

Reconstructing Mechanistic Models of Cognition via Simultaneous

MINDy Modeling for Resting-State and Task fMRI.

Matthew F. Singh^{1,2,3}, Anxu Wang^{12,3}, ShiNung Ching^{3,4} & Todd S. Braver^{1,2}

1. Dept. of Neuroscience 2. Dept. of Psychology 3. Dept. of Electrical and Systems Eng. 4. Dept. of Biomedical Eng.



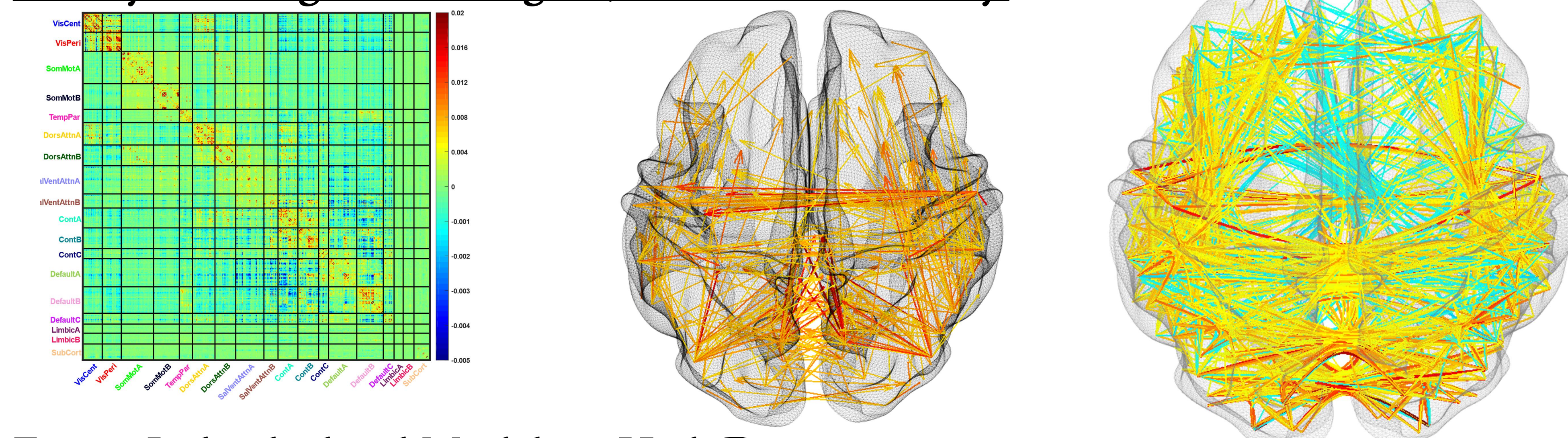
Background: Big data initiatives have enabled dynamical models of neural activity¹ while also empowering the study of individual differences². However, there remains a gap between dynamical models which have enabled mechanistic hypothesis-testing of circuit function and statistical models that dominate data driven studies of individual differences. **We aim to bridge this gap with MINDy modeling.**

Mesoscopic Individualized NeuroDynamic (MINDy)

modeling: The entire brain is modeled as a network of **neural-mass models**³ (1/region: "n" total) with 3 components each:

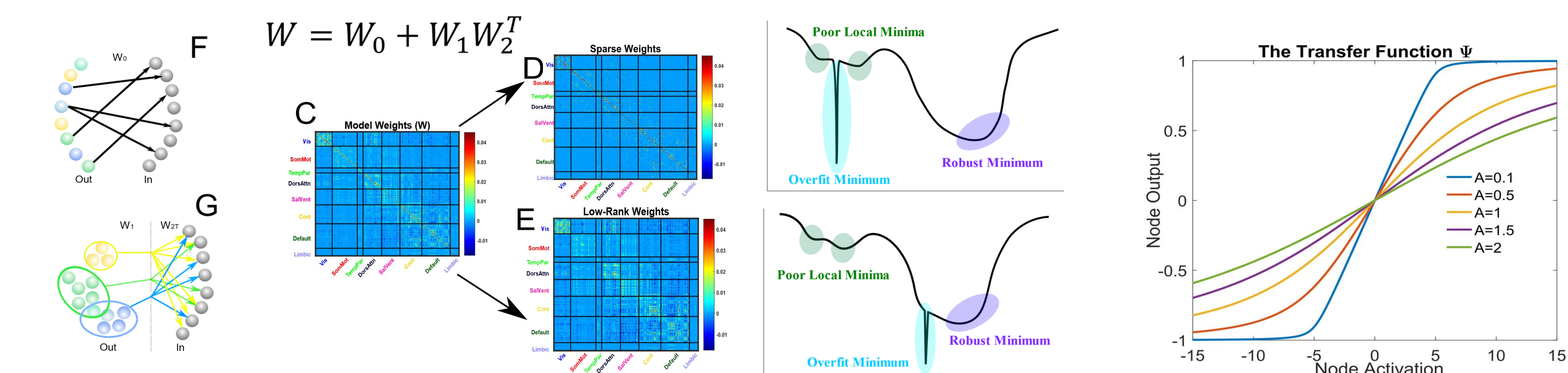
1. A **weight matrix** of connectivity: W : (nxn)
 2. A **transfer function** transforms local neural activity into output signals: $\Psi(X)$: (nx1)→(nx1)
 3. A **decay coefficient** describes how quickly each neural mass returns to baseline activity: D : (nx1)
- $x(t)$: activation vector (all regions): $dx/dt = W\psi(x) - Dx$

MINDy Modeling Produces Signed, Directed Connectivity:

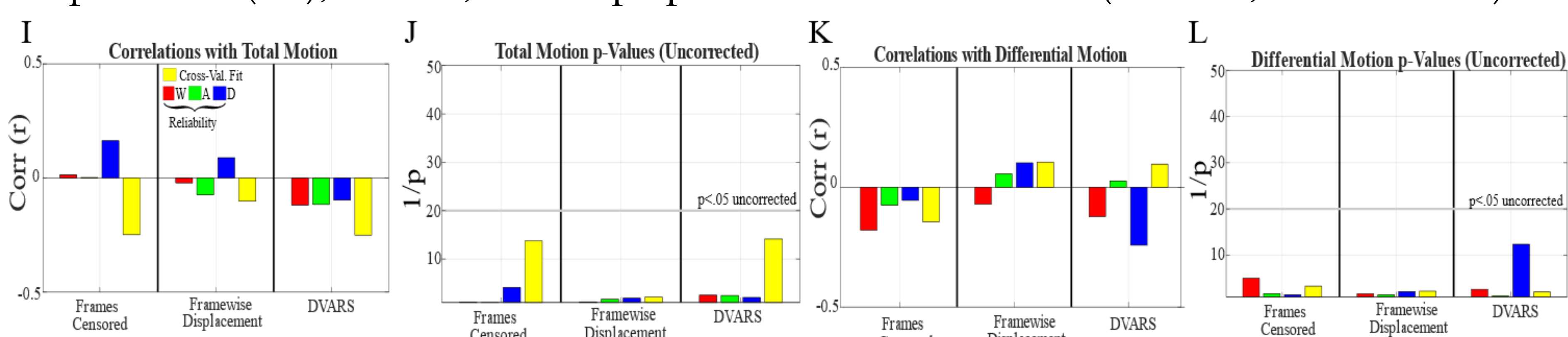


Fitting Individualized Models in High Dimensions:

1. Decompose the weight matrix into sparse (W_0) and low-rank/diffuse components ($W_1W_2^T$)
2. Stochastic gradient descent with adaptive momentum (NADAM)
3. Allow region specific **curvature** (A) in the transfer function: $\Psi(x) = \sqrt{A + (bx + \frac{1}{2})^2} - \sqrt{A + (bx - \frac{1}{2})^2}$



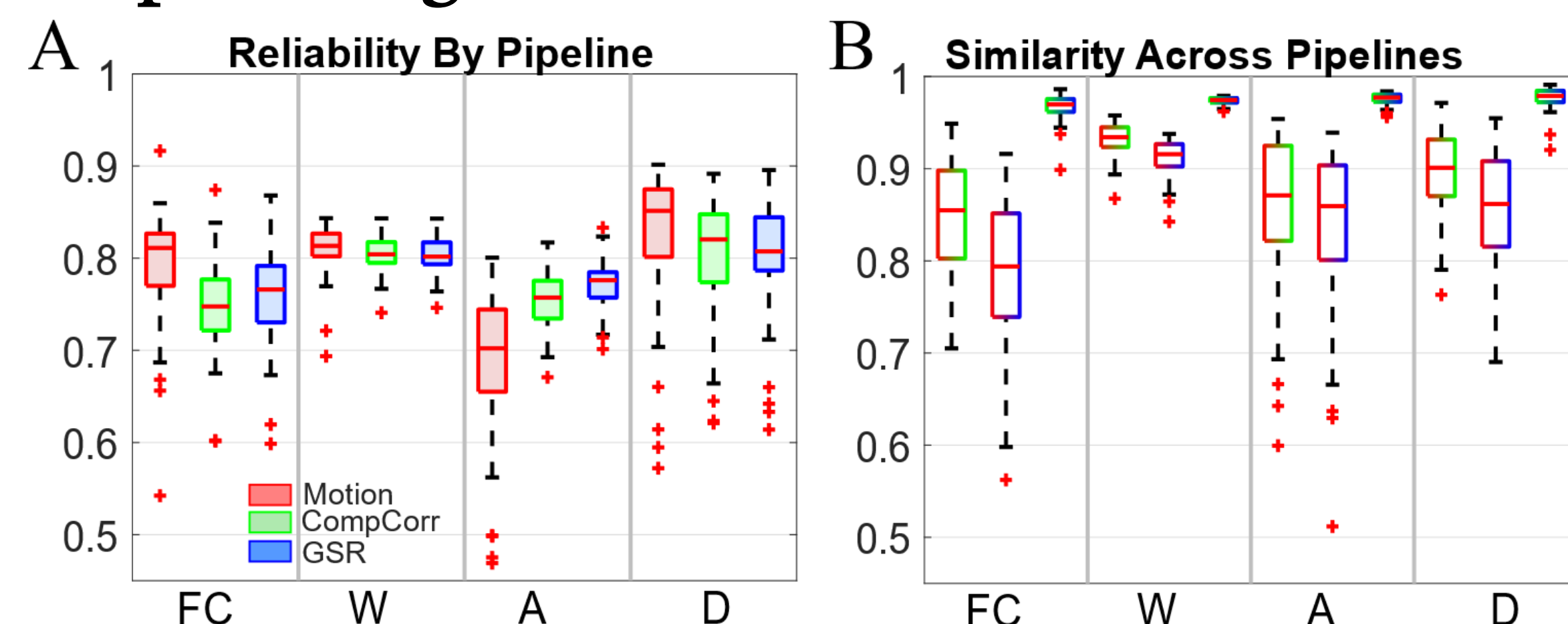
MINDy is Robust to Motion Artifact: MINDy does not suffer under differences in motion (within a reasonable range) or differential motion between scans. This property holds for Frame-wise Displacement (FD), DVARS, and the proportion of censored frames (from FD, DVARS cutoff).



MINDy Parameters are Robust to Preprocessing Choices:

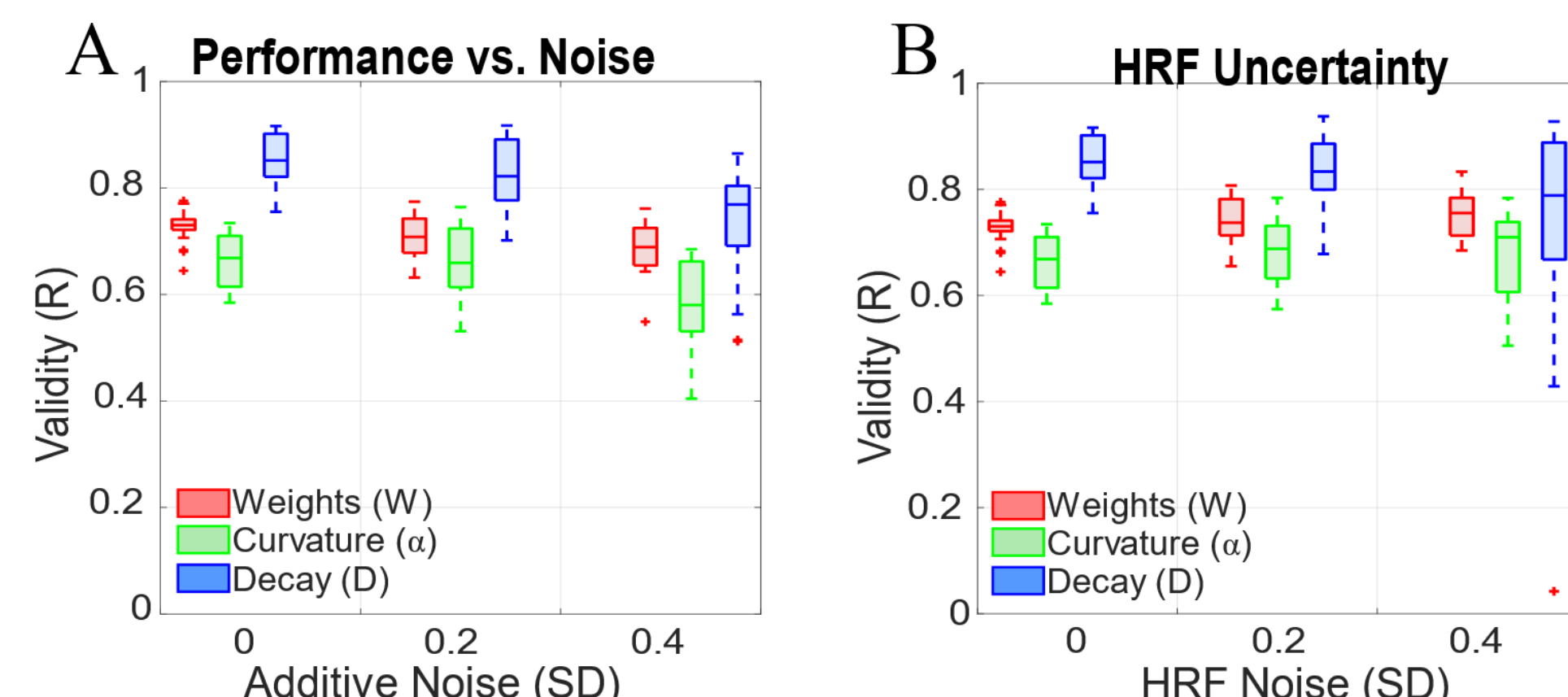
Considered 3 levels:

1. **Motion only**⁴: (scrubbing and censoring with DVARS and Frame Displacement)
2. **+CompCorr**⁵: White matter and CSF principle components regressed out.
3. **+Global Signal**: Mean signals for white matter, CSF and grey matter regressed out in addition to CompCorr



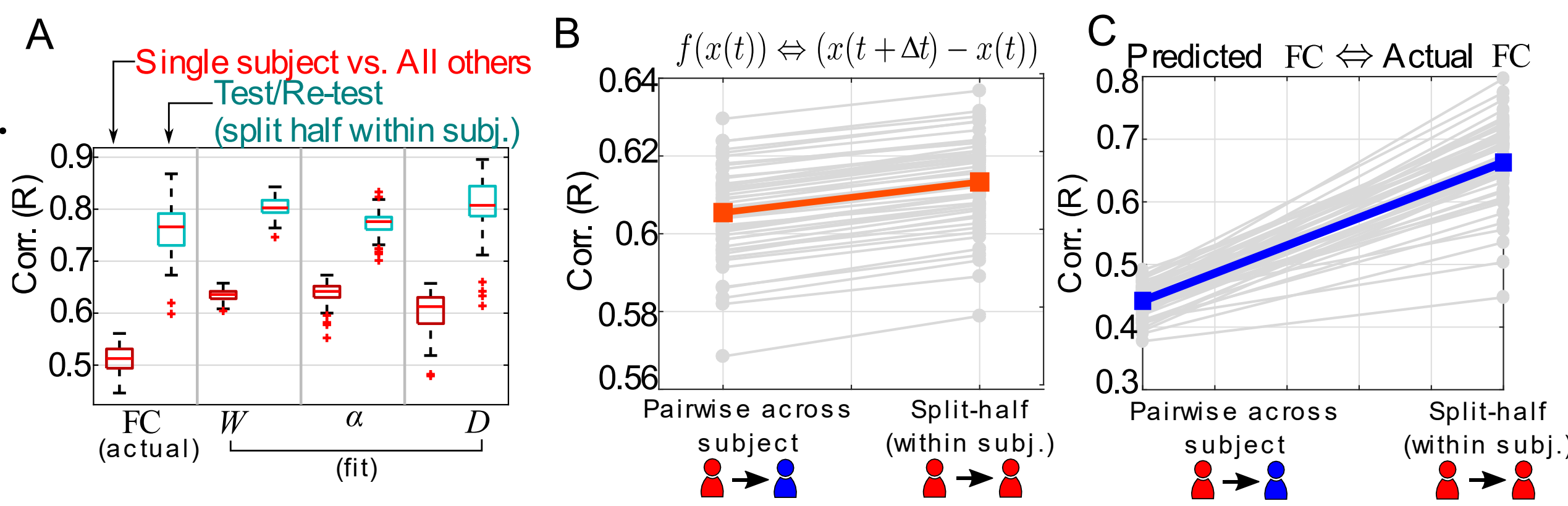
MINDy Retrieves Ground-Truth Connectivity and Decay Under Realistic HRF Uncertainty and Noise:

- Simulated MINDy with **parameters randomly selected from individuals**
- Retrieved parameters while varying measurement noise and variability in HRF



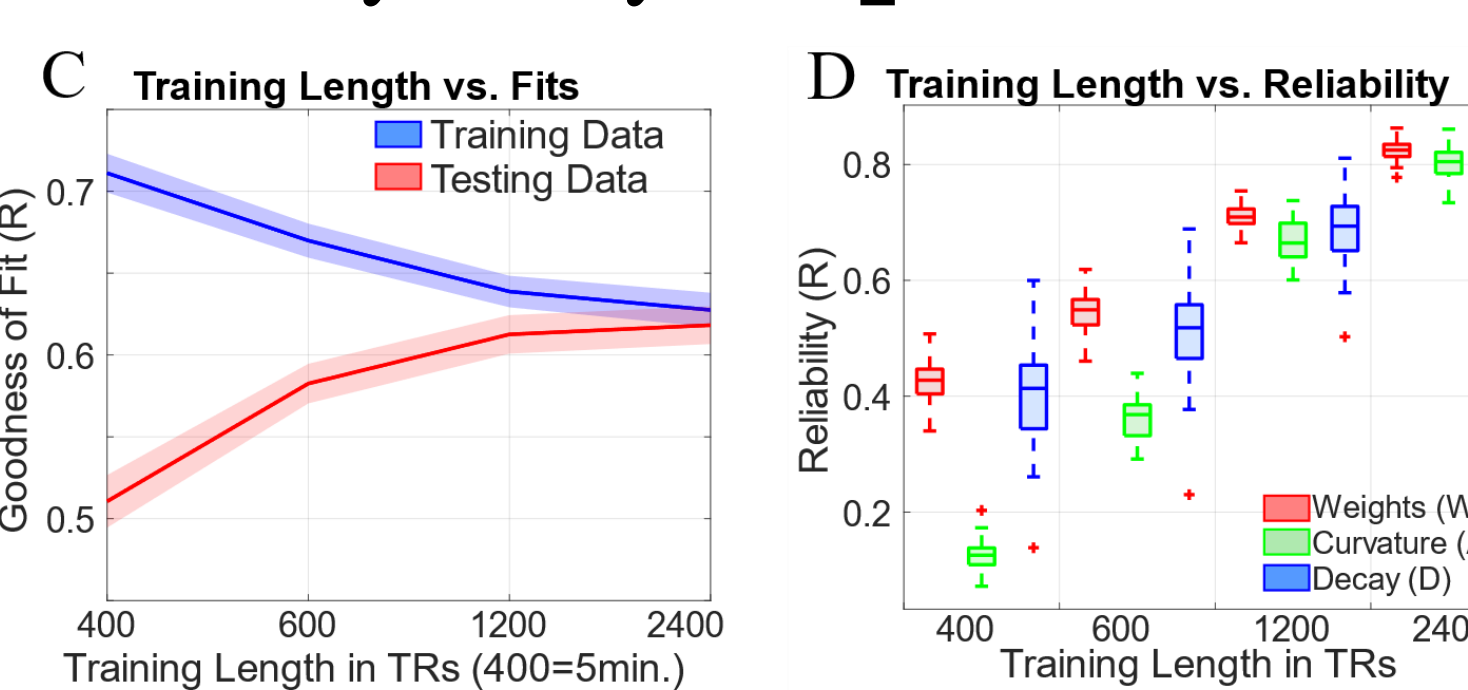
MINDy Models & Parameters Differentiate Individuals

- "Fingerprinting" analysis compared within-subject vs. between subject similarity
- Parameter similarity and cross-validated model fits uniquely identify individuals



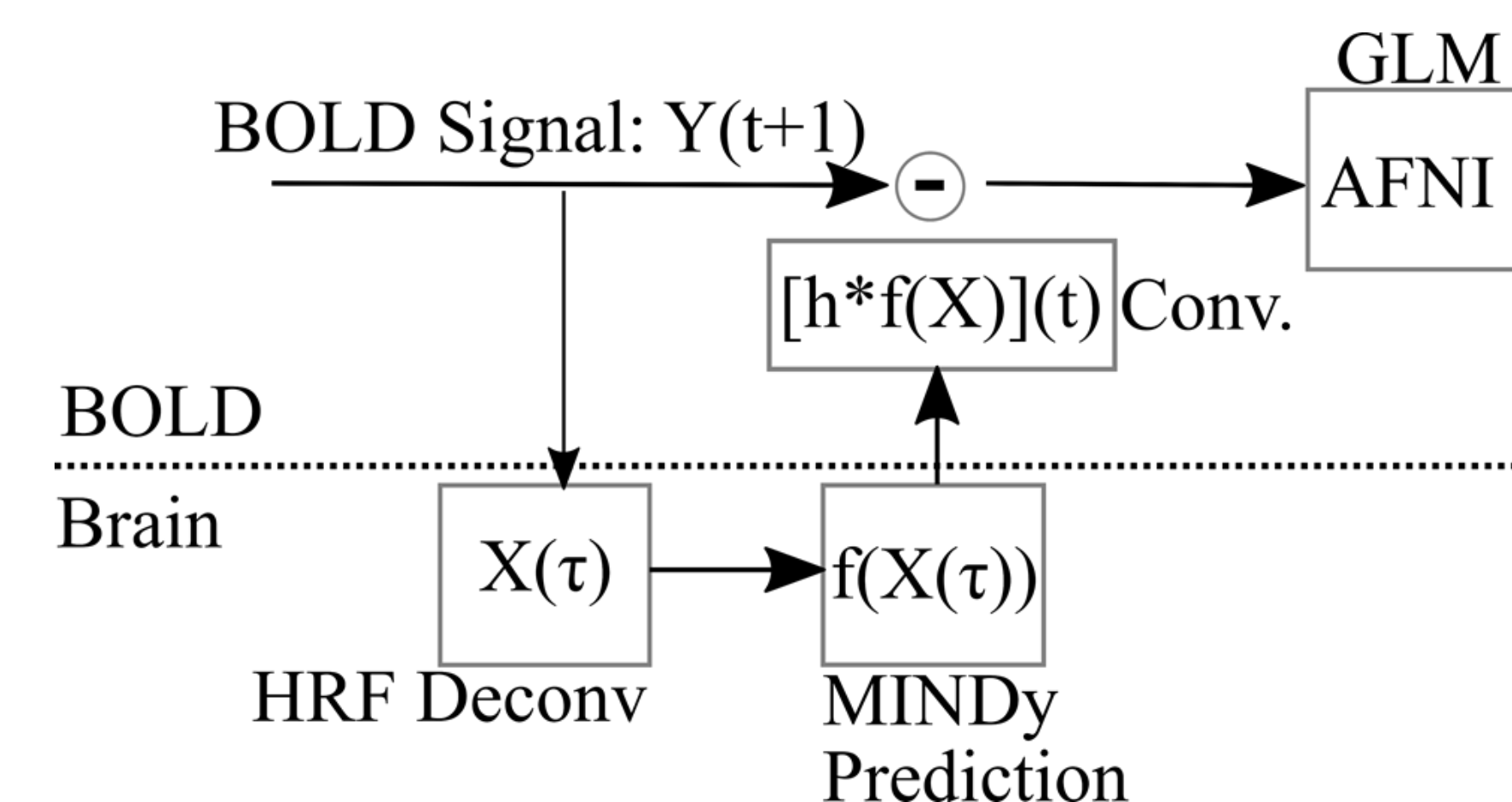
MINDy Only Requires 15 Minutes of Scan Time

- Divided full data into **variable length segments**
- Compared cross-validated model fits and parameter reliabilities
- Performance was strong at 15 minutes., but more data improves reliability.



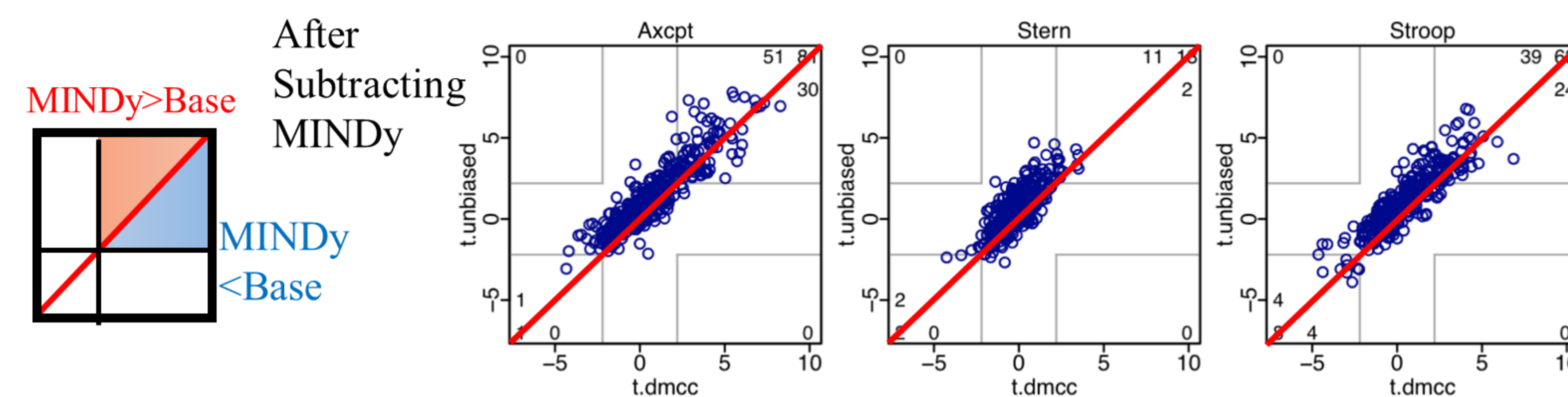
Isolating Task Effects with MINDy

- Activity during task consists of direct task-modulation and the flow of this activity through brain networks.
- By filtering-out the resting-state model predictions, we better isolate task-modulation.



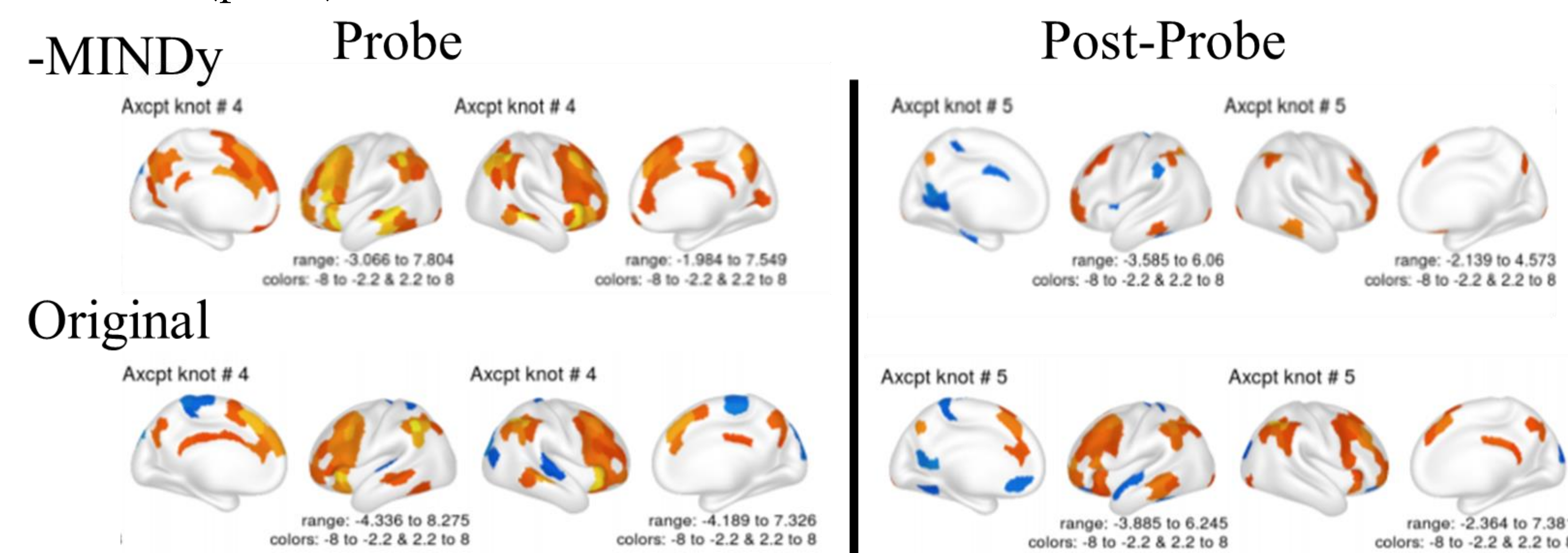
Isolating Cognitive Conflict Signatures

- High vs. low conflict conditions in three tasks:
- 1. AX-CPT, 2. Sternberg, 3. Stroop
- Same AFNI GLM applied to either the original BOLD time-series or after subtracting MINDy (resting-state) predictions.
- Compared group-level t-Tests across parcels



Removing Intrinsic Dynamics Improves Temporal Precision

- Compared GLM estimates for the effect of cognitive conflict during and after the probe period.
- After filtering intrinsic dynamics (via MINDy), task effects are centered about the period of cognitive conflict (probe).



Applications: We have validated a powerful new tool for directly fitting high-dimensional dynamic networks to individual subject's data and envision the following applications:

1. An improved **measure of effective connectivity**
2. Nonlinear **analysis of human brain dynamics**
3. A more general method to **isolate task-related brain signals**: unlike Dynamic Causal Modeling⁶, we generate large models using only resting state, so we need not constrain task dynamics. Subtracting model predictions leaves a full time-series of task-induced changes.

References: 1. Van Essen et al. (2013), *N.Image*. 2. Sanz Leon et al. (2013), *Front. Neuroinform*. 3. Wilson & Cowan (1972), *Biophys.J*. 4. Siegel et al. (2013), *HBM*. 5. Salimi-Khorshidi (2013) *N.Image*. 6. Friston (2003), *N.Image*.

Acknowledgements: MS was partially funded by NSF DGE-1745038. TB acknowledges R37 MH066078 from the US National Institute of Health. SC holds a Career Award at the Scientific Interface from the Burroughs-Wellcome Fund. Portions of this work were supported by AFOSR 15RT0189, NSF ECCS 1509342 and NSF CMMI 1537015, from the US Air Force Office of Scientific Research and the US National Science Foundation, respectively. Data were collected by the Human Connectome Project WU-MINN consortium (NIH 1U54MH091657)