



Correction to: The Moderating Influence of School Achievement on Intelligence in Young Adulthood

Emilie Rune Hegelund^{1,2,3} · Erik Lykke Mortensen² · Trine Flensburg-Madsen² · Jesper Dammeyer¹ · Kaare Christensen⁴ · Wendy Johnson³

Published online: 4 January 2022
© Springer Science+Business Media, LLC, part of Springer Nature 2022

Correction to: Behavior Genetics (2021) 51:45–57
<https://doi.org/10.1007/s10519-020-10027-7>

In the article “The Moderating Influence of School Achievement on Intelligence in Young Adulthood” by Emilie R. Hegelund, Erik L. Mortensen, Trine Flensburg-Madsen, Jesper Dammeyer, Kaare Christensen, and Wendy Johnson (*Behavior Genetics*, Vol. 51, No. 1, pp. 45–57. <https://doi.org/10.1007/s10519-020-10027-7>), we estimated the gene-environment interaction model referred to as the ‘full moderation model’ using the `umxGxEbiv` function from the `umx` package (version 3.0.5; Bates et al. 2019) in R.

Since the publication of our article, Prof Timothy Bates, the developer of the `umxGxEbiv` function, has discovered that the function produced incorrect expected covariance matrices because it reversed the moderator and outcome variables at one point in the script (personal correspondence with Prof Timothy Bates, 7 July 2021; Bates 2021). Rerunning our statistical analyses using the `OpenMx` package (version 2.19.5) in R led to differences from the full moderation model results, presented in Table 2 and Fig. 3 in the Results section as well as in Tables 4 and 5 in the Appendix of our above paper. The corrected tables and figures are presented below.

As can be seen, the best-fitting version of the full moderation model investigating the extent to which grade point average (GPA) in lower secondary school moderated the genetic and environmental influences on IQ scores suggested only moderation of the common genetic influences. More specifically, the model suggested that the genetic variance in IQ scores was greater among individuals with low GPAs (Table 2 and Fig. 3). The genetic variance was 0.74 among individuals with a GPA of one standard deviation below the mean, 0.62 among individuals with an average GPA, and 0.52 among individuals with a GPA of one standard deviation above the mean. The shared environmental variance and the non-shared environmental variance were constant across the range of GPA (0.06 and 0.20, respectively).

Though the corrected full moderation model fit the empirical data much better than the full moderation model estimated using the `umxGxEbiv` function from the `umx` package (version 3.0.5), the published article’s central message still holds. That message is that neither of the applied models generated results that described the data well, and this is very common when the two variables are highly correlated, especially when reciprocally so. We need better statistical models of gene-environment interplay because this kind of situation is common for many important developmental characteristics related to health and wellbeing and of much

The original article can be found online at <https://doi.org/10.1007/s10519-020-10027-7>.

✉ Emilie Rune Hegelund
emhe@sund.ku.dk

¹ Department of Psychology, University of Copenhagen, Copenhagen, Denmark

² Department of Public Health, University of Copenhagen, Copenhagen, Denmark

³ Department of Psychology, The University of Edinburgh, Edinburgh, UK

⁴ The Danish Twin Registry, University of Southern Denmark, Odense, Denmark

Table 2 Parameter estimates from the best-fitting full moderation model and derived variance components and genetic and environmental correlations

Parameter	umx (version 3.0.5)			OpenMx (version 2.19.5)		
	Estimate (95% CI)			Estimate (95% CI)		
Common genetic influences						
Common A	0.11 (– 0.02, 0.24)			0.59 (0.51, 0.68)		
Common A moderation	0.00 ^a			– 0.09 (– 0.12, – 0.06)		
Common shared environmental influences						
Common C	0.49 (0.42, 0.56)			0.25 (0.15, 0.35)		
Common C moderation	0.00 ^a			0.00 ^a		
Common non-shared environmental influences						
Common E	0.29 (0.25, 0.33)			0.10 (0.06, 0.14)		
Common E moderation	0.00 ^a			0.00 ^a		
Unique genetic influences						
Unique A	0.05 (– 0.01, 0.10)			0.52 (0.46, 0.58)		
Unique A moderation	– 0.42 (– 0.47, – 0.36)			0.00 ^a		
Unique shared environmental influences						
Unique C	0.43 (0.36, 0.49)			0.00 (– 0.31, 0.31)		
Unique C moderation	0.00 ^a			0.00 ^a		
Unique non-shared environmental influences						
Unique E	0.42 (0.39, 0.45)			0.44 (0.41, 0.47)		
Unique E moderation	0.00 ^a			0.00 ^a		
Variance components						
	– 1SD	0 SD	1 SD	– 1SD	0 SD	1 SD
Genetic	0.23	0.01	0.15	0.74	0.62	0.52
Shared environmental	0.42	0.42	0.42	0.06	0.06	0.06
Non-shared environmental	0.26	0.26	0.26	0.20	0.20	0.20
Correlations						
	– 1SD	0 SD	1 SD	– 1SD	0 SD	1 SD
Genetic	0.23	0.92	0.29	0.80	0.75	0.70
Shared environmental	0.75	0.75	0.75	1.00	1.00	1.00
Non-shared environmental	0.57	0.57	0.57	0.22	0.22	0.22

^aParameter was fixed to 0

Fig. 3 Variance in IQ scores as a function of grade point average (GPA) in lower secondary school, by source of variance. *Note* A refers to genetic variance, C to shared environmental variance, and E to non-shared environmental variance. The dotted line shows the empirical variance.

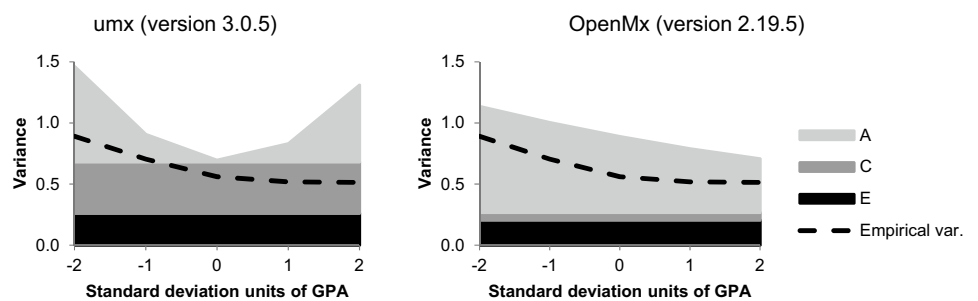


Table 4 Parameter estimates from the full moderation model with all moderation paths fixed to 0 (Cholesky model)

Parameter	umx (version 3.0.5)	OpenMx (version 2.19.5)
	Estimate (95% CI)	Estimate (95% CI)
a_c	0.22 (0.04, 0.40)	0.57 (0.48, 0.66)
c_c	0.60 (0.53, 0.66)	0.28 (0.17, 0.39)
e_c	0.28 (− 0.24, 0.32)	0.10 (0.06, 0.15)
a_u	5.41×10^{-6} (− 0.77, 0.77)	0.55 (0.52, 0.57)
c_u	0.50 (0.42, 0.57)	0.00 (− 0.32, 0.32)
e_u	0.50 (0.46, 0.53)	0.44 (0.41, 0.47)

Table 5 Fit statistics from the full moderation models of variance components

Model	− 2xLL	df	χ^2	Δ df	<i>p</i>	AIC	BIC
umx (version 3.0.5)							
All parameters free	11,231.9	17	–	–	–	11,265.9	11,352.8
Fix common A, C, and E, unique C and E moderation paths to 0 ^a	11,241.9	12	10.0	5	0.08	11,265.9	11,327.2
Fix all moderation paths to 0	11,354.8	11	113.0	1	<0.001	11,376.9	11,433.1
OpenMx (version 2.19.5)							
All parameters free	11,093.3	4856	–	–	–	11,127.3	11,214.2
Fix common C and E, unique A, C, and E moderation paths to 0 ^a	11,096.6	4861	3.3	5	0.65	11,120.6	11,182.0
Fix all moderation paths to 0	11,123.7	4862	27.1	1	<0.001	11,145.7	11,201.9

A refers to genetic influences, C to shared environmental influences, and E to non-shared environmental influences. There are possible common and unique moderation paths for each of A, C, and E. Best-fitting model is indicated by superscript 'a'. Fixed moderation paths were constrained to 0, which means that those sources of influence were present but did not vary across the level of GPA. *AIC* Akaike Information Criterion, *BIC* Bayesian Information Criterion

interest to behaviour genetics researchers. In particular, such models need to be able to distinguish uniform main effects from moderated covariance.

Bates TC, Maes H, Neale MC (2019) umx: twin and path-based structural equation modeling in R. *Twin Res Hum Genet* 22(1):27–41. <https://doi.org/10.1017/thg.2019.2>

Publisher's Note Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

References

Bates TC (2021) Releases · tbates/umx. GitHub. <https://github.com/tbates/umx/releases>