



Correction to: The Augmented Classical Twin Design: Incorporating Genome-Wide Identity by Descent Sharing Into Twin Studies in Order to Model Violations of the Equal Environments Assumption

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Published online: 27 May 2021
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Correction to: Behavior Genetics (2021) 51:223–236
<https://doi.org/10.1007/s10519-021-10044-0>

In the original version of this article, Fig. 2 was inadvertently published with a typographic error. In Fig. 2, the covariance matrix between DZ twins should include the components $V_{C_{DZ}}$ and $V_{E_{DZ}}$ in the formulae for the variances and not

$V_{C_{MZ}}$ and $V_{E_{MZ}}$ as originally presented. This typographic error does not affect the results or conclusions of the manuscript. The original version of Fig. 2 has been corrected by publishing this correction article.

The correct Fig. 2 is shown below.

The original article can be found online at <https://doi.org/10.1007/s10519-021-10044-0>.

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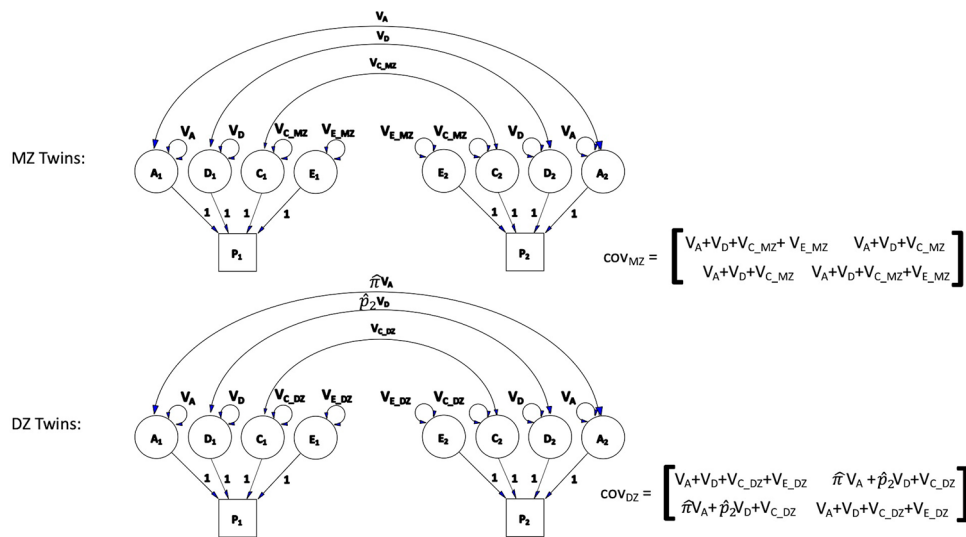


Fig. 2 Extension of the Augmented Classical Twin Design to Include Genetic Dominance. Phenotypes for each twin (P1, P2) are modelled as a function of latent additive genetic (A), dominance genetic (D), common environmental (C) and unique environmental (E) sources of variation. The variance of each latent variable is estimated and the path coefficients between the latent and observed variables are constrained to one. The additive genetic covariance between MZ twins is estimated as VA whilst the additive genetic covariance between the ith DZ twin pair is modelled as a function of their estimated genome-wide proportion of alleles IBD ($\hat{\pi}$) multiplied by the additive genetic variance. The dominance genetic covariance between MZ twins is

estimated as VD whilst the dominance genetic covariance between the ith DZ twin pair is modelled as a function of the estimated proportion of the genome in which they share both alleles IBD (\hat{p}_2) multiplied by the dominance genetic variance. Common environmental and unique environmental variables in MZ and DZ twin pairs are allowed to have different variances with the constraint that the total environmental variance in MZ and DZ twins is the same (i.e. VC_MZ + VE_MZ = VC_DZ + VE_DZ). The expected phenotypic covariances under the full model for each zygosity are displayed. Under this formulation, a test of the EEA is whether common and unique environmental variance components

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