



European **Association** of Methodology







A comparison of algorithms for tests of variance in genetic ACE models Olivier Vivier¹ & Pier-Olivier Caron²

Intro

Genetic and environmental similarities can be decomposed into: A: Additive genetic C: Common environment E: Unique

Three algorithms exist to identify the final ACE model using likelihood ratio tests

1-Saturated:

environment

Comparison of a saturated model to components of the ACE (i.e., ACE, AE, CE and E models)

2-Components:

Nested comparison of the ACE components

3-Estimates: Testing the significance of the component's estimate

Objective

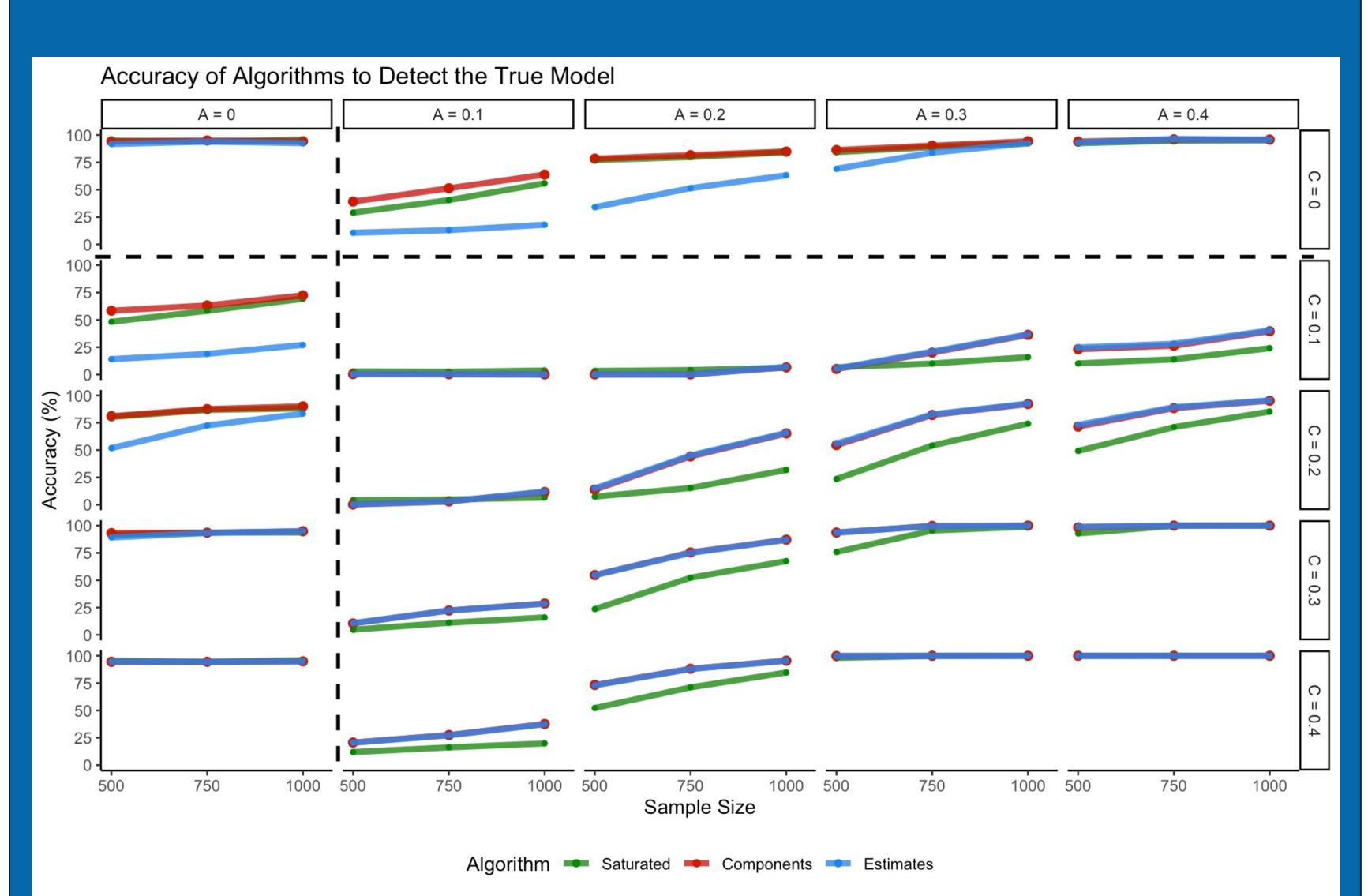
Examine the accuracy and bias of the algorithms

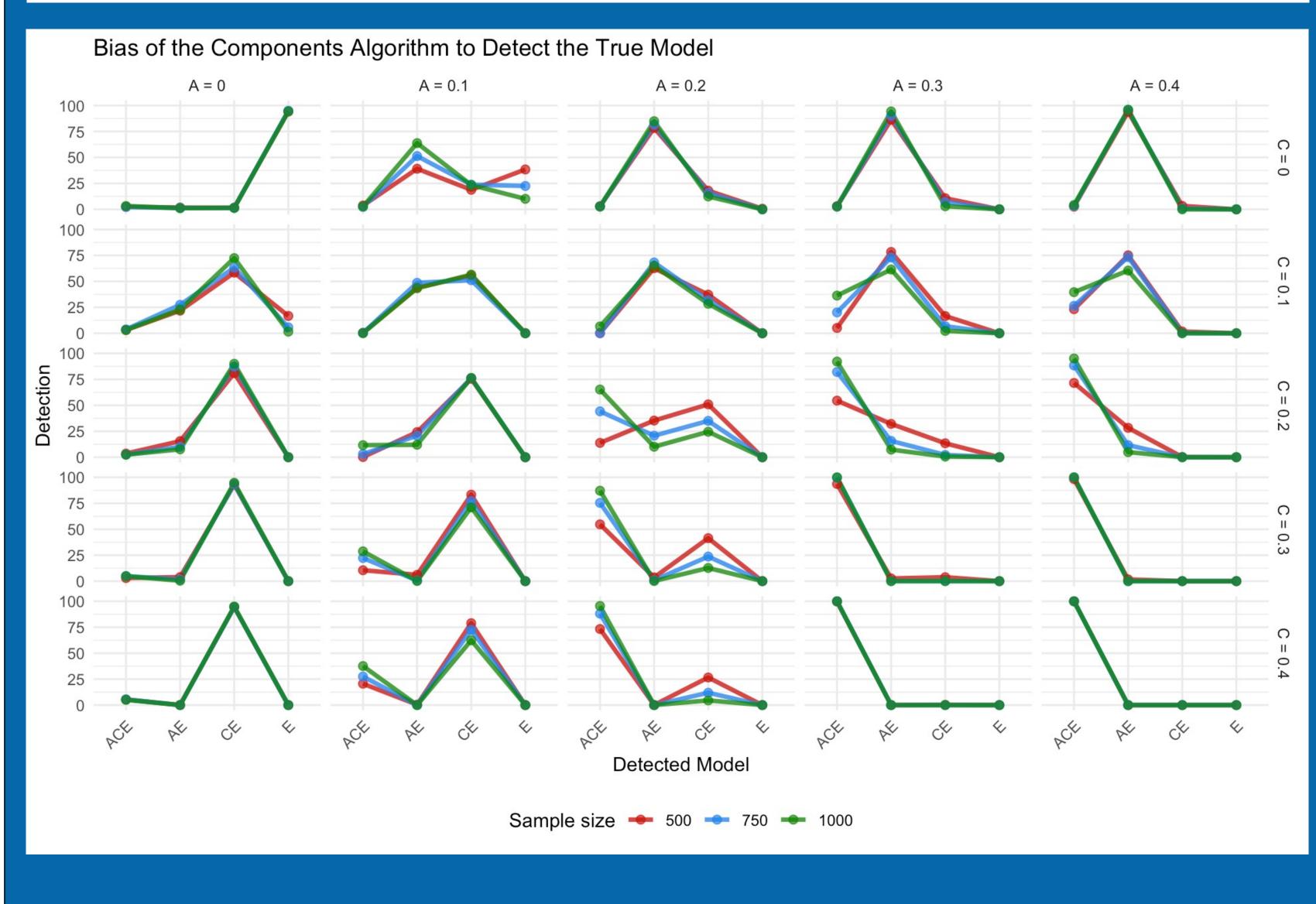


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Testing ACE model vs nested comparisons performs better than other algorithms.





Method **Monte Carlo** simulations

Manipulating the A and C parameters: 0, .1, .2, .3 and .4.

Three sample sizes for twin pairs: 1000, 1500, 2000

Discussion

These results shed light on the **need** for improvement.

- Saturated:

struggles to identify ACE models.

- Components:

struggles to identify ACE models when parameters are low.

- Estimates:

struggles to identify AE and CE models when parameters are low.

The Components algorithm had the best accuracy over the different cases.

Very large sample sizes are required to reach sufficient accuracy.



















