Estimating task structure by maximizing similarity between task-state and resting-state functional connectivity

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Introduction

- The brain flexibly reconfigures in response to task demands[1].
- Task designs induce time-locked changes in the blood oxygen-level dependent (BOLD) response and are reflected in functional connectivity[2].
- Removing variance of the task's structure yields stronger associations between task-removed and resting-state functional connectivity (trFC, rsFC)[2, 3].

Can we identify an existing task structure in a data-driven way by maximising the relationship between rsFC and trFC?

Methods

Input data
from the HCP-YA dataset[4]
(100 unrelated subjects)

Voxel time series
from working memory n-back task (0-back and 2-back)
- 2 phase-encoding runs (RL/LR)
  - 5:11 min. each
- 8 task blocks (25s each)

Group rsFC (from day 1)
- 2 phase-encoding runs (RL /LR)
  - 15 min. each
- 300 regions[5]

Output (per phase-encoding run)
Task structure with the highest achieved similarity after 200 iterations

Task structure identification pipeline (based on a genetic algorithm [GA] framework)

1. Define potential task structures (n=100)
- initial definition is random
- each structure has 8 onset times (in sec.)

per task structure

2. Build a task model
- Double gamma HRF convolution (duration of 25s, amplitude of 1, incl. dispersion and first derivative)

3. Regress the task model from voxel time series of all subjects (incl. 12 motion regressors)

extract residual time series

4. Calculate trFC per subject
Subject task-removed voxel time series
Pearson's r
Subject trFC (300 regions)[5]

average across subject trFC

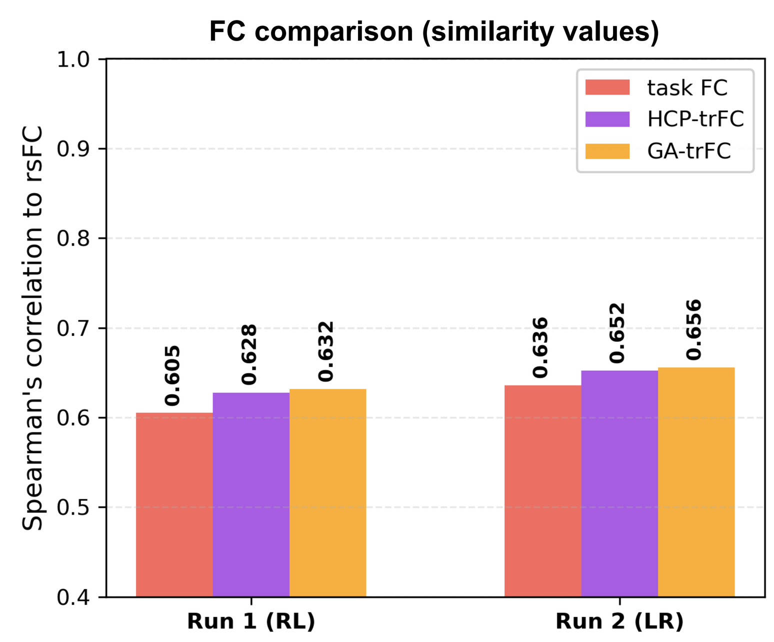
5. Compute similarity (on group level FC)
Group rsFC (300 regions)[5]
Spearman's ρ
Group trFC (300 regions)[5]

6. Propagate
- best 5 structures are used in next generation
- other 95 structures are recombined and/or slightly changed

repeat for 200 iterations

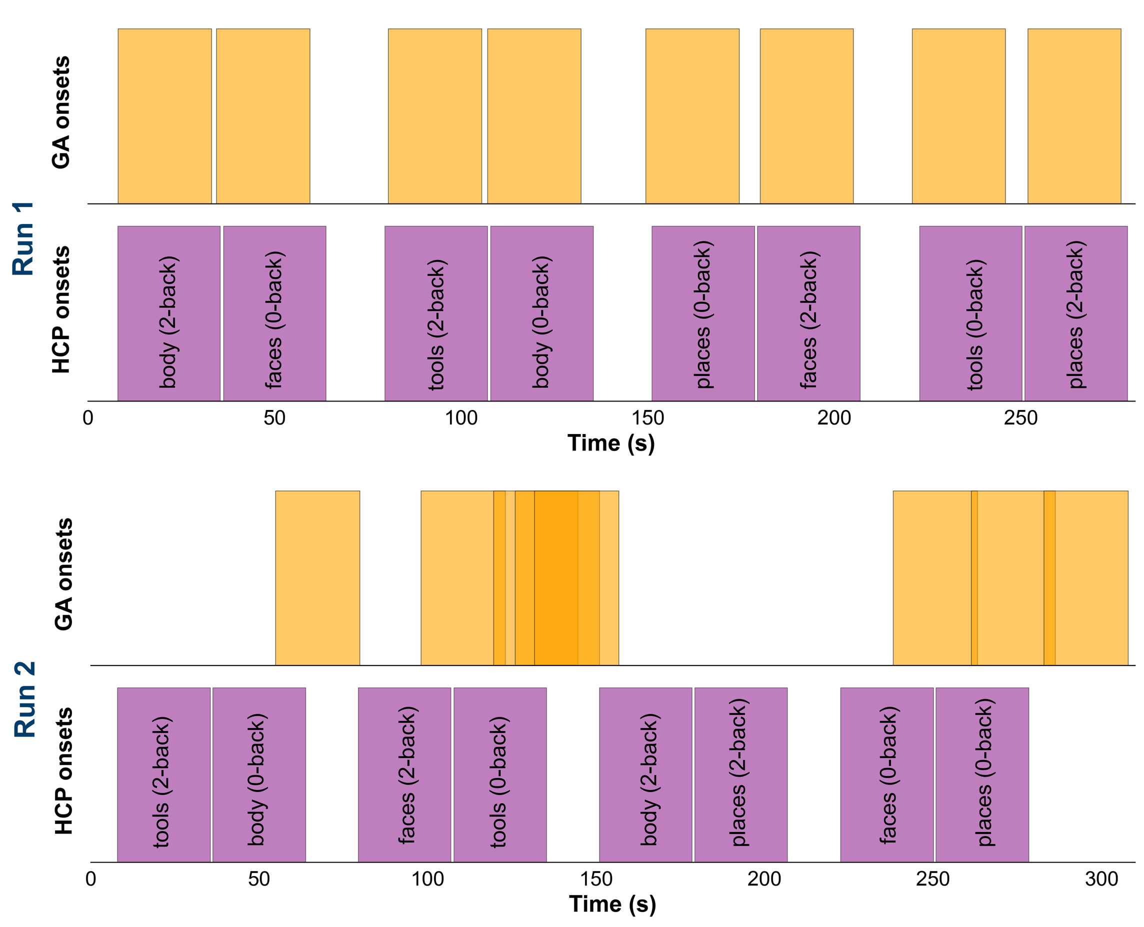
Results

1. TrFC with the highest similarity to rsFC surpassed HCP ground truth

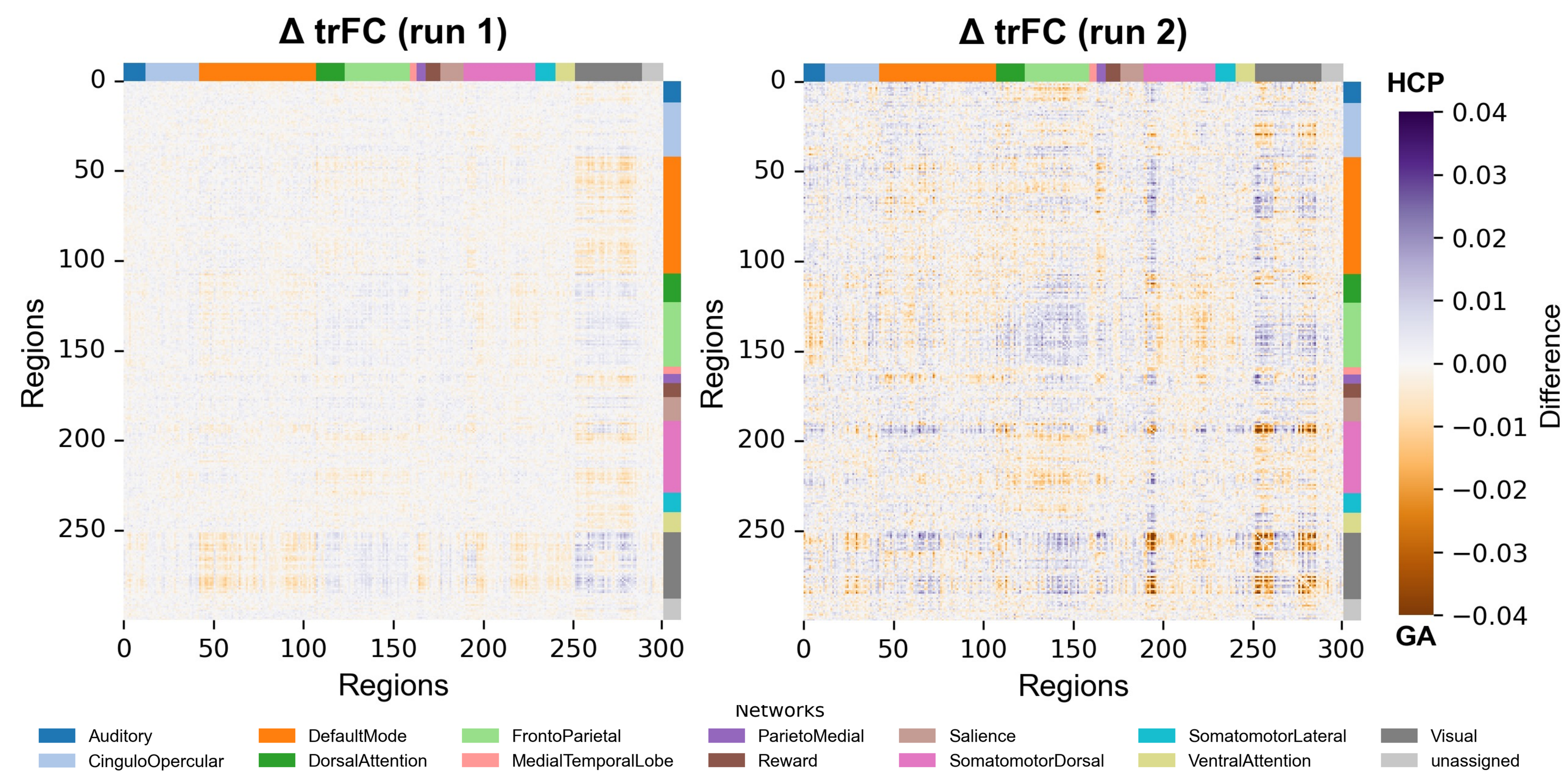


FC similarities (Spearman's ρ) to rsFC for both phase-encoding runs. Task FC (red, left) was built from the task BOLD signal. HCP-trFC (purple, middle) was built from residuals after removal of the empirical task structure. GA-trFC (orange, right) was built from residuals after removal of the identified task structure with the highest similarity to rsFC after 200 iterations.

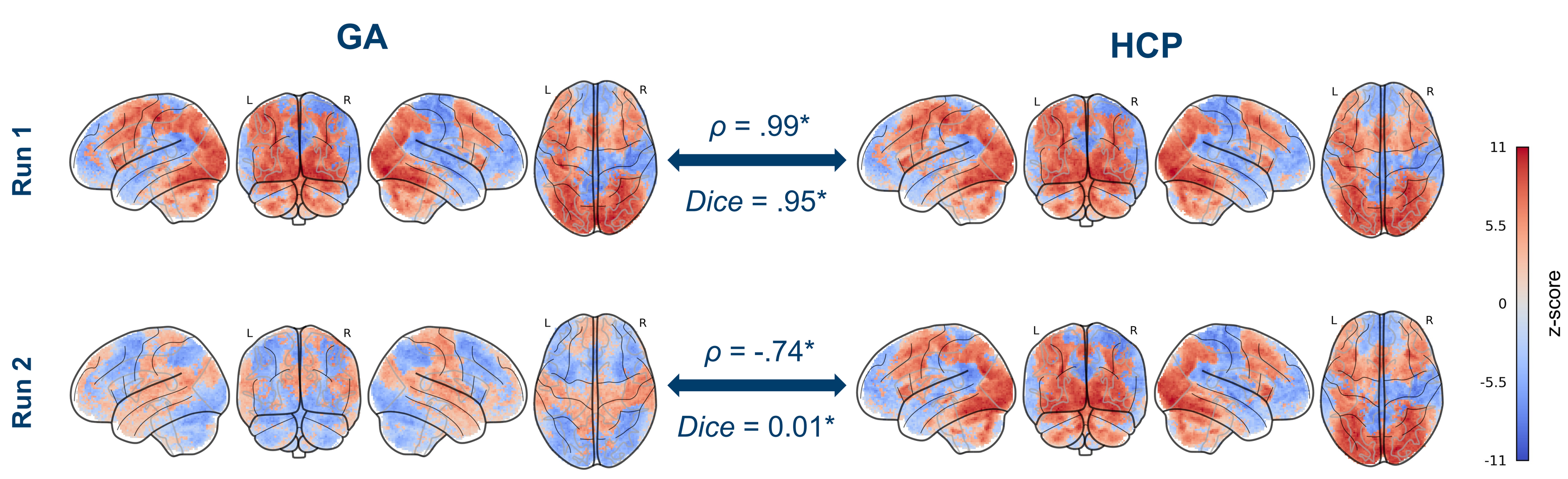
2. Identified task structure only matches the HCP ground truth in run 1



3. TrFC differences (HCP - GA) are numerically larger in run 2

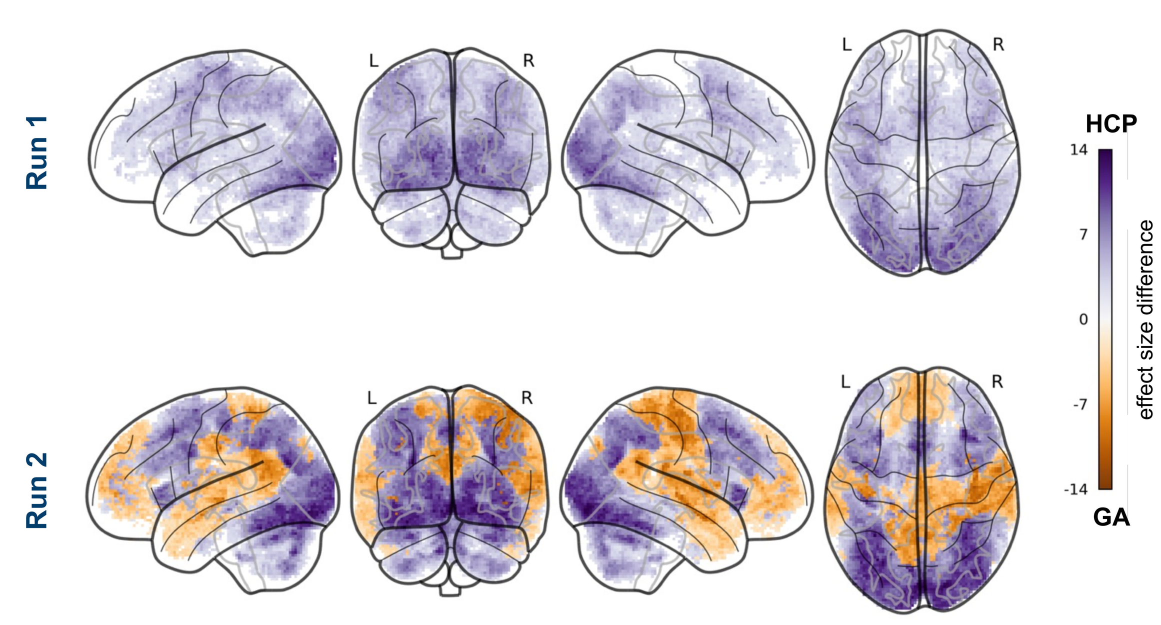


4. Mismatching task structure in run 2 translates into inverted spatial activation patterns



Unthresholded group-level spatial activation maps generated from GA (left) and HCP (right) task structure in data from run 1 (top) and run 2 (bottom). The task contrast was defined as GA or HCP > baseline.
**Spearman's correlation or dice coefficient (top 90% values) are significant at p < .005 (5k spins).*

5. Mismatching task structure in run 2 captures larger effect sizes of spatial activation in task-deactivated regions



Cluster-thresholded (at p < .05) group-level difference maps between effect sizes of task contrasts (task > baseline) generated from HCP and GA task structure separately.
Run 1 (top): Effect sizes of the task contrast were exclusively larger using the HCP task structure.
Run 2 (bottom): Effect sizes of the task contrast from the HCP task structure were larger in task-activated regions and larger for the GA task structure in task-deactivated regions.

Conclusions

1. Yes, we can identify a task structure by maximizing the similarity between trFC and rs FC

2. A higher similarity to rsFC does not guarantee precise temporal alignment with the empirical task structure[6]

3. Task-related network reconfigurations may not always reflect BOLD signal changes associated with empirical task onset[2]

4. Spatial activation patterns from maximized onsets can reflect activity in task-deactivated brain regions

References

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