

Xuan Li^{1,2}, Maiwenn Fleig¹, Patrick Friedrich^{1,2}, Simon B. Eickhoff^{1,2}, Susanne Weis^{1,2}

¹Institute of Systems Neuroscience, Heinrich Heine University Düsseldorf, Düsseldorf, Germany;

²Institute of Neuroscience and Medicine (INM-7: Brain and Behaviour), Research Centre Jülich, Jülich, Germany
xu.li@fz-juelich.de

#213

Introduction

- Naturalistic viewing (NV) paradigms, i.e., watching movie in the scanner, provide a promising tool for studying individual differences [1].
- Individual differences in brain activity evoked during NV are associated with individual differences in personal traits and clinical symptoms [2].
- Sex differences are of great interest to both cognitive and clinical neurosciences [3].
- To what extent brain activity evoked during NV reflect sex differences remains largely unknown.

AIM:

- To investigate sex differences in brain function during NV
- Characterising individual differences by the data-driven topography-based predictive framework (TOPF) [4]
- Prediction of sex under multiple NV conditions using machine learning

Subjects:

- Human Connectome Project (HCP) [5] 7T subset (N = 178, age = 29.40±3.32 years, 108 females/ 70 males)

NV fMRI data:

- 7T Siemens scanner ; TR = 1 s;
- Preprocessed by HCP standard pipelines;
- Voxel-averaged time series extracted for each ROI of a whole-brain parcellation [6]

Movie clips:

- 12 clips from 4 movie runs, each containing 3 different movie clips (length > 3 mins)
- Independent films (runs 1 and 3) vs. Hollywood films (runs 2 and 4)
- All clips truncated to the same length (3 mins, 180 TRs)

Methods

Sex prediction with TOPF [4]:

- Identify response time courses shared across subjects by principal component analysis (PCA) for each ROI
- Individual expression levels of shared responses (i.e., PC loadings) of all ROIs used as features
- Three sets of features: PC1 loadings (268), PC2 loadings (268), PC1+2 loadings (268*2)

Performance evaluation:

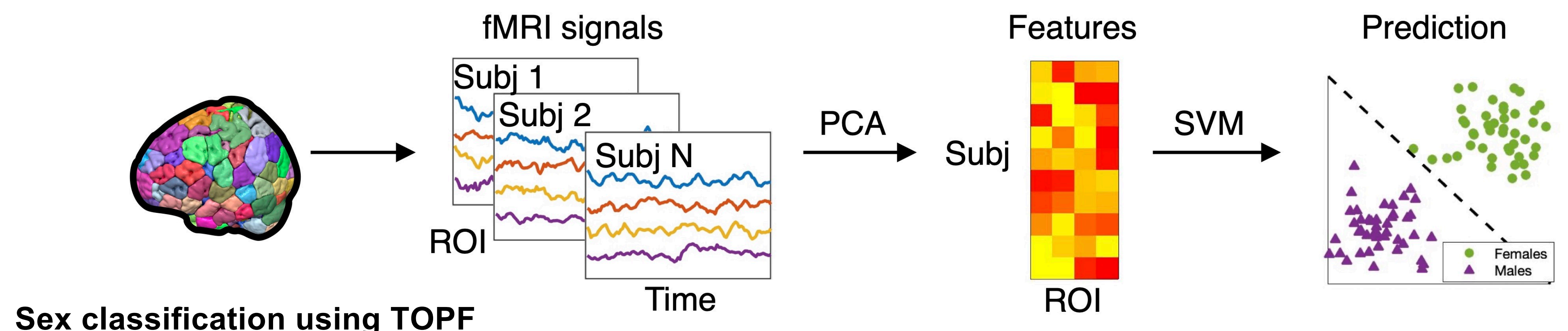
- Nested 10-fold cross-validation with 10 repetitions
- SVM with RBF kernel [3]
- Balanced accuracy (ACC) and area under the curve (AUC)

Data leakage prevention

- Training/test separation before feature extraction
- Control for family structure

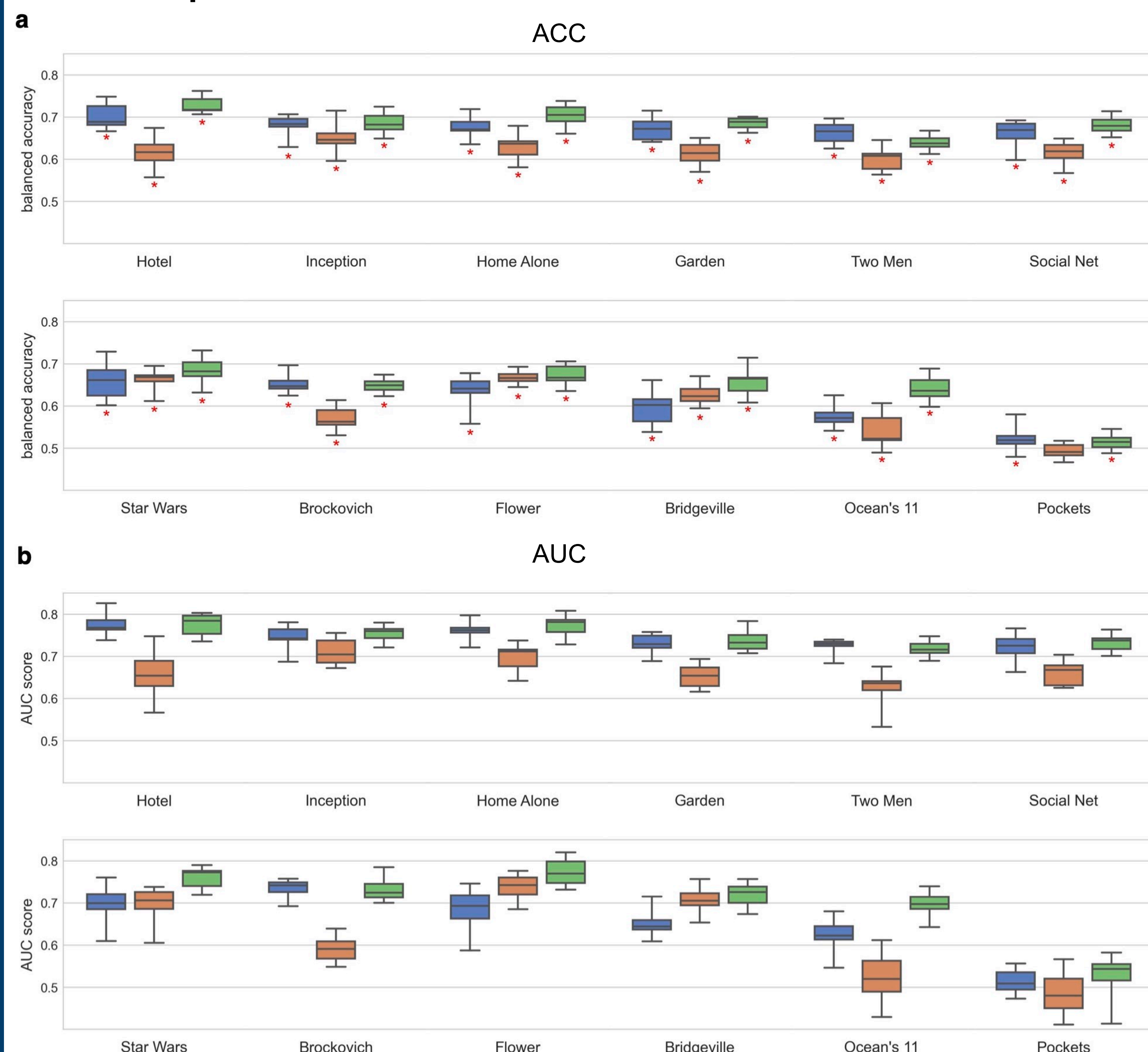
Importance of predictive features

- Permutation feature importance



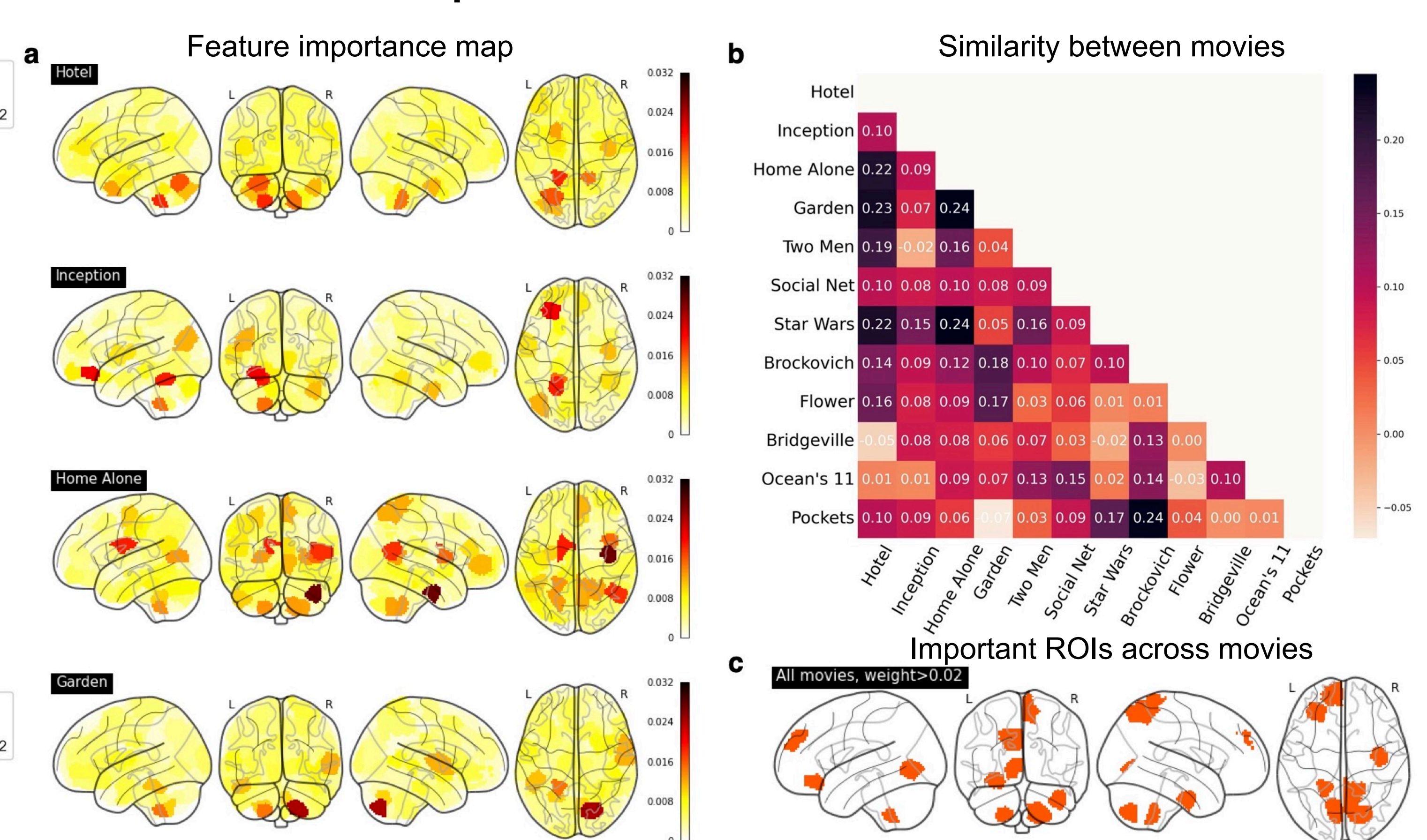
Results

Prediction performance



*: significant results (permutation-based $p < 0.05$, 500 iterations)

Permutation feature importance



a, Feature importance maps for the top 4 movie clips. b, Similarity (Pearson r) in feature importance maps between movie clips. c, Most predictive (importance > 0.02) parcels shared across all movie clips.

Main findings

- Sex was significantly predicted (permutation-based $p < 0.01$) for most movie clips using all feature sets
- Prediction performance varied across movie clips.
- Predictive models and important features varied across movie clips.

Discussion

- The successful prediction of sex suggests that systematic sex differences exist in brain function under NV conditions.
- Prediction performance varied largely across movie clips, with “Hotel” (ACC: 70.0%) and “Pockets” (ACC: 52.2%) achieving the highest and lowest scores, respectively.
- Brain regions that are most important for sex prediction are mainly located in prefrontal, superior parietal, inferior temporal and cerebellum regions.
- These brain regions are associated with various cognitive processes, e.g., language and semantic processing [7,8].
- The variations in predictive models and important features suggest that

different movie stimuli may elicit distinct brain states and emphasise different aspects of the same brain-behaviour relationship.

- In sum, these results show the potential of NV conditions for phenotype prediction and for facilitating our understanding of sex differences in brain function.
- However, further investigation is needed to understand differences between movie stimuli and how they influence the study of individual differences and brain-behaviour relationships.

[1] Sonkusare, S. (2019), Naturalistic stimuli in neuroscience: Critically acclaimed, Trends Cogn. Sci. 23, 699–714.

[2] Finn, E.S. (2020), Idiosyncrony: From shared responses to individual differences during naturalistic neuroimaging, Neuroimage 215, 116828.

[3] Weis, S. (2020), Sex classification by resting state brain connectivity. Cereb. Cortex 30, 824–835.

[4] Li, X. (2023), A topography-based predictive framework for naturalistic viewing fMRI. Neuroimage 277, 120245.

[5] Van Essen, D.C., Smith S.M., Barch D.M., Behrens T.E., Yacoub E., Ugurbil K. (2013), The WU-Minn Human Connectome Project: An overview, Neuroimage 80, 62–79.

[6] Shen, X., Tokoglu F., Papademetris X., Constable R.T. (2013), Groupwise whole-brain parcellation from resting-state fMRI data for network node identification, Neuroimage 82, 403–415.

[7] Jung-Beeman, M. (2005), Bilateral brain processes for comprehending natural language. Trends Cogn. Sci., 9, 512–518.

[8] Ralph, M. A. L. (2017), The neural and computational bases of semantic cognition. Nat. Rev. Neurosci., 18, 42–55.