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Poster

A comparison of algorithms for tests of variance components in genetics ACE models

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Abstract

Using structural equation modeling, the genetic and environmental similarities (and dissimilarities) between monozygotic and dizygotic twins can be decomposed into three components: additive genetics (A), common environment (C) and unique environment (E). After identifying the ACE model, model fitting is examined to evaluate the improvement of the model after dropping one or more of the components to assess whether they should be retained (Maes, 2014). Three approaches, hereafter referred to as Saturated, Components and Estimates are used : a) comparison of a saturated model to components of the ACE model (i.e., ACE, AE, CE and E models); b) nested comparison of the ACE model's components, and; c) assessing the component based on its parameters estimates in the ACE model. To our knowledge, these three approaches found in the scientific literature were never compared, yet, they may vary in their accuracy and may lead to different conclusions regarding the optimal model. This Monte Carlo simulation study aimed to examine the accuracy of these different algorithms when varying specifications of the ACE model's components and sample sizes. Overall, the results show that the Components algorithm is the best to recover the correct models. However, they also show that the different algorithms struggle to identify ACE models even when parameters are moderate (A = .30, C = .30) and sample sizes are large (ns <= 500) . The Components algorithm approach outperforms the other algorithms when A or C is at zero whereas the Estimates and Components algorithms perform similarly when both A and C are non-zero. The saturated algorithm had the poorest performance overall being only better than Estimates in the A=0 or C=0 conditions, but still much worse than Components. However, in all cases, very large sample sizes are required to reach sufficient accuracy. The current results shed light on the absence of consensus and lack of directives on tests of variance components in ACE models.

Keywords

ACE models, genetics, simulation

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