Low Rank Mixup Augmentations for Contrastive Learning of Phenotypes from Functional Connectivity

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Introduction

- Functional magnetic resonance imaging (fMRI) and fMRI-derived metrics such as functional connectivity (FC) allow for unmatched analysis of human cognition in vivo.
- Contrastive learning (CL) has shown state of the art results in the computer vision domain as well as in integration of images with genomics.

Problem

Many frameworks that utilize CL depend on image augmentations, a technique that is not present in FC.

Solution

We present a robust mixup-style augmentation strategy for FC based on eigendecomposition.

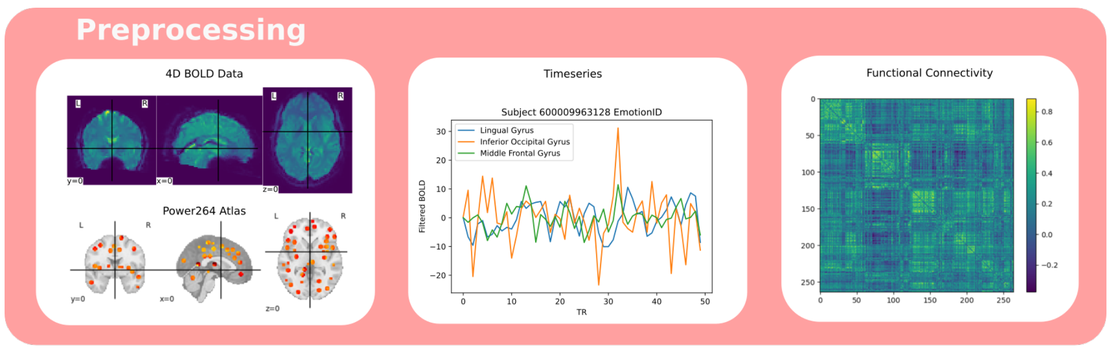
- We find that the rank-1 approximation of FC cannot be used for accurate prediction of phenotypes and thus can be used as non-informative noise in mixup augmentations.
- We test our augmentation strategy on the Philadelphia Neurodevelopmental Cohort (PNC) and Bipolar and Schizophrenia Network for Intermediate Phenotypes (BSNIP) datasets.

We perform an eigendecomposition to get a rank-N approximation of FC. $\mathbf{X}$ = positive semidefinite subject FC matrix

$$\mathbf{X} = \mathbf{V}\mathbf{\Lambda}\mathbf{V}^\mathsf{T}$$

$$\hat{\lambda}_{ii} = \begin{cases} \lambda_{ii}, & i \leq N \\ 0, & \text{otherwise} \end{cases} \tag{1}$$

$$\mathbf{X}^{(N)} = \mathbf{V}\hat{\mathbf{\Lambda}}\mathbf{V}^\mathsf{T}$$



We then mix up the first component based on matching of demographic variables $m_{y,i}(j) = \mathsf{I}[y_i == y_j]$.

$$\mathbf{p}_{y,i} = \text{Softmax}(\mathbf{m}_{y,i}), \quad \mathbf{p}_i = \text{Softmax}(\prod_y^{N_y} \mathbf{p}_{y,i})$$

$$\tilde{\mathbf{X}}_i = \mathbf{X}_i - \mathbf{X}_i^{(1)} + \mathbf{X}_j^{(1)}, \quad j \sim \text{Categorical}(\mathbf{p}_i) \tag{2}$$

Model trained by minimizing the combination of three losses:

$$\mathcal{L}_{NCE} = -\frac{1}{NM}\sum_{n,i}^{N,M} \log \frac{e^{\mathbf{q}_i^\mathsf{T}\mathbf{k}_i^+/\tau}}{e^{\mathbf{q}_i^\mathsf{T}\mathbf{k}_i^+/\tau} + \sum_{j=1}^{K} e^{\mathbf{q}_i^\mathsf{T}\mathbf{k}_{i,j}^-/\tau}}$$

$$\mathcal{L}_{CE} = -\frac{1}{N}\sum_{i}^{N}(y_{i,0}\log(p_{i,0}) + y_{i,1}\log(p_{i,1})) \tag{3}$$

$$\mathcal{L}_{RMSE} = \left(\frac{1}{N}\sum_{i}^{N}(y_i - \hat{y}_i)^2\right)^{1/2}$$

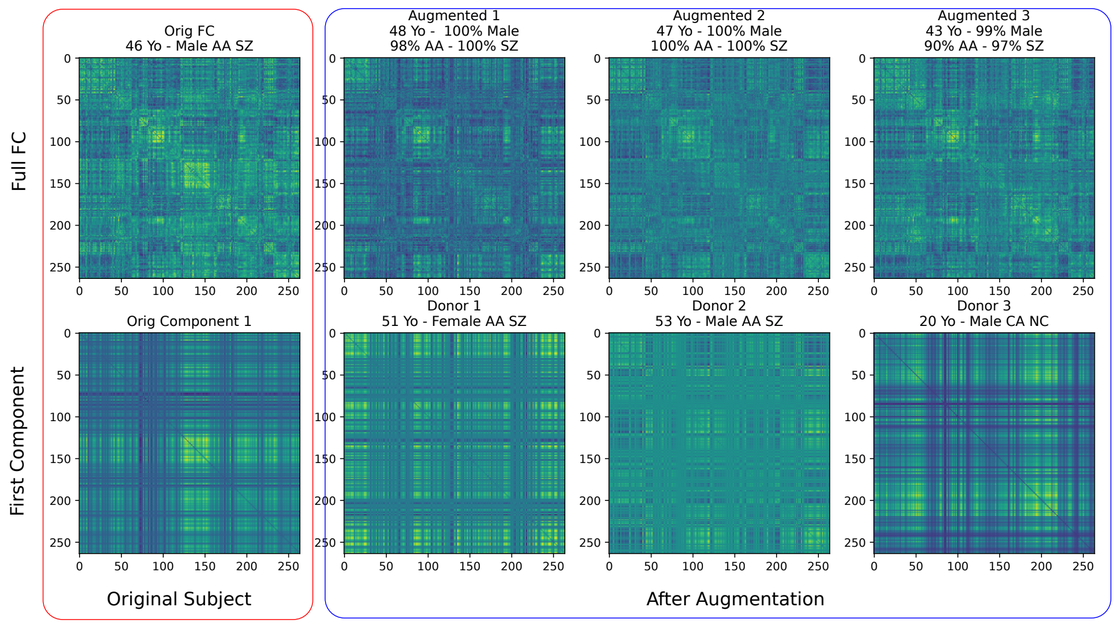
Combined with contrastive learning, our augmentation strategy outperforms basic MLP and GCN models.

Table: Phenotype prediction using CL with low rank augmentations compared to MLP and GCN.

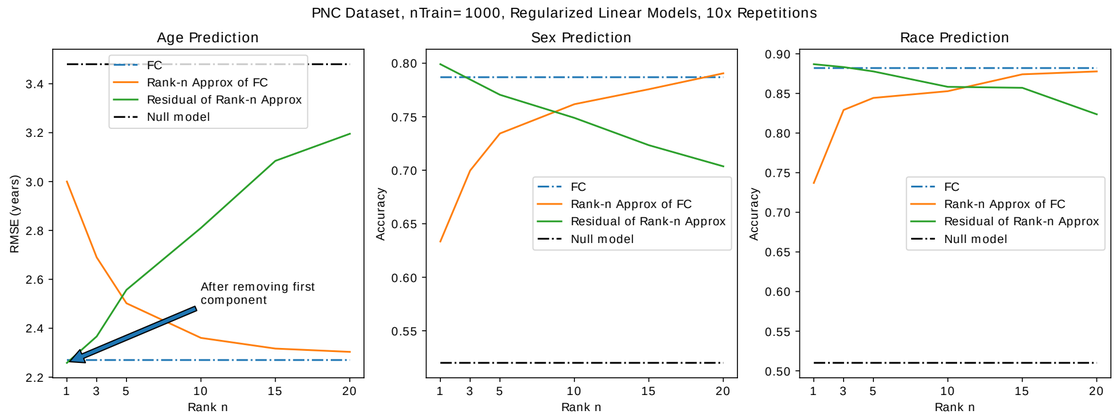
Dataset	Phenotype	Metric	MLP	GCN	CL-LRAug	p-value
BSNIP	Age	RMSE (yr)	11.82 ± 0.62	11.07 ± 0.67	$\mathbf{10.25 \pm 0.64}$	< 0.001
BSNIP	Sex	Accuracy	68.1 ± 4.6	66.4 ± 6.1	$\mathbf{71.7 \pm 5.1}$	0.003
BSNIP	Race	Accuracy	76.0 ± 3.8	72.4 ± 6.1	$\mathbf{77.7 \pm 4.4}$	0.026
BSNIP	SZ	Accuracy	75.2 ± 3.6	71.2 ± 6.7	$\mathbf{76.9 \pm 4.4}$	0.017
PNC	Age	RMSE (yr)	2.62 ± 0.14	2.44 ± 0.12	$\mathbf{2.18 \pm 0.07}$	< 0.001
PNC	Sex	Accuracy	77.9 ± 2.0	73.7 ± 9.8	$\mathbf{79.7 \pm 2.2}$	< 0.001
PNC	Race	Accuracy	87.7 ± 1.6	86.6 ± 3.8	$\mathbf{89.8 \pm 1.9}$	< 0.001

This works because phenotype prediction is largely invariant to first component of FC. AA=African Ancestry, CA=Caucasian Ancestry, SZ=Schizophrenia, NC=Normal Control

Predictions are Largely Invariant to First Component of FC



We find that residual of FC minus first component contains as much information as full FC and is easier for predictive models to use.



Conclusion

- We find that CL using low-rank augmentations outperforms MLP and GCN models by 2-10% across all predictive tasks.
- Removing the first component either increases or has no impact on predictive accuracy among all phenotypes in the PNC and BSNIP datasets.