

## A universal method of controlling for confounds in MVPA

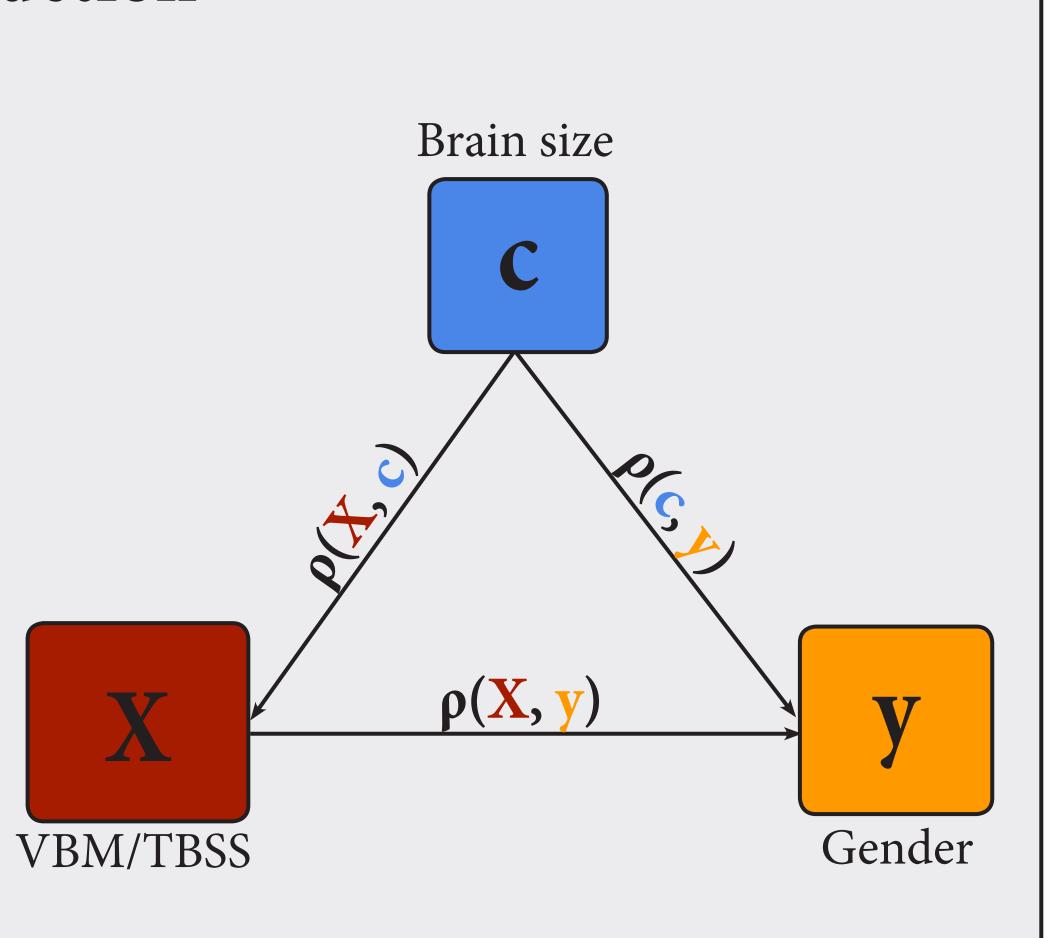
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### Introduction

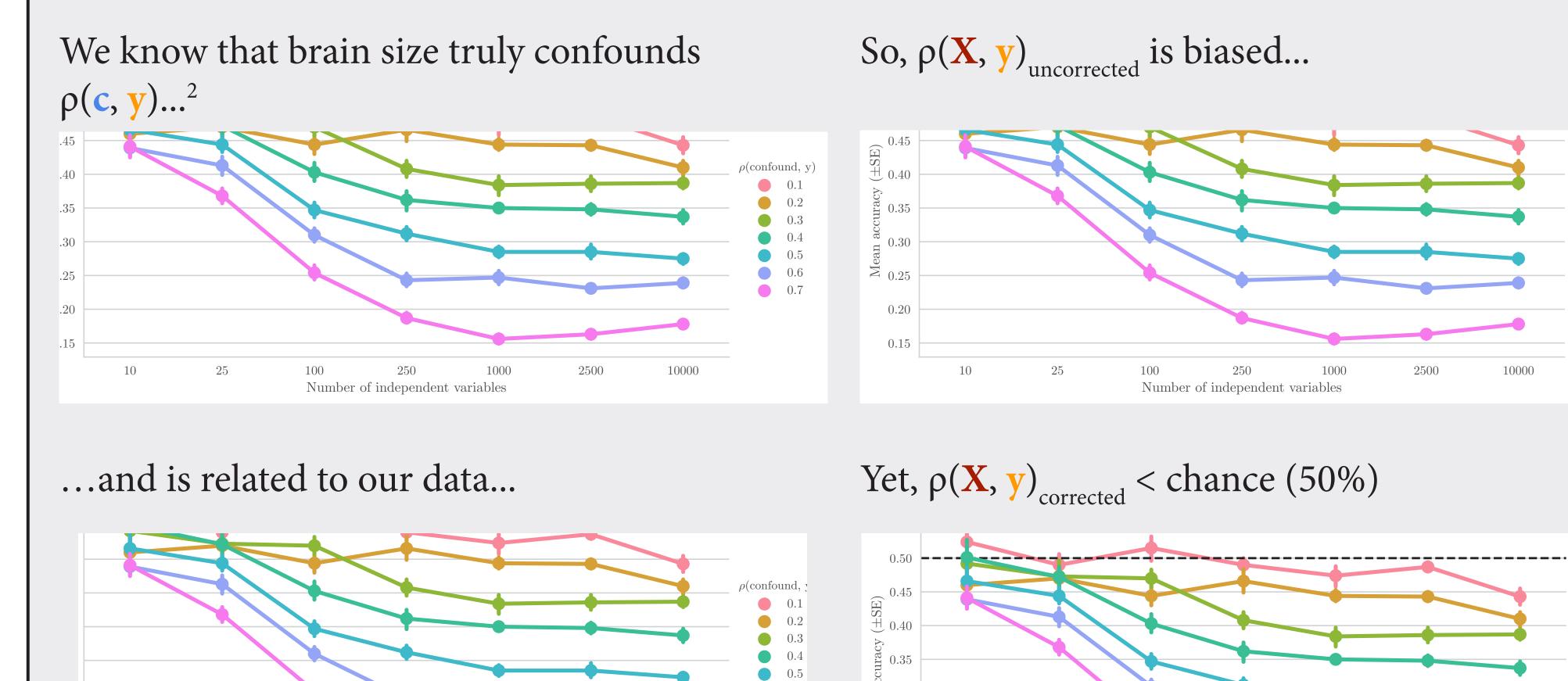
- Contrary to mass-univariate analyses, where confounds are widely controlled for, it is unclear how to handle confounds in MVPA
- This poses a serious threat to the generalizability of MVPA results in both clinical and fundamental research - especially because MVPA is arguably more sensitive to confounds<sup>1</sup>
- Here, we show how a previously proposed<sup>2,3</sup> method of dealing with confounds ("confound regression") leads to bias<sup>4</sup>, and causes belowchance accuracy<sup>3</sup>
- We introduce a universal and unbiased method of dealing with confounds in MVPA

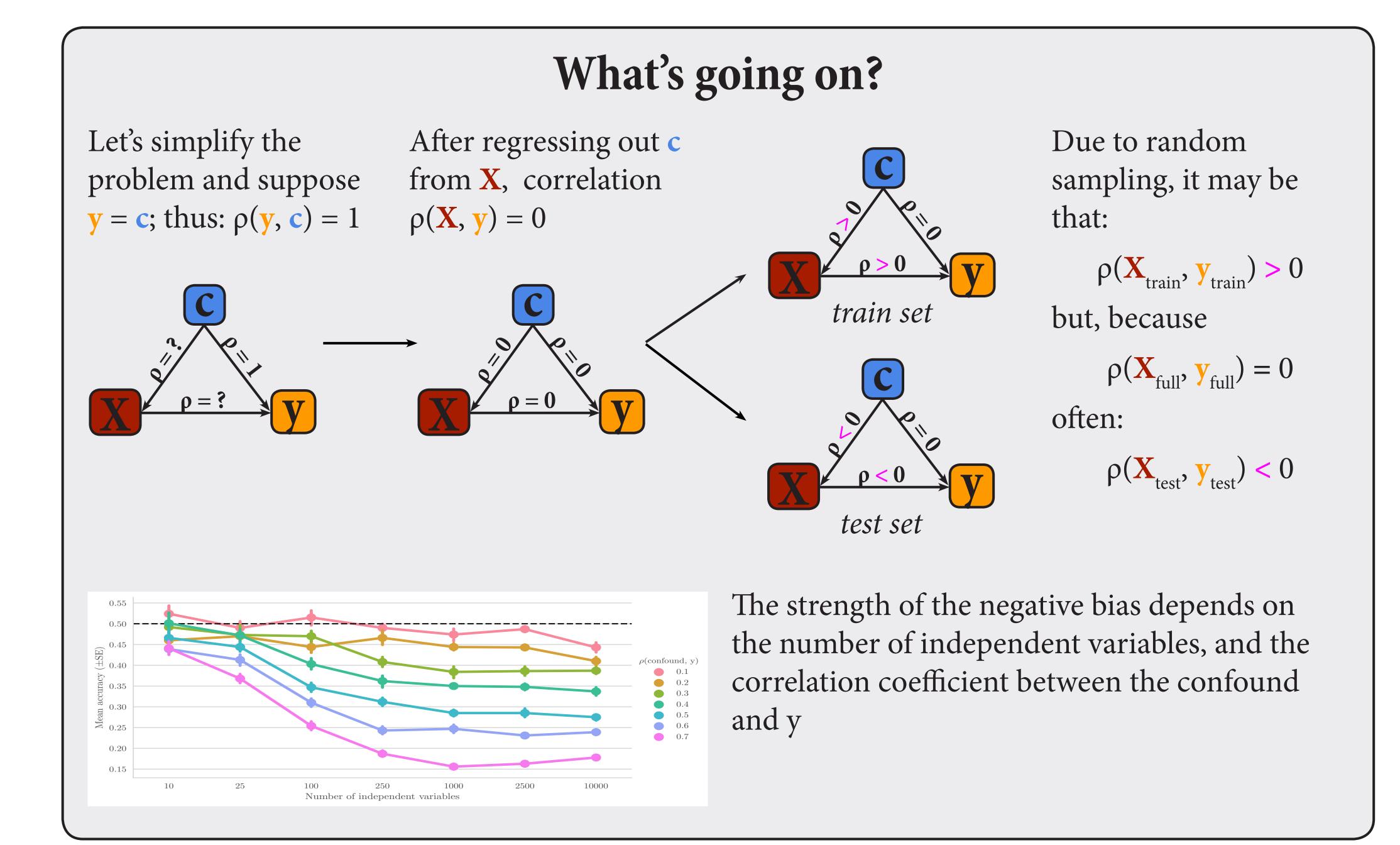
Number of independent variables



# What's the problem?

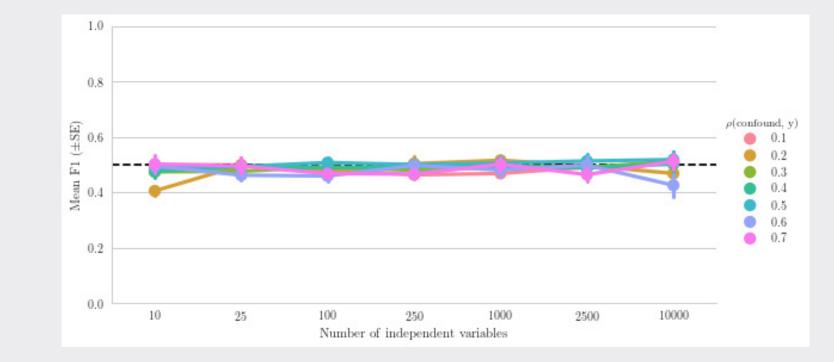
Following the example to predict gender (y) from VBM and TBSS-data (X) in the face of the "confound" brain size (c)...



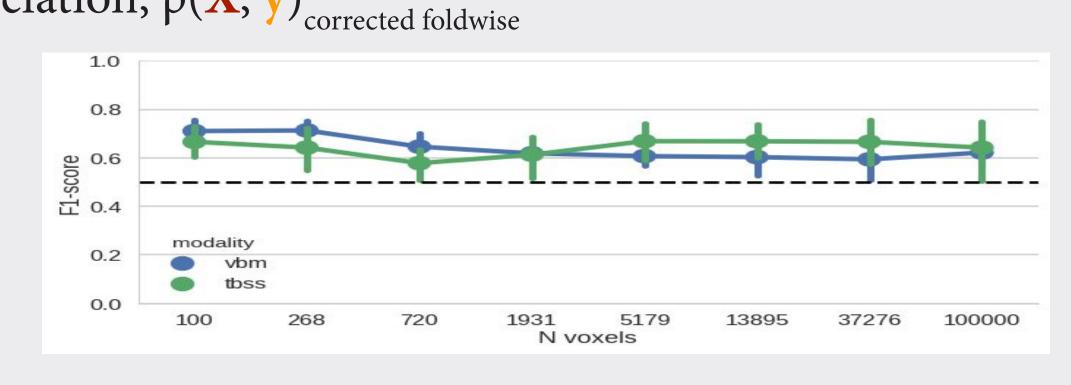


### Solution

The problem can easily be solved by regressing out c from X within each fold! In simulations without a correlation  $\rho(X, y)$ ...



...and in our empirical example, where there is a relation,  $\rho(X, y)$  corrected foldwise



### Conclusion

- Confound regression introduces bias in cross-validated MVPA pipelines, especially when many voxels are used
- Regressing out confounds foldwise is a universal and simple method, enhancing the generalizability of MVPA results

#### 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