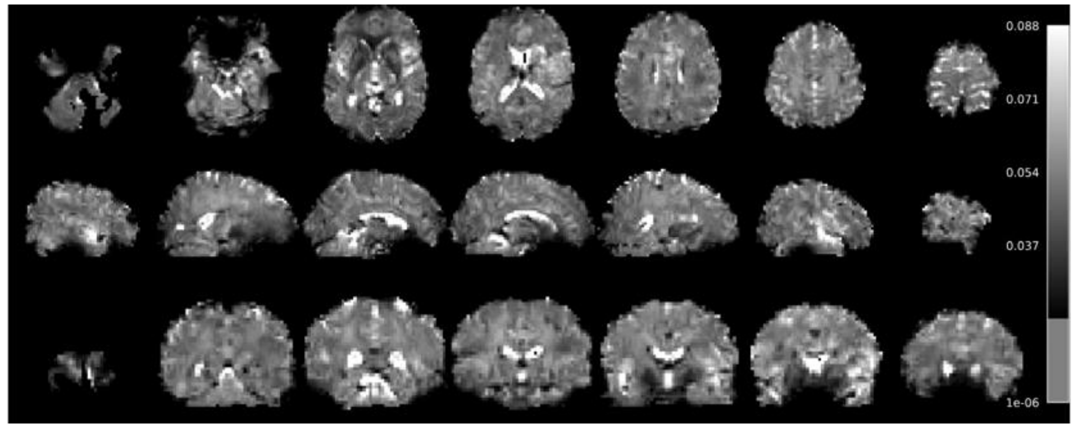
TSNR



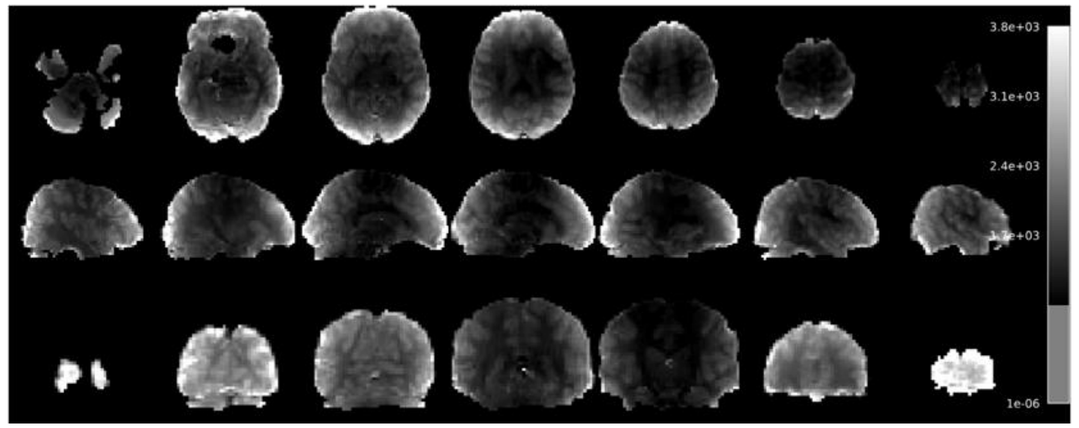
QA for ME-data: Why? (II)



Component Selection



T2* Estimation



S0 Estimation

QA for ME-data: Why? (III)

- Higher Temporal Signal-to-Noise Ratio

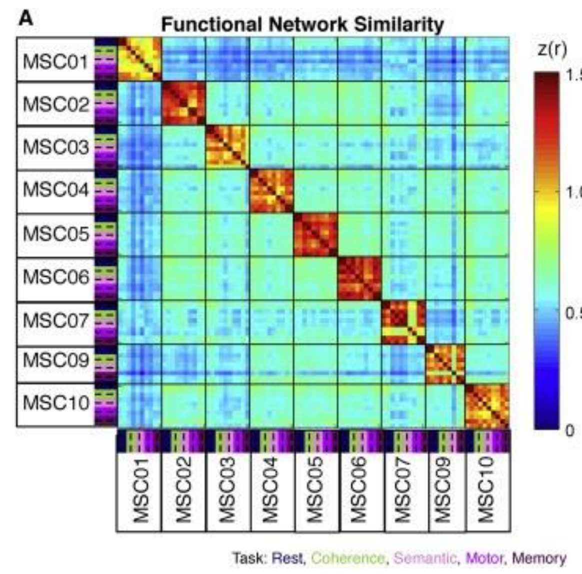
As we remove noise-related variance, TSNR increases

Yet, as we remove variance of interest, TSNR also increases

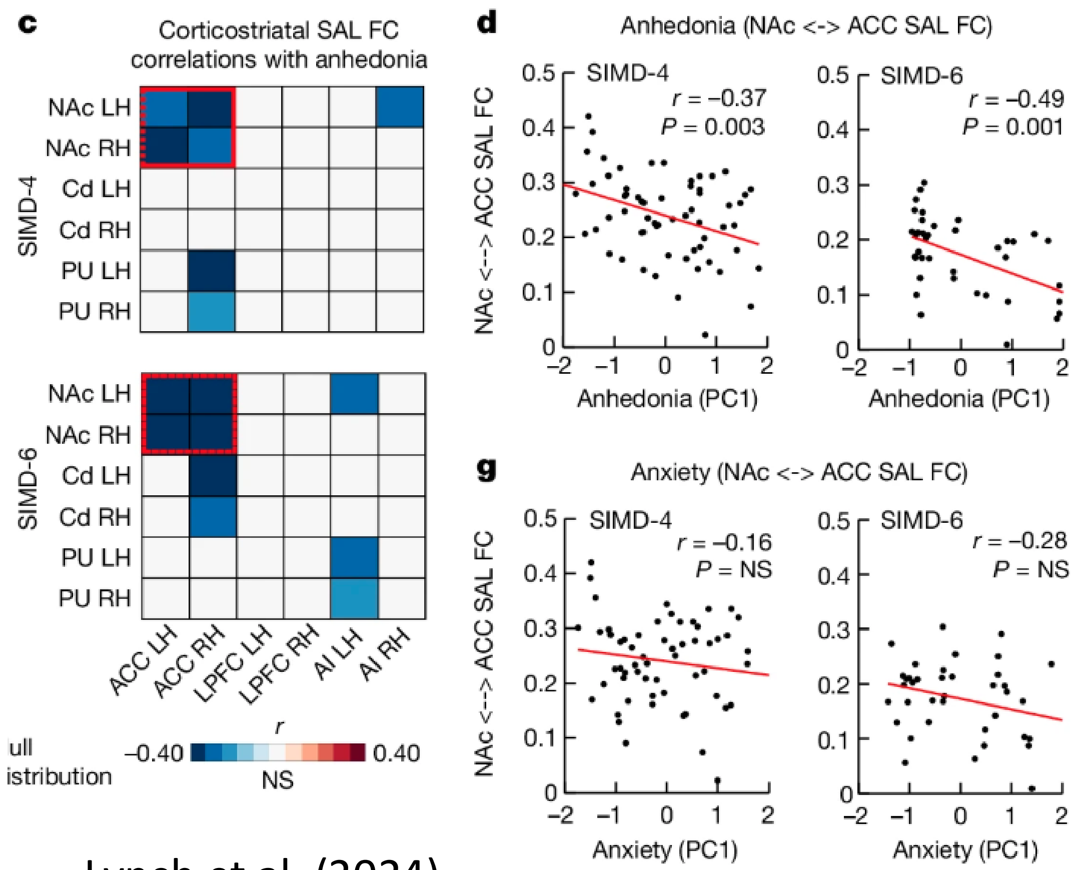
- Higher Test-Retest Reliability

Functional patterns of interest should be stable in time

Yet, some changes are clinically relevant



Gratton et al. (2018)



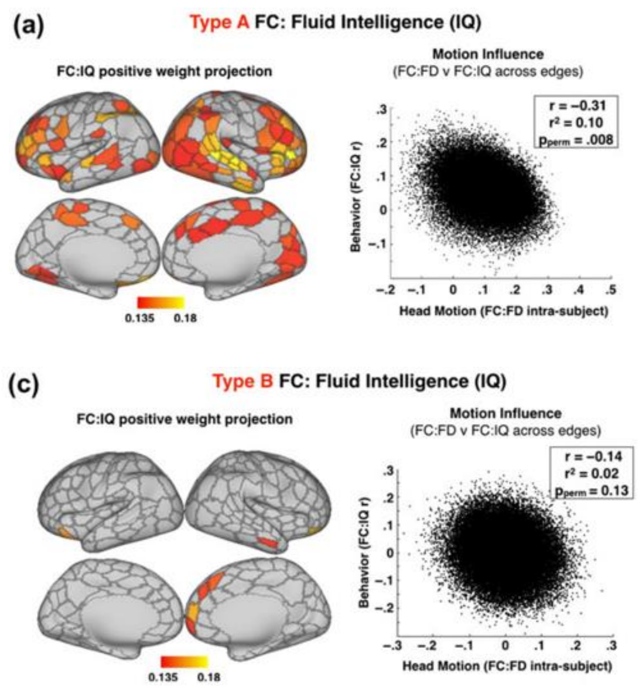
Lynch et al. (2024)

- Higher Correlation with an external phenotype

Stronger brain-behavior relationships signal better data

Yet, systematic differences in nuisance factors can alter this relation

Subject measures	Pearson r
ReadEng (AgeAdj)	−0.23
ReadEng (Unadj)	−0.23
Vocabulary (AgeAdj)	−0.19
Dexterity (Unadj)	−0.18
CardSort (Unadj)	−0.18
Dexterity (AgeAdj)	−0.18
CardSort (AgeAdj)	−0.18
Education	−0.17
Fluid intelligence	−0.17
Spatial orientation	−0.17
Vocabulary (unadjj)	−0.17
Emotion recognition	−0.16
DSM somatic problems (pct)	0.16
DSM antisocial (raw)	0.16
ASR externalizing (raw)	0.16
DSM somatic problems (raw)	0.16
Tobacco use 7 day	0.18
Diastolic blood pressure	0.18
ASR externalizing	0.18
Tobacco use today	0.2
Systolic blood pressure	0.23
Weight	0.52
Body mass index (BMI)	0.66



Siegel et al. (2017)

- More significant voxels are better

Not always

QA for ME-data: How?

Signal at voxel/ROI ‘x’, timepoint ‘t’ and echo ‘k’

BOLD fluctuations

$$S(x,t,TE_k) = S_o(x,t) \cdot e^{-R_2^*(x,t) \cdot TE_k} + n(x,t)$$

Fluctuations in net magnetization

Thermal Noise

Data free of fluctuations in net magnetization and thermal noise is better data

***p**$_{BOLD}$* ~ probability of data being dominated by BOLD fluctuations

Gonzalez-Castillo et al. BioRxiv (2026)

QA for ME-data: Correlation across TEs | Theory

$s_{x,i} \approx \Delta\rho_x - \Delta R_x \cdot TE_i$ ← Signals at two ROIs [*x* and *y*] acquired at two different TEs [*i* and *j*] → $s_{y,j} \approx \Delta\rho_y - \Delta R_y \cdot TE_j$

$$R(s_{x,i}, s_{y,j}) = R_{xi,yj} = \frac{\sum\left(s_{x,i} - \overline{s_{x,i}}\right)\cdot\left(s_{y,j} - \overline{s_{y,j}}\right)}{\sqrt{\sum\left(s_{x,i} - \overline{s_{x,i}}\right)^2 \cdot \sum\left(s_{y,i} - \overline{s_{x,i}}\right)^2}} \xrightarrow{\overline{s_{x,i}}=\overline{s_{y,j}}=0} \frac{\sum s_{x,i}\cdot s_{y,j}}{\sqrt{\sum\left(s_{x,i}\right)^2 \cdot \sum\left(s_{y,i}\right)^2}}$$

$$R_{xi,yj} = \frac{\sum(\Delta\rho_x - \Delta R_x \cdot TE_i)\cdot\left(\Delta\rho_y - \Delta R_y \cdot TE_j\right)}{\sqrt{\sum(\Delta\rho_x - \Delta R_x \cdot TE_i)^2} \cdot \sqrt{\sum\left(\Delta\rho_y - \Delta R_y \cdot TE_j\right)^2}}$$

BOLD-DOMINATED REGIME

$\Delta\boldsymbol{\rho}_x \ll \Delta\boldsymbol{R}_x \;\&\; \Delta\boldsymbol{\rho}_y \ll \Delta\boldsymbol{R}_y$

$$R_{xi,yj} = \frac{\cancel{TE_i}\cdot\cancel{TE_j}\cdot\sum\left(\Delta R_x \cdot \Delta R_y\right)}{\cancel{TE_i}\cdot\cancel{TE_j}\cdot\sqrt{\sum(-\Delta R_x)^2}\cdot\sqrt{\sum\left(-\Delta R_y\right)^2}}$$

R is TE-independent

S_0-DOMINATED REGIME

$\Delta\boldsymbol{\rho}_x \gg \Delta\boldsymbol{R}_x \;\&\; \Delta\boldsymbol{\rho}_y \gg \Delta\boldsymbol{R}_y$

$$R_{xi,yj} = \frac{\sum \Delta\rho_x \cdot \Delta\rho_y}{\sqrt{\sum(\Delta\rho_x)^2}\cdot\sqrt{\sum\left(\Delta\rho_y\right)^2}}$$

R is TE-independent

Gonzalez-Castillo et al. BioRxiv (2026)

QA for ME-data: Covariance across TEs | Theory

$s_{x,i} \approx \Delta\rho_x - \Delta R_x \cdot TE_i$ ← Signals at two ROIs [*x* and *y*] acquired at two different TEs [*i* and *j*] → $s_{y,j} \approx \Delta\rho_y - \Delta R_y \cdot TE_j$

$$C_{xi,yj} = \frac{1}{N_t - 1} \cdot \sum \left(s_{x,i} - \overline{s_{x,i}}\right) \cdot \left(s_{y,j} - \overline{s_{y,j}}\right) \xrightarrow{\overline{s_{x,i}} = \overline{s_{y,j}} = 0} \frac{1}{N_t - 1} \cdot \sum s_{x,i} \cdot s_{y,j}$$

$$C_{xi,yj} = \frac{1}{N_t - 1} \cdot \sum (\Delta\rho_x - \Delta R_x \cdot TE_i) \cdot \left(\Delta\rho_y - \Delta R_y \cdot TE_j\right)$$

BOLD-DOMINATED REGIME

$\boldsymbol{\Delta\rho_x \ll \Delta R_x \;\&\; \Delta\rho_y \ll \Delta R_y}$

$$C_{xi,yj} = \frac{TE_i \cdot TE_j}{N_t - 1} \cdot \sum \Delta R_x \cdot \Delta R_y$$

C is a function of contributing echoes

S_0-DOMINATED REGIME

$\boldsymbol{\Delta\rho_x \gg \Delta R_x \;\&\; \Delta\rho_y \gg \Delta R_y}$

$$C_{xi,yj} = \frac{1}{N_t - 1} \cdot \sum \Delta\rho_x \cdot \Delta\rho_y$$

C is TE-independent

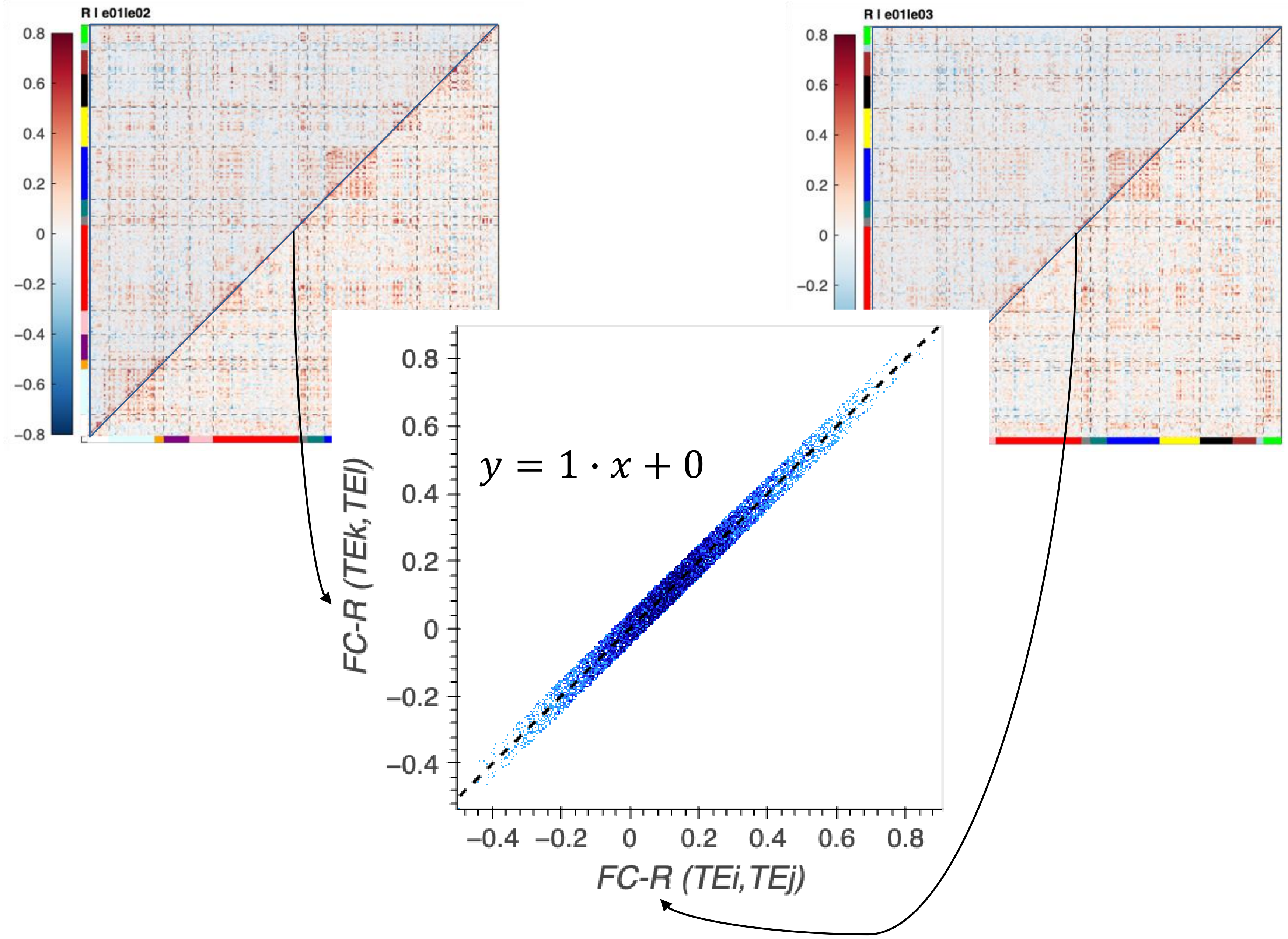
Gonzalez-Castillo et al. BioRxiv (2026)

QA for ME-data: R and Cov across TEs | Theory

FC as Pearson's Correlation

FC-R is TE-independent for both BOLD and So dominated data

$$R_{xk,yl} = R_{xi,yj} \;\forall i,j,k,l$$



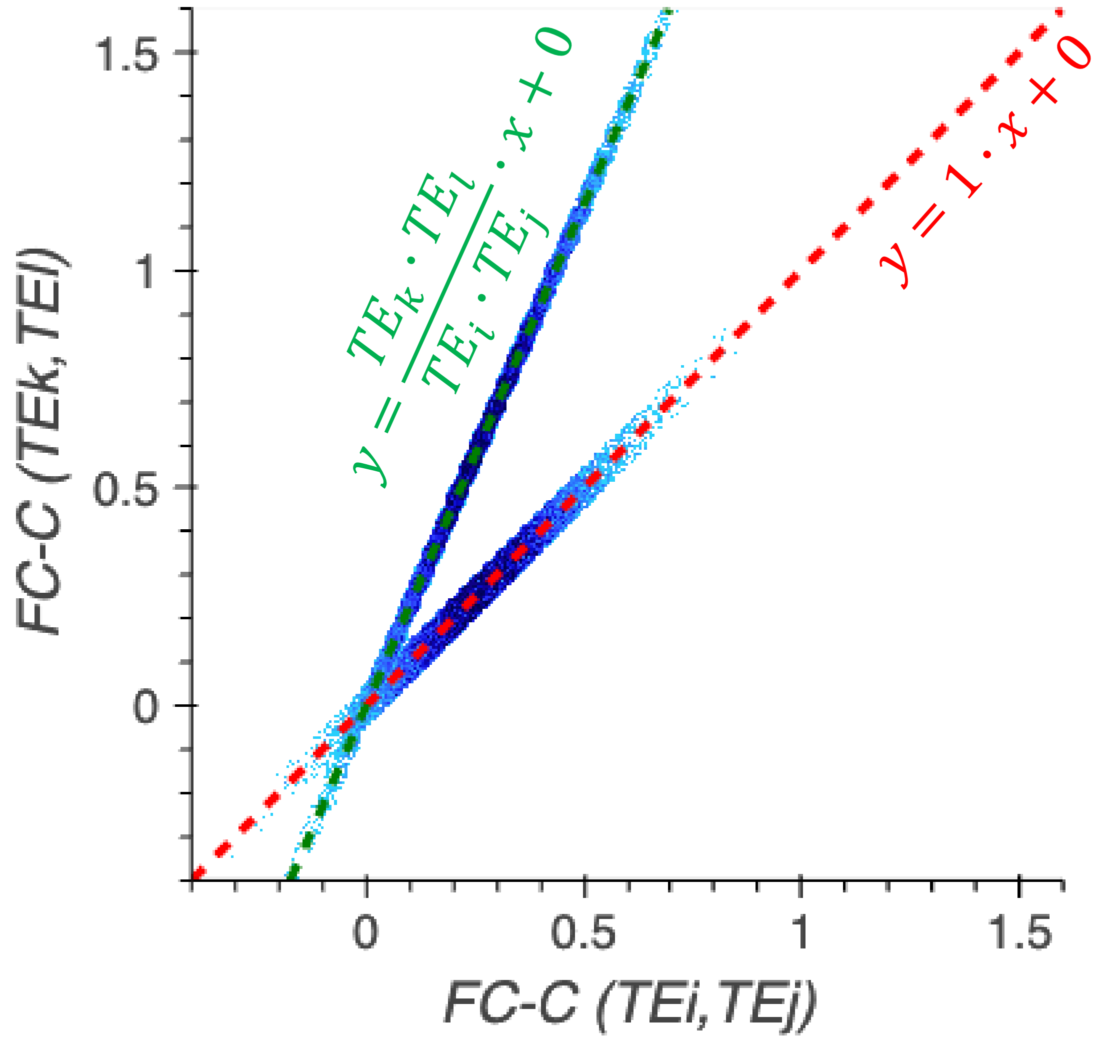
FC as Covariance

FC-C is TE-independent for So dominated data

$$C_{xk,yl} = C_{xi,yj} \;\forall i,j,k,l$$

FC-C is TE-dependent for BOLD dominated data

$$C_{xk,yl} = \frac{TE_k \cdot TE_l}{TE_i \cdot TE_j} \cdot C_{xi,yj}$$



Gonzalez-Castillo et al. BioRxiv (2026)

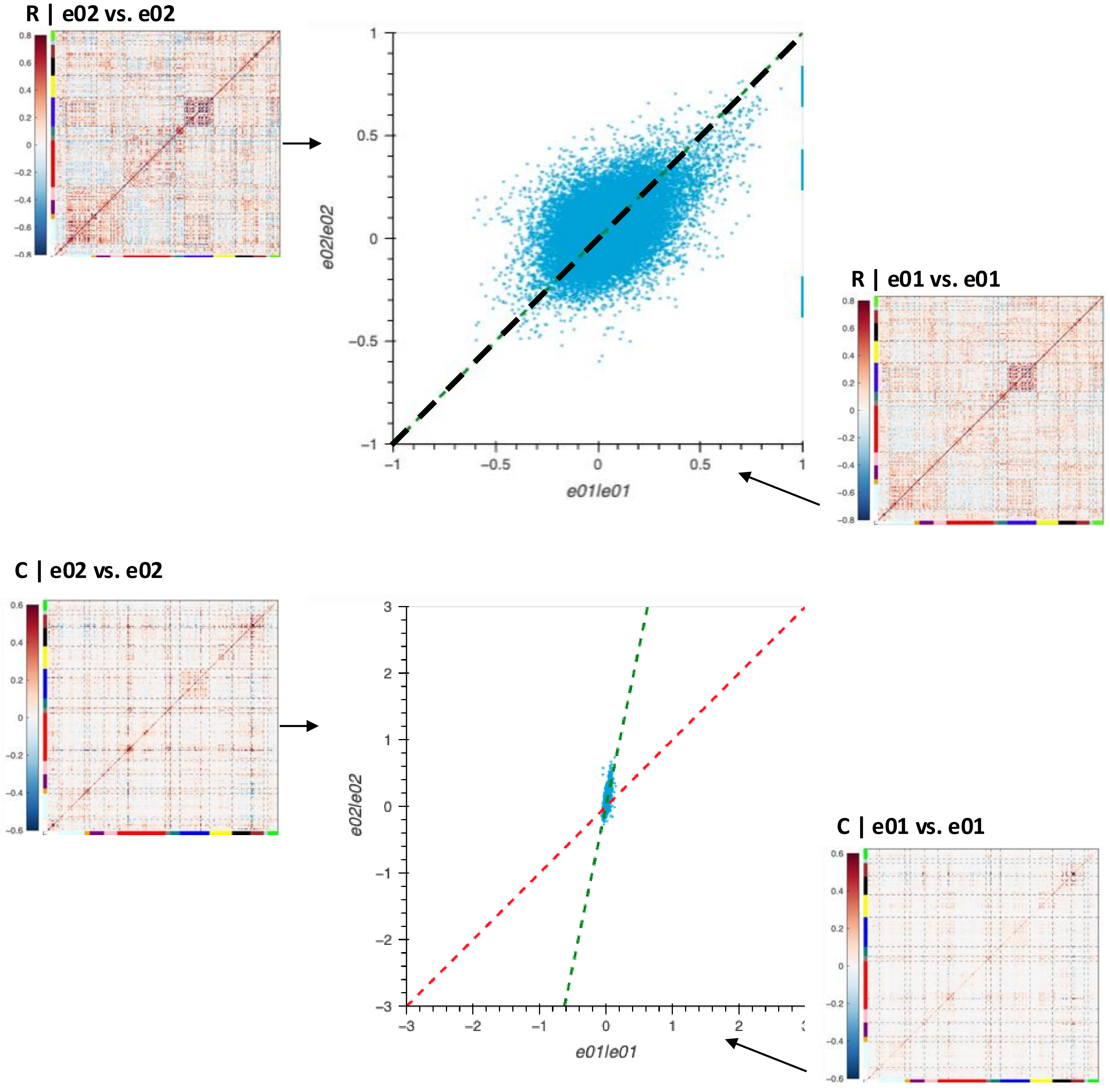
R and Cov across TEs – Empirical Data

BOLD Dominated Data:
Constant TR + Low Motion + Tedana Denoising

Non-BOLD Dominated Data:
Variable TR + Basic Denoising

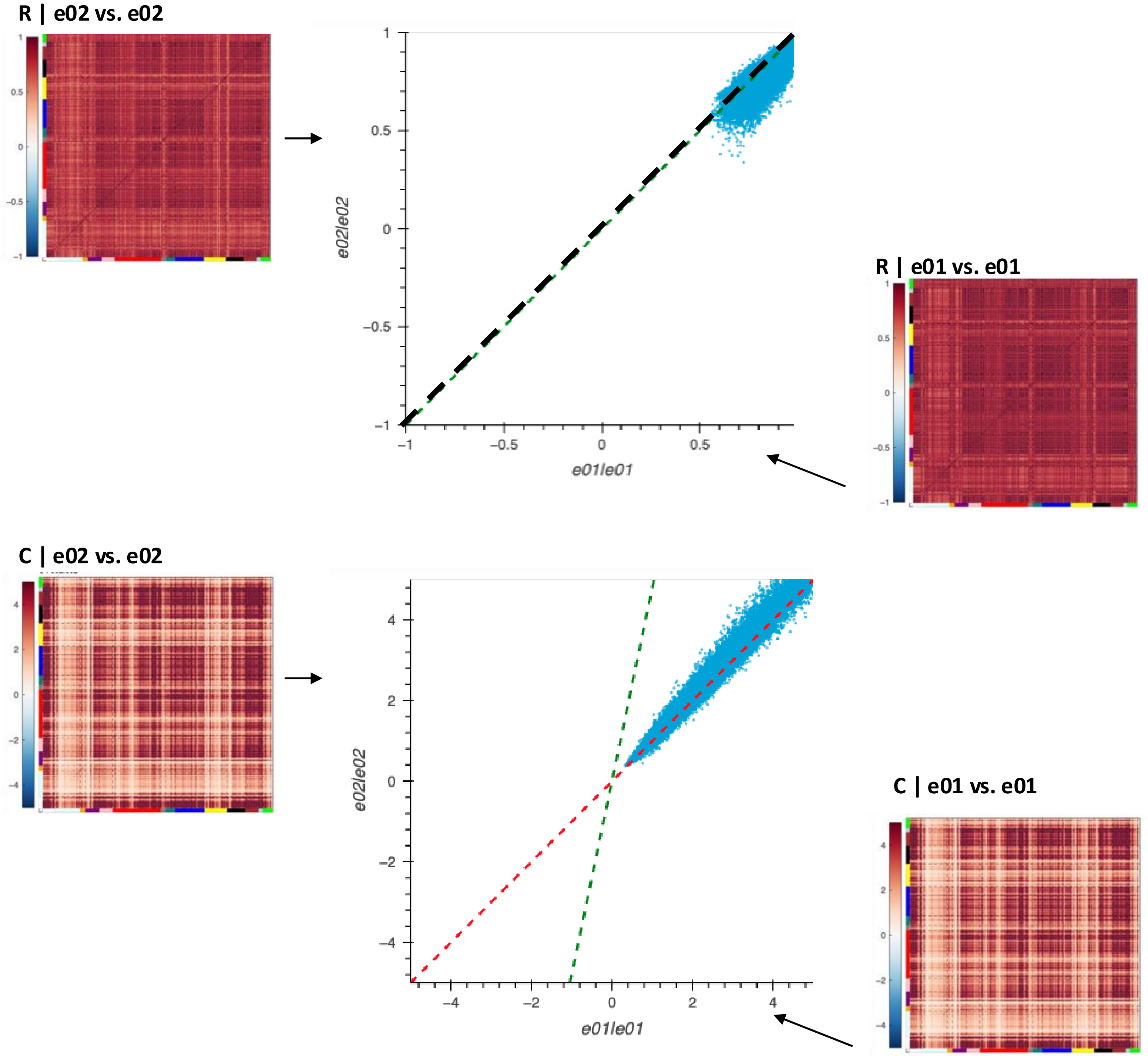
FC as Pearson's Correlation

FC as Covariance



Same Behavior

Differential Behavior



Gonzalez-Castillo et al. BioRxiv (2026)

How to quantify this: p_{BOLD}

1) Compute $FC_C[(x,y), TE_i, TE_j]$

2) Compute $FC_C[(x,y), TE_k, TE_l]$

3) Create scatter plot

4) Estimate d_{So} $\forall edges$

5) Estimate d_{BOLD} $\forall edges$

6) Given d_{So}, d_{BOLD} & $\delta = 10^{-3}$,
compute pref. towards BOLD line:

$$pref\_to\_BOLD_{(x,y)} = \begin{cases} 1 \; if \; dBOLD_{(x,y)} > dSo_{(x,y)} + \delta \\ 0 \; if \; dBOLD_{(x,y)} < dSo_{(x,y)} + \delta \\ 0.5 \; otherwise \end{cases}$$

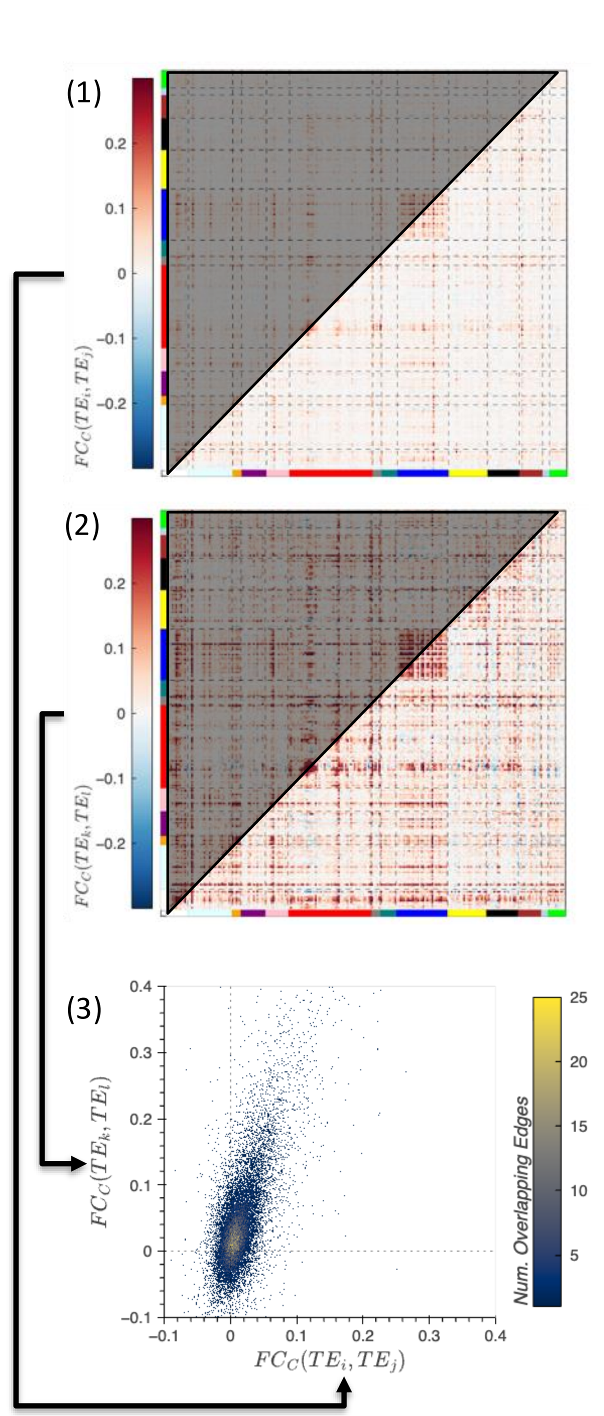
7) To minimize the influence of edges near the origin, we weight BOLD preference by distance to the origin ($w_{(x,y)}$).

$$Wpref\_to\_BOLD_{(x,y)} = w_{(x,y)} \cdot pref\_to\_BOLD_{(x,y)}$$

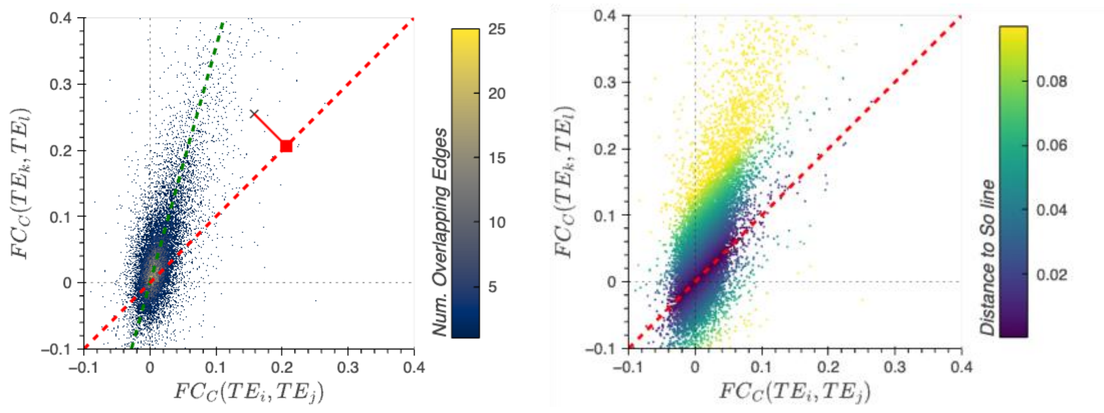
8) Average across all edges

$$p_{BOLD_{(TE_i,TE_j),(TE_k,TE_l)}} = \frac{\sum_{\forall(x,y)} w_{(x,y)} \cdot pref\_towards\_BOLD_{(x,y)}}{\sum_{\forall(x,y)} w_{(x,y)}}$$

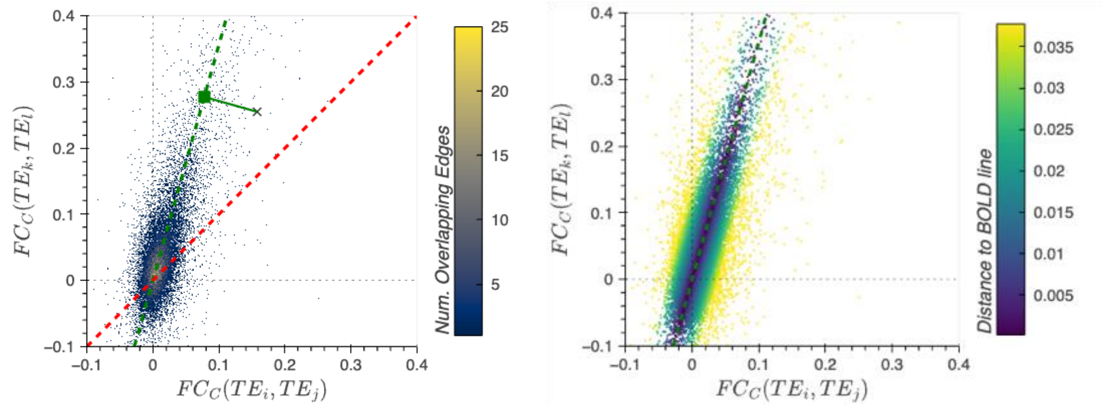
Steps 1 - 3



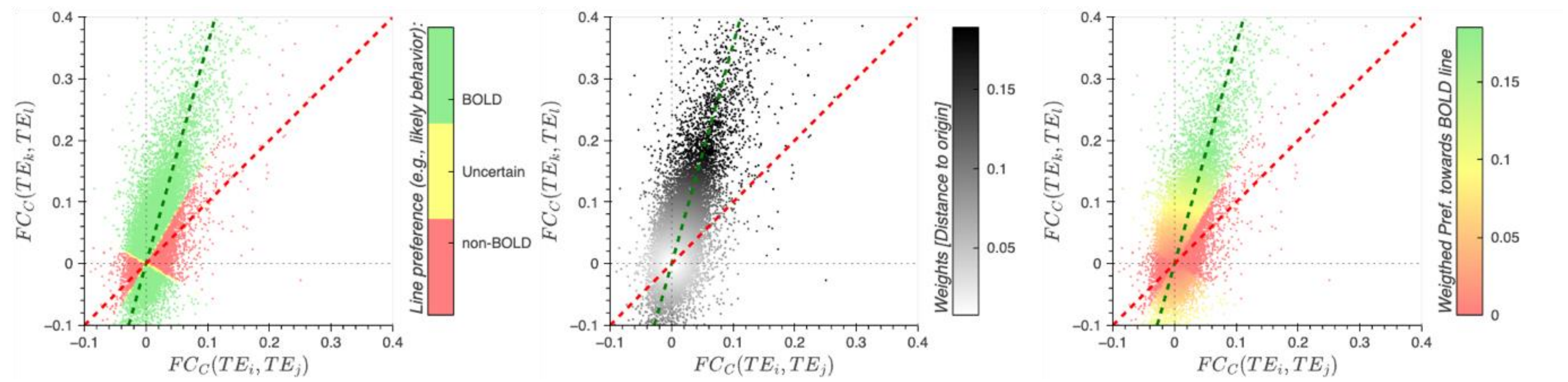
Step 4 | Distance to line indicating So dominated data



Step 5 | Distance to line indicating BOLD dominated data



Steps 6 - 7 | Weighted Preference towards the BOLD line



Gonzalez-Castillo et al. BioRxiv (2026)

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2) Compute $FC_C[(x, y), TE_k, TE_l]$

3) Create scatter plot

4) Estimate d_{So} $\forall edges$

5) Estimate d_{BOLD} $\forall edges$

6) Given d_{So}, d_{BOLD} & $\delta = 10^{-3}$, compute pref. towards BOLD line:

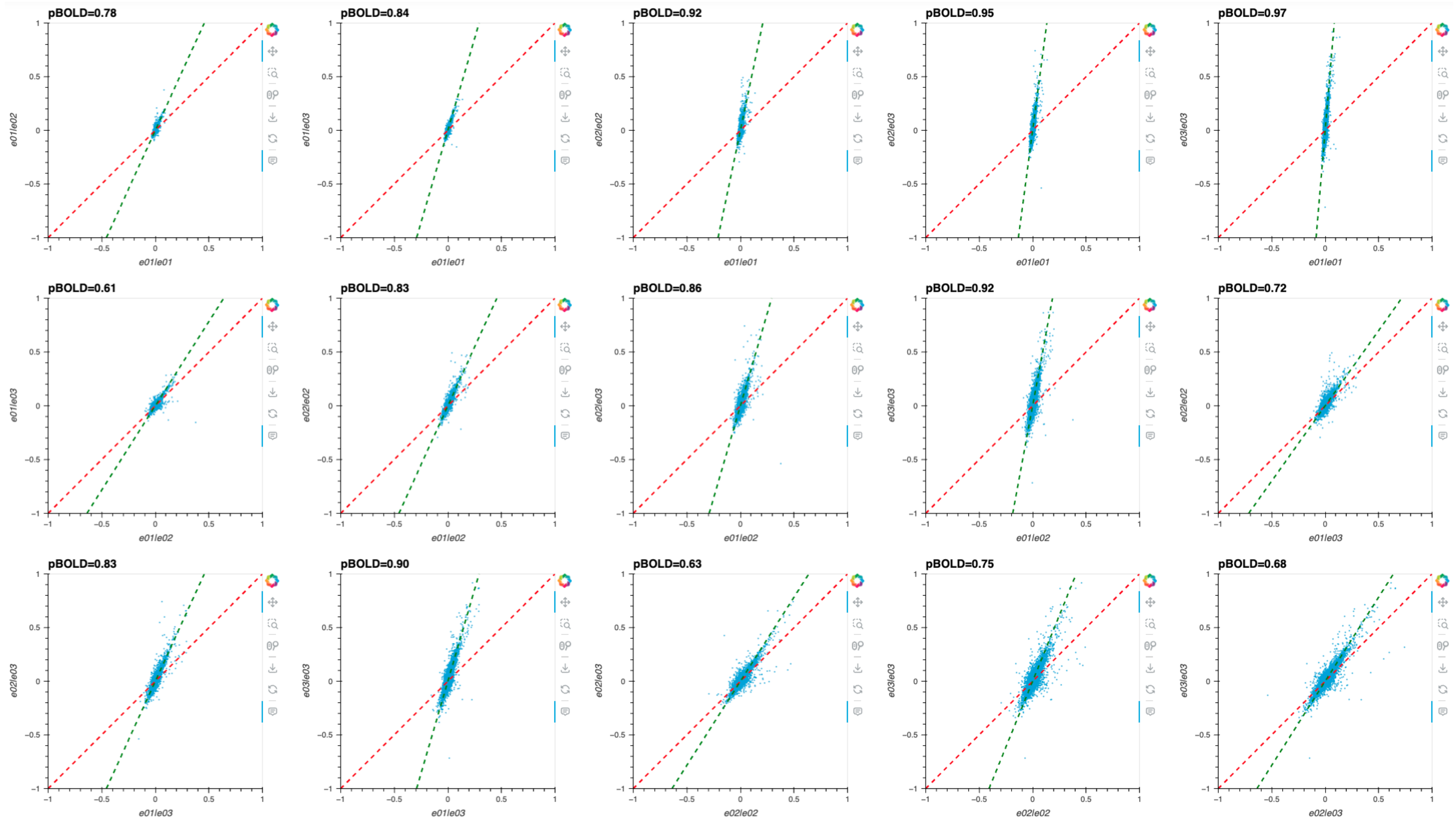
$$pref\_to\_BOLD_{(x,y)} = \begin{cases} 1 \; if \; dBOLD_{(x \cdot y)} > dSo_{(x,y)} + \delta \\ 0 \; if \; dBOLD_{(x \cdot y)} < dSo_{(x,y)} + \delta \\ 0.5 \; otherwise \end{cases}$$

7) To minimize the influence of edges near the origin, we weight BOLD preference by distance to the origin ($w_{(x,y)}$).

$$Wpref\_to\_BOLD_{(x,y)} = w_{(x,y)} \cdot pref\_to\_BOLD_{(x,y)}$$

8) Average across all edges

$$p_{BOLD}{}_{(TE_i, TE_j),(TE_k, TE_l)} = \frac{\sum_{\forall (x \cdot y)} w_{(x,y)} \cdot pref\_towards\_BOLD_{(x,y)}}{\sum_{\forall (x \cdot y)} w_{(x,y)}}$$



Gonzalez-Castillo et al. BioRxiv (2026)

How to quantify this: p_{BOLD}

1) Compute $FC_C[(x,y),TE_i,TE_j]$

2) Compute $FC_C[(x,y),TE_k,TE_l]$

3) Create scatter plot

4) Estimate d_{So} $\forall edges$

5) Estimate d_{BOLD} $\forall edges$

6) Given d_{So}, d_{BOLD} & $\delta = 10^{-3}$, compute pref. towards BOLD line:

$$pref\_to\_BOLD_{(x,y)} = \begin{cases} 1 \text{ } if \text{ } dBOLD_{(x,y)} > dSo_{(x,y)} + \delta \\ 0 \text{ } if \text{ } dBOLD_{(x,y)} < dSo_{(x,y)} + \delta \\ 0.5 \text{ } otherwise \end{cases}$$

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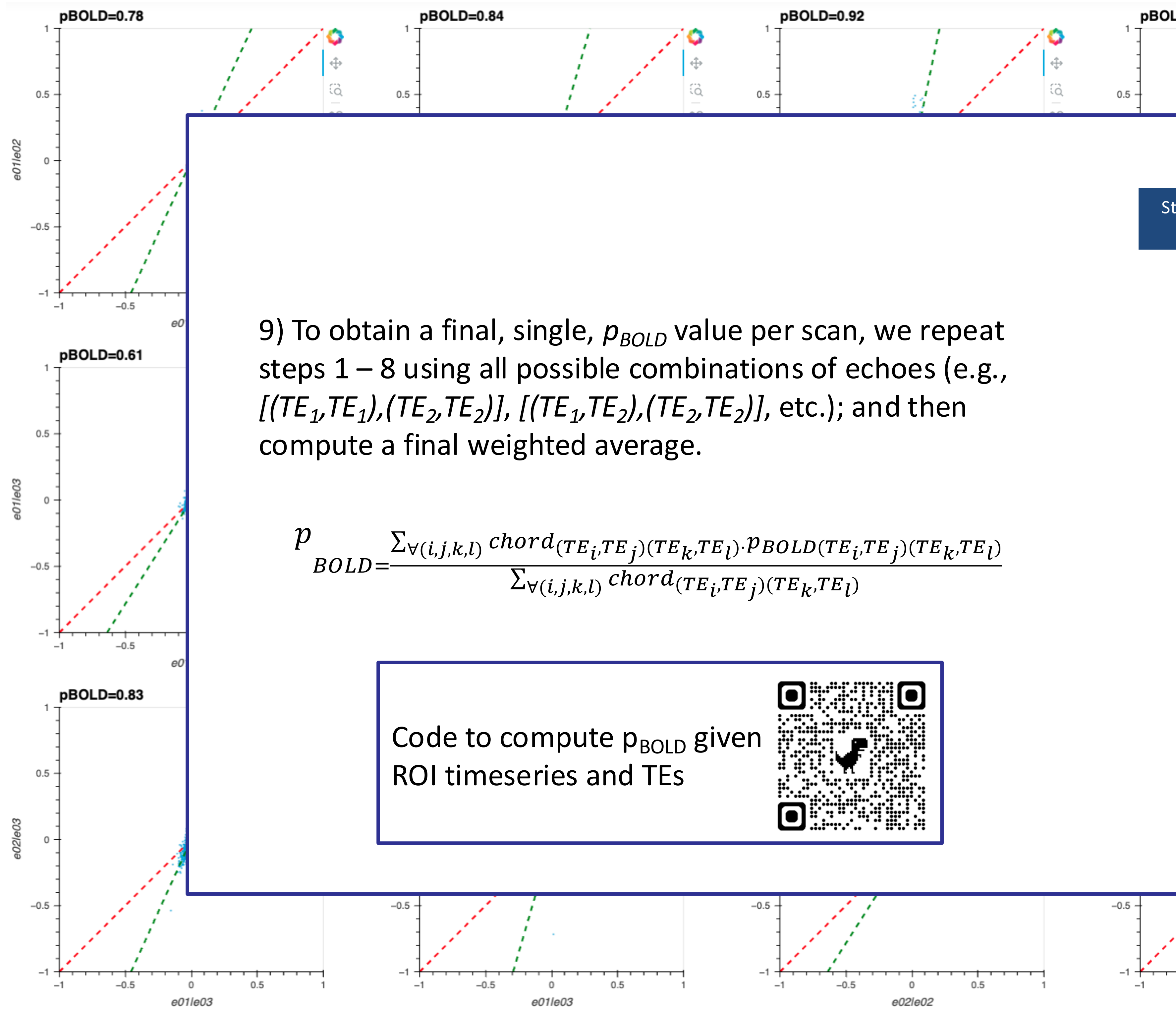
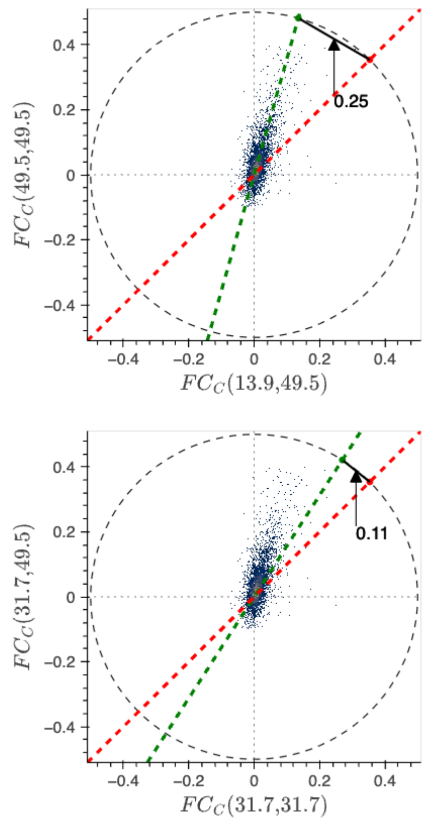


9) To obtain a final, single, p_{BOLD} value per scan, we repeat steps 1 – 8 using all possible combinations of echoes (e.g., $[(TE_1,TE_1),(TE_2,TE_2)]$, $[(TE_1,TE_2),(TE_2,TE_2)]$, etc.); and then compute a final weighted average.

$$p_{BOLD} = \frac{\sum_{\forall(i,j,k,l)} chord_{(TE_i,TE_j)(TE_k,TE_l)} \cdot p_{BOLD(TE_i,TE_j)(TE_k,TE_l)}}{\sum_{\forall(i,j,k,l)} chord_{(TE_i,TE_j)(TE_k,TE_l)}}$$

Step 9 | Final weighting across all possible scatter plots



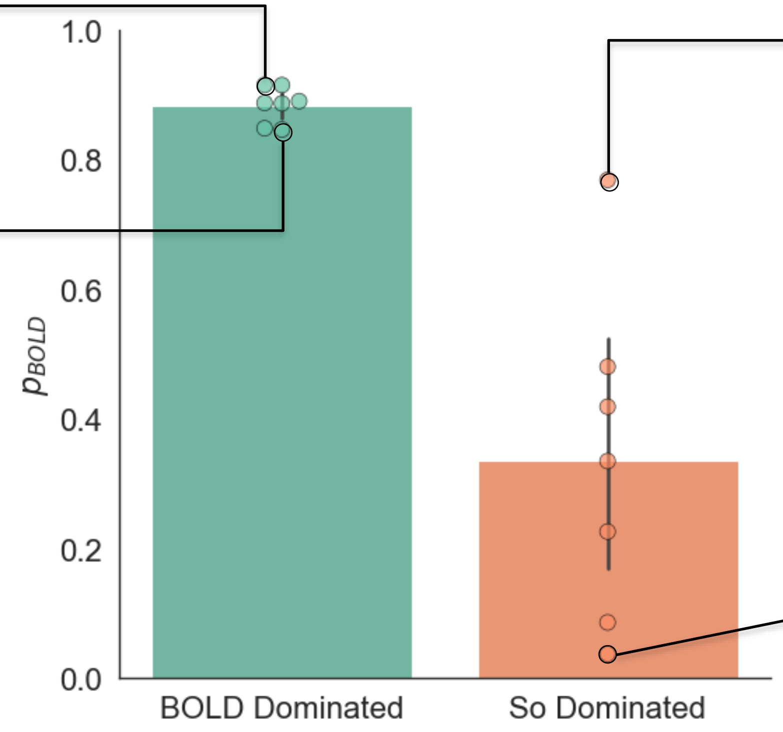
Code to compute p_{BOLD} given ROI timeseries and TEs

Gonzalez-Castillo et al. BioRxiv (2026)

R and Cov across TEs – Empirical Data

Constant-gated scans + Tedana Pre-processing

Cardiac-gated scans + Basic Pre-processing



Gonzalez-Castillo et al. BioRxiv (2026)

R and Cov across TEs – Empirical Data

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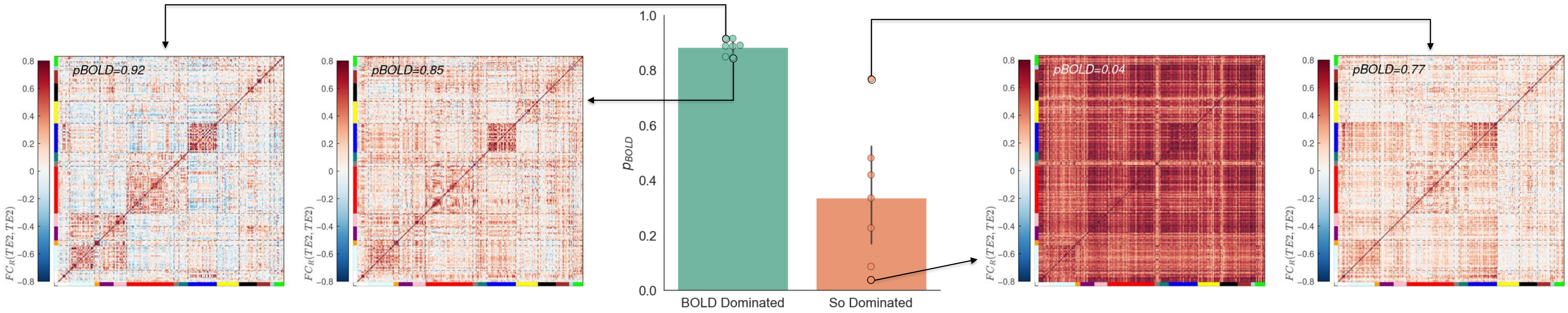
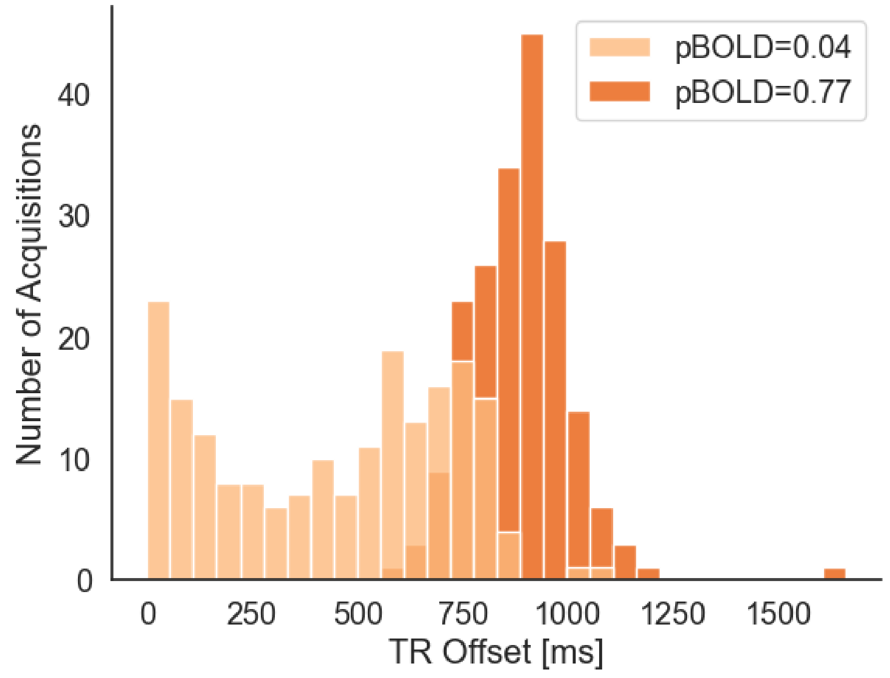
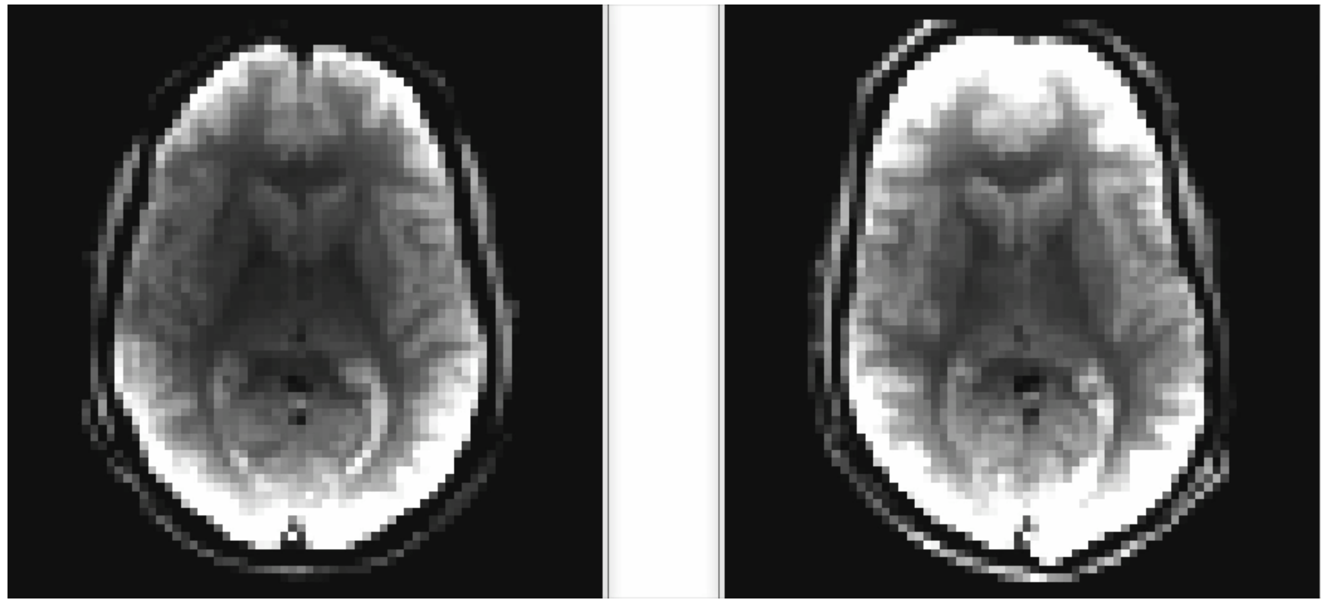


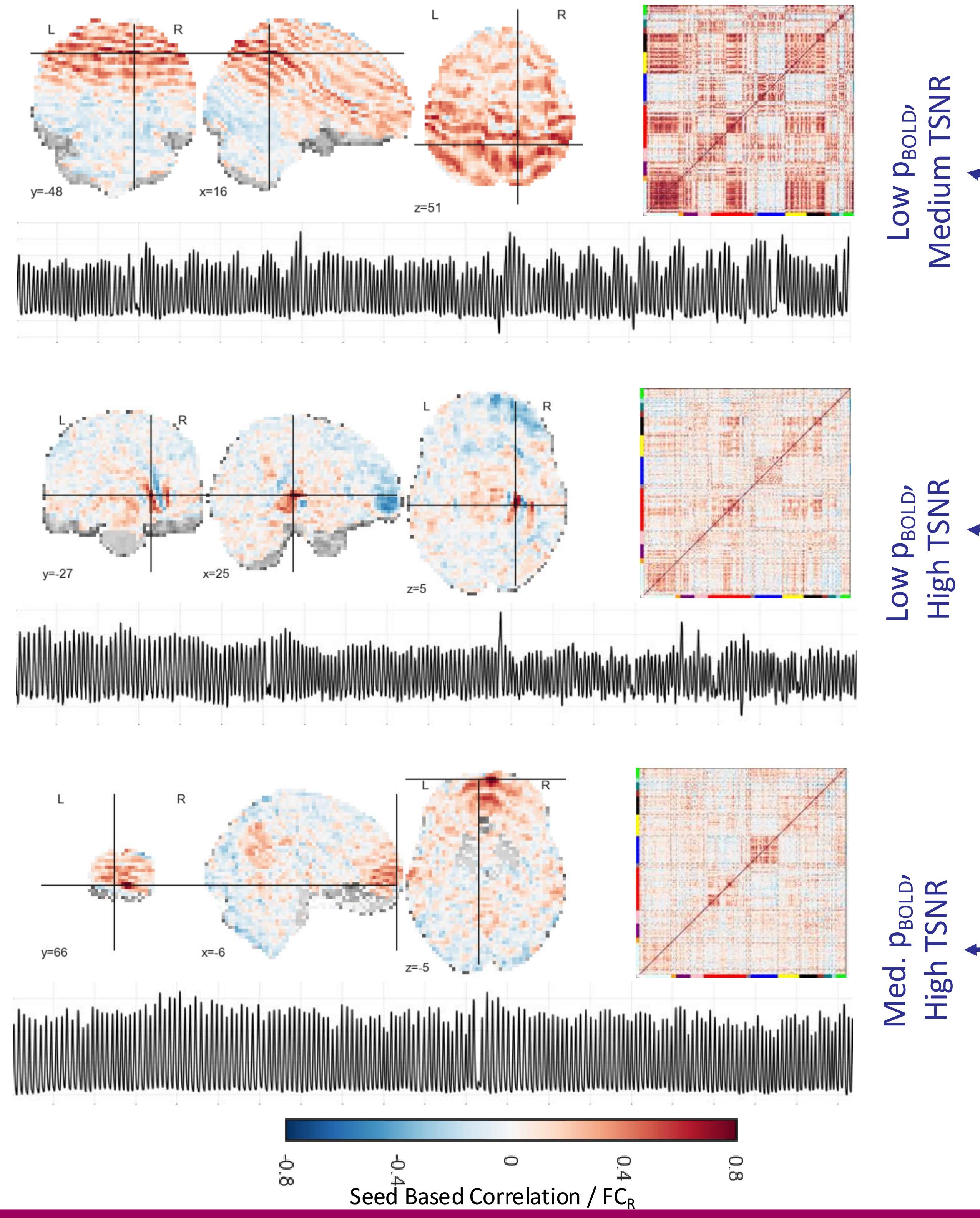




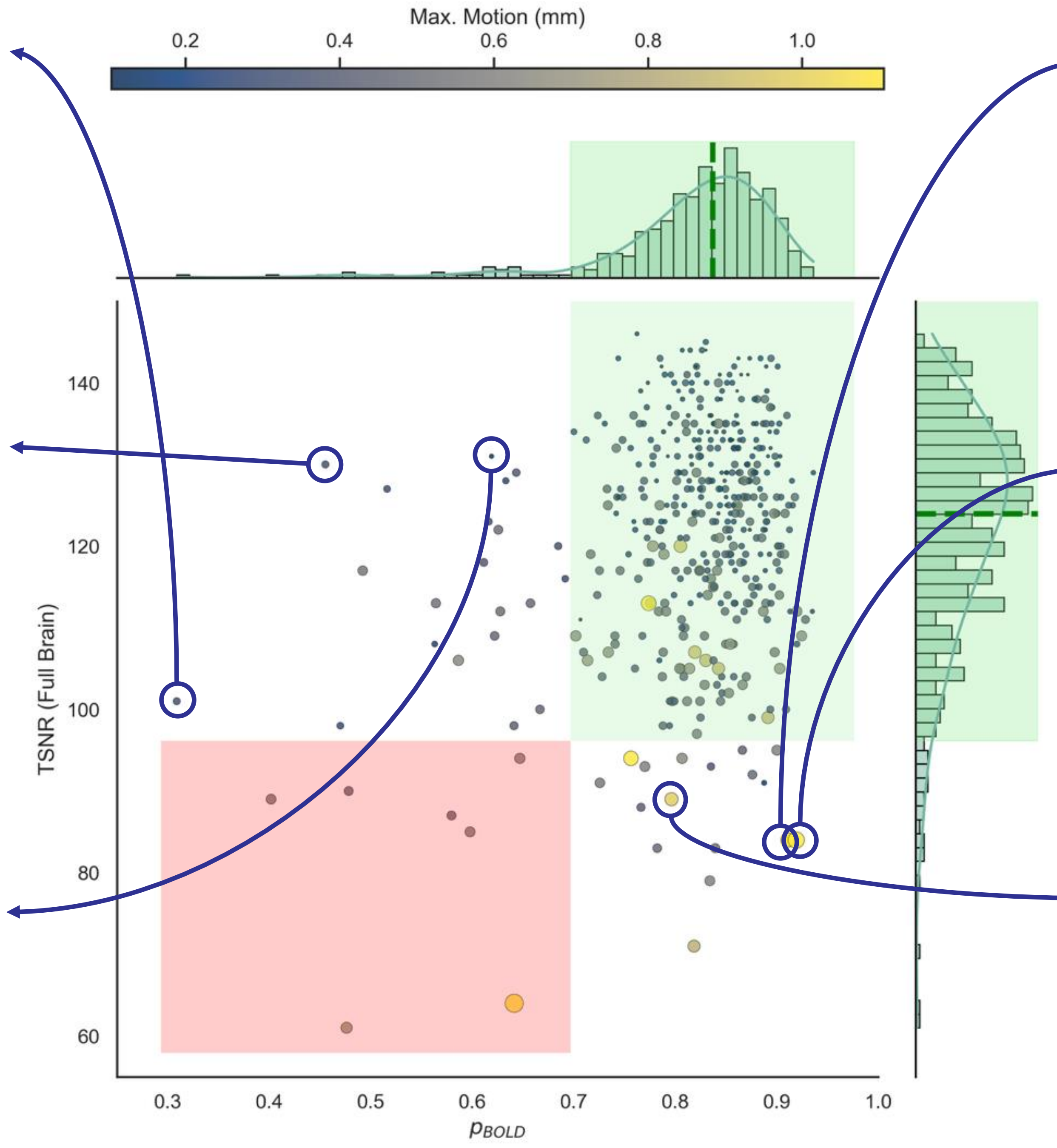
Gonzalez-Castillo et al. BioRxiv (2026)

p_{BOLD} Applications: Evaluate Individual Scans

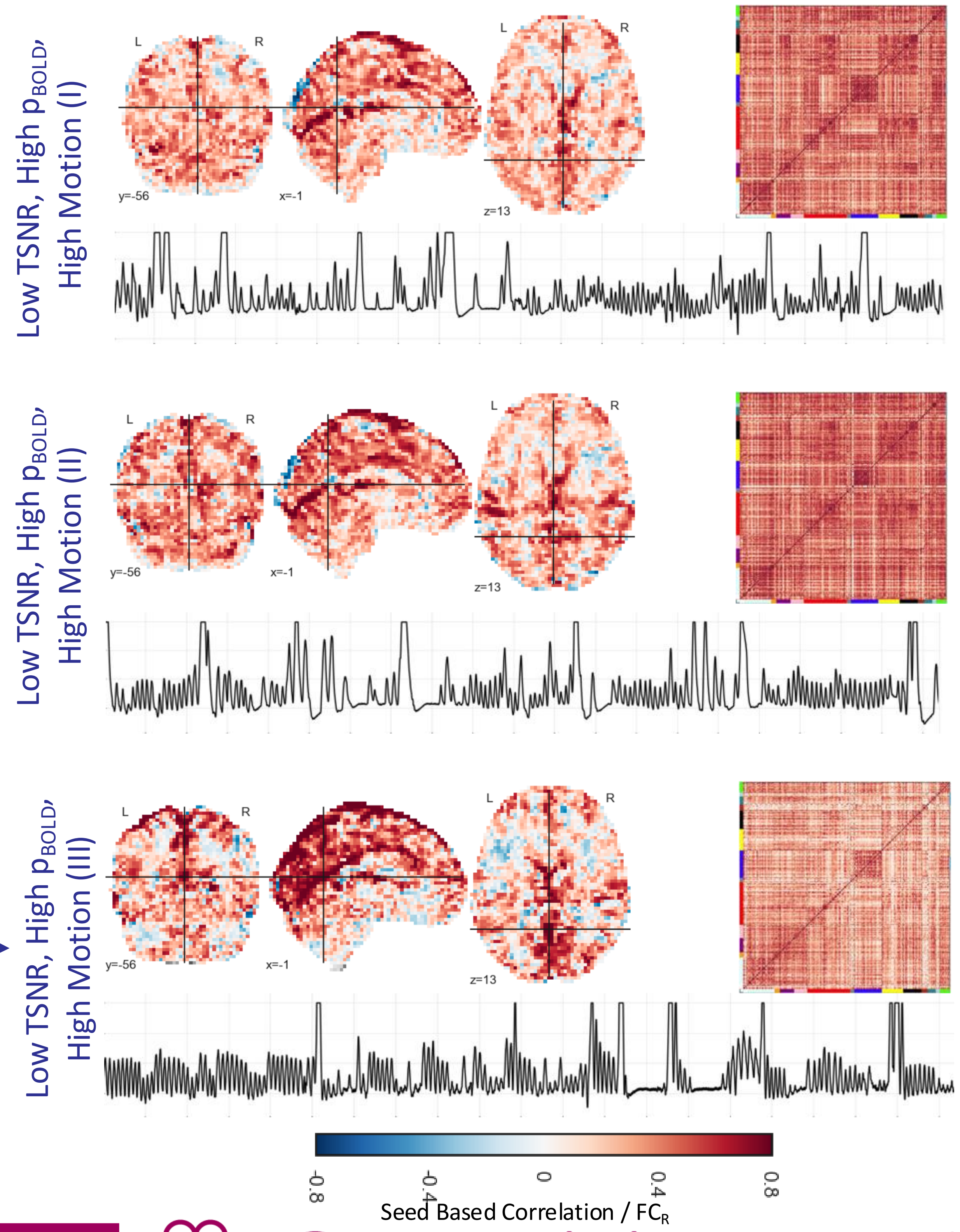
Scans deemed problematic only by p_{BOLD}



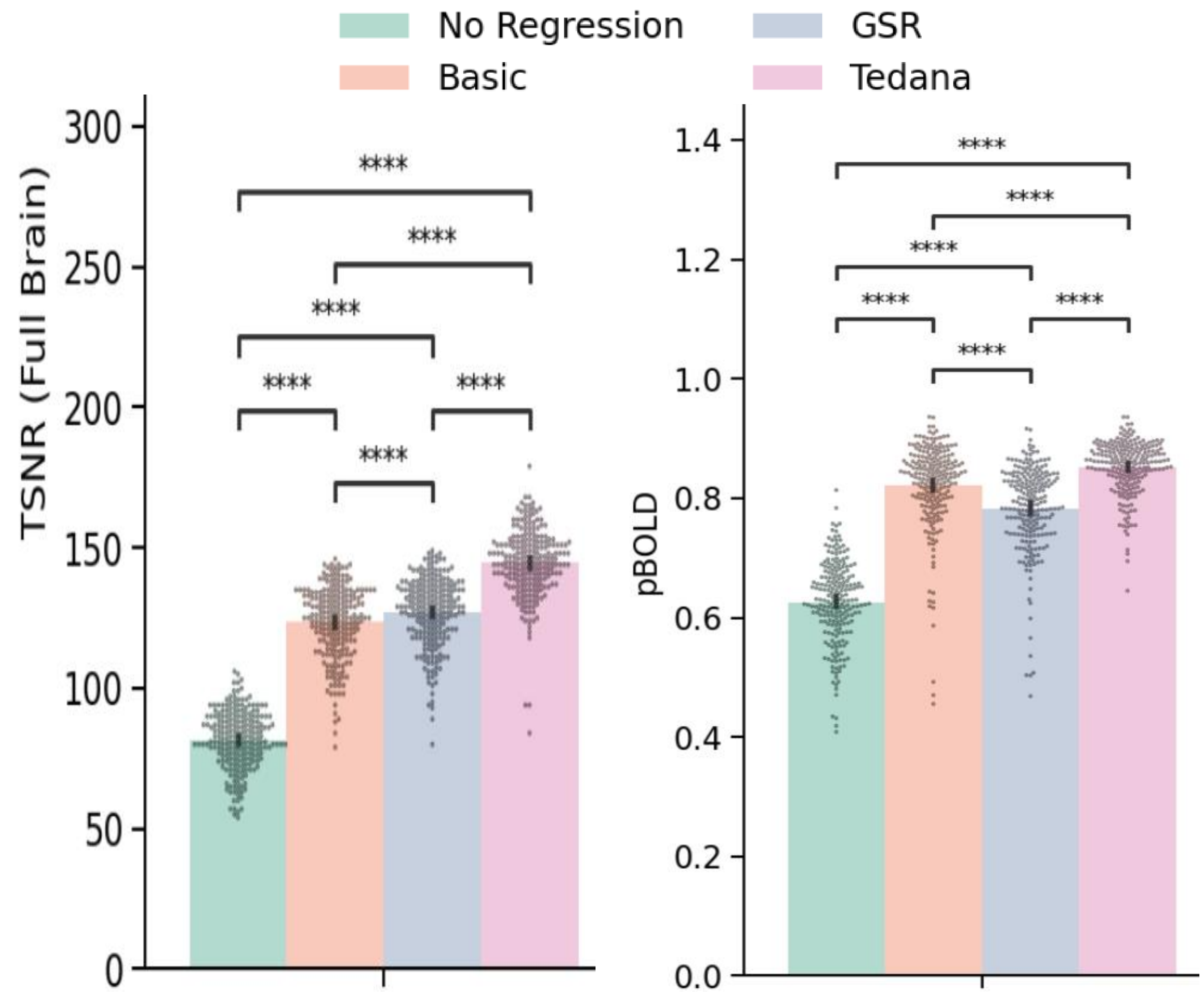
- Site 1 from Spreng et al.: 3T GE MR750 | 32-Channels Coil
- 436 rs-fMRI scans from 221 subjects
- Scan Duration = 10m6s | TR = 3s | # Acqs = 201
- TEs = 13.7 / 30 / 47 ms | Spatial Resolution = 3x3x3 mm^3
- Includes behavioral assessments (IQ, personality, etc.)



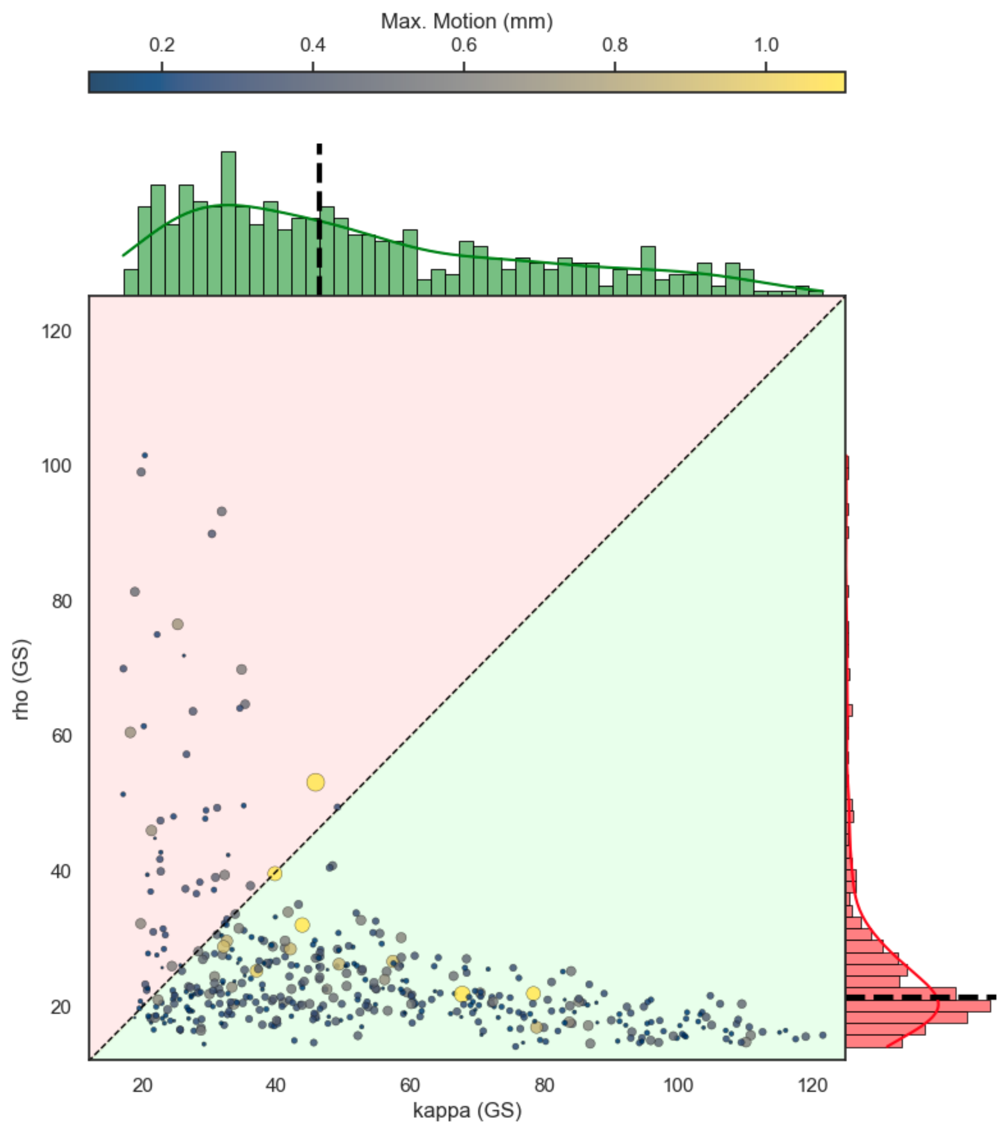
Scans deemed problematic only by TSNR



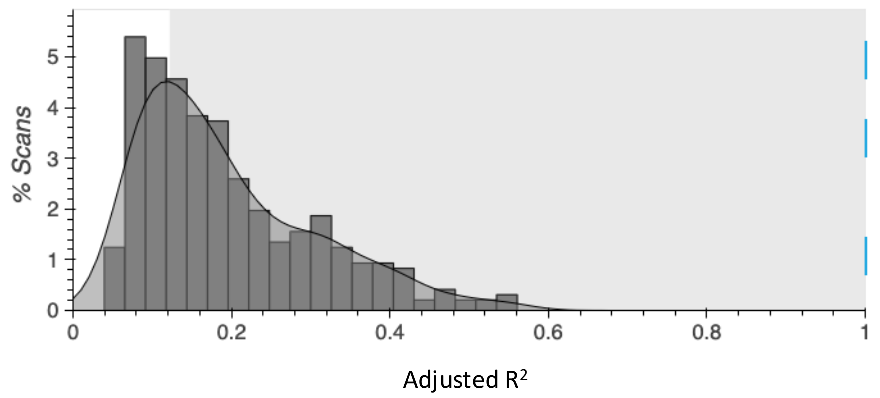
p_{BOLD} Applications: Evaluate Pipelines



"BOLDness" of the Global Signal



Relationship to Physiological Regressors



Gonzalez-Castillo et al. BioRxiv (2026)

QA for ME-data: Conclusions

- We can leverage the additional information present in ME data to better assess the quality of our data.
- The proposed metric (p_{BOLD}) provides complementary information to TSNR.
- Demonstrated p_{BOLD} applications in two scenarios:
  - Detection of problematic scans.
  - Comparison of pre-processing pipelines.
- Because not all BOLD is good BOLD, p_{BOLD} ought to be interpreted cautiously.
- The same principle applies to voxel-wise covariance → working on an alternative metric at the voxel level.

Preprint

Code to compute p_{BOLD} given ROI timeseries and TEs

How to take advantage of all this extra info

Automatic Denoising (tedana, ME-ICA, tedana + NN)

ME Hemodynamic Deconvolution

ME Quality Assurance (p_{BOLD})

Study signals from non-GM compartments

How to take advantage of all this extra info

Automatic Denoising (tedana, ME-ICA, tedana + NN)

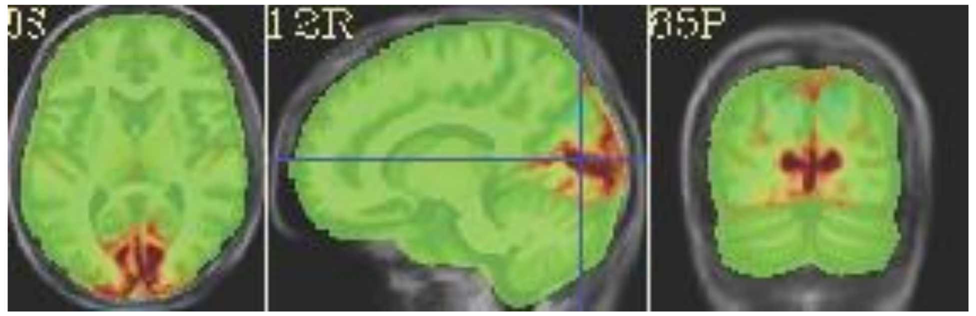
ME Hemodynamic Deconvolution

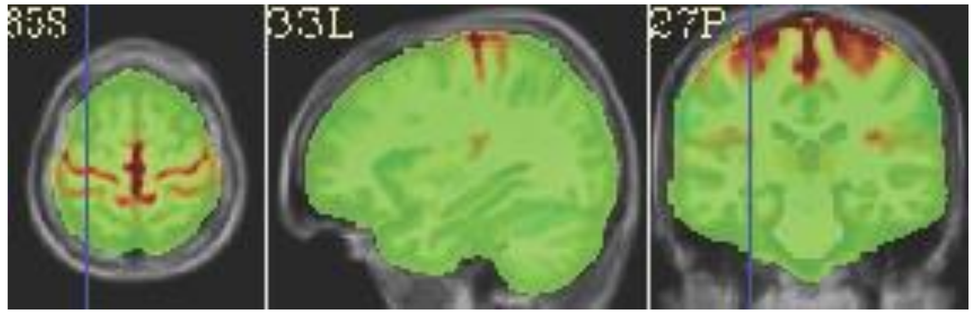
ME Quality Assurance (ρ_{BOLD})

Study signals from non-GM compartments

ME Components Exploration

Components of interest





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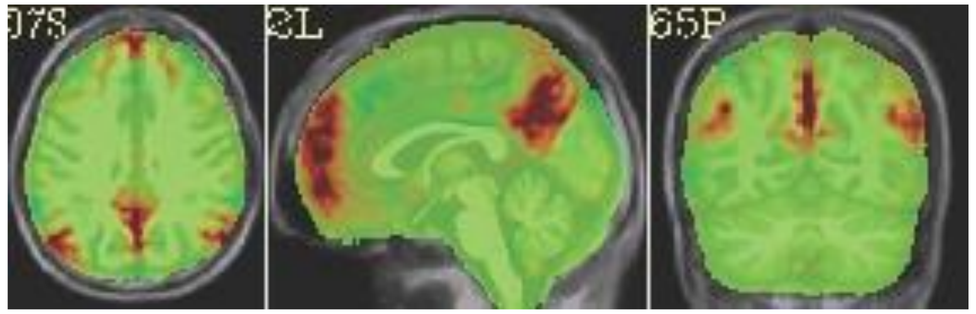
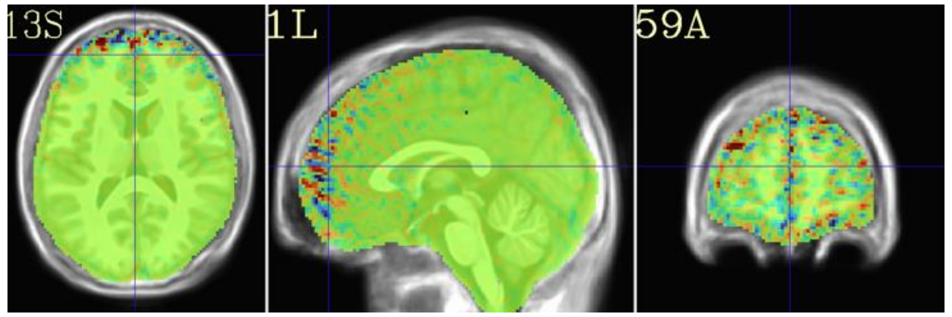
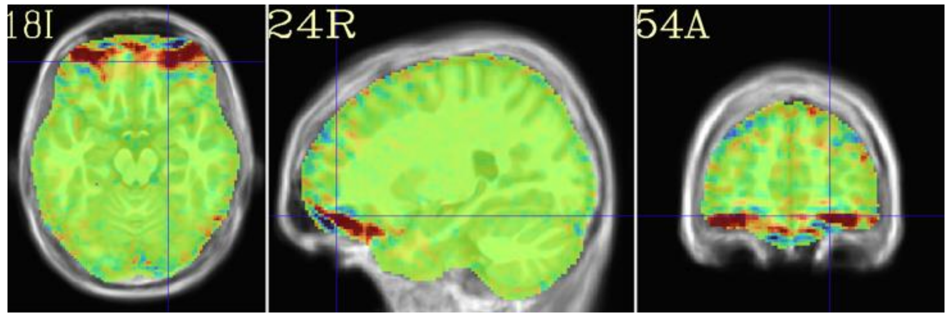


Components to remove





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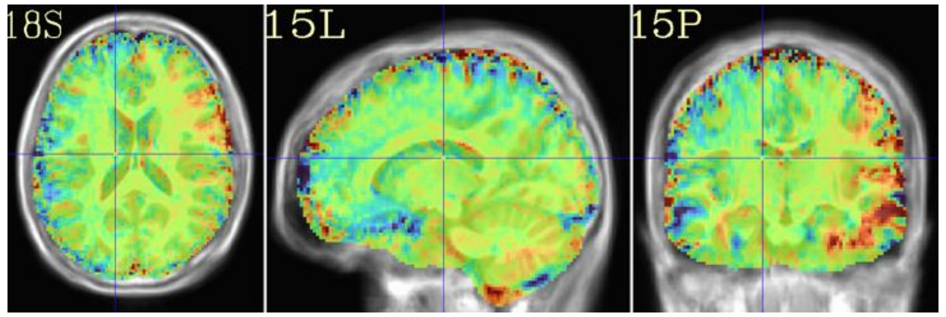
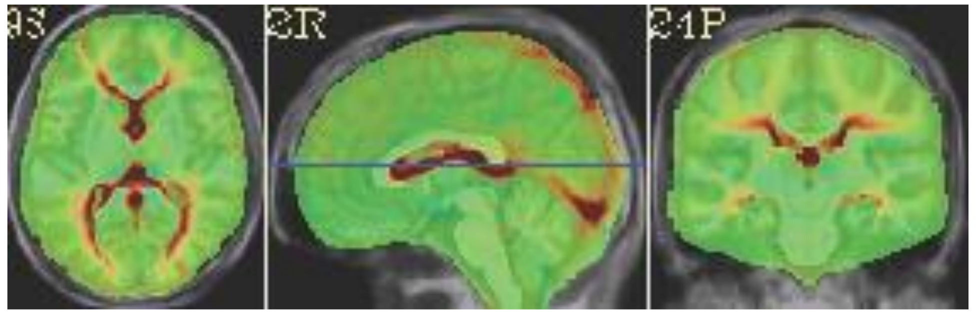
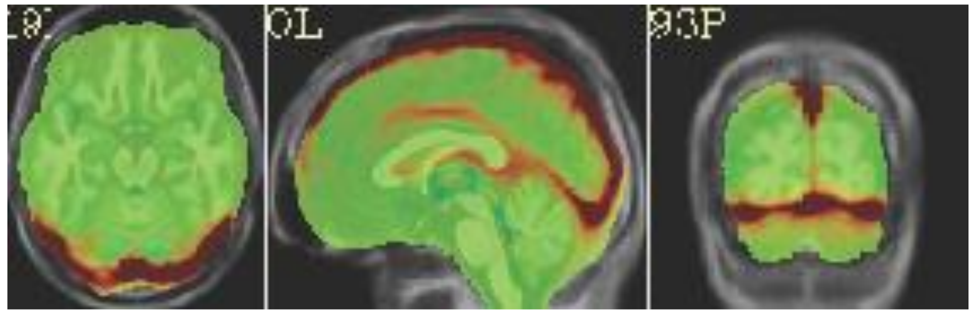


Other Components





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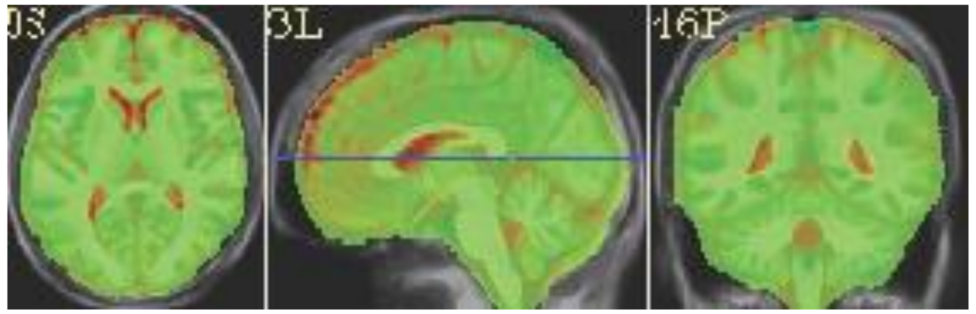
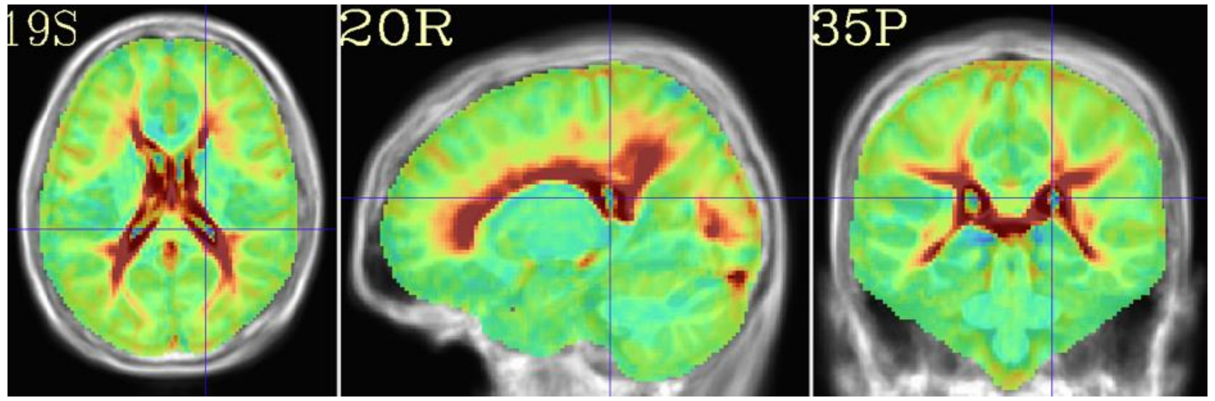


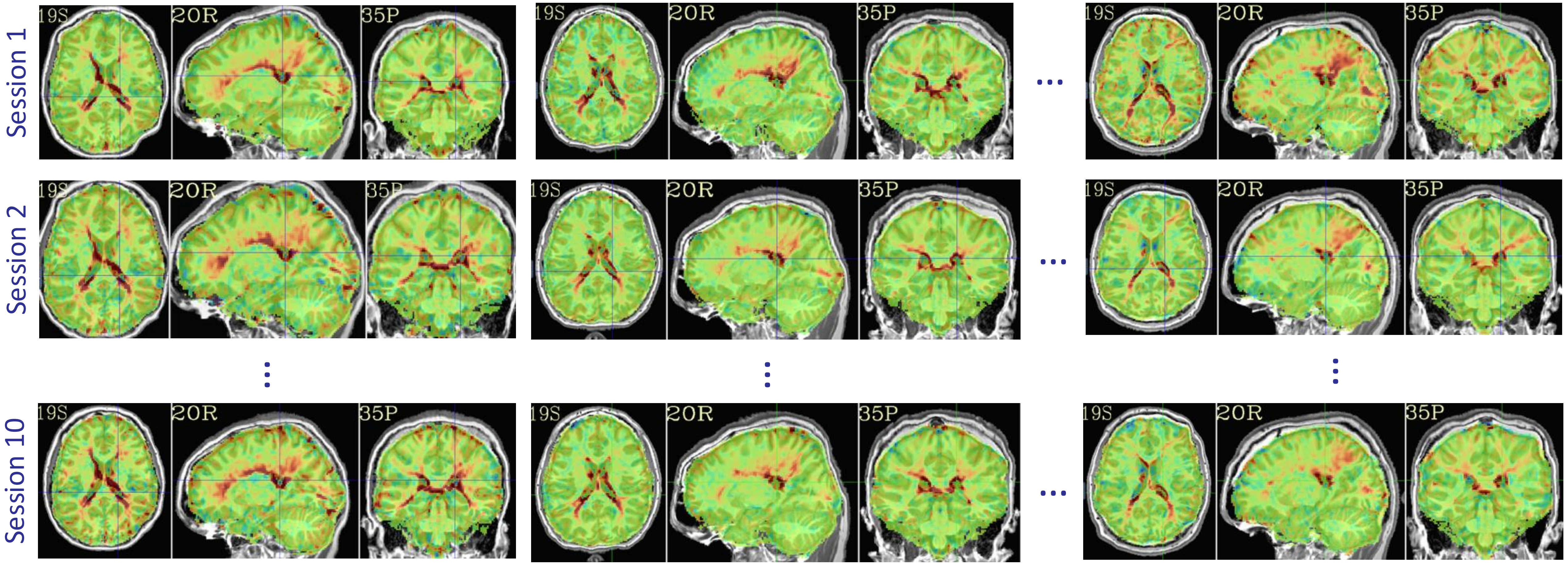
Example: Periventricular + WM Component

Group-Level (gRAICAR)



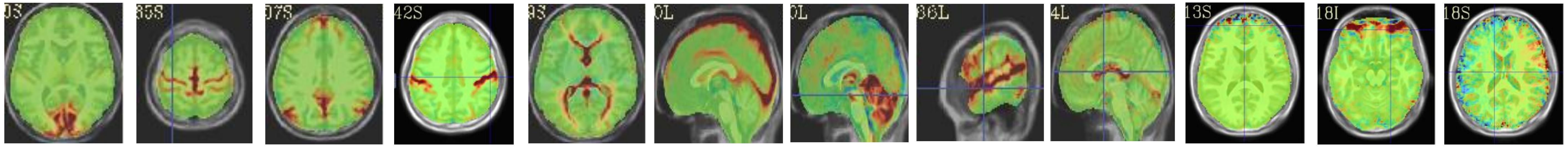
Reproducible across subjects and sessions? ✓

Subject 1 Subject 2 Subject 10



Other components of interest…

	Visual	SomatoMot.	DMN	DAN	Periv/WM	Deep & Lat. Sinuses	Cerebellar Spaces	Superficial Veins	Periventricular Vasculature	Noise IC1	Noise IC2	Noise IC3
T2* (ms) Unimodal?	False	False	False	False	True	False	False	False	False	False	False	False
T2* (ms) Long Tails?	True	True	True	True	True	True	True	True	True	True	True	True
T2* (ms) [StDev]	7.7	16.1	12.8	11.4	60.2	18.1	35.7	12	75.6	18.2	24	17.1
T2* (ms) [Median]	45.4	57.3	52	54.3	66.7	31.4	52.1	42.6	70.4	39.5	29.8	34.7
Rejection Rate	0	0	0	0	0	48.7	0	0	22.5	76.9	87.2	95
Acceptance Rate	100	100	100	100	100	51.3	100	100	77.5	23.1	12.8	5
Average Rho	8.6	9	8.7	8.6	9.2	12.1	10.1	9.4	16.3	11.5	34.8	19.6
Average Kappa	123.9	113.2	132.1	120.8	63.1	42.1	45.1	72	30.6	42.4	29.8	27.6



Visual | SomatoMot. | DMN | DAN | Periv/WM | Deep & Lat. Sinuses | Cerebellar Spaces | Superficial Veins | Periventricular Vasculature | Noise IC1 | Noise IC2 | Noise IC3

ICs of Interest | Vascular/CSF ICs | Noise ICs

Poster #2481 (Wednesday / Thursday)

Now that I have ME data, what can I do?

Automatic Denoising (tedana, ME-ICA, tedana + NN)

Improve data quality, increase sensitivity, scan less…

ME Hemodynamic Deconvolution

Reliably detect individual events without a priori information about their timing

Estimates have interpretable units [s^{-1}] that proved to be within physiologically plausible limits

Paper

Code

ME Specific QA

Inter-regional covariance as a way to quantify how much BOLD dominates over other fluctuations (p_{BOLD})

Provides complementary information to TSNR

Scenarios: problematic scan detection, pipeline evaluation

Preprint

Code

Characterize Non-GM components with ME

Kappa, Rho, etc. provide information about BOLD content

T2* map provide information about contributing tissue compartments

Reliably detect components for WM vasculature, deep and lateral sinuses, and superficial veins

Poster #2481
(Wednesday / Thursday)

Thank You

National Institute
of Mental Health

Peter
Bandettini

Daniel
Handwerker

Marly
Rubin

Puja
Panwar

BASQUE CENTER
ON COGNITION, BRAIN
AND LANGUAGE

Cesar
Caballero-Gaudes

Stefano
Moia
(now @ Maastricht University)

Eneko
Uruñuela
(now @ Univ. of Calgary)

OHBM 2026