

A comparison of algorithms for tests of variance in genetic ACE models

Olivier Vivier¹ & Pier-Olivier Caron²

¹Université du Québec à Montréal

²Université TÉLUQ



Intro

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

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

1-**Saturated** :
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

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**.

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

