

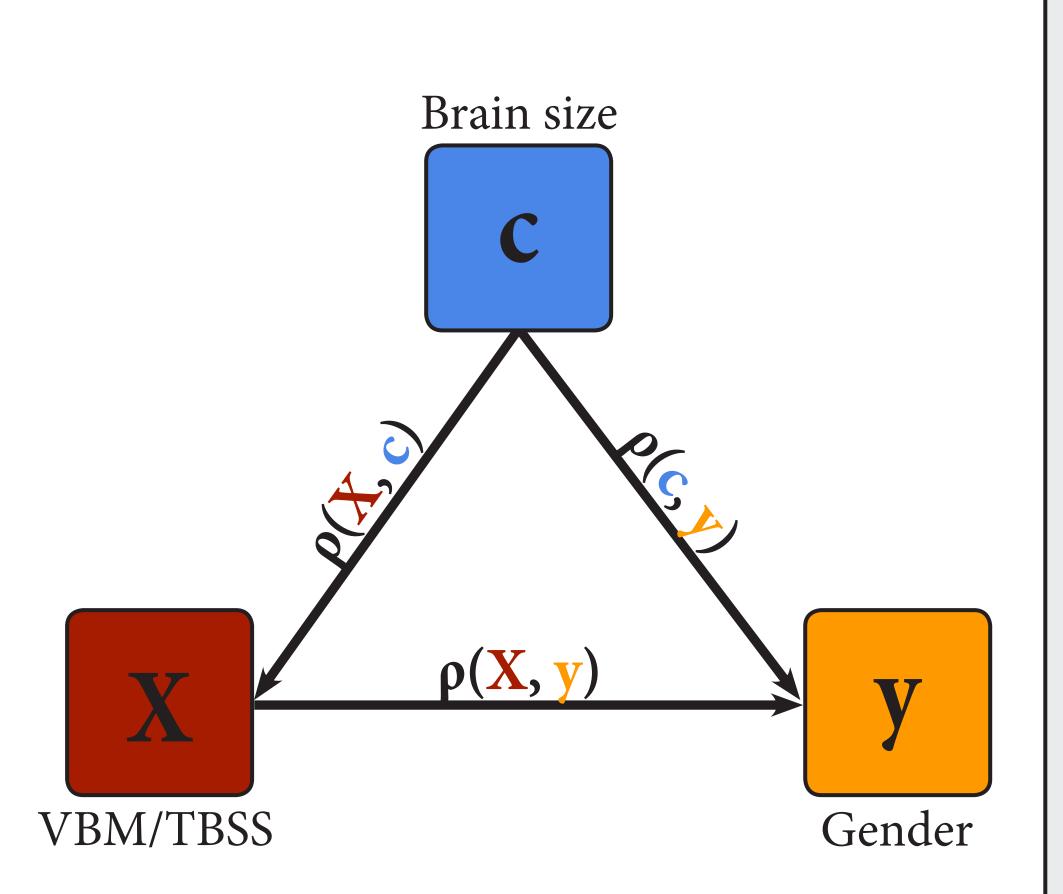
# A universal method of controlling for confounds in MVPA

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



## Introduction

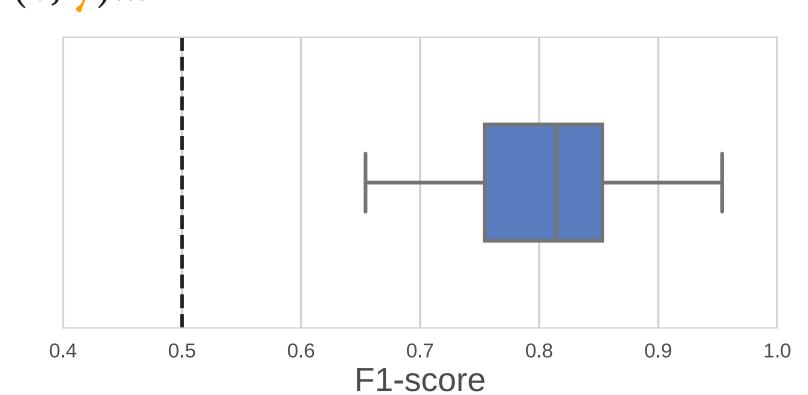
- Contrary to mass-univariate analyses, where confounds are often controlled for, it is unclear how to handle confounds in MVPA<sup>1,2</sup>
- This poses a serious threat to the **generalizability of MVPA results** in both clinical and fundamental research especially because MVPA is arguably **more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



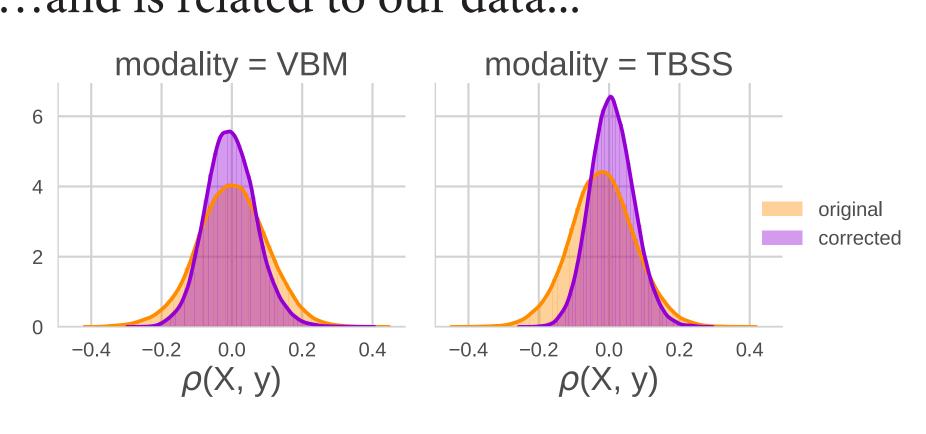
## What's the problem?

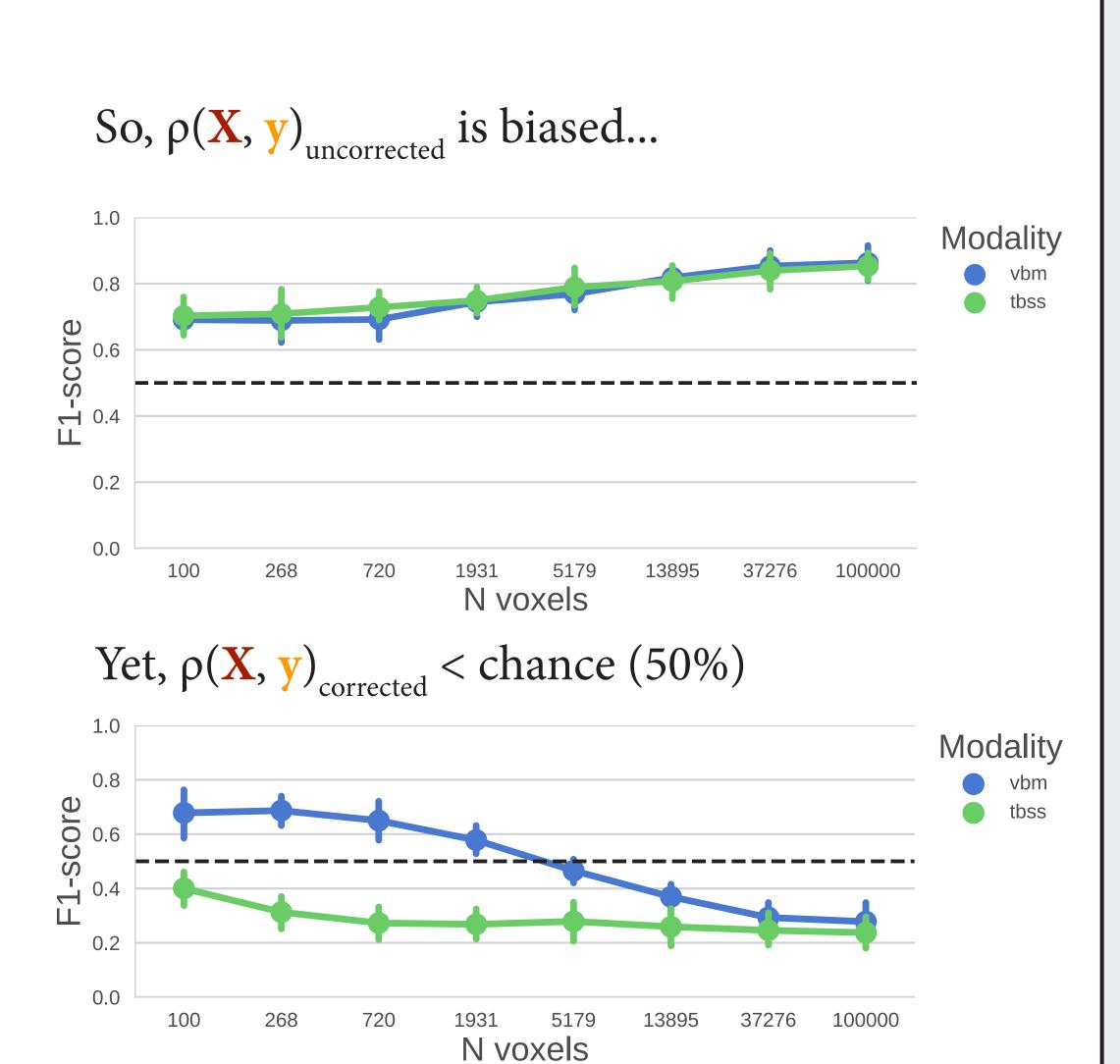
Following the example to predict gender (y) from VBM and TBSS-data (X) in the face of the "confound" brain size (c)...

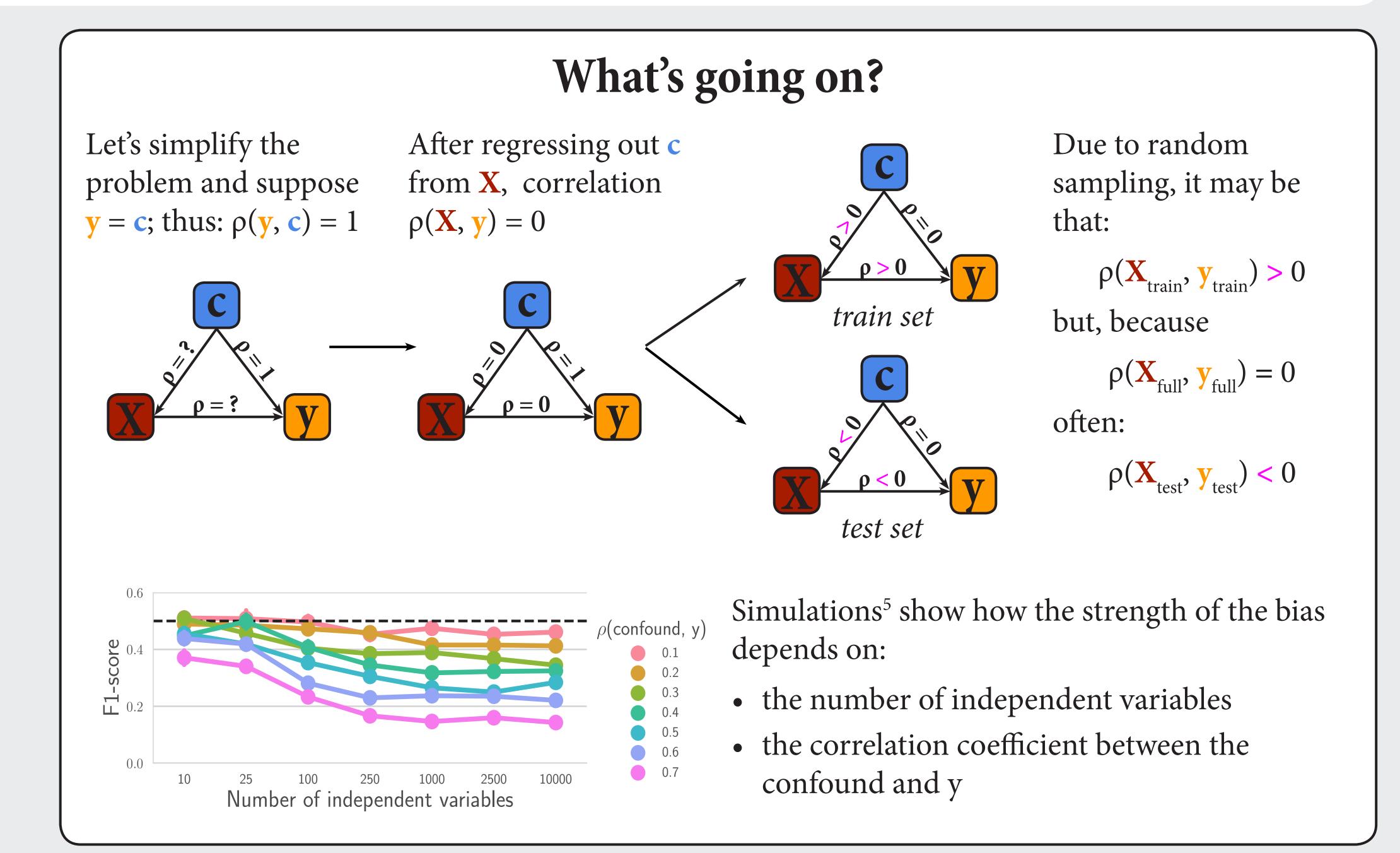
We know that brain size truly confounds  $\rho(c, y)...^2$ 



...and is related to our data...

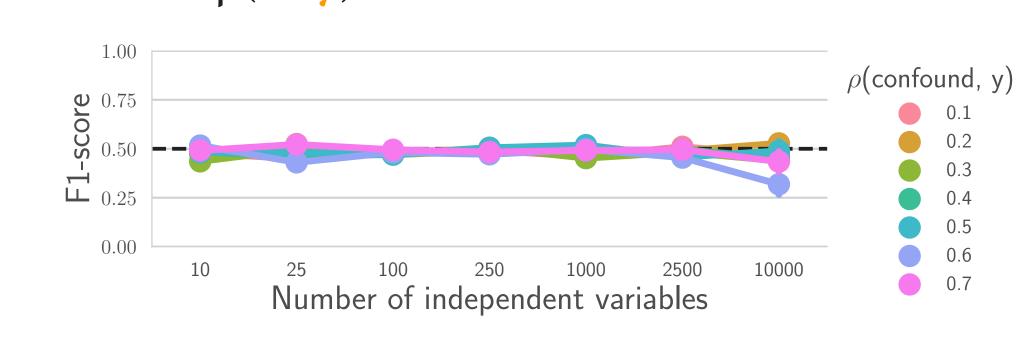




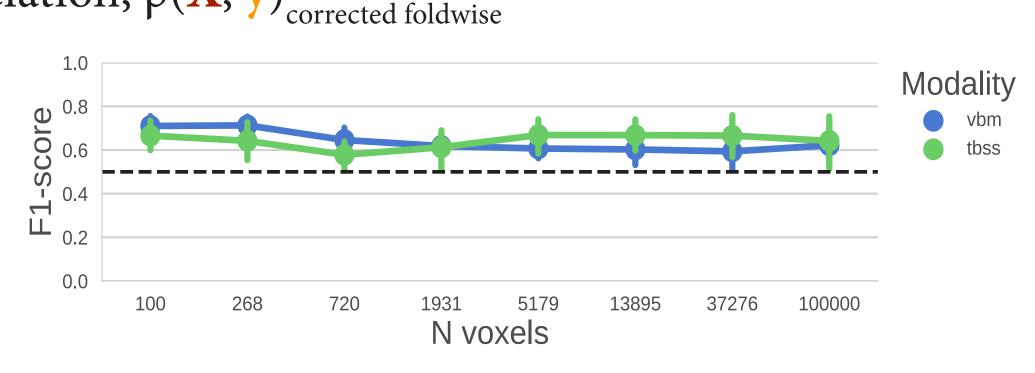


## Solution

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,  $\rho(\mathbf{X}, \mathbf{y})_{\text{corrected foldwise}}$ 



## Conclusion

- Confound regression introduces bias in cross-validated MVPA pipelines<sup>4</sup>, especially when many voxels are used
- Regressing out confounds foldwise is a universal and easy method, improving the generalizability of MVPA results

#### References

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