KERNEL PARTIAL LEAST SQUARES REGRESSION FOR RELATING FUNCTIONAL BRAIN NETWORK TOPOLOGY TO CLINICAL MEASURES OF BEHAVIOR

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We propose a method for analyzing relationships between functional brain networks and behavioral phenotypes.

We map **topological data features** extracted from resting-state fMRI networks to a kernel space and use kernel partial least squares (kPLS) regression to quantify their relationship to autism. The advantages are:

Kernel Partial Least Squares

PLS projects two datasets, X and Y, of sizes $n \times N$ and $n \times M$ down to p latent dimensions that maximally covary. kPLS [1] extends this, assuming that X is mapped by Φ to a higher dimensional inner product space \mathcal{F} .

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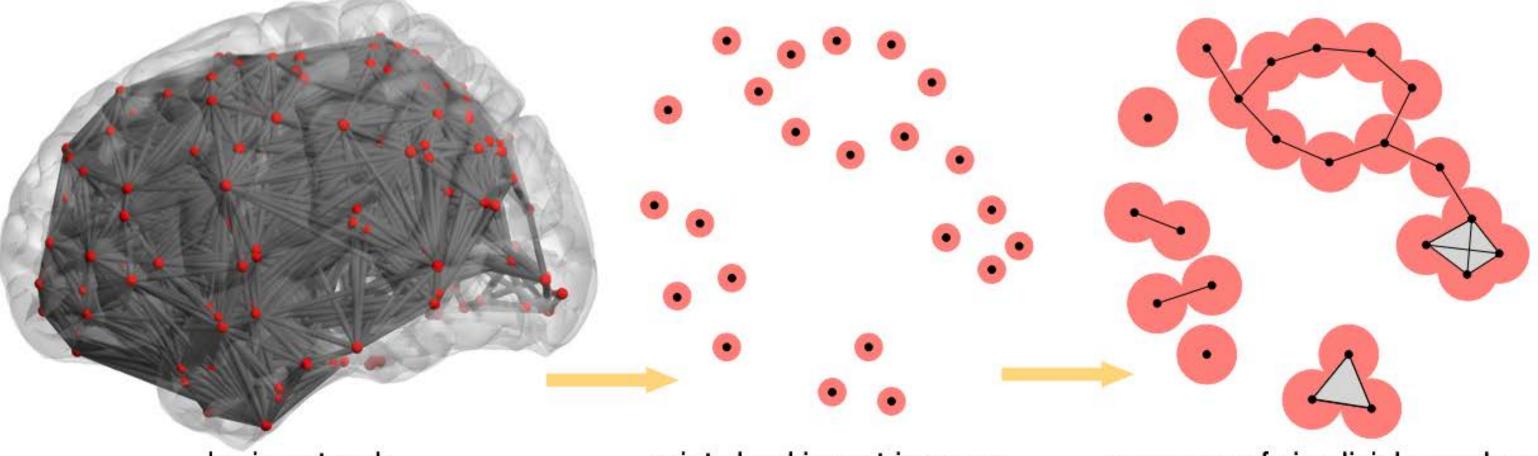
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kPLS Algorithm

 $t = \Phi(x) \Phi(x)^T u = K u$

- Typical correlation-based methods use thresholds to determine the existence of an edge in the network. Topological features capture network organization across all threshold values.
- Multiple image features can be easily combined by a summation of kernels.

Topology of Brain Networks



$\iota = \Psi(x)\Psi(x)$	$u = \kappa u$
$\ t\ \to 1$	$K: \operatorname{Gram} \operatorname{matrix} \operatorname{of} X$
$c = Y^T t$	$K(x, x') : \langle \Phi(x), \Phi(x') \rangle_{\mathcal{F}}$
u = Yc	t, u: covarying latent variables
$\ u\ \to 1$	c : loadings for Y

Once all the latent dimensions are found, the regression from kernel to Y is $\hat{Y} = \Phi(x)B = KU(T^TKU)^{-1}T^TY$.

TDA Kernel

We take all subject persistence barcodes to construct a multiscale topological kernel [2] with stability properties,

$$K_{\sigma}^{TDA}(A,B) = \frac{1}{8\pi\sigma} \sum_{p \in A, q \in B} e^{-\frac{||p-q||^2}{8\sigma}} - e^{-\frac{||p-\bar{q}||^2}{8\sigma}}$$

where for every $q = (a,b) \in B, \ \bar{q} := (b,a).$

brain network

point cloud in metric space

sequence of simplicial complexes

t=5

t=5.6

Procedure:

t=0

• For each subject, map the nodes from a brain network to points in a metric space using the distance measure,

 $d(u, v) = \sqrt{(1 - corr(u, v))}.$

- Grow the radius of a neighborhood around each point. Neighborhoods begin to merge.
- Track the o-,1-,2-dim topological features (connected components, holes, and voids) that appear and disappear over time.

Persistent homology follows the birth and death times of these features, which can be visualized as a barcode.

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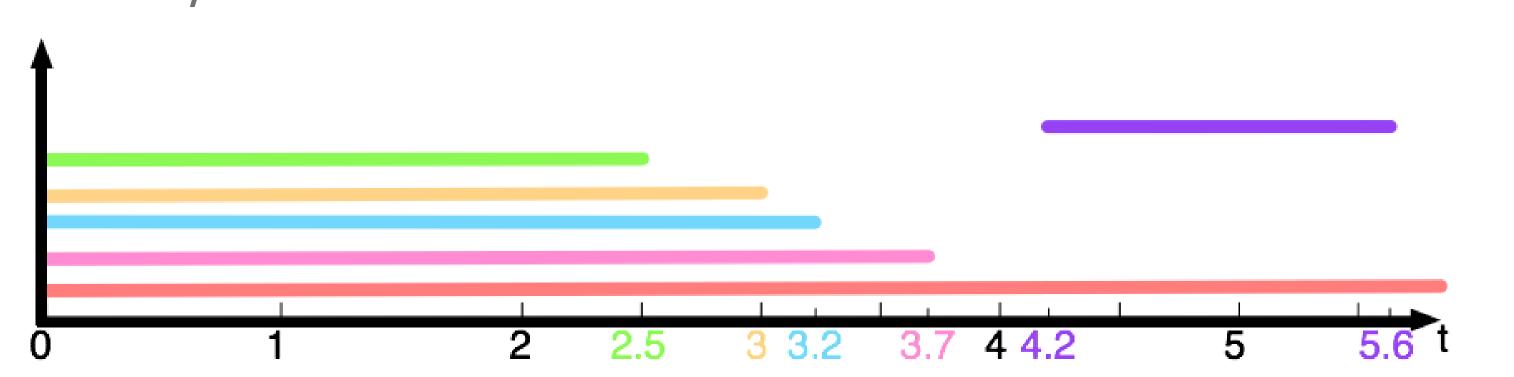
Experiments

Goal Predict ADOS score from resting state fMRI using data from one site in the ABIDE dataset (30 control, 57 ASD subjects) **Results** Compared with using just raw correlations from 264 ROIs (d=34716), augmentation with topological features improves predictive power.

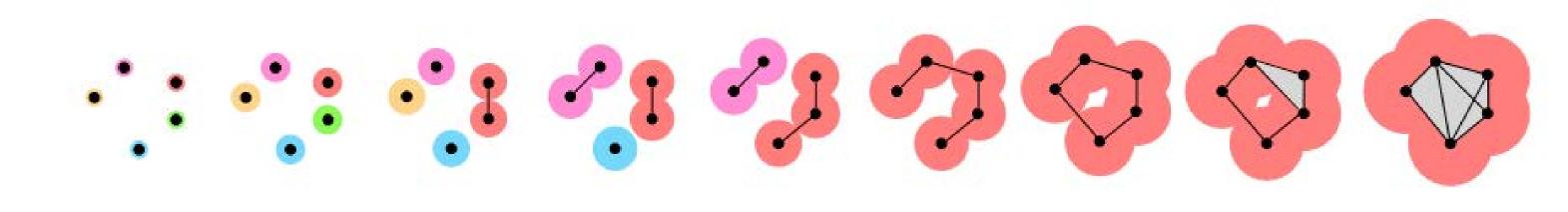
We did LOOCV and evaluated the RMSE of the predictions. We used the following comparisons:

- $K^{\rm cor}$: Linear kernel from correlation matrices by taking Euclidean dot products between subjects
- K^{TDA_0} and K^{TDA_1} : o-,1-dim TDA feature kernels
- $K^{\text{TDA}+\text{cor}} = w_0 K^{\text{TDA}_0} + w_1 K^{\text{TDA}_1} + (1 w_0 w_1) K^{\text{cor}}$:

the combined kernel with 4 parameters to cross validate over. Weights w_0, w_1 in the range o to 1 by 0.05, and log



It is equivalent to capturing the topological changes of the *Rips complexes*, formed by connecting the points in intersecting neighborhoods with pairwise edges.



References

[1] Rosipal, Roman, and Leonard J. Trejo. "Kernel partial least squares regression in reproducing kernel hilbert space." The Journal of Machine Learning Research 2 (2002): 97-123. [2] Reininghaus, Jan, et al. "A stable multi-scale kernel for topological machine learning." Proceedings of the IEEE Conference on Computer Vision and Pattern Recognition. 2015.

- kernel sizes $\log_{10}(\sigma_0)$, $\log_{10}(\sigma_1)$ from -8 to 6 by 0.2
- ADOS mean baseline: mean from n-1 subjects to predict leave-out subject. We also looked at random noise which performed worse than this baseline.

	RMSE	ADOS mean	K^{TDA}	$K^{\rm cor}$
ADOS mean	6.4302	_	_	_
K^{TDA}	6.3553	0.316	_	_
$K^{\rm cor}$	6.0371	0.055	0.095	_
$K^{\mathrm{TDA+cor}}$	6.0156	0.048	0.075	0.288

We used permutation tests to get a p-value for the significance of the results.

Acknowledgements This work was supported by NSF grants IIS-1513616 and IIS-1251049.