

Spatial Reorganization of fMRI Functional Networks Encodes Task- and Participant-Specific Features

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Background

Need: personalized biomarkers improve targeted brain stimulation in psychiatric disorders.

Current Limits: fMRI networks are promising, but group-averaged methods reduce individualization and underuse task data.

Our Approach: PROFUMO co-estimates networks from rest and task data, at group and individual-levels, allowing networks to spatially reorganize for each individual.

Objective

Extract functional biomarkers from PROFUMO networks derived from resting-state and task fMRI data.

Methods

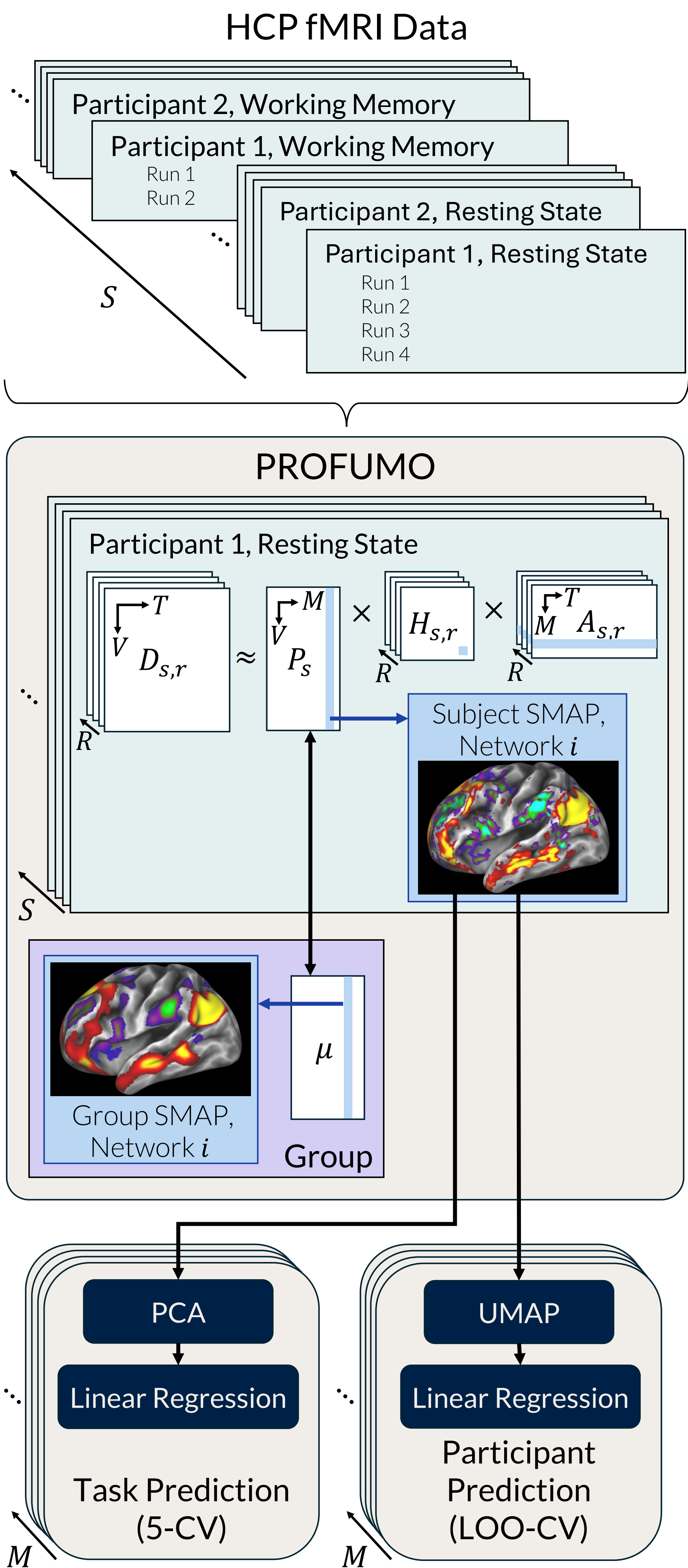


Figure 1. For each participant-task pair (s), sPROFUMO¹ derived 40 network SMAPs (group: μ , subject: P_s). Each network's SMAPs were dimension-reduced, then used to predict participant- or task-identity via cross-validated multinomial linear regression. (S : # pairs = 954 participants \times 8 tasks; V : # voxels; T : # fMRI timepoints; R : # runs; M : # networks; $D_{s,r}$: fMRI data for run r of task-participant subject s ; $H_{s,r}$: networks' amplitude; $A_{s,r}$: networks' timecourses.)

Key Results

In certain PROFUMO networks, task-specific reorganization is captured by maximal variance, while participant-specific reorganization is captured by UMAP embeddings

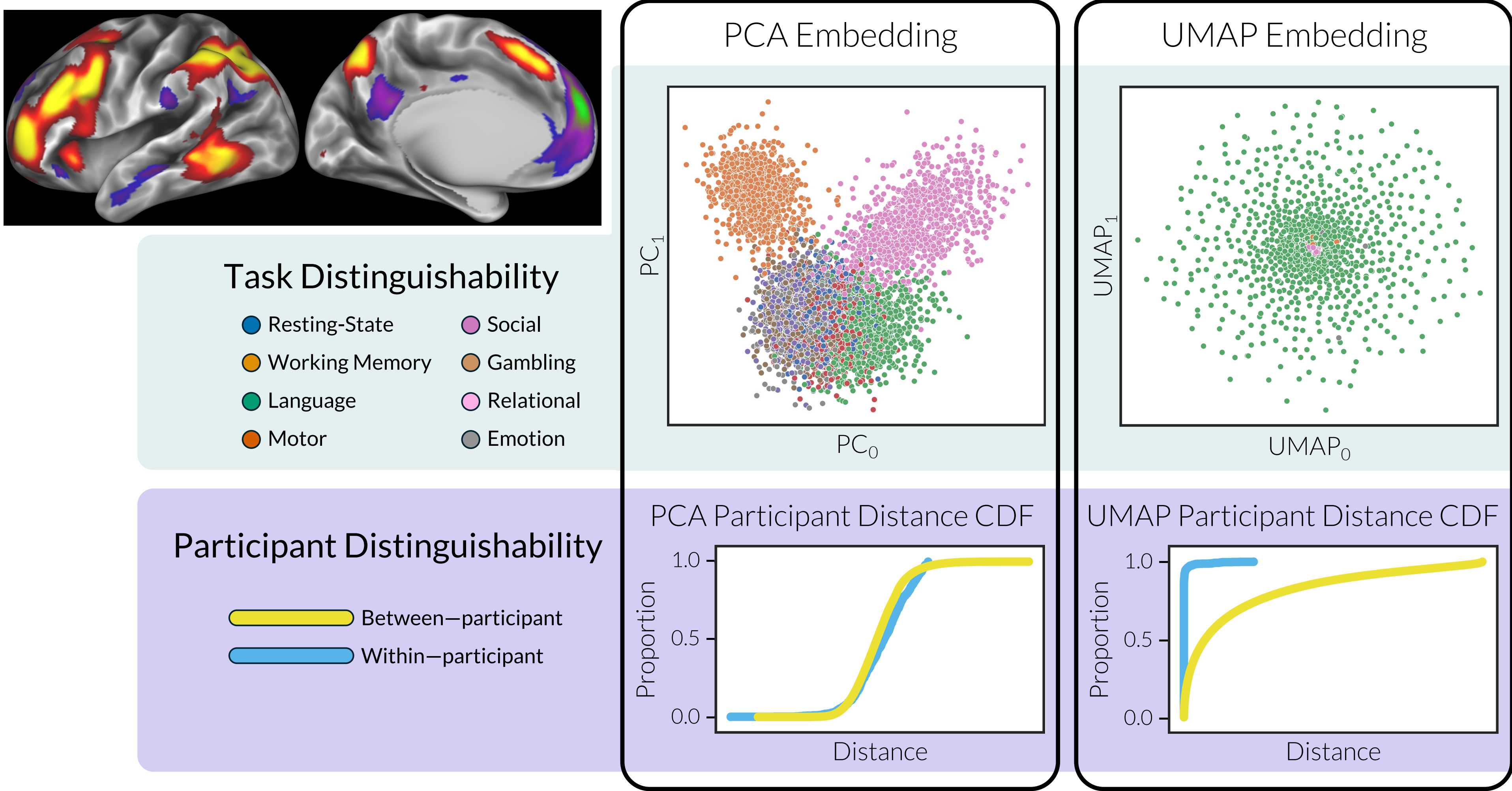


Figure 2. Different embeddings of subject SMAPs capture distinct patterns of spatial reorganization in an example PROFUMO network (containing CN & DAN regions), revealing task and participant features. PCA embeddings cluster by task, while UMAP embeddings separate by participant (the cumulative distribution function (CDF) of the UMAP within-participant distances are noticeably smaller than the between-participant distances).

This network reorganization pattern enables robust task and participant prediction

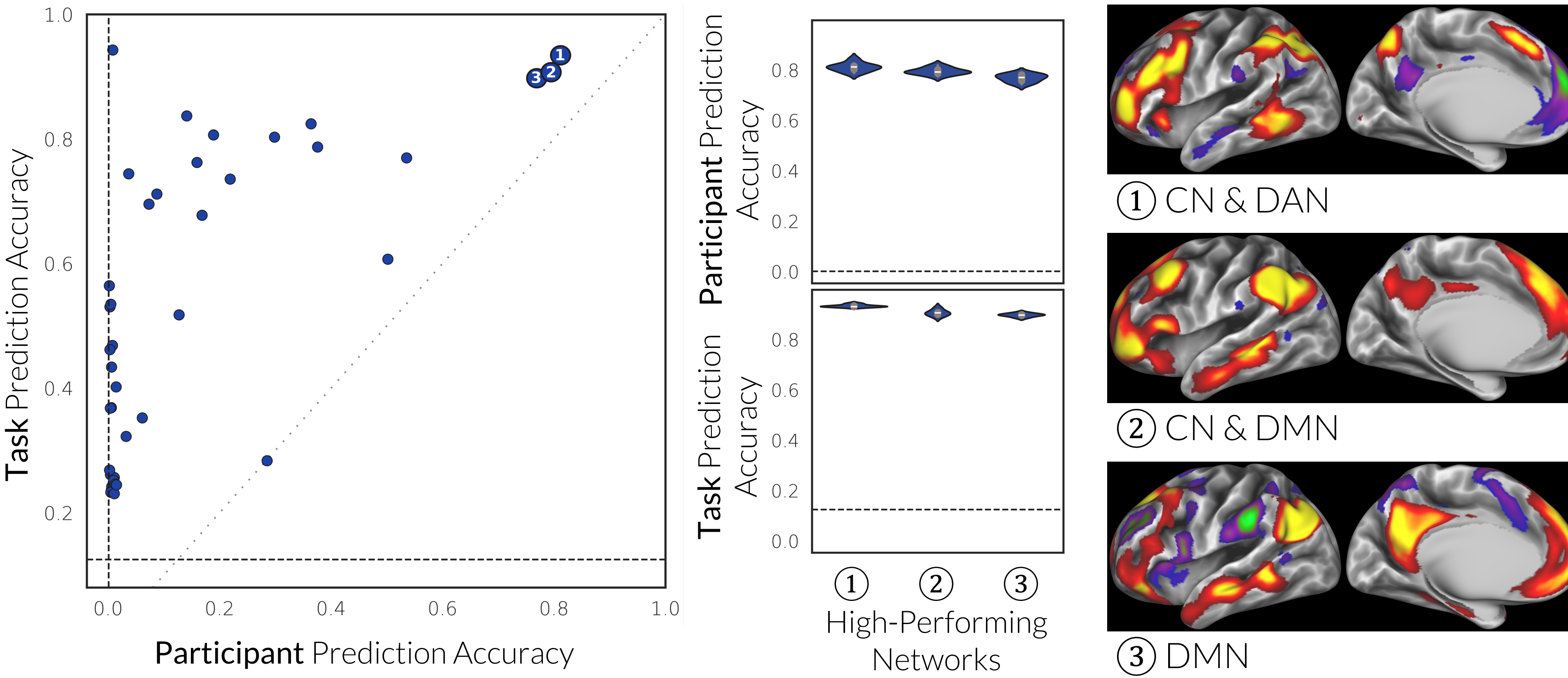


Figure 3. PROFUMO networks that robustly predict participant-identity also robustly predict task-identity (marked ①, ②, ③). Left: participant vs task average prediction accuracies for each network (blue circles). (Dashed lines: null accuracies; Dotted line: task = participant prediction accuracy). Middle: the top-performing networks show consistent high performance across cross-validation folds for both prediction accuracies. Right: group SMAPs for the top-performing networks.

Abbreviations

SMAP	Spatial Map
HCP	Human Connectome Project - Young Adult
PCA	Principal Component Analysis
UMAP	Uniform Manifold Approximation and Projection
5-CV	Nested 5-fold Cross-Validation
LOO-CV	Leave-One-Out Cross-Validation
DAN	Dorsal Attention Network
DMN	Default Mode Network
CN	Control Network

Key References

1. Farahibozorg, S.-R. et al. Hierarchical modelling of functional brain networks in population and individuals from big fMRI data. *NeuroImage* 243. Publisher: Elsevier, 118513. ISSN: 1053-8119 (Nov. 2021).

Discussion & Conclusions

- Spatial reorganization of PROFUMO's functional networks reliably captures individual- and task-level information.
- Networks with this dual reorganization pattern overlap with clinically relevant networks (CN, DAN, & DMN).
- These PROFUMO networks derived from rest and task fMRI data are promising personalized biomarkers.

Future Directions

Use PROFUMO networks to inform targeted neurostimulation paradigms.