Individual brain activity topographies during naturalistic viewing predict individual traits

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Individual brain activity topographies during naturalistic viewing predicts individual traits

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#WTh011

Introduction

- Naturalistic viewing (NV) fMRI (i.e., watching movies in the scanner), opens a new window into brain function under realistic conditions [1].
- Brain activity evoked during NV synchronises across individuals [2] while showing substantial individual differences [3].
- Understanding these individual differences in brain activity and their relationship with behaviour is of great interest.

AIM:

- Provide a novel approach for facilitating our understanding of individual differences and brain-behaviour relationships on NV fMRI data, by

  (i) identification of individual evoked activity topographies in a data-driven manner;

  (ii) phenotype prediction using a machine learning framework.

Methods

Subjects & Data:

- Human Connectome Project (HCP) [4] 7T subset (N = 179, age = 29.43±3.35 years, 108 females/ 71 males)
- **NV fMRI** (7T): Siemens scanner ; TR = 1 s; 3 movie clips: Two men (4'05"); Bridgeville (3'41"); Pockets (3'08")
- **Task fMRI** (3T): TR = 720 ms; 4 tasks: Motor (3'34"); Social (3'27"); Working memory (5'01"); Language (3'57")
- **Phenotypes** (8): fluid intelligence; working memory; personality (5 dimensions); emotion recognition

Preprocessing:

- HCP pipelines with standard processing
- Extract and normalise voxel-averaged time series for each parcel in a whole-brain parcellation [5]

Activity topography identification:

- Principal component analysis (PCA) on data across subjects within each parcel separately
- Dimensionality reduction on subject dimension

Phenotype prediction:

- Ridge regression model, Julearn python package
- Nested 10-fold cross-validation; 10 repetitions

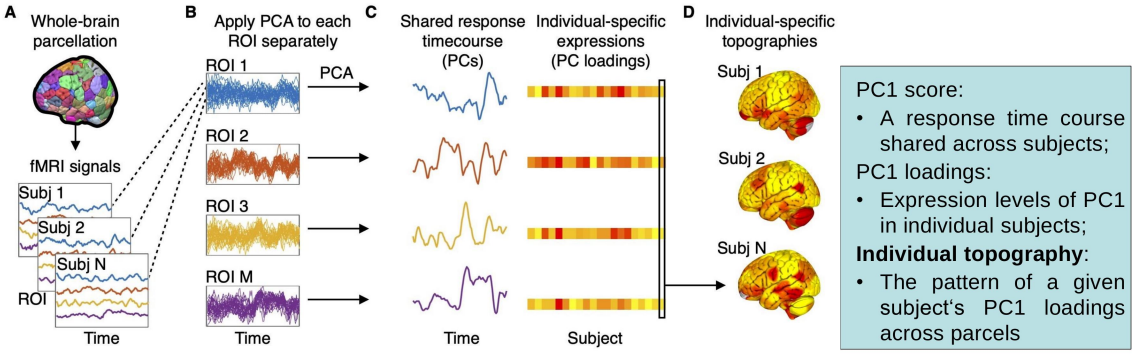

Fig.1 Schematic for identification of individual activity topographies

Results

Prediction performance

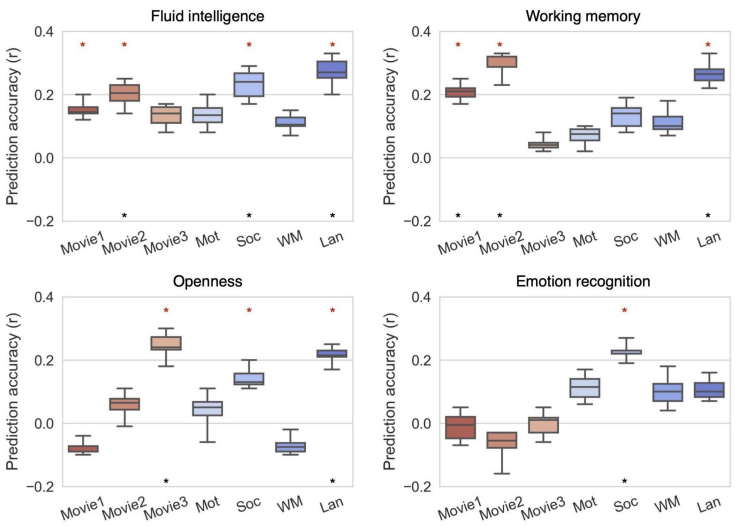

Fig.2 Prediction accuracy of phenotypes with significant results (p<0.05)

Movie1: Two men; Movie2: Bridgeville; Movie3: Pockets; Mot: motor task; Soc: social task; WM: working memory task; accuracy: Pearson correlation between predicted and observed scores over all subjects after regressing out sex, age and head motion from both scores. Significant results before and after FDR correction are marked in red and black stars respectively. Significance is determined by using permutation tests with 5000 iterations.

Important brain regions

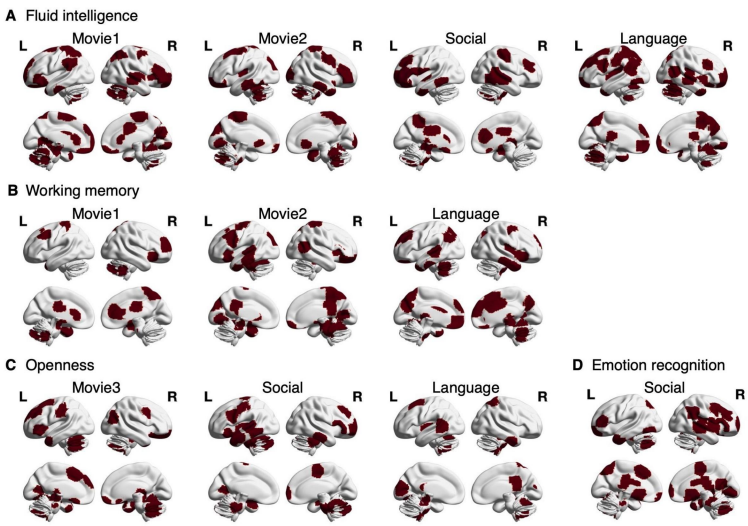

Fig.3 Important brain regions for significant predictions

*Important brain regions are identified based on their permutation feature importance. Only the brain regions for which the permutation feature importance (computed on test data of each fold averaged over 100 iterations) is significantly (permutation-based p<0.05, corrected; 1000 iterations) larger than zero over all 100 fitted models (10 folds*10 repetitions) are shown here.*

Discussion

- Together, we propose a useful data-driven, machine learning-based tool for understanding individual differences and brain-behaviour relationships on NV fMRI data.
- Individual activity topographies characterised by our proposed approach reflect meaningful individual differences in behaviour.
- Results also demonstrate the great potential of using NV fMRI data for studying brain-behaviour relationships.
- The dependence of the prediction performance on movie contents indicates that different movies may be suitable for investigating different research questions.
- Identified important brain regions are partially consistent with previous findings, demonstrating the promising interpretability of the proposed approach; e.g., frontal-parietal regions support cognitive ability, and temporal parietal junction supports emotion recognition.
- Highly variable patterns of these important regions among fMRI paradigms may reflect unique neural processes related to the same behaviour.
- The proposed approach works well for not only NV but also task fMRI data, providing a flexible and unified framework.

Preprint

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