

Transcriptomic underpinnings of individual variation in brain co-activity

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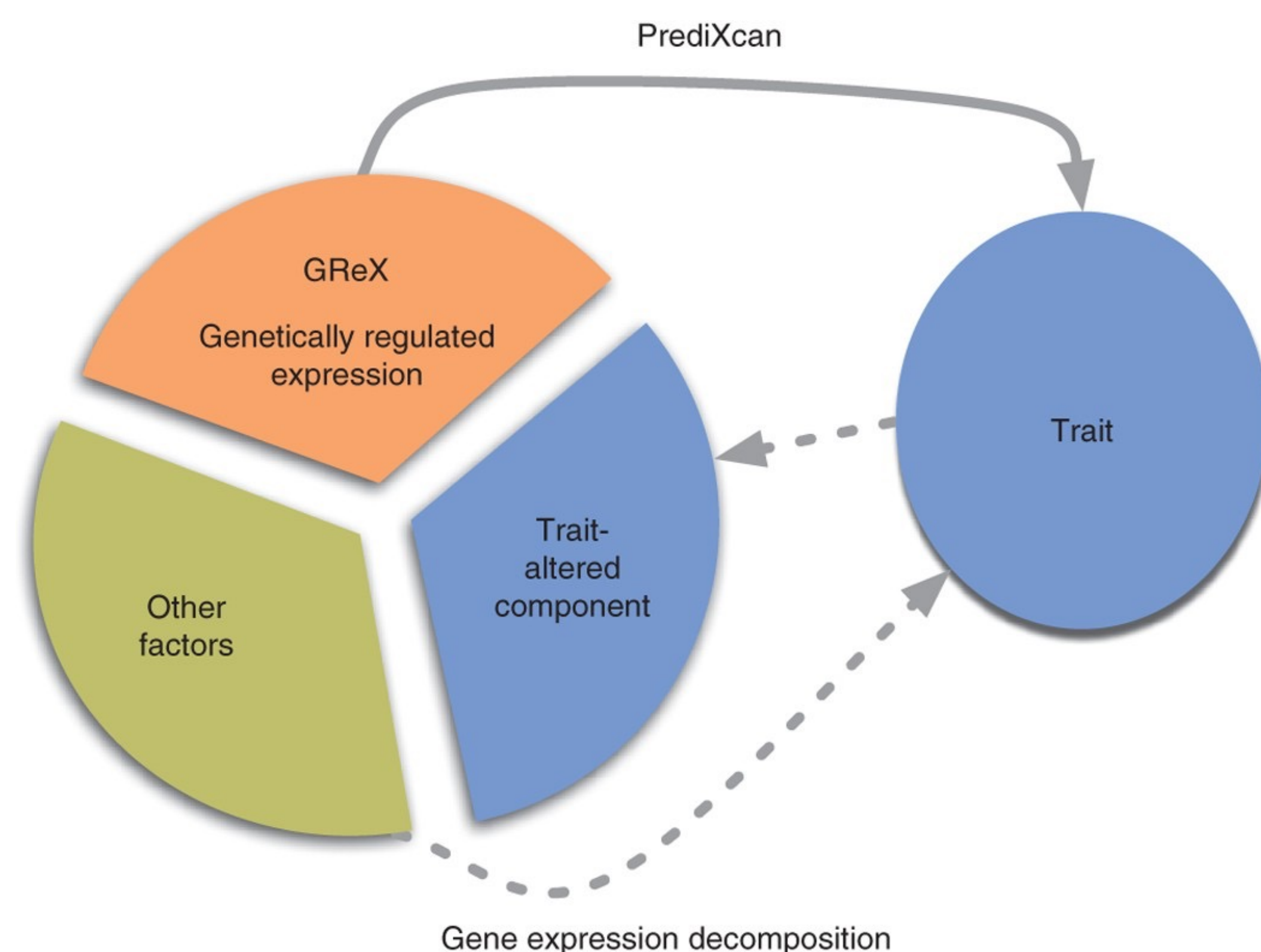
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Motivation

- Individual brain network organization is likely to be under strong genetic control.
- A lack of integrated neuroimaging and gene expression data has limited our ability to study the transcriptomic basis of this individuality.

Approach

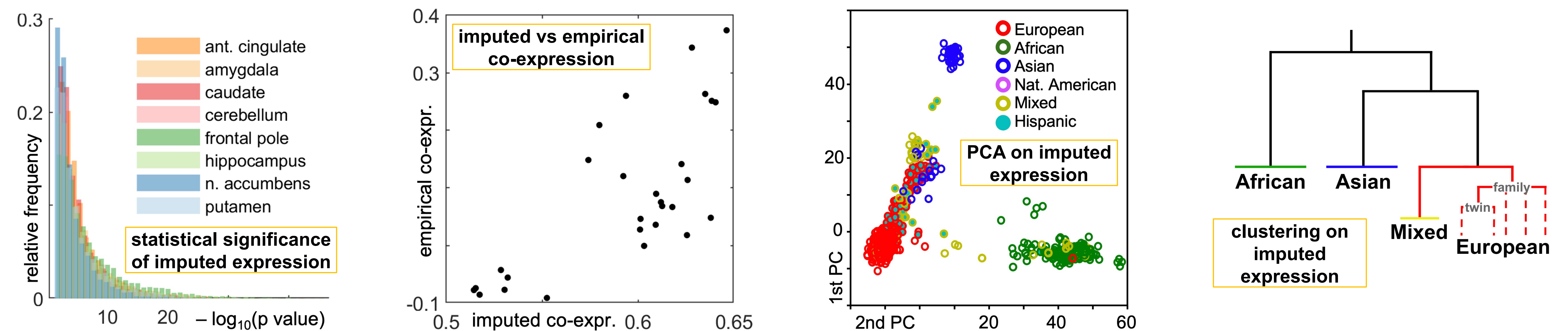
- We integrated multiple neuroimaging and genomic datasets to impute gene expression profiles of eight brain regions in healthy adults from the Human Connectome Project.
- We used PrediXcan, a statistical modeling framework, to impute heritable aspects of gene expression from genomic variation alone.



Results and Conclusions

1

Imputed gene expression captures the structure of empirical gene expression



2

Brain-network phenotypes are strongly heritable and correlate with imputed expression of several genes across several brain regions

