# Transcriptomic underpinnings of individual variation in brain co-activity

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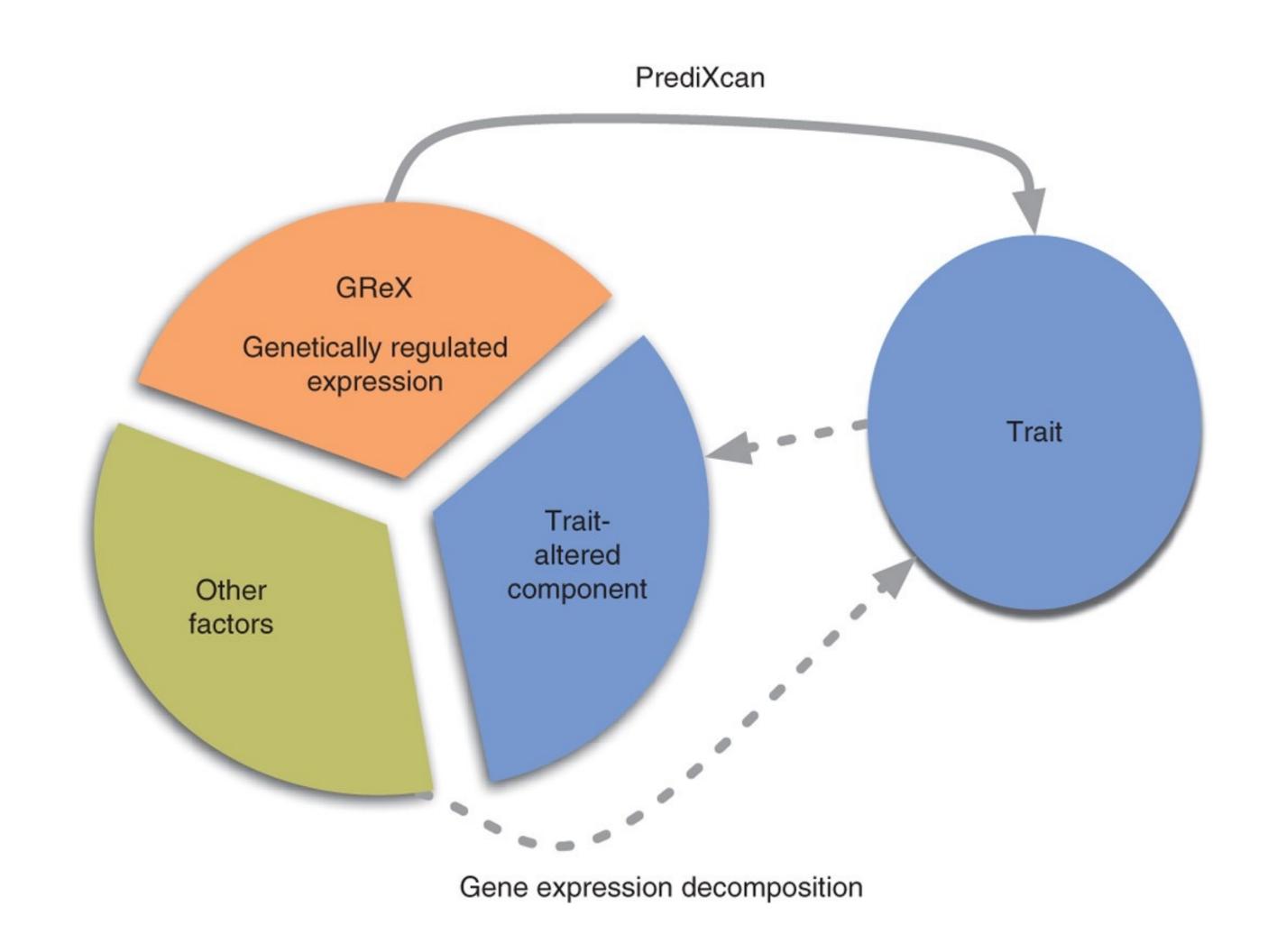
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## Motivation

- 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.

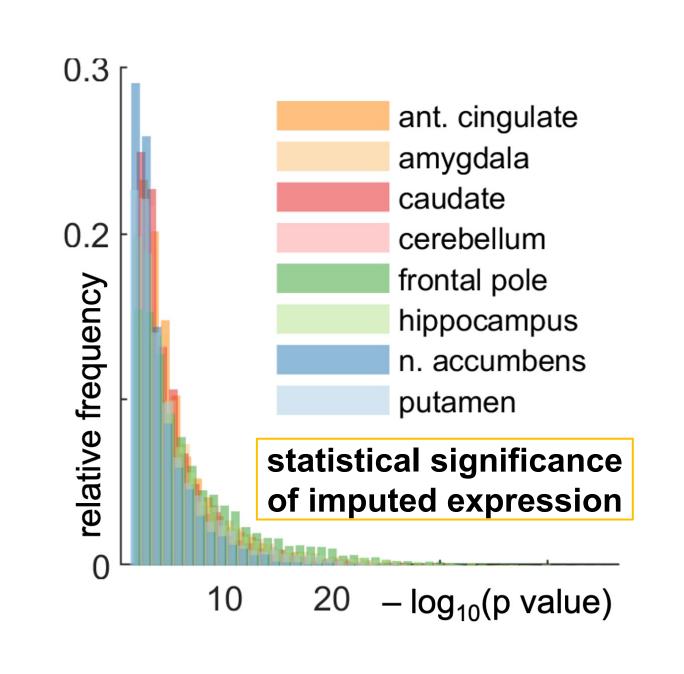
# Approach

- 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.

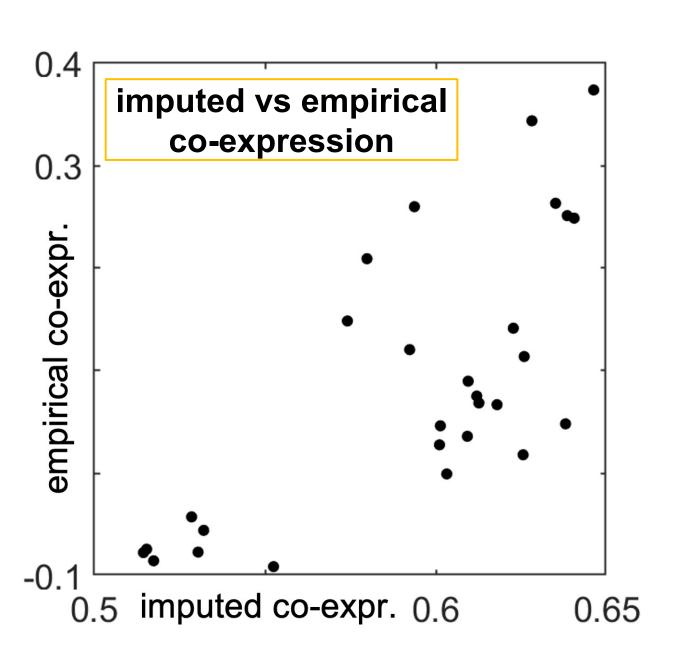


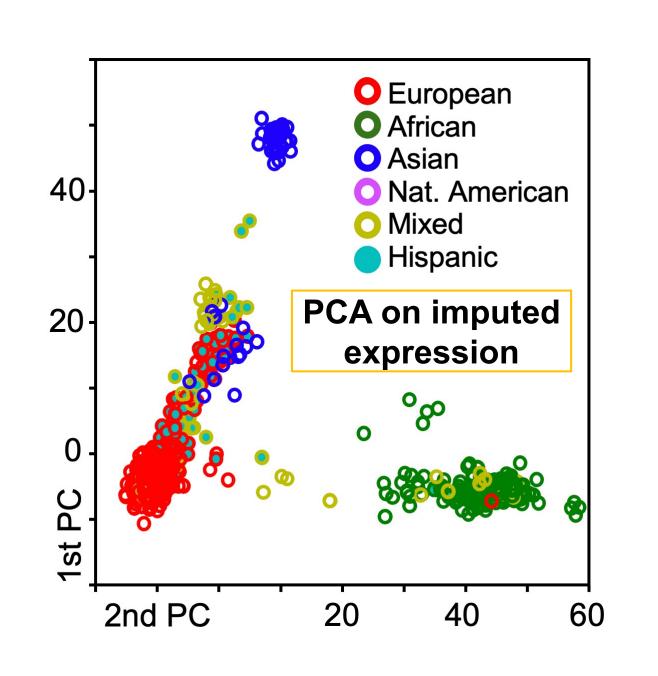
## Results and Conclusions

Imputed gene expression captures the structure of empirical gene expression

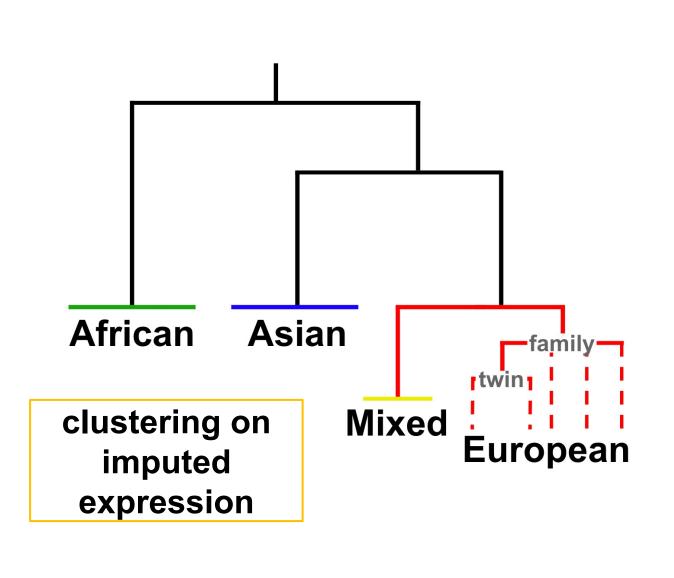


gene (ARHGAP33)





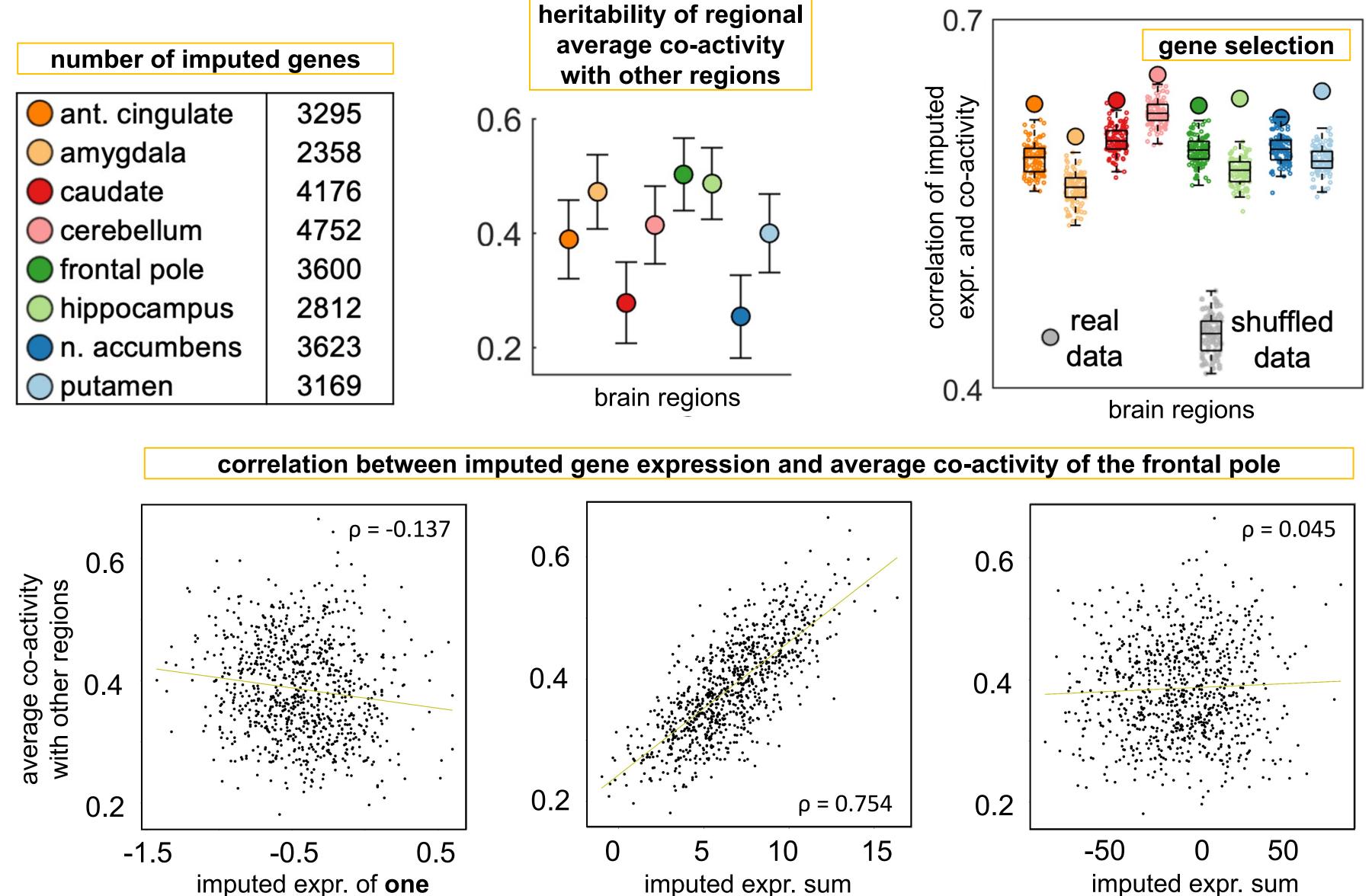
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Brain-network phenotypes are strongly heritable and correlate with imputed expression of several genes across several brain regions

of all genes



of selected genes

#### overlaps in genes selection for brain-network phenotypes ant. cingulate cerebellum amygdala caudate 70 17 64 94 14 86 111 10 113 90 21 80 7 0 5 86 116 frontal pole n. accumbens 91 17 89 101 8 101 68 23 59 115 6 111

#### Acknowledgements

average co-activity co-activity variance fractional amplitude of low-frequency fluctuations

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#### References

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