Comparing approaches for estimating regional hemodynamic timing differences in BOLD-fMRI data

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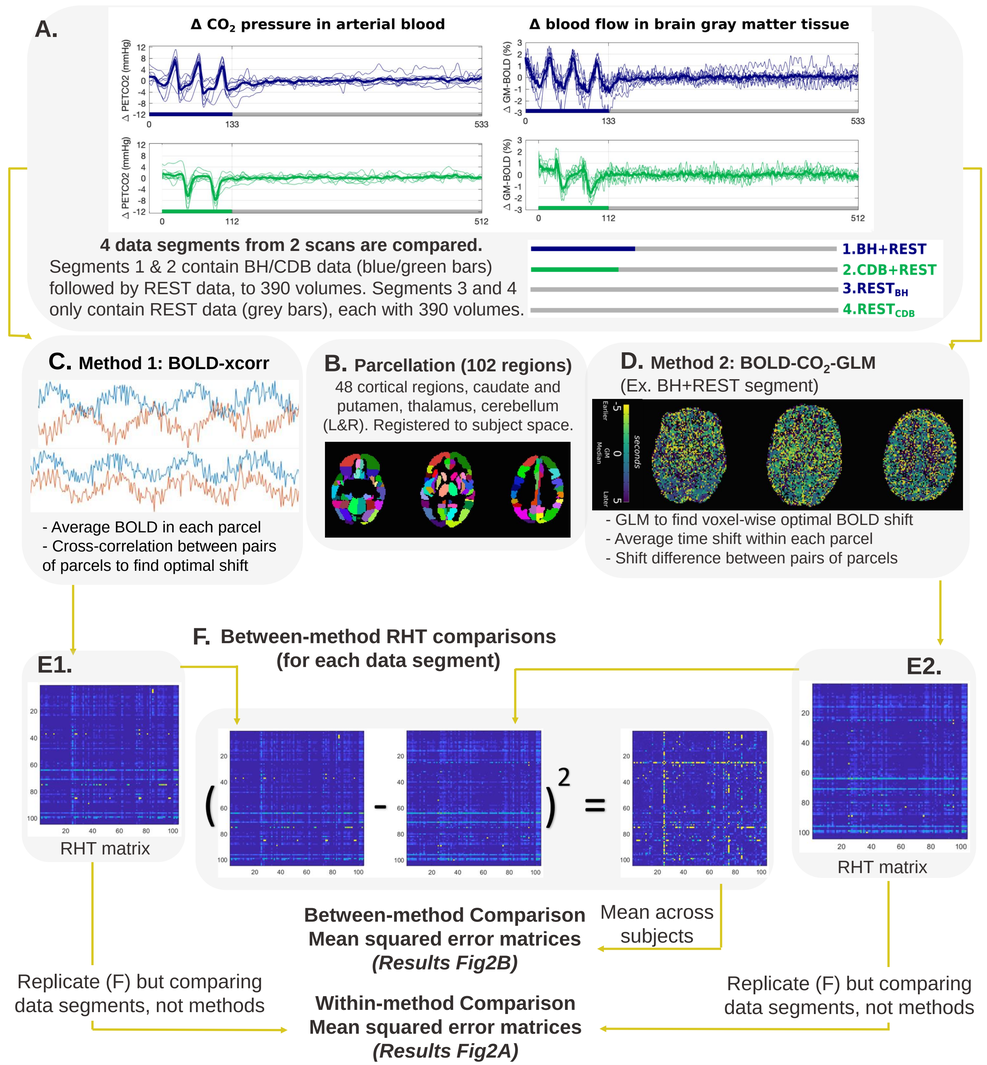
BACKGROUND

- Functional MRI (fMRI) captures functional networks formed by brain regions working together, which may be anatomically separated.
- The blood-oxygenation-level-dependent (**BOLD**) signal demonstrates variable hemodynamic delays throughout the brain that should be accounted for in rs-fMRI analysis
- CO_2 fluctuation is a major **physiological confound** in resting-state (rs) fMRI studies.[1,2]
- It is easier to estimate hemodynamic timings in BOLD-fMRI data with **breathing tasks** compared to resting-state data.[3,4]

METHODS

- 9 subjects (6 F; 26±4 years) completed 2 fMRI scans (3T-MRI, GE-EPI, TR/TE=1200/34ms, 2mm^3, 60-slices, multi-band 4), counterbalanced across subjects. Each scan included 8 mins of fixation (**REST**). Two of the scans included 2-3 mins of breathing tasks (**BH**: breath holding; **CDB**: cued deep breathing) before the fixation (Fig 1A).
- Inspired and expired CO_2 (in units of mmHg) were sampled with a nasal cannula and gas analyzer (AD Instruments) during scanning.
- We compared two approaches for estimating relative hemodynamic timings (**RHT**) in BOLD-fMRI data. (**Method 1: BOLD-xcorr; Method 2: BOLD-CO_2-GLM**)
- These approaches are compared for two scans: resting-state only and resting-state preceded by breathing tasks (**BH/CDB+REST** and **REST$_{BH/CDB}$**) to induce fluctuations in CO_2.[5,6,7]
- Figure 1 (right) shows the **main analysis steps**



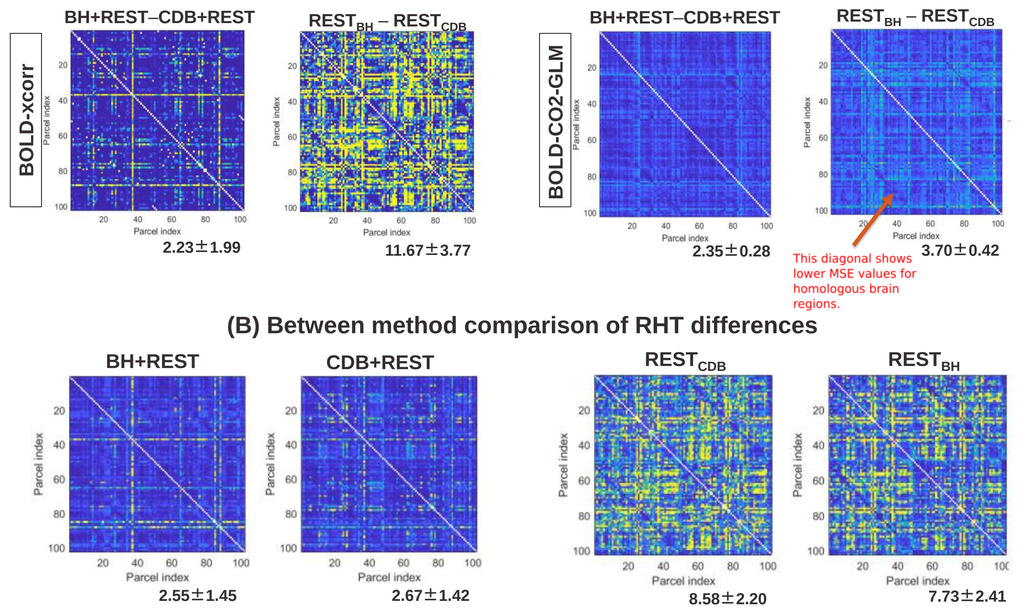


Figure 2. **Comparing relative hemodynamic timing (RHT) matrices.**
Panel A shows the within-method comparisons, comparing two breathing segments (first column) and two rest segments (second).
Panel B shows between-method comparisons, for each data segment separately. Numbers under each matrix summarize the mean±standard deviation of that matrix. Left and right refer to brain hemisphere.

RESULTS & DISCUSSION

- Better agreement in RHT is visualized by lower MSE (Fig2). Resting-state data show greater variability, both within and between methods, in measurements of Relative Hemodynamic Lag (RHT) .
- For the BOLD-xcorr method, RHT matrices agree more between breathing task segments, compared to between two REST segments. For the BOLD-CO_2-GLM method, the RHT agreement is similar for both types of data segments (Fig2A).
- Between-method agreement was better in data segments including breathing tasks compared to REST only segments (Fig2B).
- The addition of a breathing task, inducing larger fluctuations in $ETCO_2$ and therefore blood flow, results in better agreement. Further work is needed to understand the influence of single subject variability, partial volume effects and small regions of interest on these RHT estimates, as well as how either RHT measure relates to variation in task-activation hemodynamics.

NEXT STEPS

- More statistical comparisons to quantitatively describe the results we have so far and test conclusions for statistical significance.
- We will incorporate a third method, hemodynamic response function (HRF) deconvolution method, to estimate the CO2 lag times and compare with our existing methods.[8]

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