Spatial Maps of Similarity Across the Cortex

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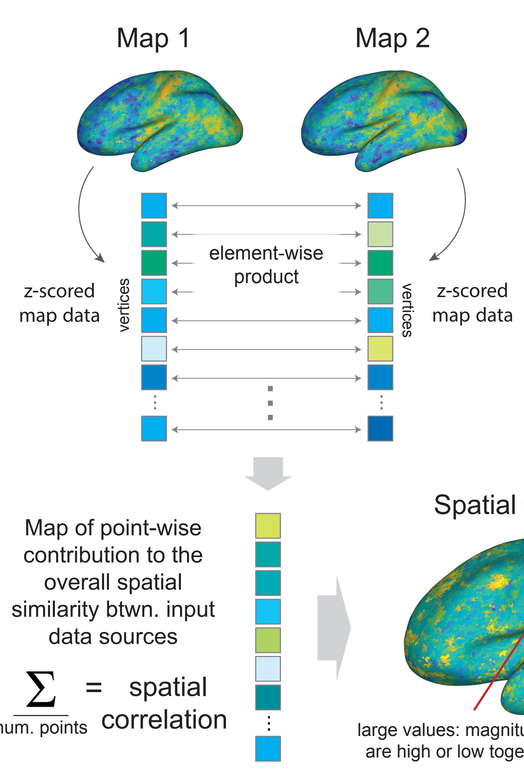
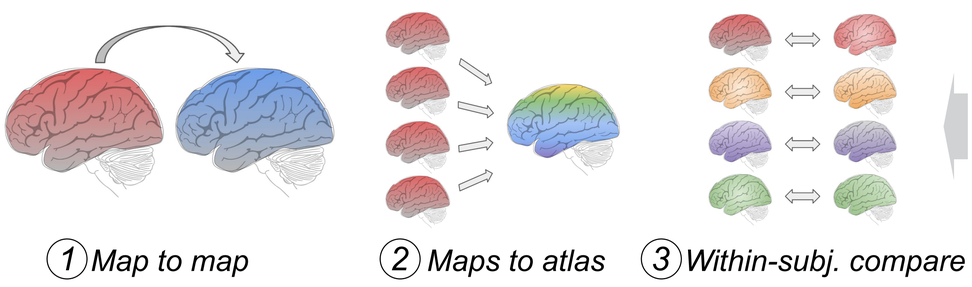
camaraderie

Introduction



- A primary goal of neuroimaging is to chart how features change across the cortex
- It's common practice to compare mapped data to:
  - A canonical reference map, like the principal gradient[9] of the functional hierarchy
  - Data from a different modality[5,7] to look for alignment of anatomical/functional indices
  - Similarly mapped data from other sessions or subjects[4,8], to situate this map among others
- Comparing maps is often performed by taking the ***Pearson correlation***
  - We previously[1] demonstrated how to "unwrap" correlation to render ***edge time series***
    - The correlation unwrapping can be applied for spatial correlations (see viz., left)
- Here, describe the process of rendering ***spatial similarity maps*** and demonstrate how the added spatial information can provide additional insights for brain mapping analyses.

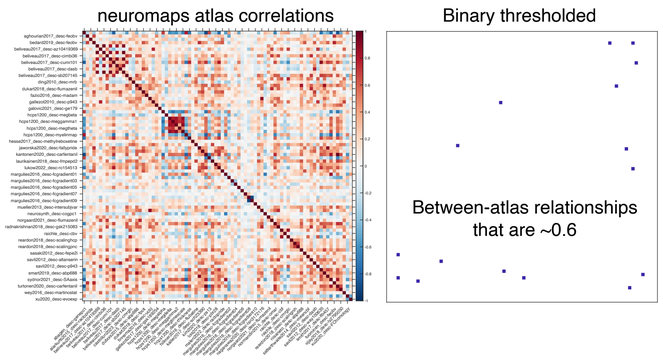


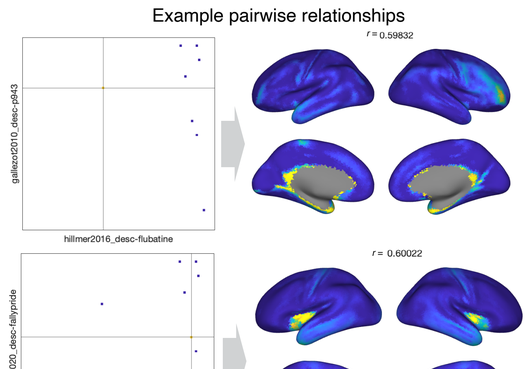
Scenarios where we demonstrate how spatial similarity maps can enhance our understanding of map comparisons

Methods

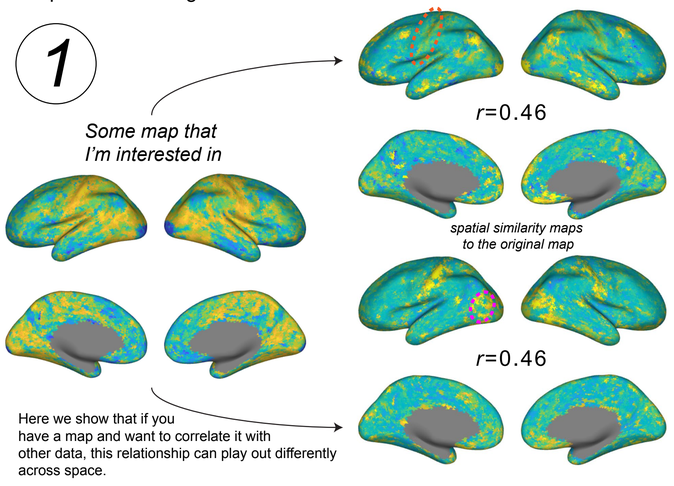
- Human Connectome Project[6] quality-controlled subset of 352 subjects
- Resting-state data (TR=0.72, 1200 TRs, ~15 min) minimally pre-processed, motion, distortion, ICA-FIX corrected, MSM-aligned, and projected to fsLR surface; bandpass (0.008 - 0.2 Hz) filtered, mean WM, mean CSF, linear, and quadratic drift removed via linear regression in one step using AfNI's 3dTproject
- REST1_LR, REST1_RL averaged for *day 1* data; REST2_RL and REST2_LR averaged for *day 2*
- Time series in fsLR space interpolated to on-avg[2] space using distance-weighted nearest-neighbors
- Structurally derived MSM-aligned data (processed by HCP) interpolated from fsLR space to on-avg space
- Within on-avg space, vertices near corpus callosum were masked out to remove edge effects in feature maps, making for a total of 18,948 vertices of surface used
- neuromaps[10] downloaded from repository, transformed to fsLR w/ included tools, and interpolated to on-avg space

Results





We downloaded all possible maps that could be projected to on-avg space (n=82). From this matrix, we identified edges within 0.002 of a 0.6 correlation, and rendered their spatial similarity maps. Examples are plotted to the right.



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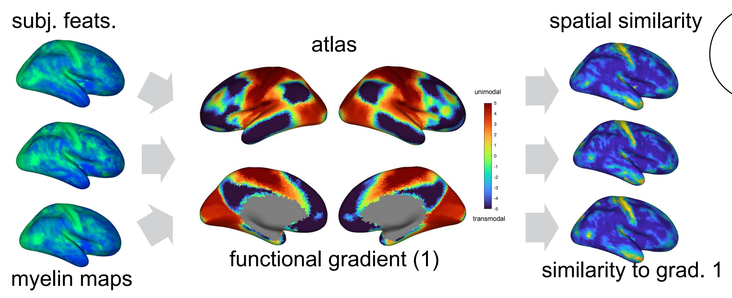
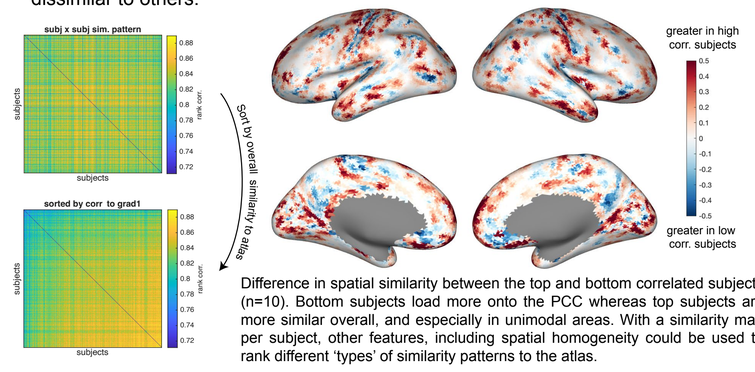
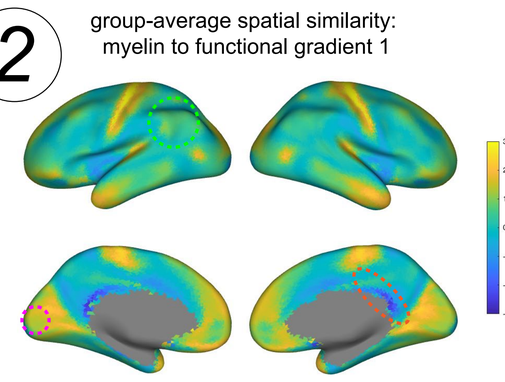


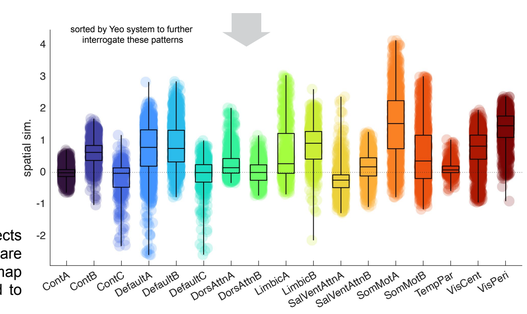
Here we render the spatial similarity when comparing multiple feature maps (myelin) to a common reference atlas. Since we get a map per subject, subjects' patterns can be interrelated (below). Sorting by overall similarity reveals a core-periphery structure[3], where the myelin maps with the lowest similarity to grad. 1 are dissimilar to others.



Difference in spatial similarity between the top and bottom correlated subjects (n=10). Bottom subjects load more onto the PCC whereas top subjects are more similar overall, and especially in unimodal areas. With a similarity map per subject, other features, including spatial homogeneity could be used to rank different 'types' of similarity patterns to the atlas.

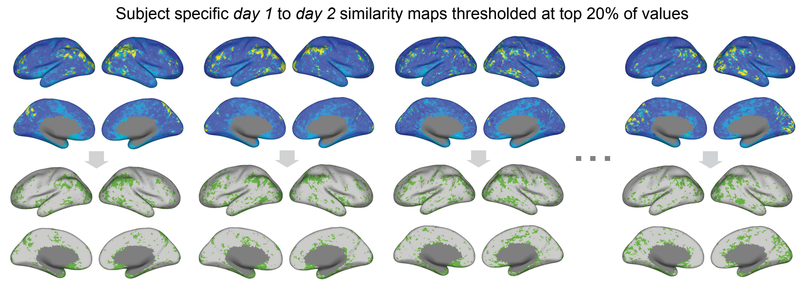


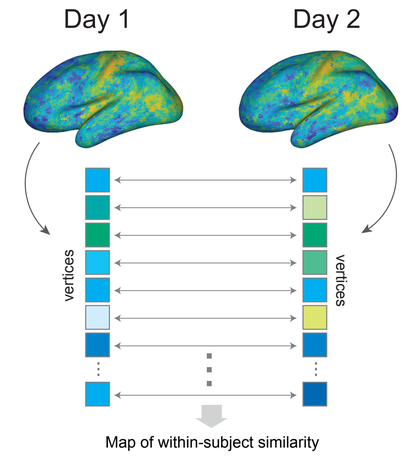
Note patterns of the group-averaged similarity can highlight locations of differential similarity. For example, highlighted in orange we see the retrosplenial cortex, which has high myelin content and yet is considered transmodal according to gradient 1. This discordance is shown as dark blue.

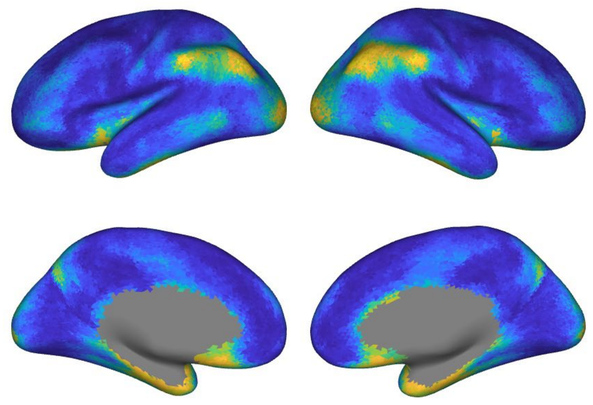


Data collected in the same subjects on two different occasions allows us to compute the reliability. Here, we can compare maps to see where within-subject similarity is greatest, using *time series autocorrelation* half-width at half-maximum[11] as the exemplar feature.

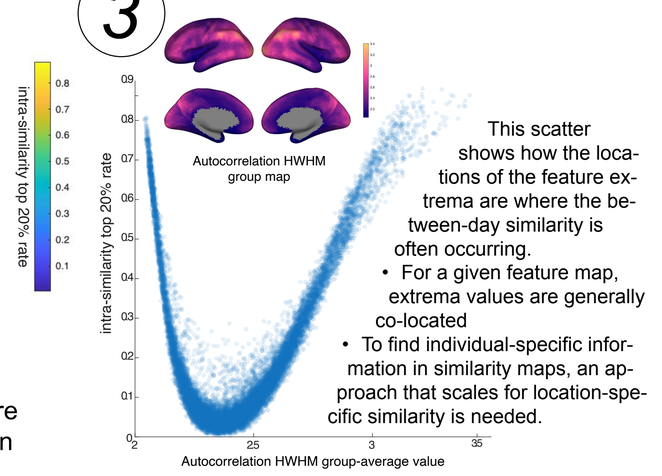
Subject specific *day 1* to *day 2* similarity maps thresholded at top 20% of values





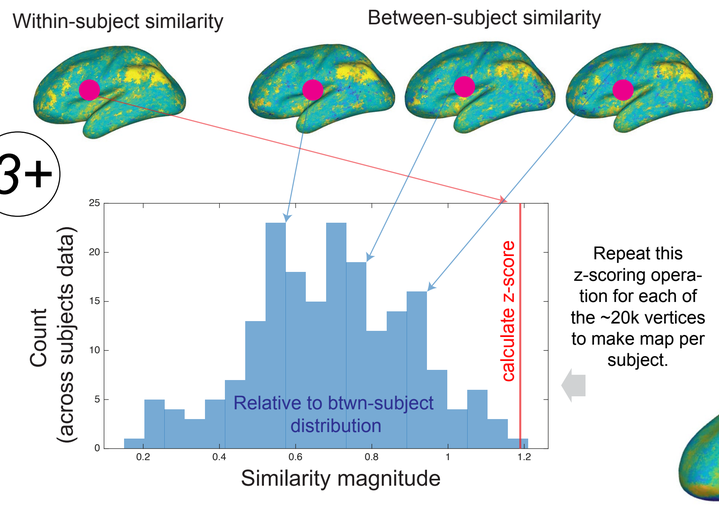


Group-average spatial similarity map showing where within-subject similarity is in the top 20% most often

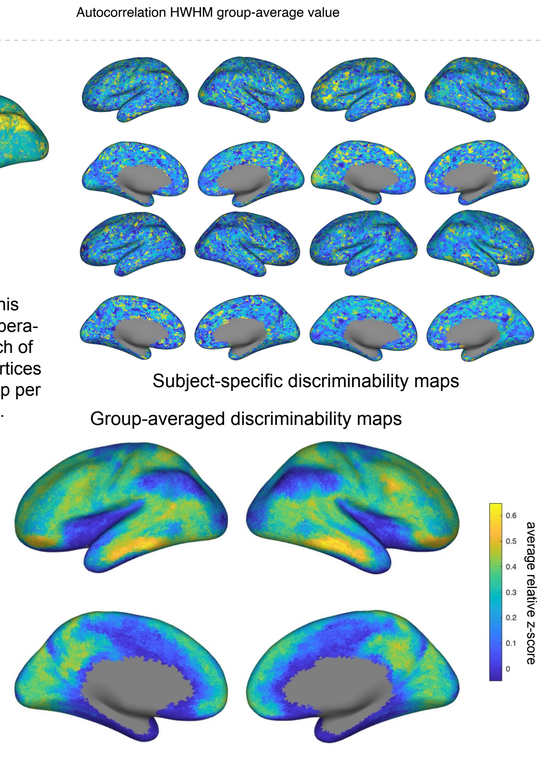


This scatter shows how the locations of the feature extrema are where the between-day similarity is often occurring.

- For a given feature map, extrema values are generally co-located
- To find individual-specific information in similarity maps, an approach that scales for location-specific similarity is needed.



Repeat this z-scoring operation for each of the ~20k vertices to make map per subject.



Note the different spatial topography of within-subject similarity map (previous panel) compared to the discriminability map (right). The discriminability map highlights areas where subjects have self-similarity that substantially exceeds the distribution formed by between-subjects similarity[4,8].

Discussion

- There are many (infinite!) similarity patterns that can result in a correlation of a specific magnitude (e.g., *r*=0.46)
- Rather than measuring similarity with one *r* value, we can use the correlation unwrapping approach to see how similarity loads across the cortex. This information can be used for:
  - Exploratory data analysis, to better understand where maps relate highly or to spot potential biases. In our examples we can see how comparing PET feature maps might be influenced by SnR in insular regions, or how the retrosplenial cortex is an area of notable dissimilarity when comparing myelin and the primary functional gradient.
  - Quantitatively describing different similarity patterns, whether via comparing patterns or by deriving a feature of the spatial similarity maps that co-varies with a behavior or phenotype. Comparing myelin-to-grad1 similarities across subjects shows that low-correlation subjects have mapped patterns that are more dissimilar to all other patterns.
- Future work will look to relate this approach to other neuroimaging methods, like VBM or spatial registration, to see how spatial similarity can be used to complement other sorts of mapped changes (especially for the case of warp fields).
- Additional future work will seek to relate spatial similarity patterns, as well as discriminability maps, to behavioral and phenotypic information. We seek to use similarity to narrow down the patches where this information resides, which could potentially boost statistical power