A universal method of controlling for confounds in multivoxel pattern analyses

Steven Miletić, Lukas Snoek, & H. Steven Scholte University of Amsterdam

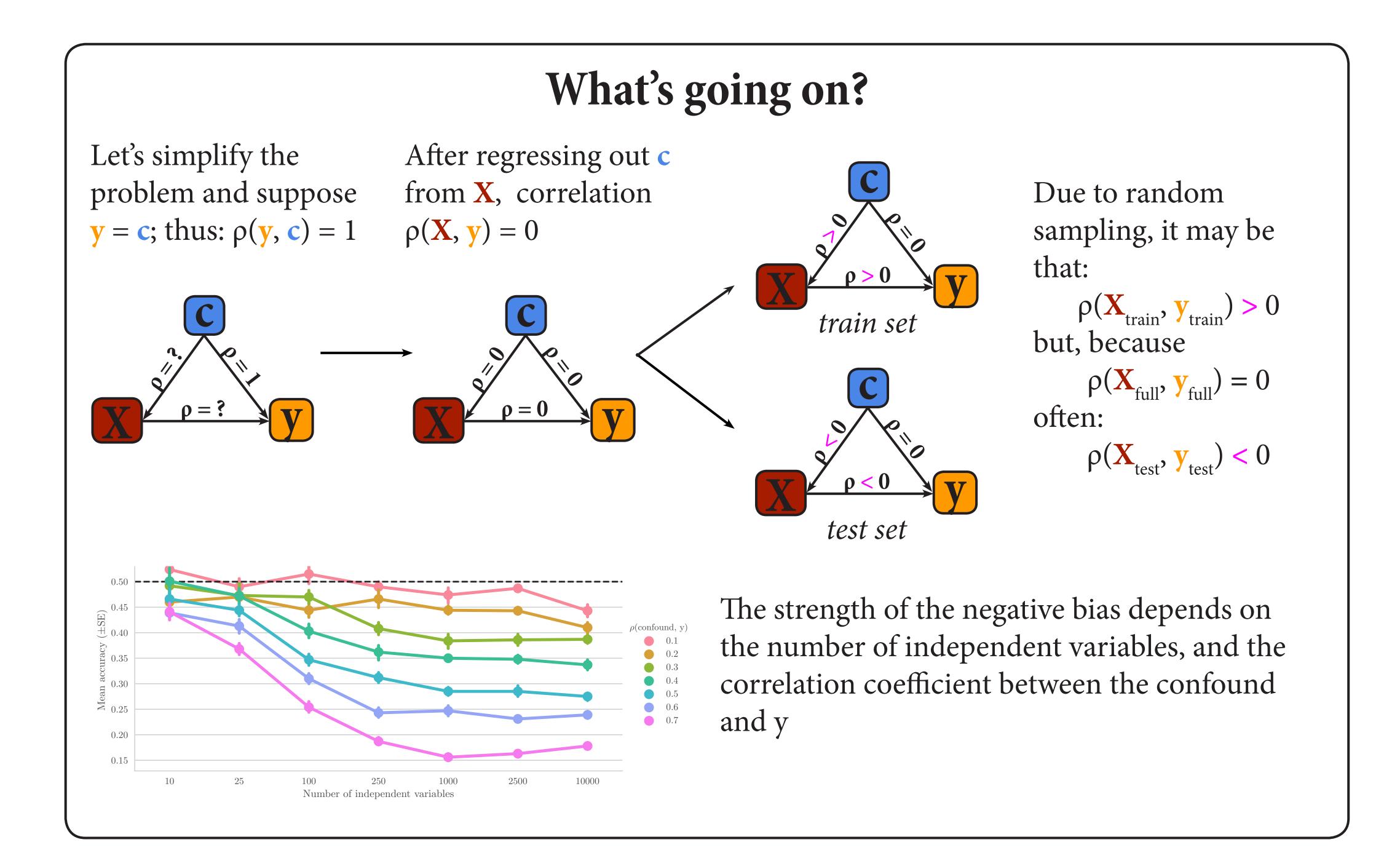
Gender

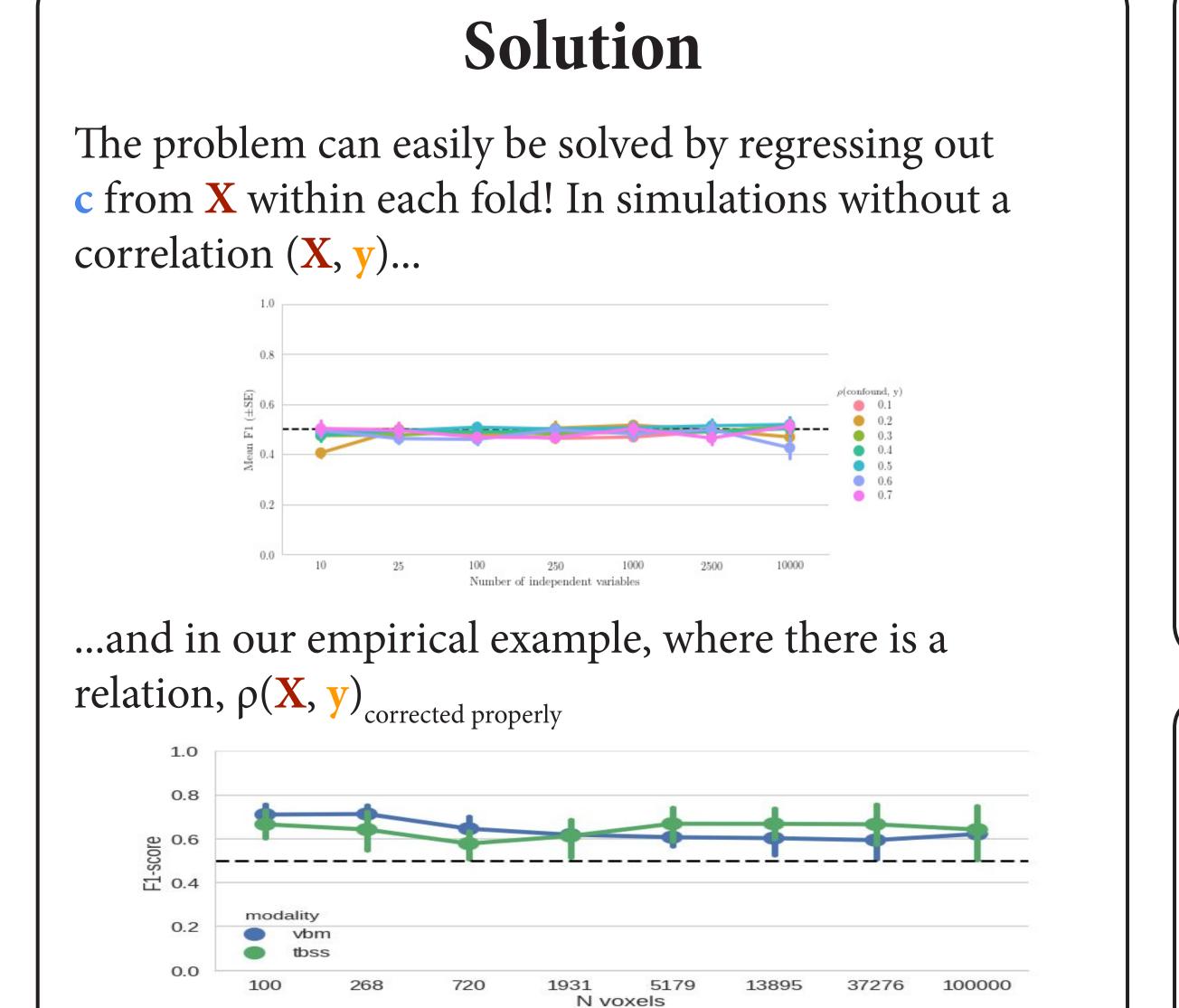
Introduction Brain size • MVPA has shown to be **more sensitive** than mass-univariate analysis, but arguably MVPA is also more sensitive to **confounds**¹ • Often, researchers deal with confounds (c) by regressing it out from the neural patterns $(X)^{2,3}$ $\rho(X, y)$ We show, however, that this introduces bias in cross-validated MVPA pipelines⁴, leading to

VBM/TBSS

below-chance accuracy³

What's the problem? Following the example to predict gender (y) from VBM and TBSS-data (X) in the face of the "confound" brain size (c)... So, $\rho(X, y)_{\text{uncorrected}}$ is biased... We know that brain size truly confounds $\rho(c, y)...^2$ 0.35 ...and is related to our data... Yet, $\rho(\mathbf{X}, \mathbf{y})_{\text{corrected}} < \text{chance } (50\%)$ 0.500.45 $\frac{1}{2}$ 0.40 $\frac{1}{2}$ 0.35 -Number of independent variables





Conclusion

- Confound regression introduces bias in cross-validated MVPA pipelines, especially when many voxels are used
- Like counterbalancing confounds⁴, confound regression should be done foldwise

References

- 1 Naselaris & Kay, TICS, 2015
- 2 Todd et al., NeuroImage, 2013
- 3 Woolgar et al., NeuroImage, 2014
- 4 Hebart & Baker, Arxiv, 2017
- 5 github.com/lukassnoek/MVCA
- 6 github.com/lukassnoek/skbold