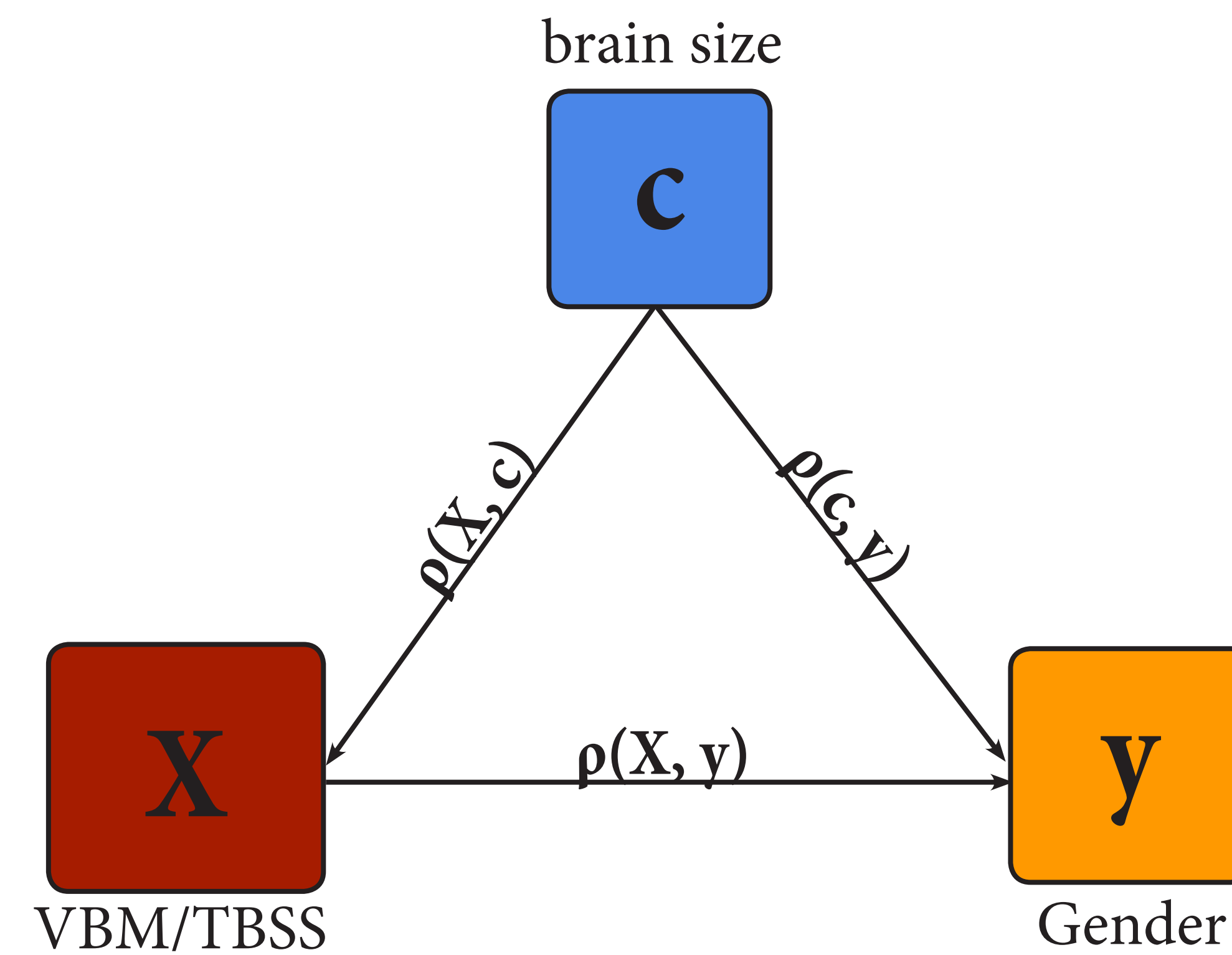


# Controlling for confounds in multivoxel pattern analyses

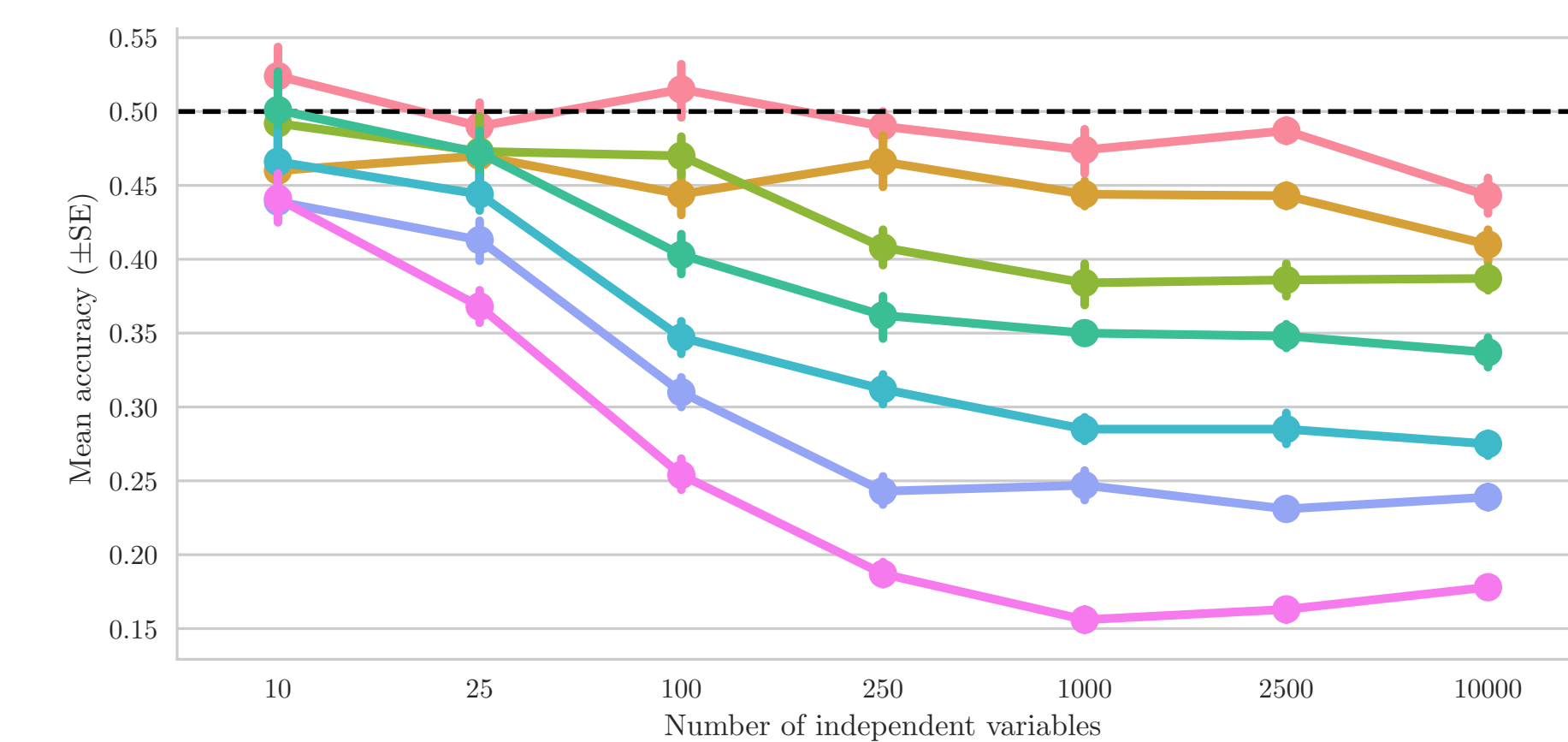
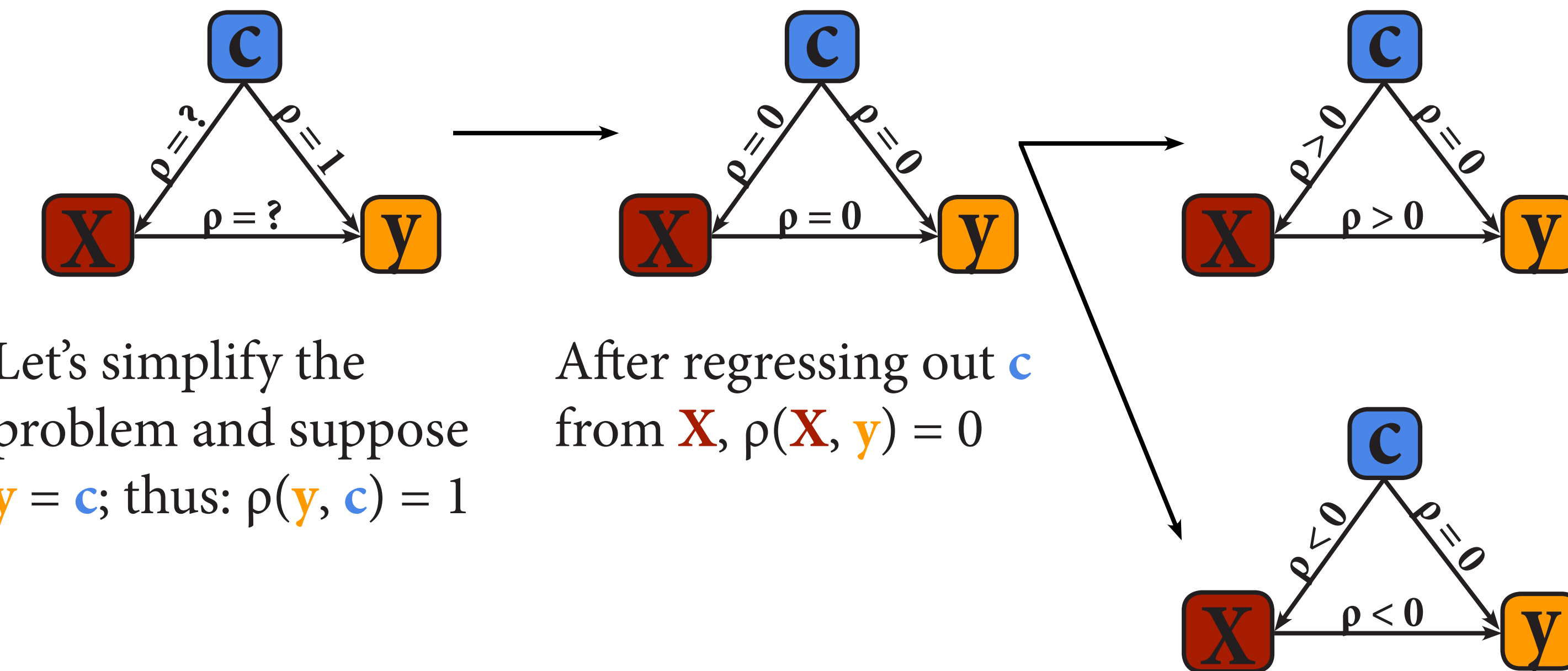
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## Introduction

- MVPA has shown to be more sensitive than mass-univariate analysis, but arguably MVPA is also more sensitive to confounds<sup>1</sup>
- Often, researchers deal with confounds ( $c$ ) by regressing it out from the neural patterns ( $X$ )<sup>2,3</sup>
- We show, however, that this introduces bias in cross-validated MVPA pipelines<sup>4</sup>, leading to below-chance accuracy<sup>3</sup>



## What's going on?

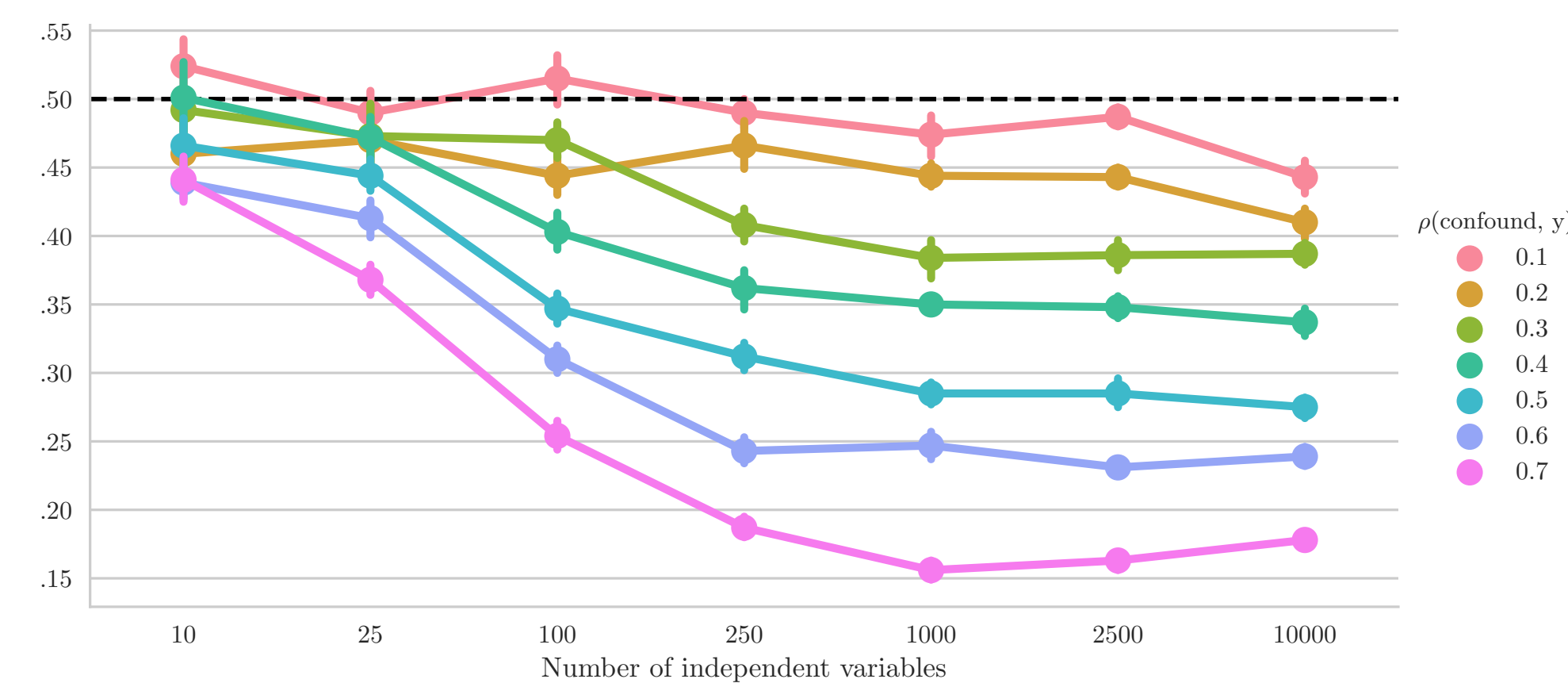


The strength of the negative bias depends on the number of independent variables, and the correlation coefficient between the confound and  $y$

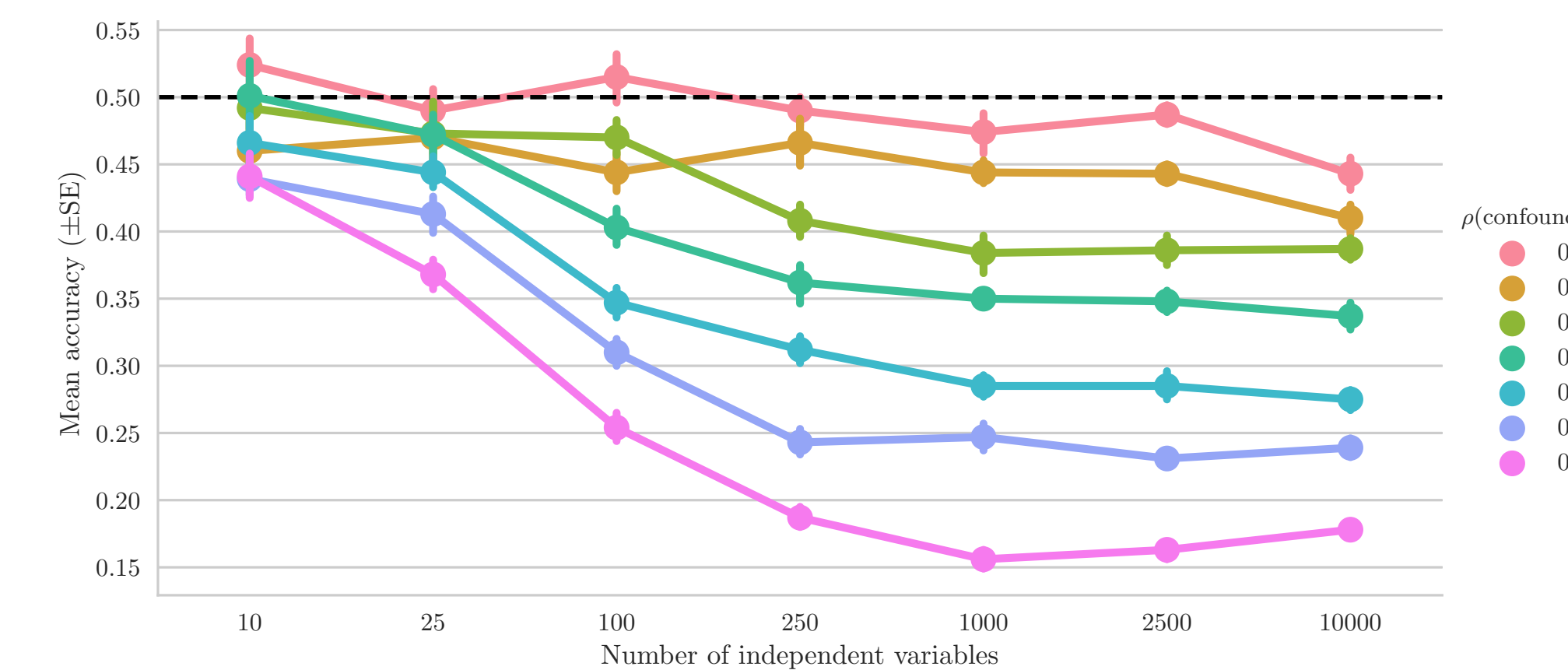
## What's the problem?

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

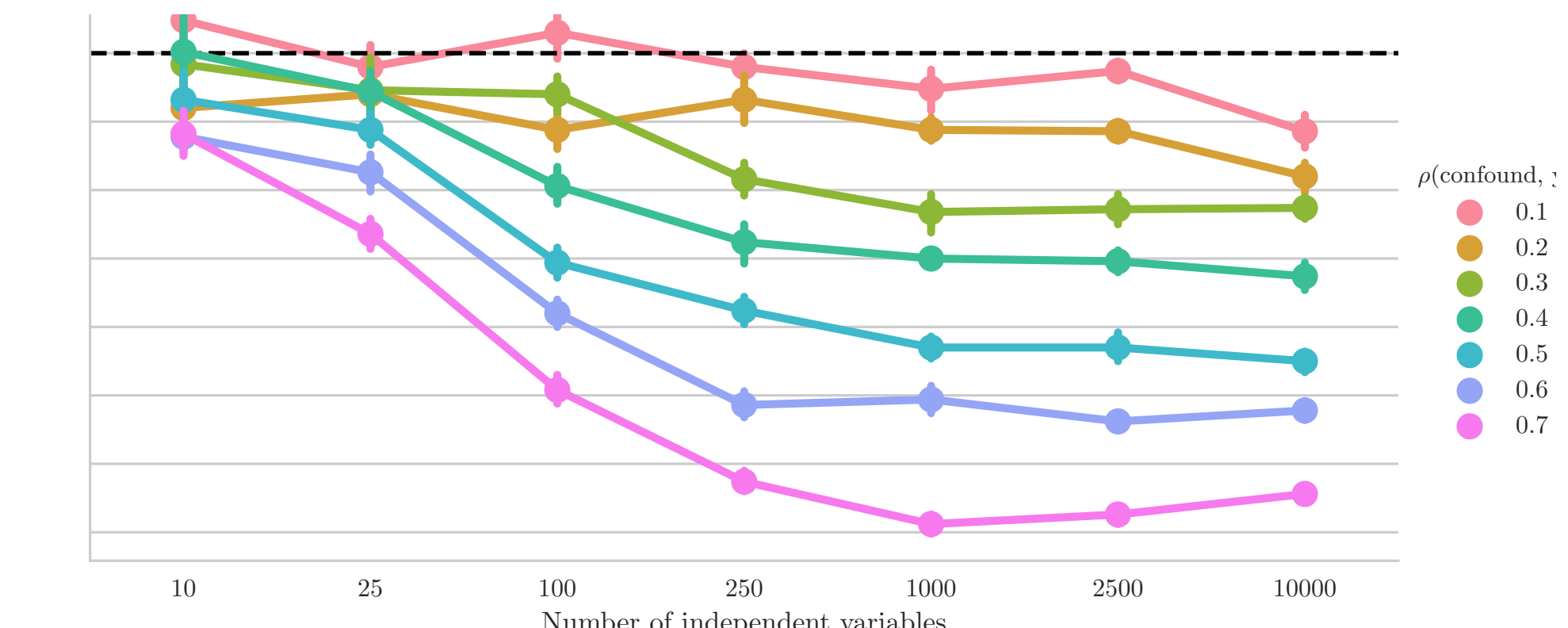
We know that brain size truly confounds  $\rho(c, y)$ ...<sup>2</sup>



So,  $\rho(X, y)$  uncorrected is biased...



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



Yet,  $\rho(X, y)$  corrected < chance (50%)

