

# Sex limitations and Moderation (*Interaction*) Models

Conor V Dolan & Eveline de Zeeuw

Boulder 2020

nature

BIOLOGY

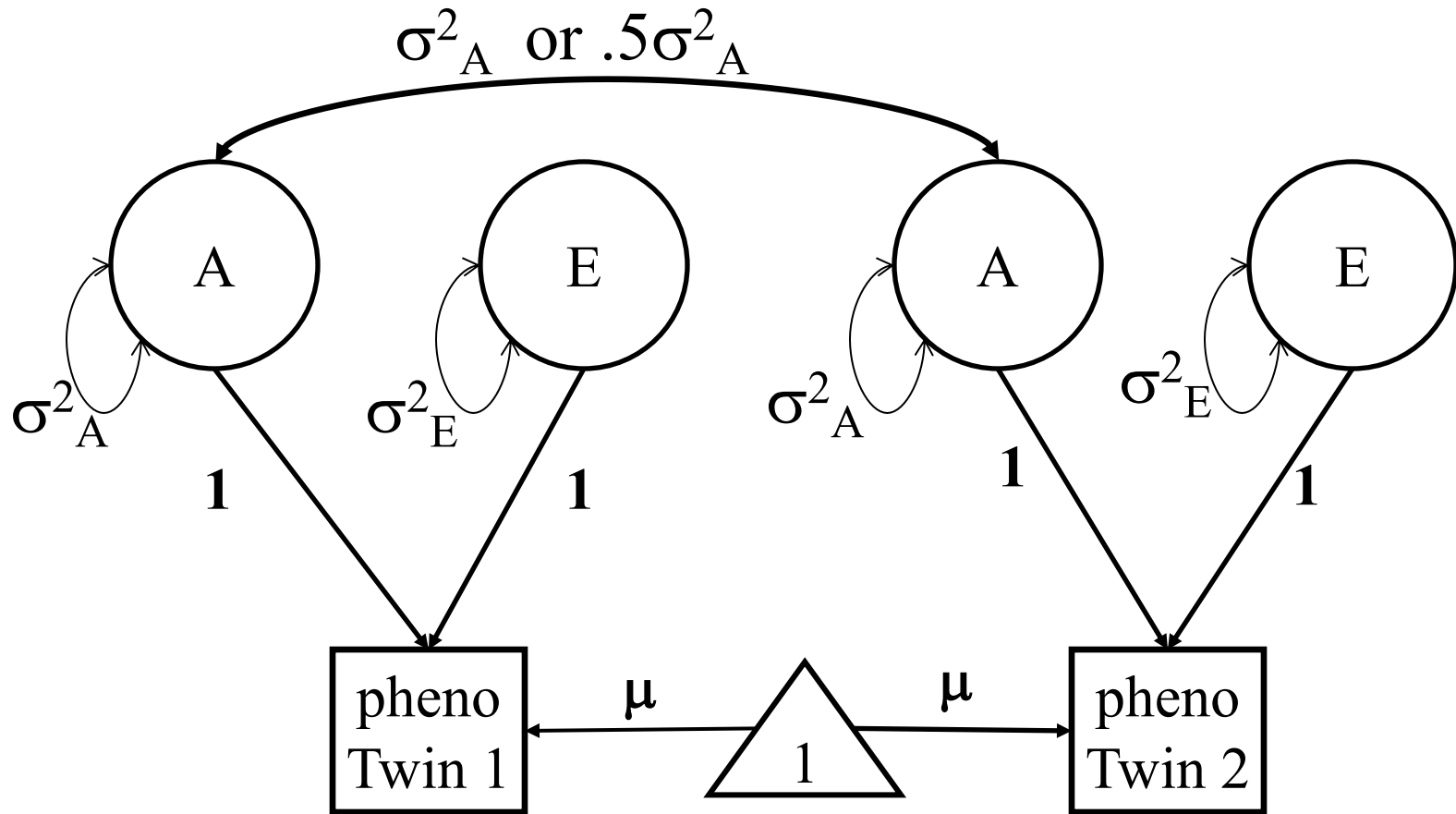
# Sex Redefined: The Idea of 2 Sexes Is Overly Simplistic

Biologists now think there is a larger spectrum than just binary female and male

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By Claire Ainsworth, Nature magazine on October 22, 2018

Standard AE model  $Ph_i - \mu = A_i + E_i$

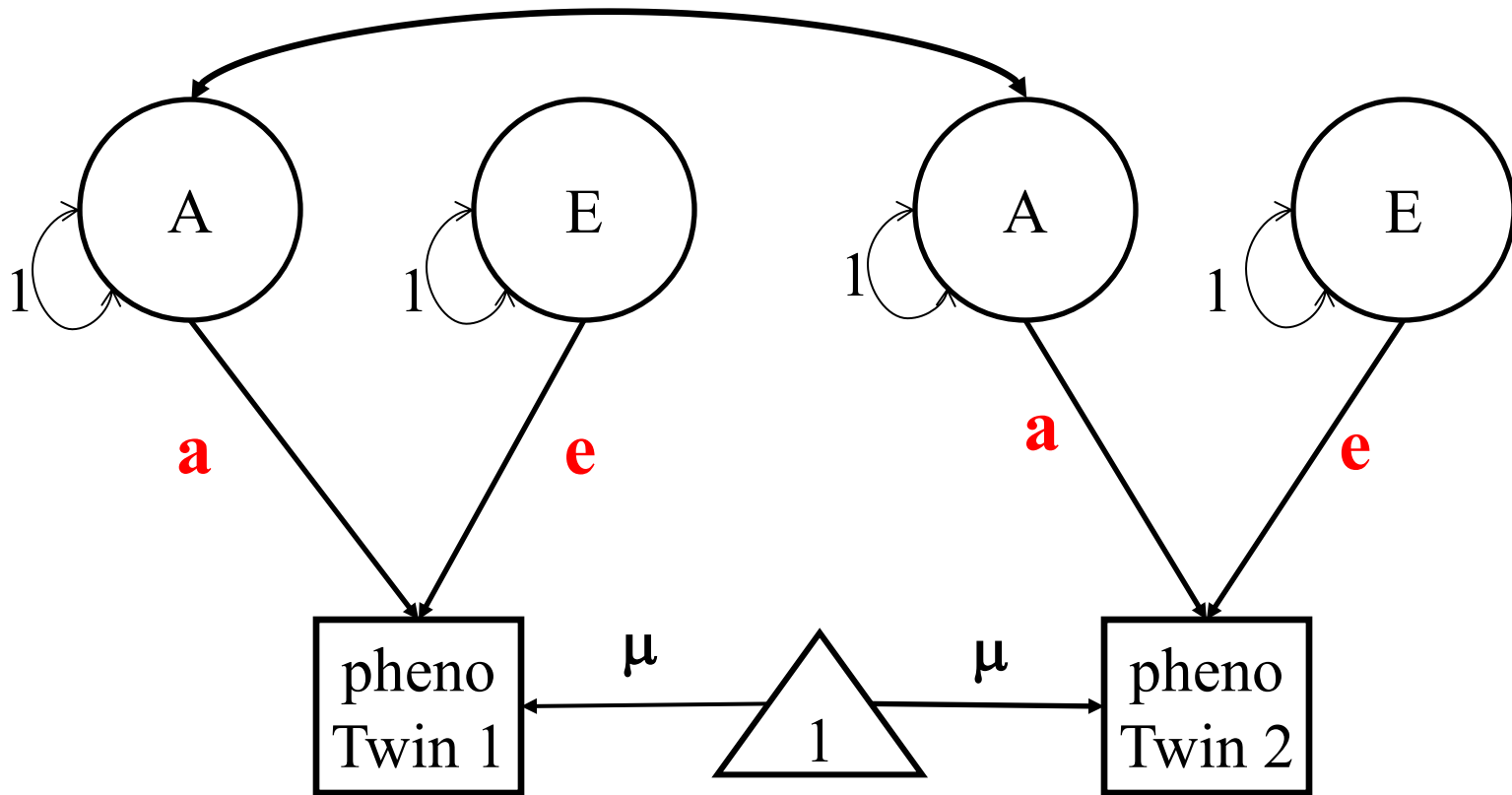


$$\text{mean}(Ph) = \mu$$

$$\text{var}(Ph) = \sigma^2_{Ph} = 1 * \sigma^2_A * 1 + 1 * \sigma^2_E * 1 = \sigma^2_A + \sigma^2_E$$

$$\text{Ph}_i - \mu = \mathbf{a}^* \mathbf{A}_i + \mathbf{e}^* \mathbf{E}_i$$

1 or .5



$$\text{mean}(\text{Ph}) = \mu$$

$$\text{var}(\text{Ph}) = \sigma^2_{\text{Ph}} = V_{\text{Ph}} = \mathbf{a}^* \mathbf{1}^* \mathbf{a} + \mathbf{e}^* \mathbf{1}^* \mathbf{e} = a^2 + e^2$$

Here's the ACE model (variance component):

$$\Sigma_{MZ} = \begin{array}{l} \sigma^2_A + \sigma^2_C + \sigma^2_E \\ \sigma^2_A + \sigma^2_C \end{array} \quad \begin{array}{l} \sigma^2_A + \sigma^2_C \\ \sigma^2_A + \sigma^2_C + \sigma^2_E \end{array}$$

$$\mu_{MZ} = \begin{array}{l} \mu \\ \mu \end{array}$$

$$\Sigma_{DZ} = \begin{array}{l} \sigma^2_A + \sigma^2_C + \sigma^2_E \\ 1/2\sigma^2_A + \sigma^2_C \end{array} \quad \begin{array}{l} 1/2 \sigma^2_A + \sigma^2_C \\ \sigma^2_A + \sigma^2_C + \sigma^2_E \end{array}$$

$$\mu_{DZ} = \begin{array}{l} \mu \\ \mu \end{array}$$

**NOTE:** When we fit this model we assume that the model holds in the **population of interest**.

- conceptually and statistically a big deal.

What if the population comprises two discernable (sub)populations of interest, e.g., males and females?

Main effect of sex on phenotype

Sex by A (genotype), E (environment) interactions

If we ignore the source of *heterogeneity*  
the estimates of  $\mu$ ,  $\sigma^2_E$ ,  $\sigma^2_A$  may be biased ...  
and even the statistical tests may be affected .... BAD!

What to do?

Include *source of heterogeneity*, moderator, in the model (sex, age, ... ANY VARIABLE **THEORY** prescribes) to render testable the moderation effects.

E.g., diathesis-stress model identifies childhood trauma as a moderator of genetic effects on depression.

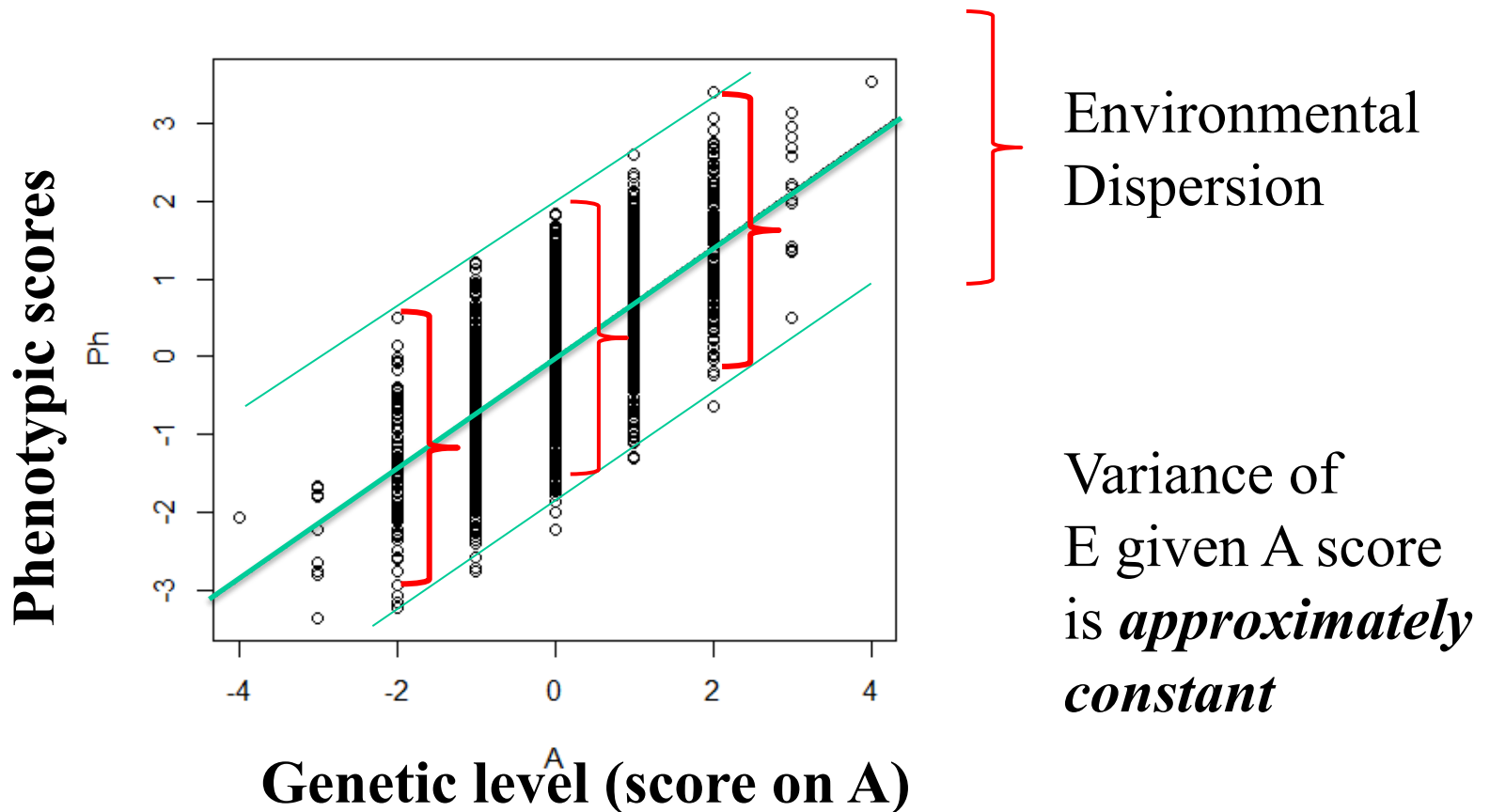
Colodro-Conde L, et al. A direct test of the diathesis-stress model for depression. *Mol. Psychiatry*. 2018;23:1590–1596. doi: 10.1038/mp.2017.130.

What is moderation (a.k.a. interaction)?

To test it (using statistics), and we define it statistically.



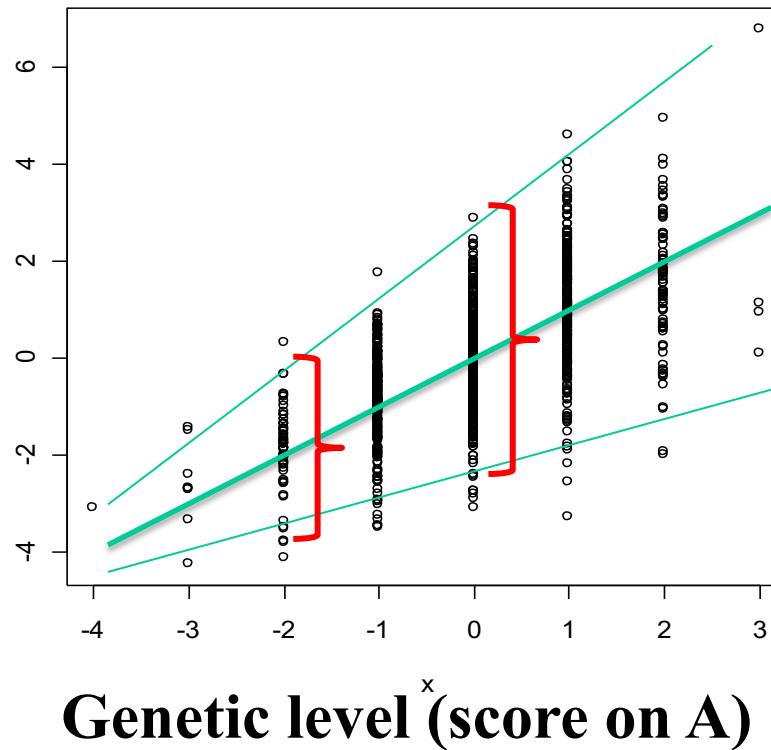
no moderation ... homoskedastic....homogeneity



$$Ph_i - \mu = \mathbf{a} * A_i + \mathbf{e} * E_i$$

**Homoskedastic model:** **e** is constant over levels of A: environmental effects are the same given any A

**Phenotypic  
scores**

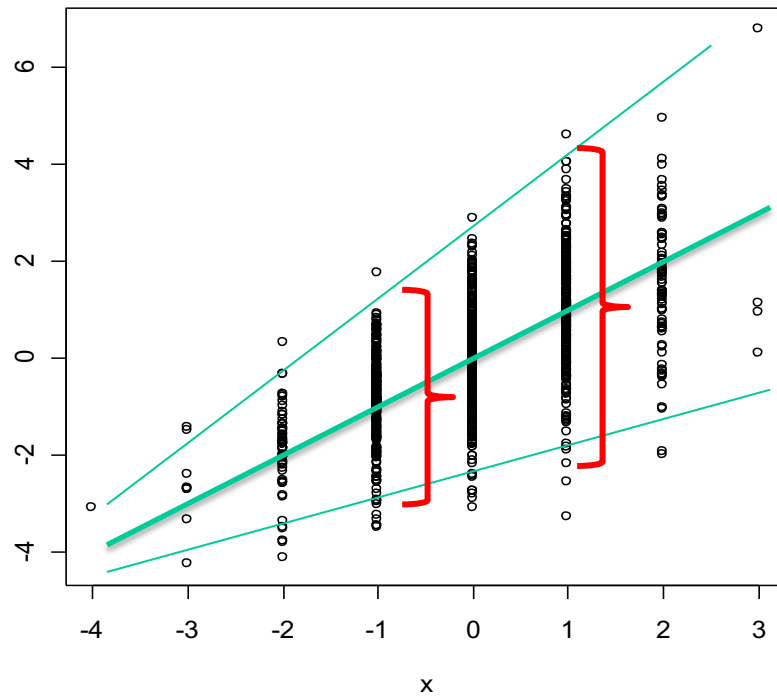


Environmental  
Dispersion

Variance of  
E given A score  
is *not constant*

A x E as “genetic control” of sensitivity to different environments: **heteroskedasticity (heterogeneity)**  
 $e=f_e(A)$  or  $\sigma^2_E =g_e(A)$  -> Environmental effects (**E**)  
systematically vary with A. A moderator ...

**Phenotypic  
scores**

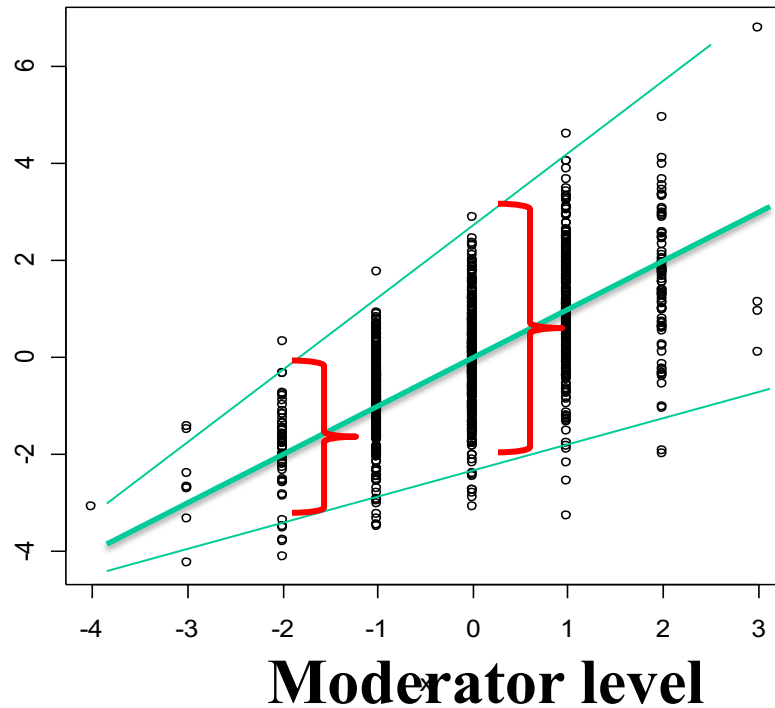


Conditional  
variance of A  
given E  
is *not* constant

**Environmental level (score on E)**

A x E as “environmental control” of genetic effects:  
heteroskedasticity ( $\mathbf{a}=f_a(E)$  or  $\sigma^2_A=g_a(E)$ ).  
E moderator

**Phenotypic scores**



Genetic variance  
or (and)  
Environmental (C and / or E) variance given M

(score on the measured moderator)

**Moderation of effects (A,C,E) by measured moderator M:**

heteroskedasticity  $\mathbf{a}=f_a(M)$ ,  $\mathbf{c}=f_c(M)$ ,  $\mathbf{e}=f_e(M)$  or

$$\sigma^2_A = g_a(M), \sigma^2_C = g_c(M), \sigma^2_E = g_e(M)$$

M moderates the effects of A, C (or D) and E

Moderators are measured variables – may be binary

A effects moderated by **marital status** (M):

Unmarried women show greater levels of genetic influence on depression (Heath et al., 1998).

A effects moderated by **religious upbringing** (M):

religious upbringing diminishes A effects on the personality trait of disinhibition (Boomsma et al., 1999).

Sex (as a binary moderator)– discussed below .

# Moderators are measured variables – may be continuous

**Age** as a moderator of A, C, E variance components (Age x A,C,E interaction)

*Research Article*



## **Large Cross-National Differences in Gene × Socioeconomic Status Interaction on Intelligence**



**Elliot M. Tucker-Drob<sup>1,2</sup> and Timothy C. Bates<sup>3</sup>**

<sup>1</sup>Department of Psychology, University of Texas at Austin; <sup>2</sup>Population Research Center, University of Texas at Austin; and <sup>3</sup>Department of Psychology, University of Edinburgh

Psychological Science

1–12

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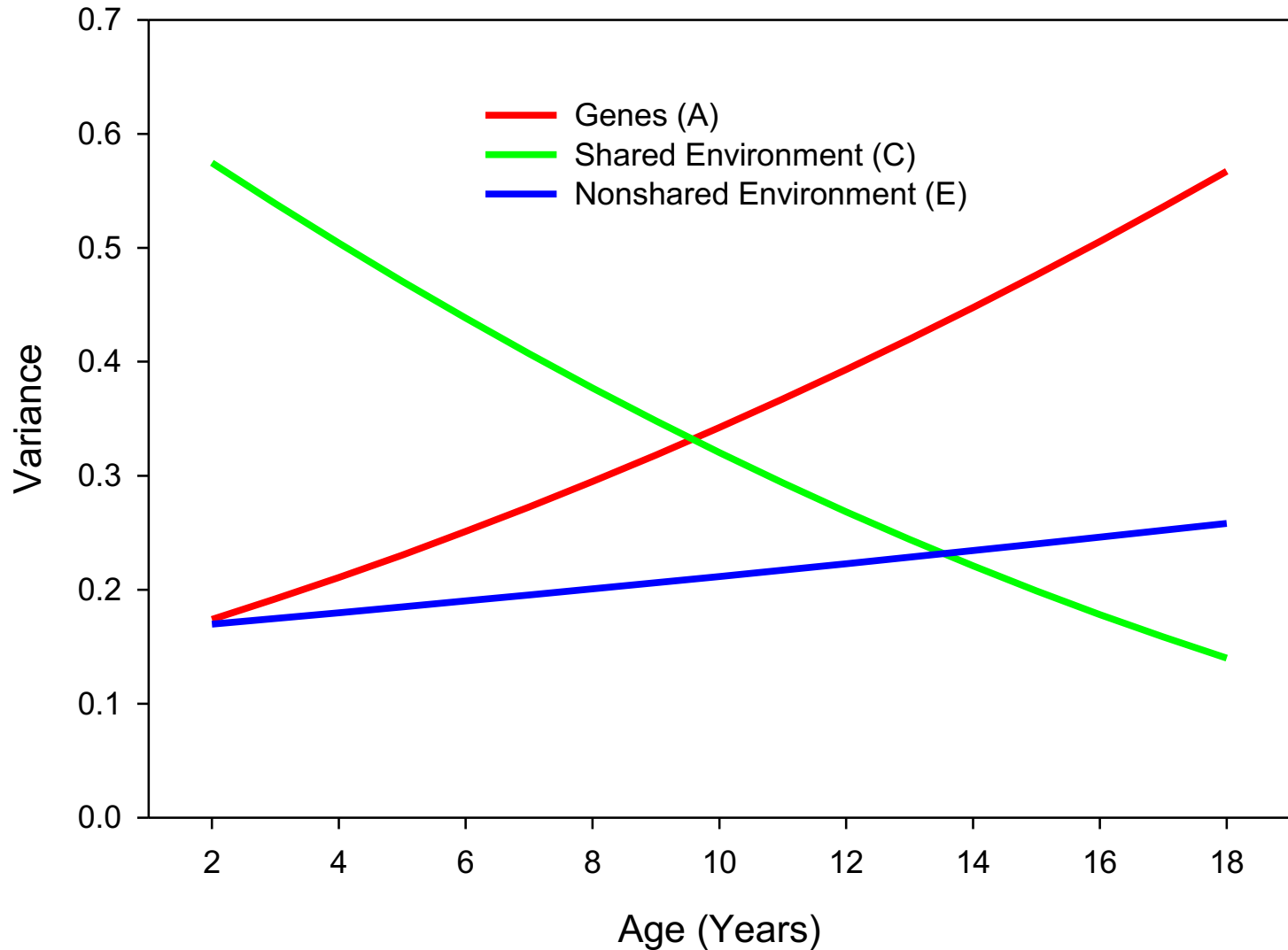
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DOI: 10.1177/0956797615612727

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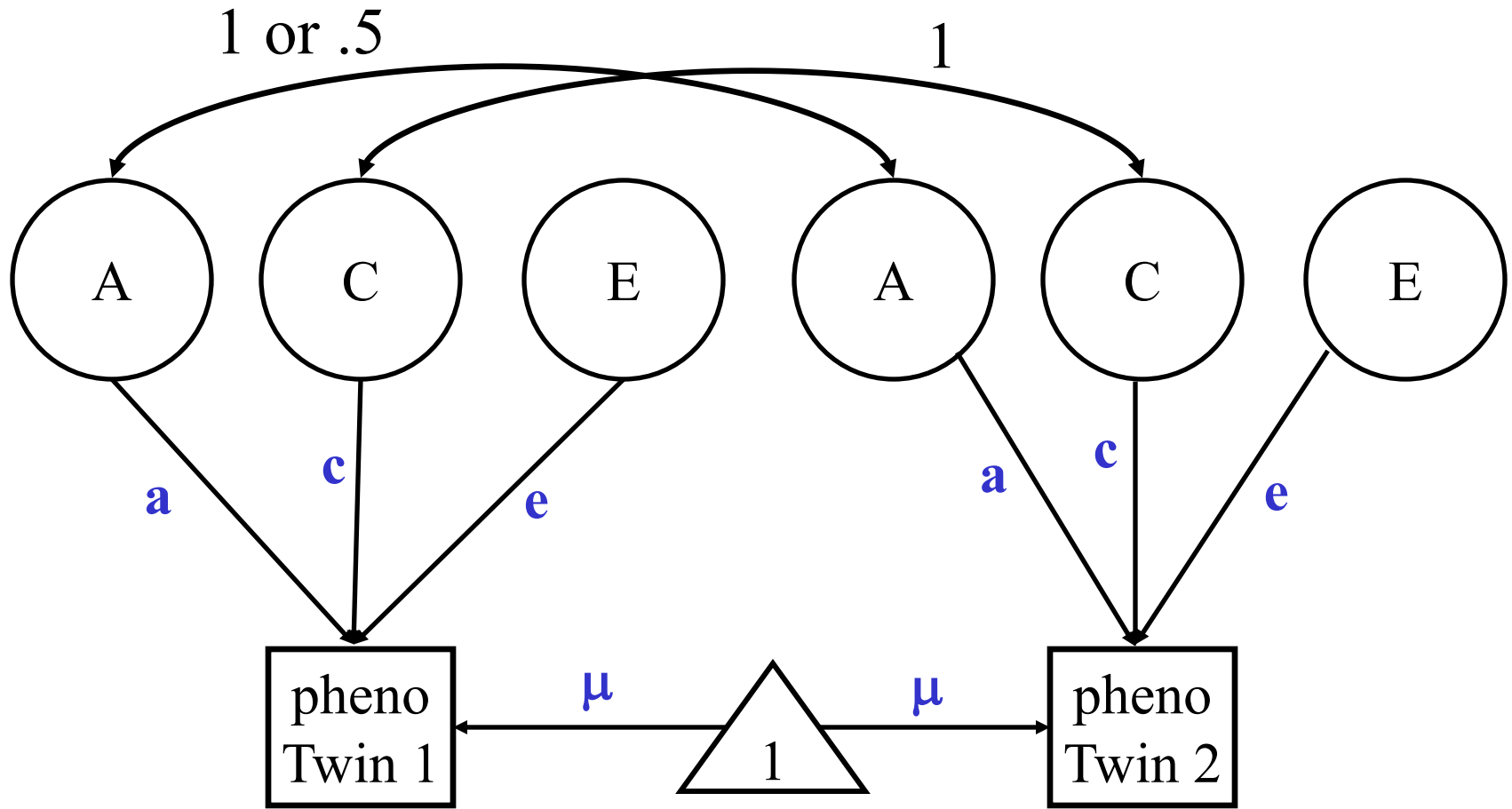


# Intelligence (western / us populations)



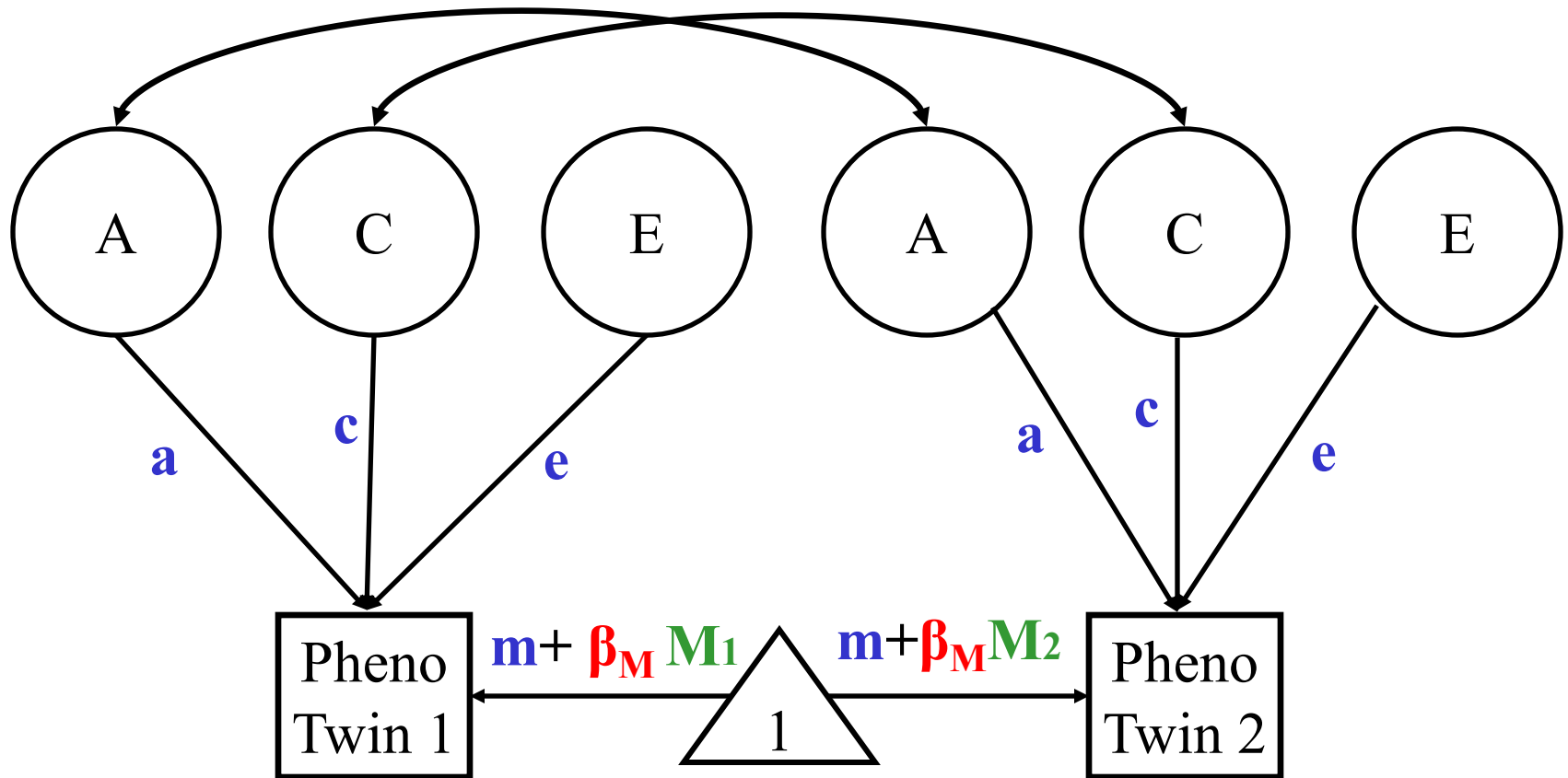
Tucker-Drob & Bates (2015)

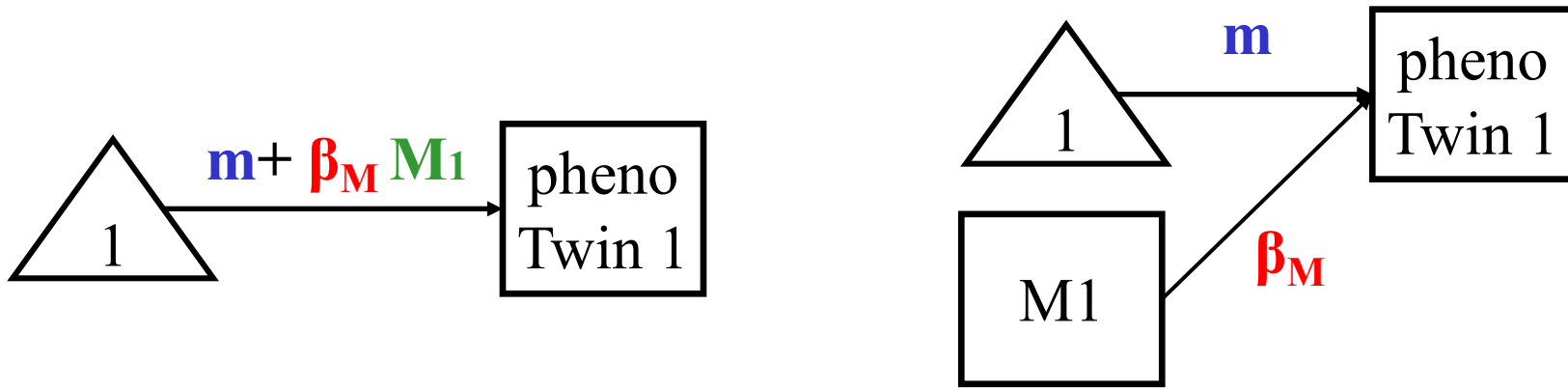
# ACE model (A,C,E standardized) continuous phenotype





# ACE model + Main effect on Means





equivalent

Two representations of the regression of Phenotype on M ...

$$\text{Pheno}_i = m + \beta_M M_{1i} + \text{residual}_i$$

# Summary stats (no moderator)

- Means vector

$$\begin{pmatrix} \mu & \mu \end{pmatrix}$$

- Covariance matrix ( $r = 1$  or  $1/2$ )

$$\begin{pmatrix} a^2 + c^2 + e^2 & \\ r * a^2 + c^2 & a^2 + c^2 + e^2 \end{pmatrix}$$

# Allowing for a main effect of the moderator M

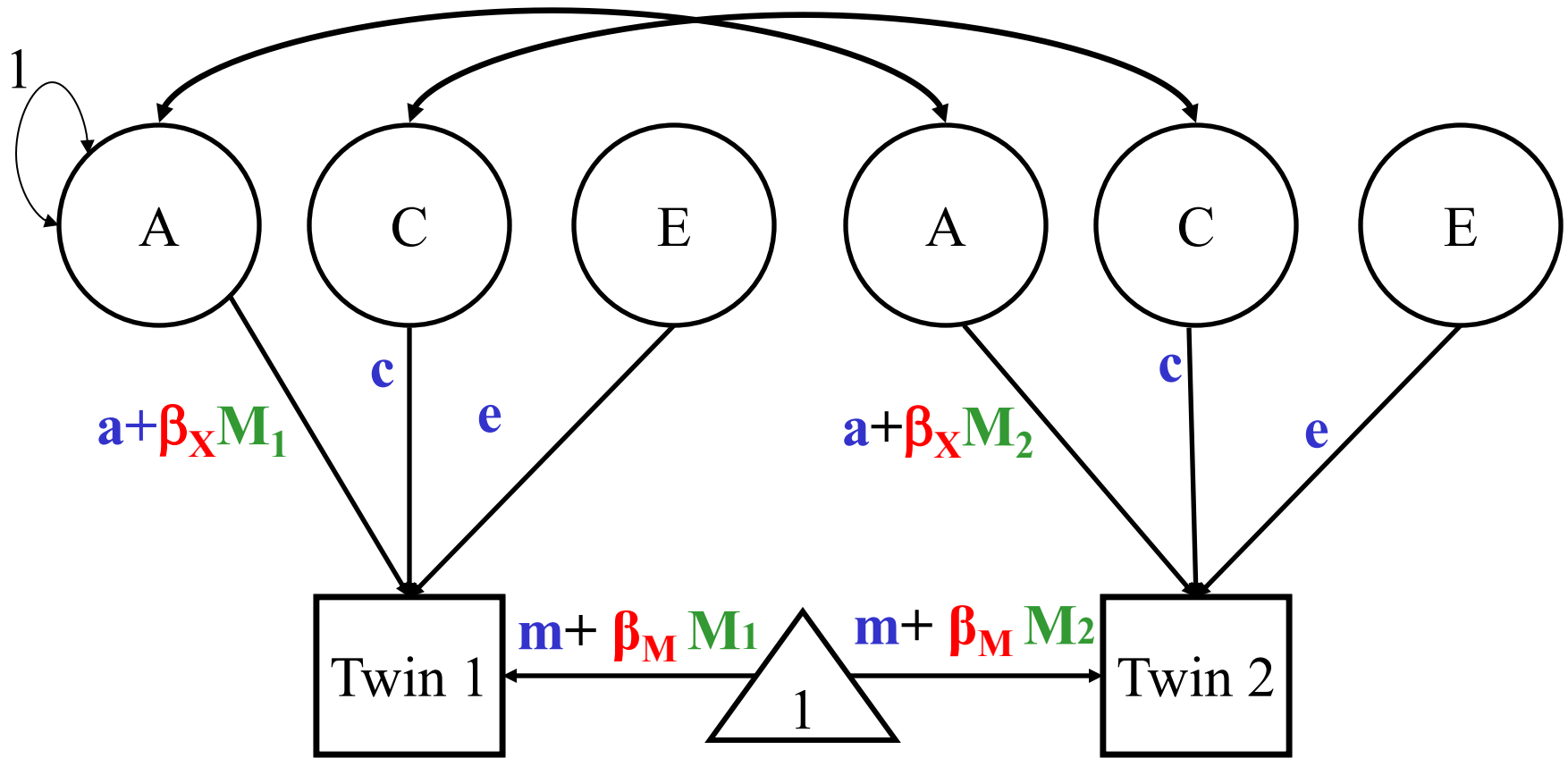
- Means vector (conditional on M)

$$\left( m + \beta_M M_{1i} \quad m + \beta_M M_{2i} \right)$$

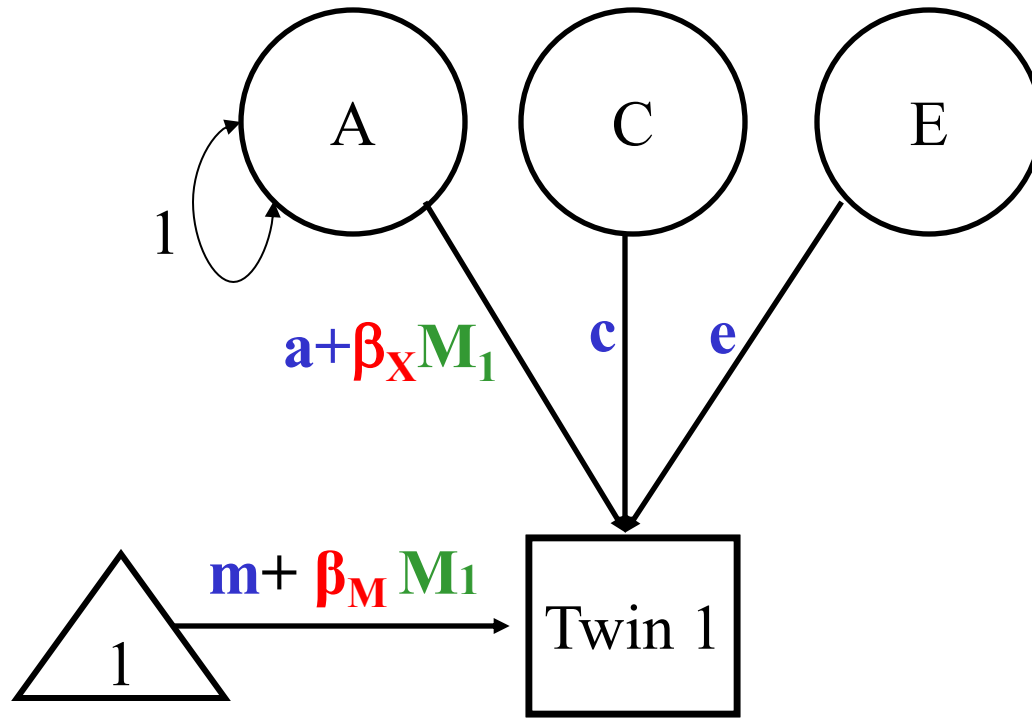
- Covariance matrix ( $r = 1$  or  $r = 1/2$ )

$$\begin{pmatrix} a^2 + c^2 + e^2 & \\ r^* a^2 + c^2 & a^2 + c^2 + e^2 \end{pmatrix}$$

# ACE model + main effect and effect on A path



M has main effect + moderation of A effect ( $a + \beta_X M_1$ )

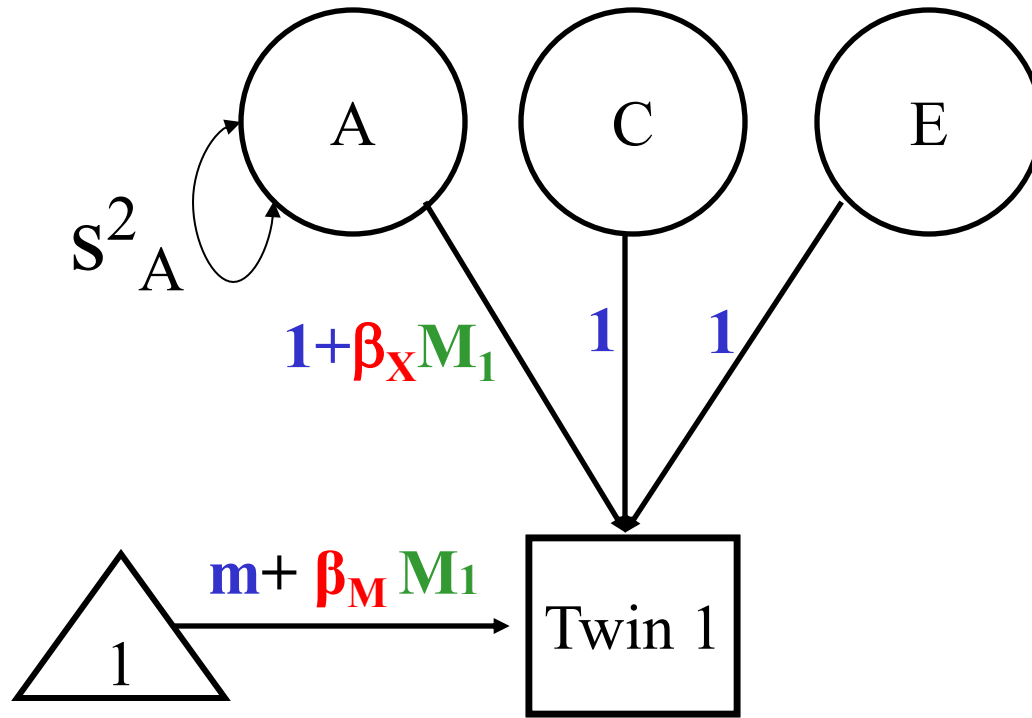


If M is binary (0/1) (instead of continuous)

$$M_1=0 \rightarrow \text{mean} = \mathbf{m} \ \& \ s^2_A = \mathbf{a}^2$$

$$M_1=1 \rightarrow \text{mean} = \mathbf{m} + \beta_M \ \& \ s^2_A = (\mathbf{a} + \beta_X M_1)^2$$

Test of moderation: test of  $\beta_X$

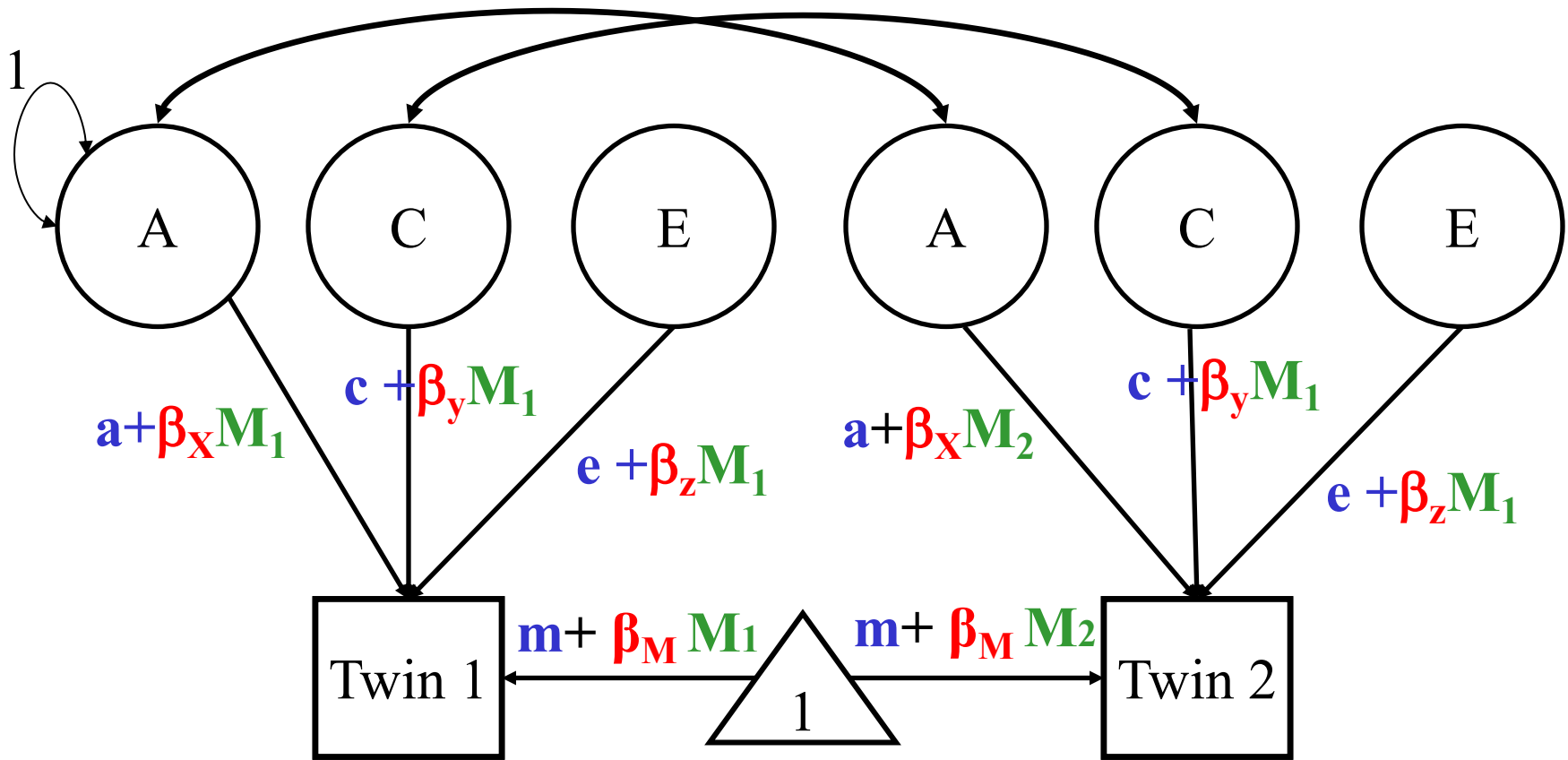


If M is binary (0/1) (instead of continuous)

$$M_1=0 \rightarrow \text{mean} = m \ \& \ s^2_A = s^2_A$$

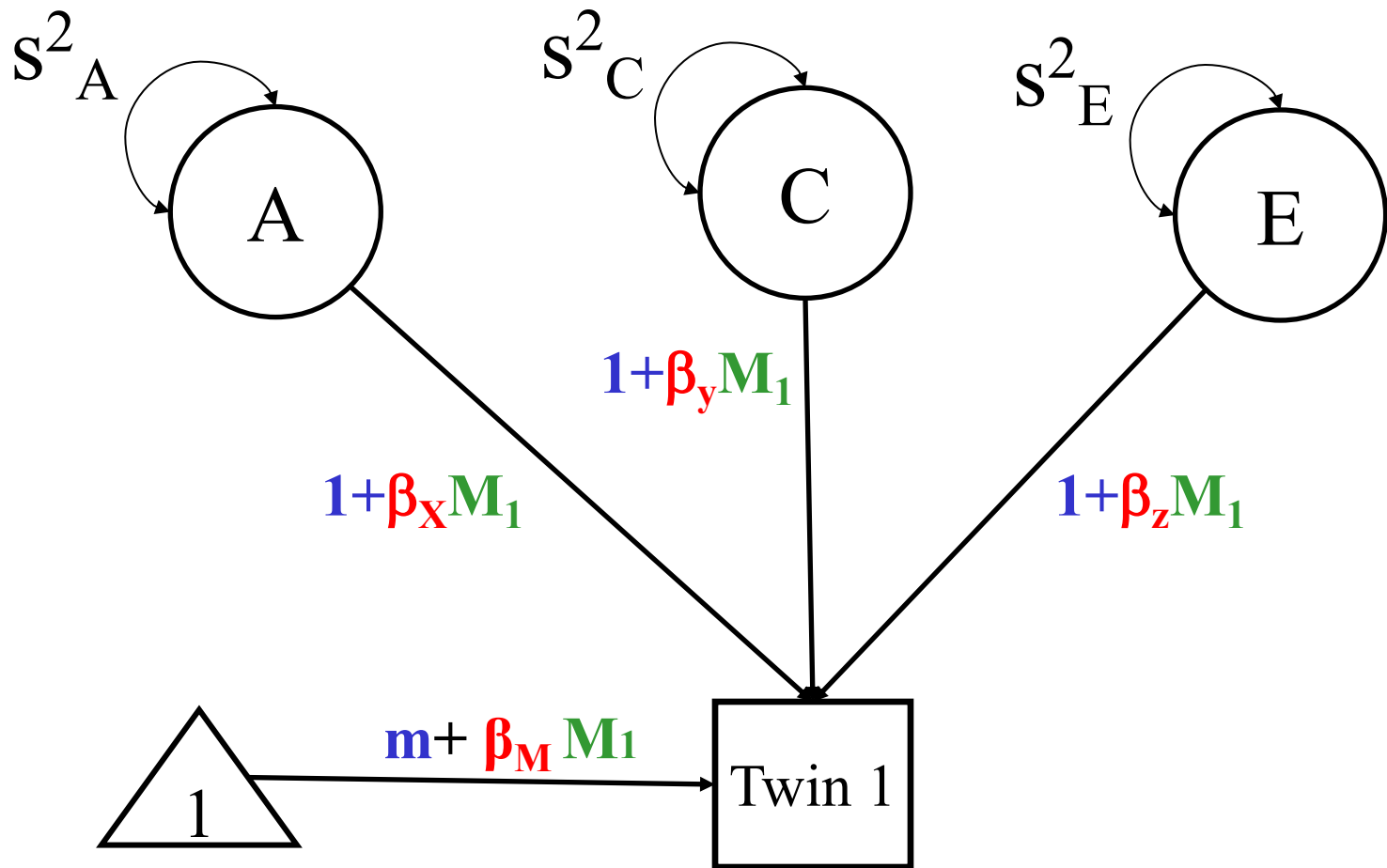
$$M_1=1 \rightarrow \text{mean} = m + \beta_M \ \& \ s^2_A = s^2_A (1 + \beta_X)^2$$

Test of moderation: test of  $\beta_X$



- Main Effect on phenotype (linear regression)
- Effect path parameters: Moderation effects (A x M, C x M, E x M interaction).
- Test of moderation: Tests of  $\beta_x$ ,  $\beta_y$ ,  $\beta_z$  (3 df omnibus test)





A variance component version  
 (just the twin 1 member)

## Conditional expected **variances**

Standard Twin Model:

$$s^2_{Ph} = a^2 + c^2 + e^2 \text{ or } s^2_A + s^2_C + s^2_E$$

Moderation Model:

$$\text{Var}(Ph|M) =$$

$$(a + \beta_X M)^2 + (c + \beta_Y M)^2 + (e + \beta_Z M)^2 \text{ or}$$

$$s^2_A(1 + \beta_X M)^2 + s^2_C(1 + \beta_Y M)^2 + s^2_E(1 + \beta_Z M)^2$$

**Ph|M** mean “the phenotype given a value on M”  
or “the phenotype conditional on M”

## Conditional expected MZ / DZ covariances

$$\text{Cov}(\text{Ph}_1, \text{Ph}_2 | M)_{MZ} = (a + \beta_X M)^2 + (c + \beta_Y M)^2$$

$$\text{Cov}(\text{Ph}_1, \text{Ph}_2 | M)_{DZ} = \frac{1}{2}(a + \beta_X M)^2 + (c + \beta_Y M)^2$$

$$\text{Cov}(\text{Ph}_1, \text{Ph}_2 | M)_{MZ} = s_A^2(1 + \beta_X M)^2 + s_C^2(1 + \beta_Y M)^2$$

$$\text{Cov}(\text{Ph}_1, \text{Ph}_2 | M)_{DZ} = \frac{1}{2}s_A^2(1 + \beta_X M)^2 + s_C^2(1 + \beta_Y M)^2$$

$$\text{Var} (P|M) = (a + \beta_X M)^2 + (c + \beta_Y M)^2 + (e + \beta_Z M)^2$$

$$h_{st}^2 |M = (a + \beta_X M)^2 / \text{Var} (P|M)$$

$$c_{st}^2 |M = (c + \beta_Y M)^2 / \text{Var} (P|M)$$

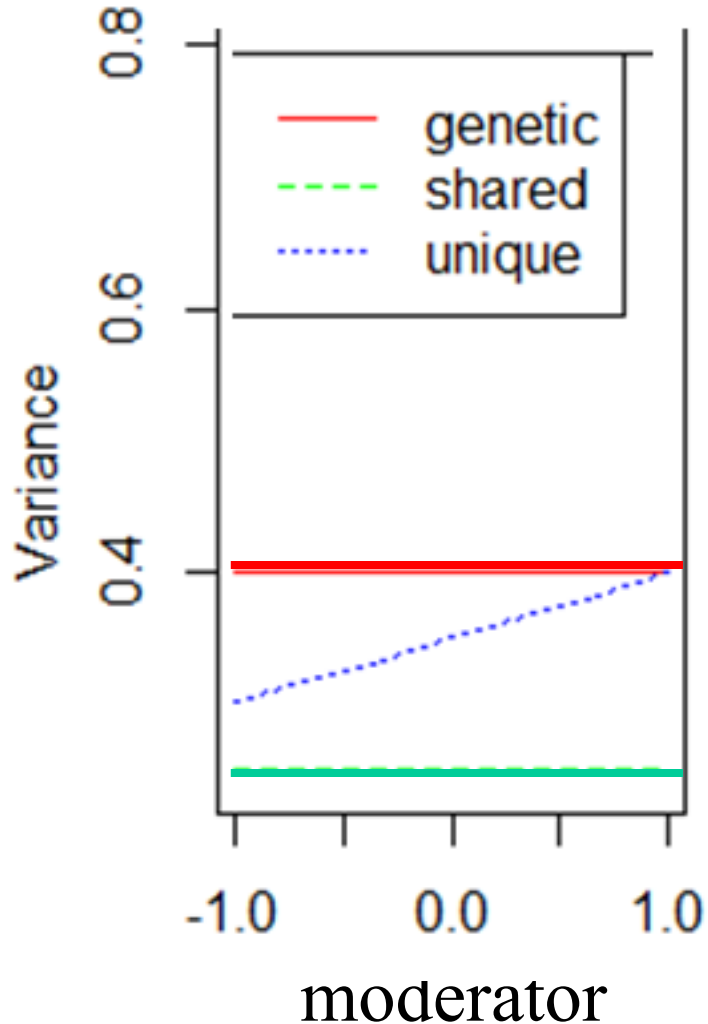
$$e_{st}^2 |M = (e + \beta_Z M)^2 / \text{Var} (P|M)$$

$$(h_{st}^2 |M + c_{st}^2 |M + e_{st}^2 |M) = 1$$

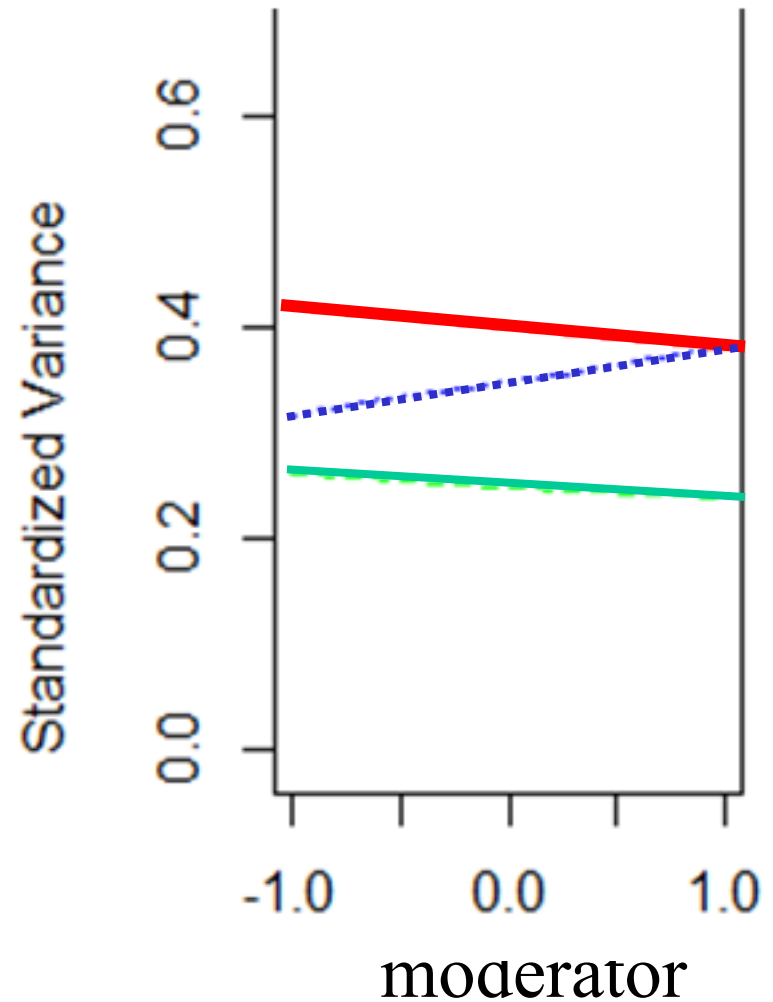
Standardized conditional on value of M..

**But**  $h_{st}^2 |M$  can vary with M while  $\beta_X = 0!$   
same applies to  $c_{st}^2 |M$  and  $e_{st}^2 |M$

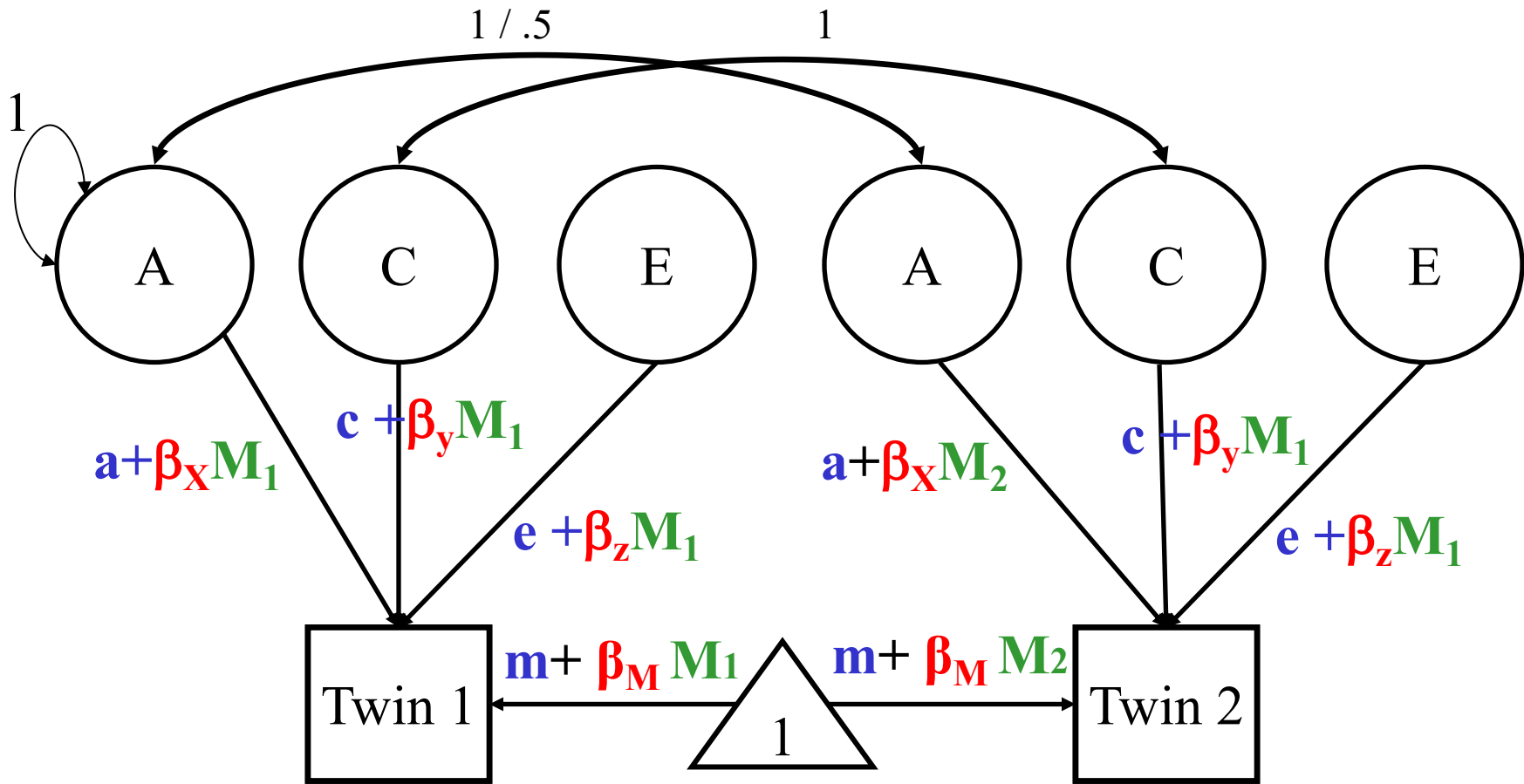
only e moderated  
(umx plots)



a,c moderated? nope!  
(umx plots)

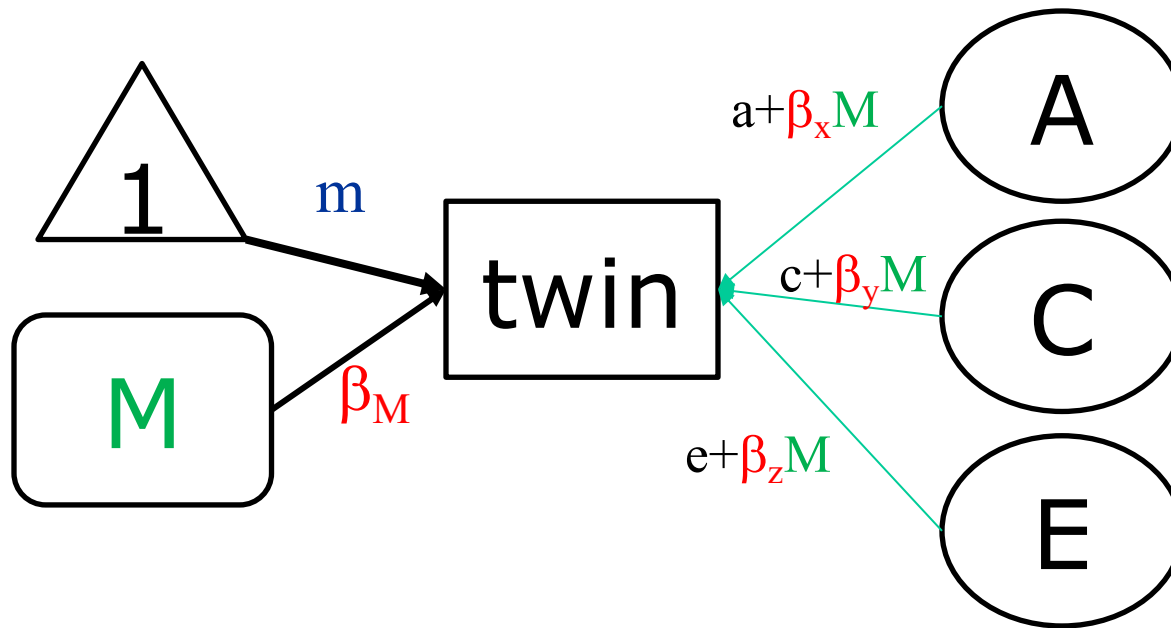


**R code in the slide notes**



But what have we assumed concerning M?  
 So far treated like a definition variable (and a fixed regressor).

# The M is a measured variable

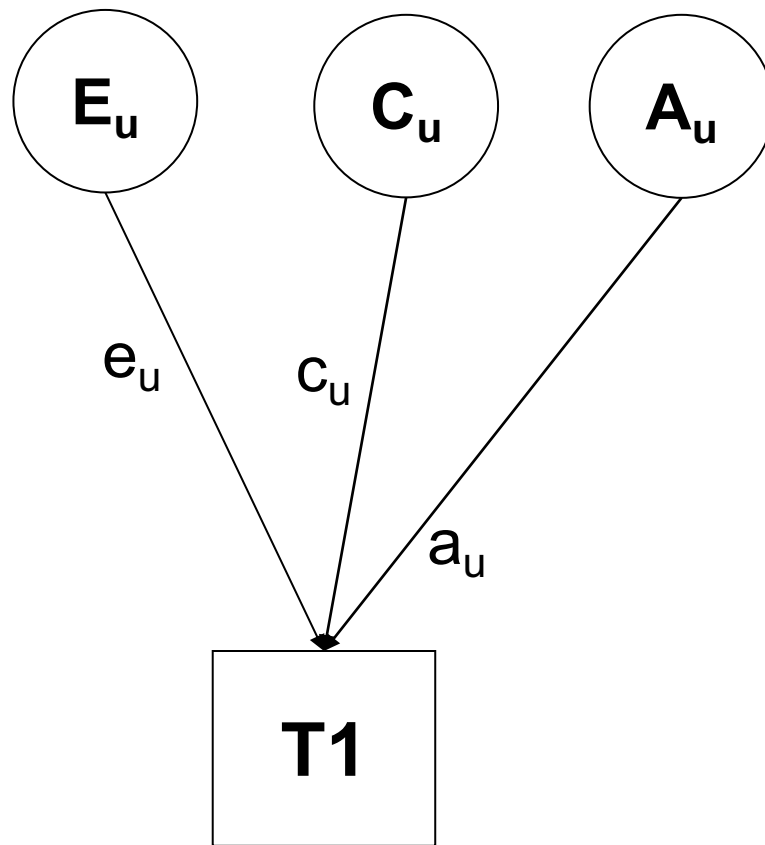
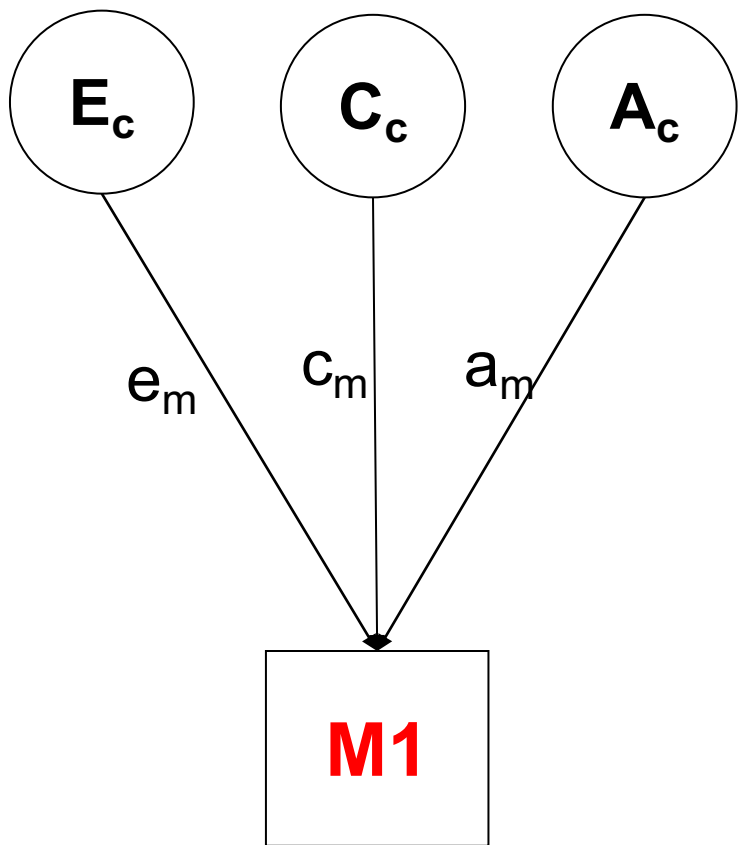


M is environmental?

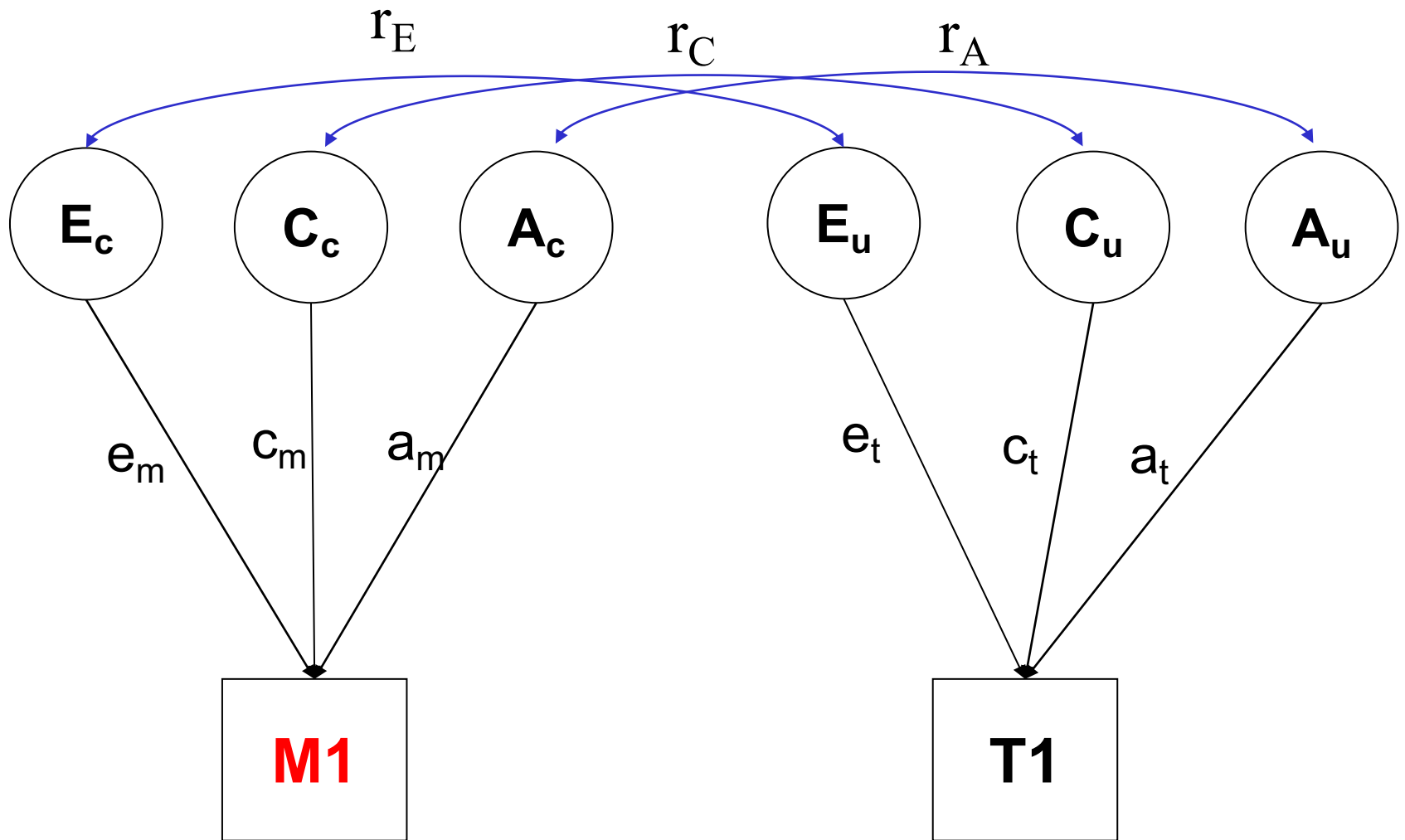
Social support? Employment status?

Marital status? (No No and No).

The weather (yes)

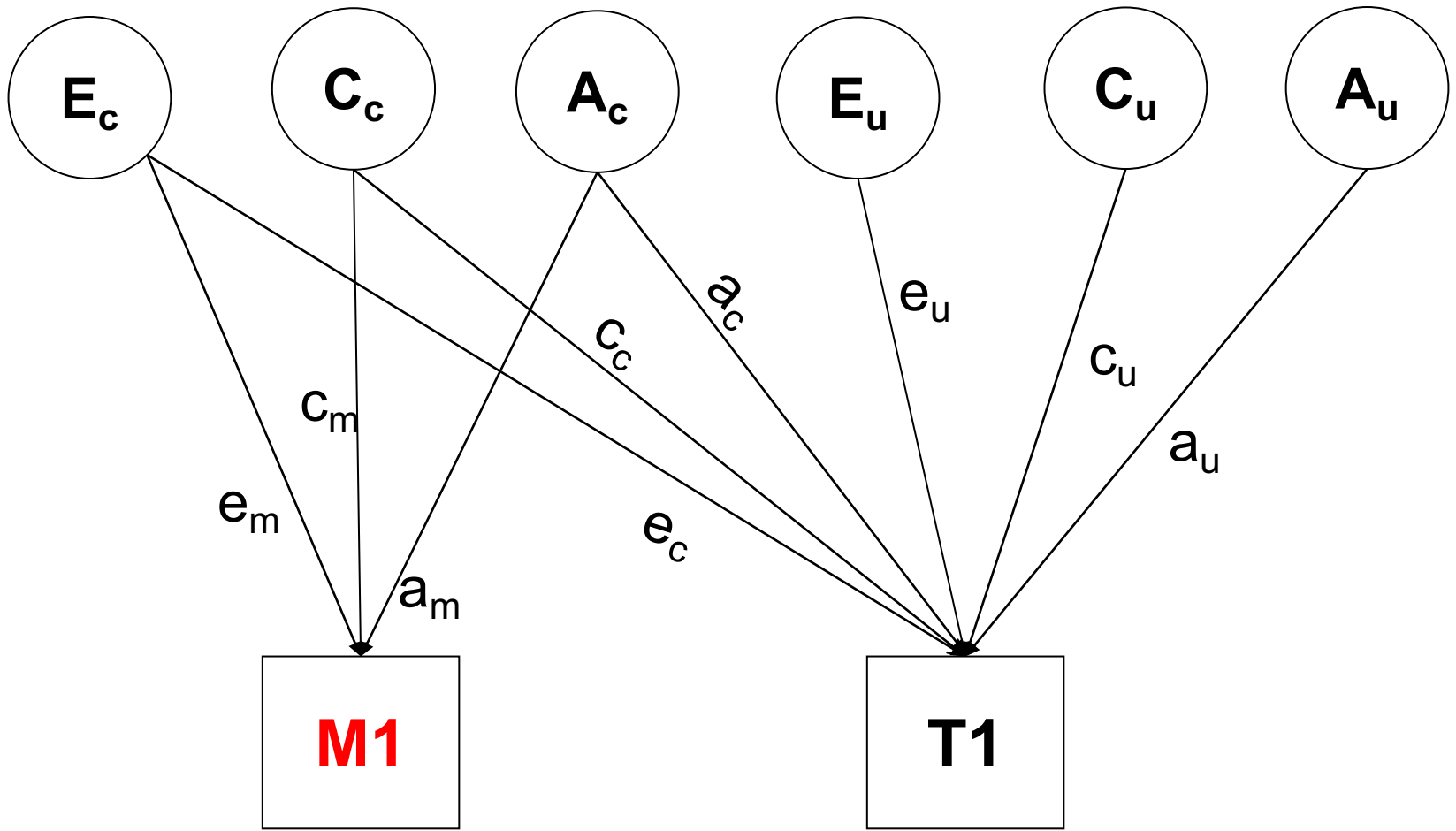






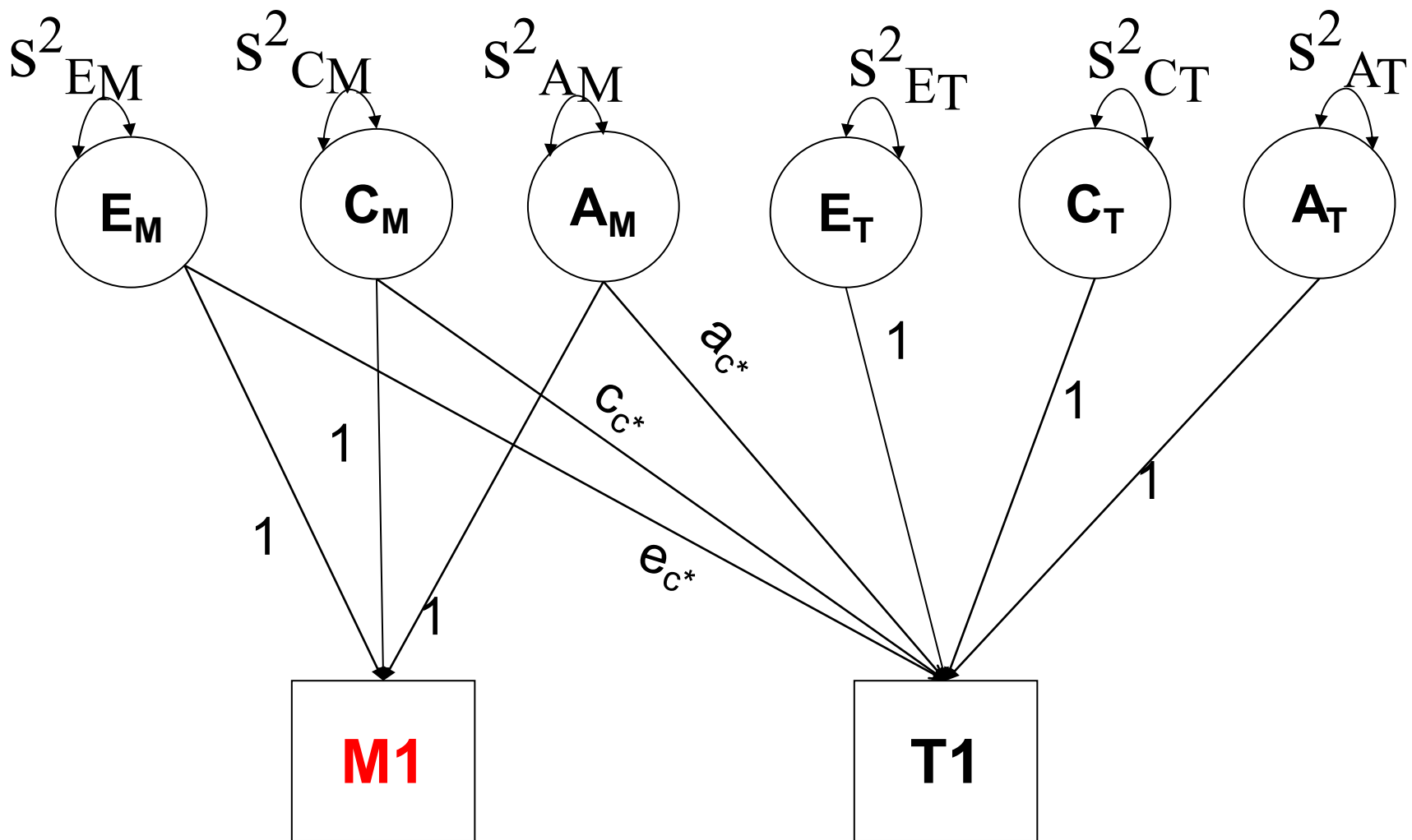
$$\text{cov}(\mathbf{M1}, \mathbf{T1}) = a_m r_E a_t + c_m r_C c_t + e_m r_E e_t$$

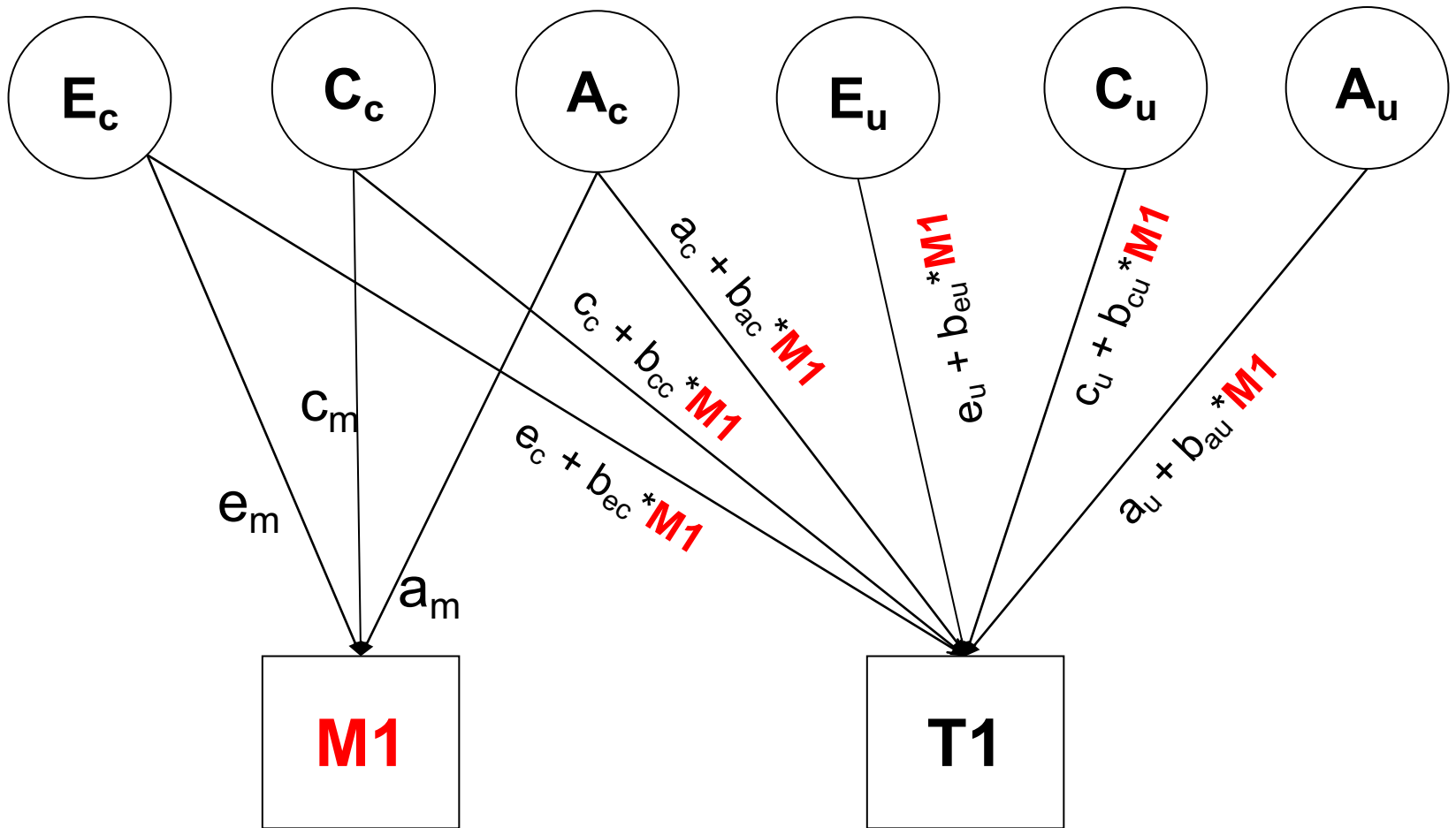
$$\text{var}(\mathbf{T1}) = a_t^2 + c_t^2 + e_t^2$$



$$\text{cov}(\mathbf{M1}, \mathbf{T1}) = \mathbf{a}_m \mathbf{a}_c + \mathbf{c}_m \mathbf{c}_c + \mathbf{e}_m \mathbf{e}_c$$

$$\text{var}(\mathbf{T1}) = \mathbf{e}_c^2 + \mathbf{c}_c^2 + \mathbf{e}_c^2 + \mathbf{e}_u^2 + \mathbf{c}_u^2 + \mathbf{e}_u^2$$





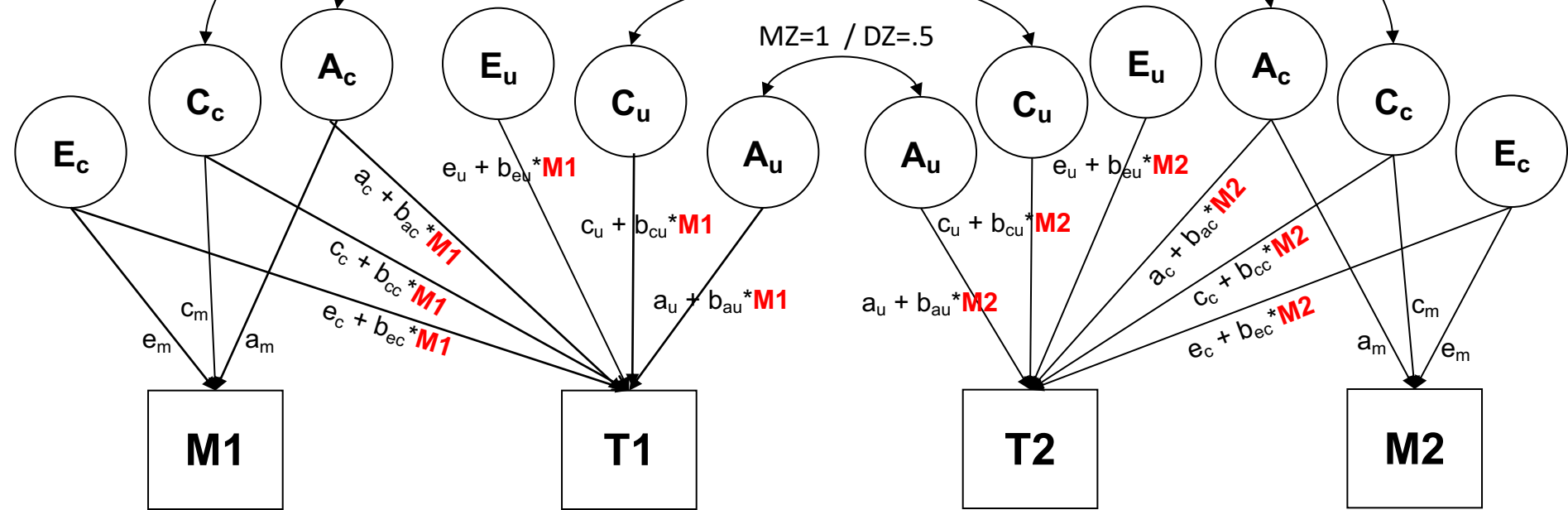
$$\text{var}(T1 | M1) = (e_c + b_{ec} * M1)^2 + (c_c + b_{cc} * M1)^2 + (a_c + b_{ac} * M1)^2 + (e_u + b_{eu} * M1)^2 + (c_u + b_{cu} * M1)^2 + (a_u + b_{au} * M1)^2$$

MZ = DZ = 1

MZ=1 / DZ=.5

MZ = DZ = 1

MZ=1 / DZ=.5



umx function available!

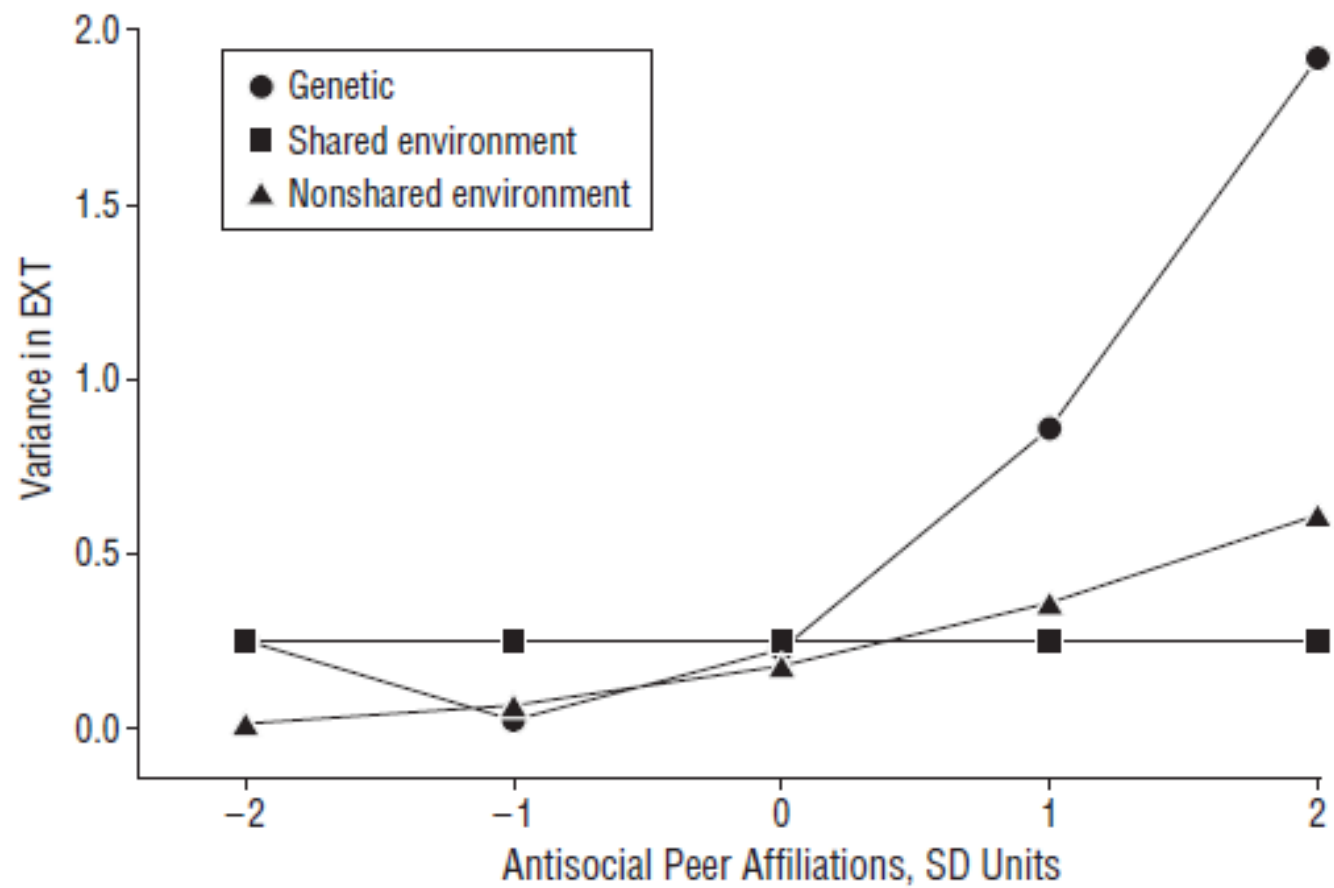
# Environmental Adversity and Increasing Genetic Risk for Externalizing Disorders

*Brian M. Hicks, PhD; Susan C. South, PhD; Ana C. DiRago, MA; William G. Iacono, PhD; Matt McGue, PhD*

**Phenotype:** externalizing behavior

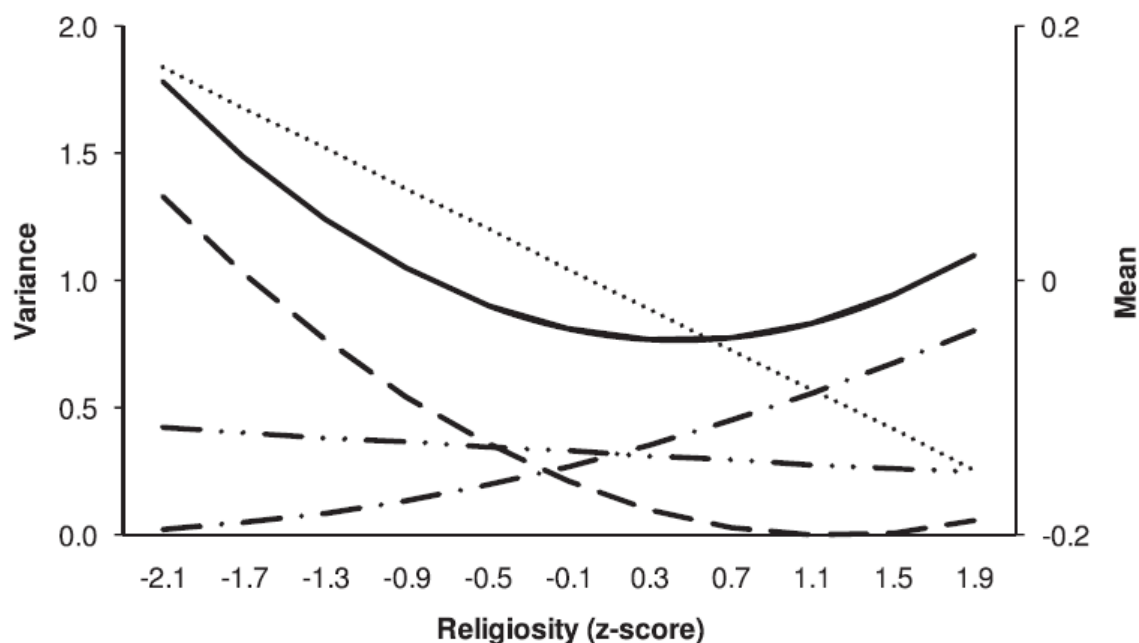
**Moderators:** academic achievement and engagement, antisocial and prosocial peer affiliations, mother-child and father-child relationship problems, and stressful life events.

*Arch Gen Psychiatry. 2009;66(6):640-648*



# The Moderating Effect of Religiosity on the Genetic Variance of Problem Alcohol Use

Tanya M. M. Button, John K. Hewitt, Soo H. Rhee, Robin P. Corley,  
and Michael C. Stallings



Adolescent male problem alcohol use

Mean ..... Phenotypic Variance \_\_\_\_\_  
 Genetic Variance - - - - - Shared Environment Variance - . - . -  
 Non-shared Environment Variance - . . - . . . . .



What about non-linear moderation? E.g., extend the model from linear to linear + quadratic.

$$e_c + b_{ec1} * \mathbf{M1} + b_{ec2} * \mathbf{M1}^2$$

What about >1 moderators?

Extend the model accordingly

$$e_c + b_{ec1} * \mathbf{SES} + b_{ec2} * \mathbf{AGE}$$

What about categorical data?

Behav Genet (2009) 39:220–229  
DOI 10.1007/s10519-008-9247-7

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BRIEF COMMUNICATION

## A Note on the Parameterization of Purcell's $G \times E$ Model for Ordinal and Binary Data

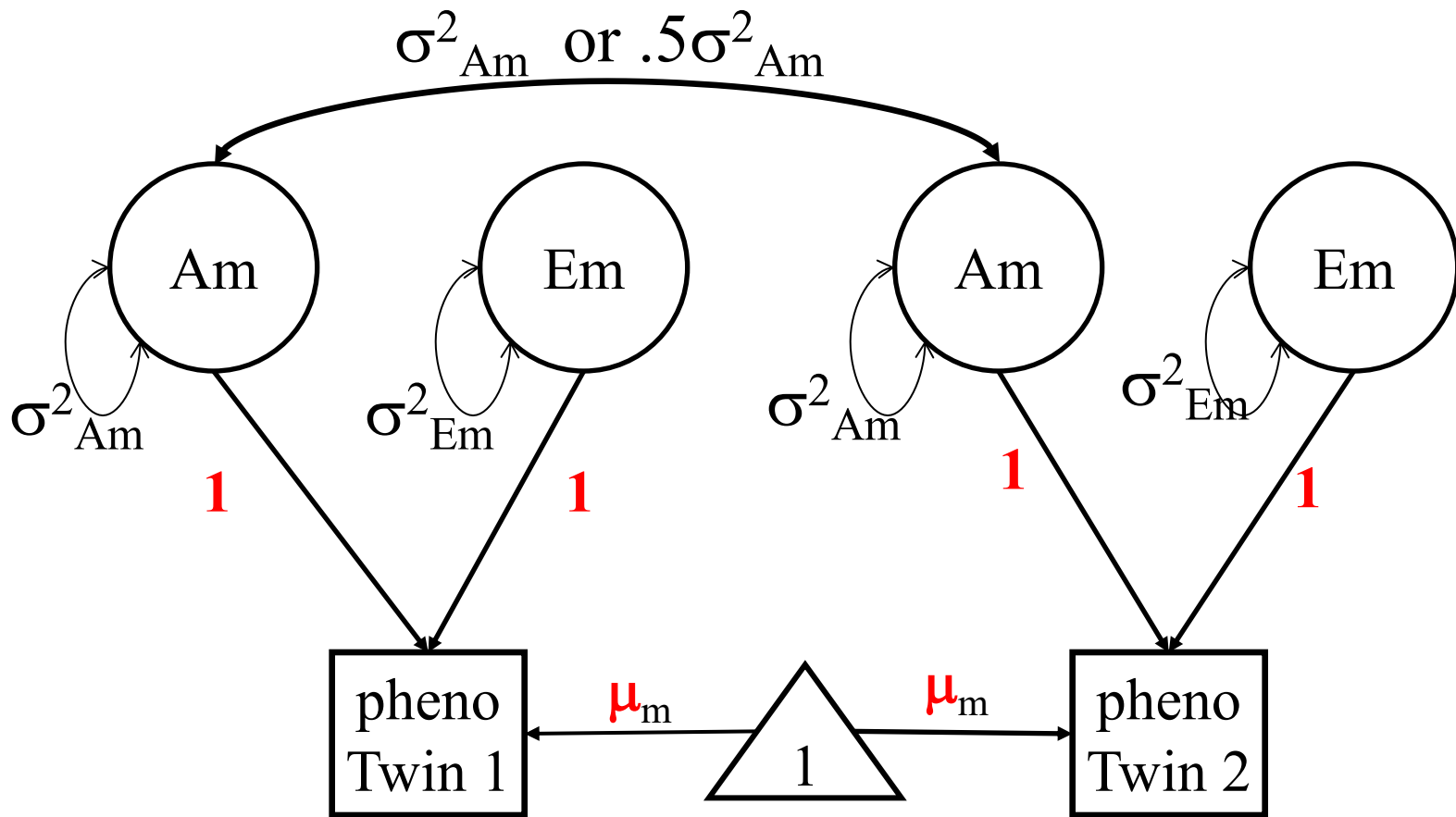
Sarah E. Medland · Michael C. Neale ·  
Lindon J. Eaves · Benjamin M. Neale

Sex special case.... DZOS!

... offer unique means to test hypotheses concerning genetic effects.

5 groups MZM, DZM, MZF, DZF, DZOS

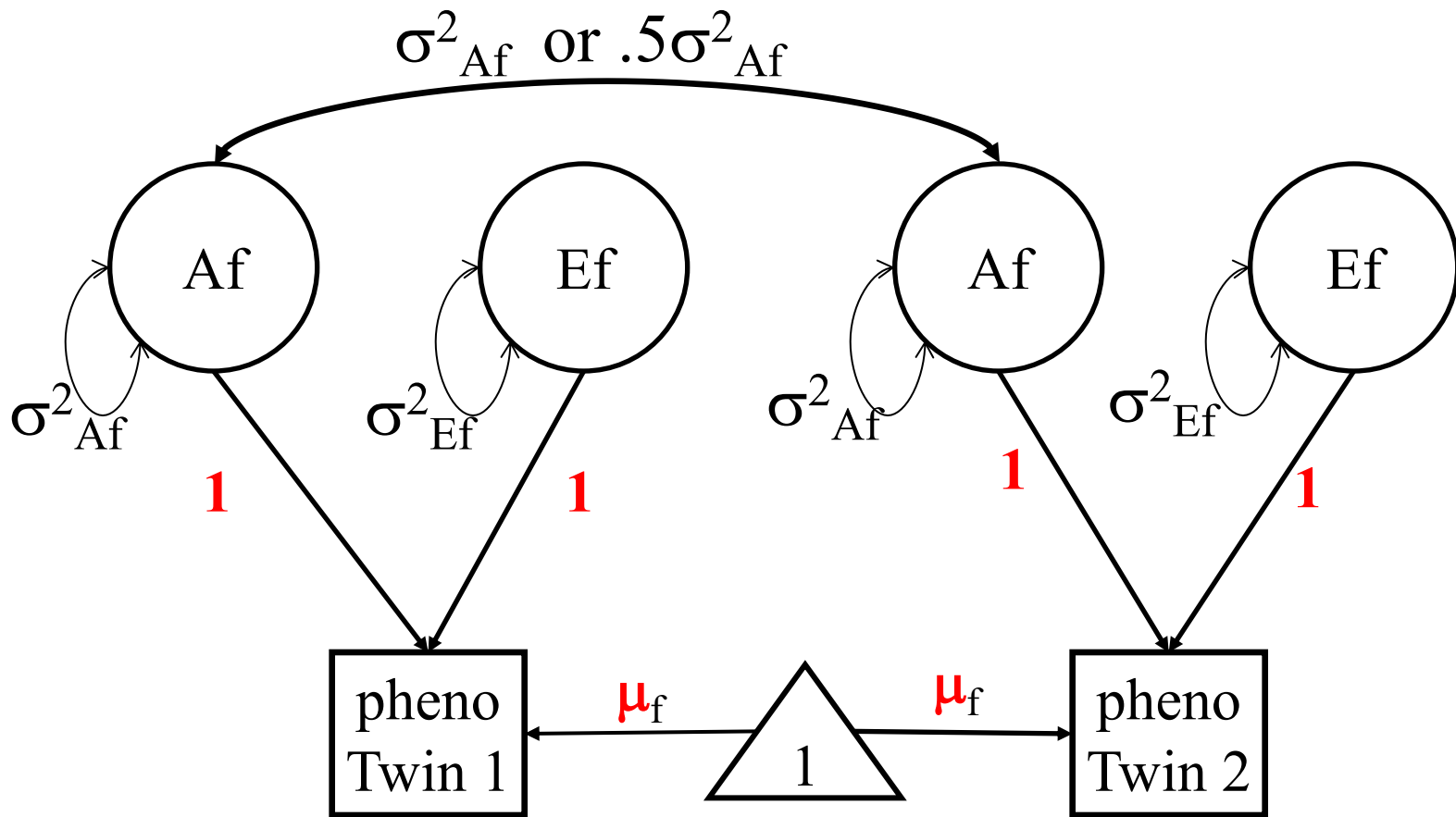
Considered in a 5 group model



$$\text{mean}(\text{Ph}_m) = \mu_m$$

$$\text{var}(\text{Ph}_m) = \sigma^2_{\text{Ph}} = \sigma^2_{\text{Am}} + \sigma^2_{\text{Em}}$$

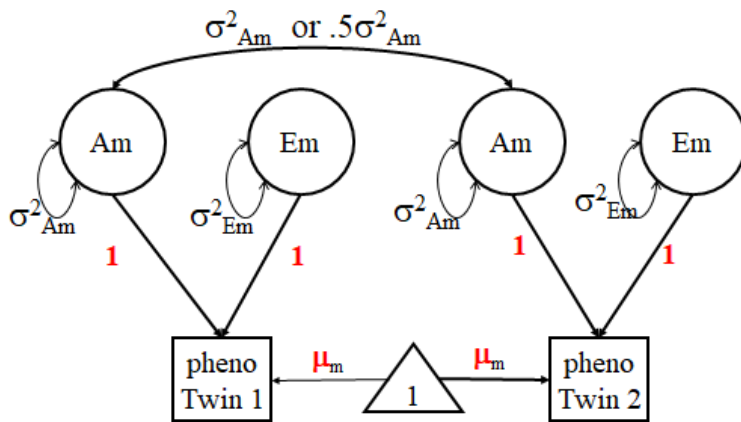
Males twins



$$\text{mean}(\text{Ph}_f) = \mu_f$$

$$\text{var}(\text{Ph}_f) = \sigma^2_{\text{Ph}} = \sigma^2_{\text{Af}} + \sigma^2_{\text{Ef}}$$

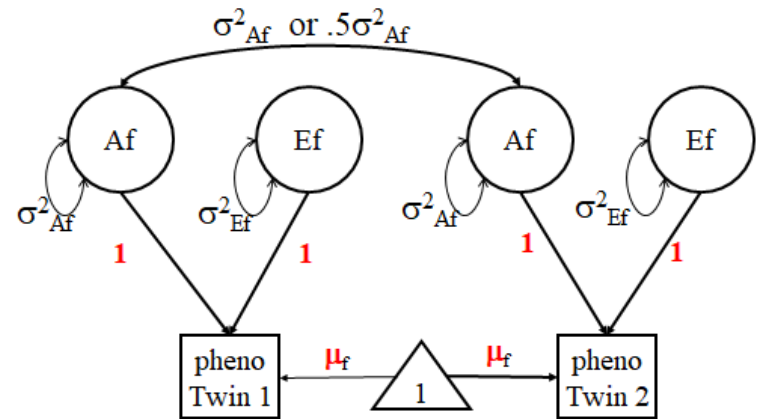
Females twins



$$\text{mean}(\text{Ph}_m) = \mu_m$$

$$\text{var}(\text{Ph}_m) = \sigma^2_{\text{Ph}} = \sigma^2_{Am} + \sigma^2_{Em}$$

Males twins



$$\text{mean}(\text{Ph}_f) = \mu_f$$

$$\text{var}(\text{Ph}_f) = \sigma^2_{\text{Ph}} = \sigma^2_{Af} + \sigma^2_{Ef}$$

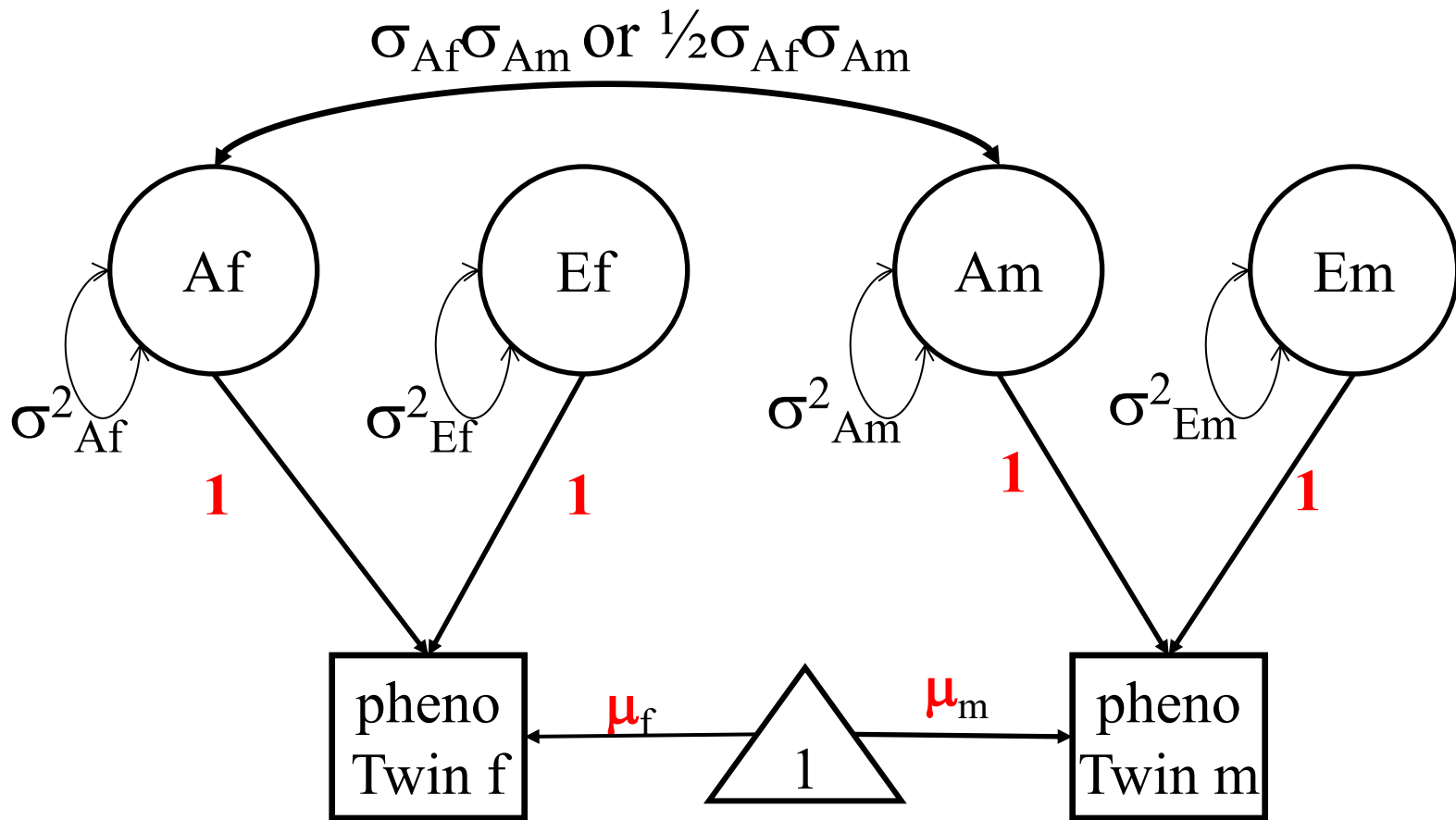
Females twins

$\mu_f = \mu_m$ ? sex differences in main effects

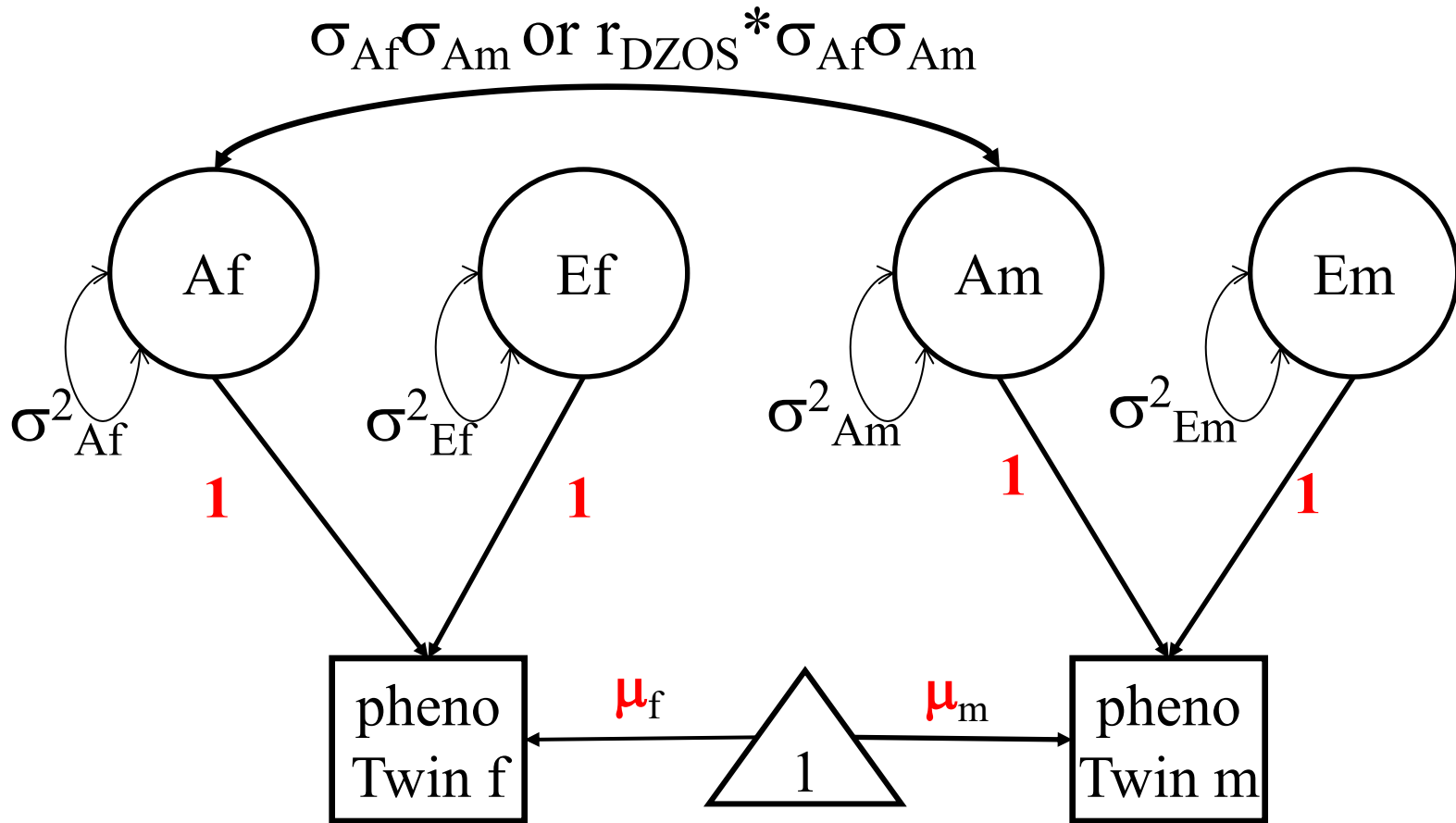
$s^2_{Af} = s^2_{Am}$ ? sex differences in A variance

$s^2_{Ef} = s^2_{Em}$ ? sex differences in E variance

(add  $s^2_{Df} = s^2_{Dm}$  or  $s^2_{Cf} = s^2_{Cm}$ )



DZOS (f,m) twins



## DZOS twins

$r_{DZOS} * \sigma_{Af}\sigma_{Am}$  note:  $r_{DZOS}$  is not necessarily  $1/2$

$r_{DZOS} = 1/2$  or  $r_{DZOS} < 1/2$  ?

# Models (ACE) (Stat or Subst)

total homogeneity (Subst)

$\mu_f = \mu_m$  (main effect absent)

$$\sigma^2_{Am} = \sigma^2_{Af} \&$$

$$\sigma^2_{Cm} = \sigma^2_{Cf} \&$$

$$\sigma^2_{Ef} = \sigma^2_{Em}$$

$$r_{DZOS} = 1/2$$

total variance homogeneity (Stat)

$\mu_f \neq \mu_m$  (main effect present)

$$\sigma^2_{Am} = \sigma^2_{Af}$$

$$\sigma^2_{Cm} = \sigma^2_{Cf} \&$$

$$\sigma^2_{Ef} = \sigma^2_{Em}$$

$$r_{DZOS} = 1/2$$



$\mu_f \neq \mu_m$  (main effect present)

**scalar sex limitation**  $r_{DZOS} = 1/2$  (Stat)

$$\begin{aligned} \sigma^2_{Am} \neq \sigma^2_{Af} \quad \& \quad \sigma^2_{Cm} \neq \sigma^2_{Cf} \quad \& \quad \sigma^2_{Ef} \neq \sigma^2_{Ef} \\ \sigma^2_{Am} = k^* \sigma^2_{Af} \quad \& \quad \sigma^2_{Cm} = k^* \sigma^2_{Cf} \quad \& \quad \sigma^2_{Ef} = k^* \sigma^2_{Ef} \end{aligned}$$

k is nonzero positive constant (to be estimated)

raw variances differ, but standardized variances are equal

$$\begin{aligned} \sigma^2_{Af} / (\sigma^2_{Af} + \sigma^2_{Cf} + \sigma^2_{Ef}) &= k^* \sigma^2_{Af} / (k^* \sigma^2_{Af} + k^* \sigma^2_{Cf} + k^* \sigma^2_{Ef}) \\ &= \mathbf{k^*} \sigma^2_{Af} / \mathbf{k^*} (\sigma^2_{Af} + \sigma^2_{Cf} + \sigma^2_{Ef}) = \sigma^2_{Af} / (\sigma^2_{Af} + \sigma^2_{Cf} + \sigma^2_{Ef}) \end{aligned}$$

parsimonious model for sex differences in variance,  
but quite restrictive (and not Subst!)

$\mu_f \neq \mu_m$  (main effect present)

## **non-scalar quantitative sex limitation**

$r_{DZOS} = 1/2$  (Subst)

$\sigma^2_{Am} \neq \sigma^2_{Af}$  &/or  $\sigma^2_{Cm} \neq \sigma^2_{Cf}$  &/or  $\sigma^2_{Ef} \neq \sigma^2_{Ef}$

$\sigma^2_{Am} \neq \sigma^2_{Af}$  & genetic effects are different, but  $r_{DZOS} = 1/2$  implies same genes in males and females.

So: sex moderates genetic effects (e.g., gene expression).

$\mu_f \neq \mu_m$  (main effect present)

**non-scalar qualitative sex limitation**

$r_{DZOS} \neq 1/2$  (Subst)

$\sigma^2_{Am} \neq \sigma^2_{Af}$  &/or  $\sigma^2_{Cm} \neq \sigma^2_{Cf}$  &/or  $\sigma^2_{Ef} \neq \sigma^2_{Ef}$

$\sigma^2_{Am} \neq \sigma^2_{Af}$  genetic effects are different, and  $r_{DZOS} \neq 1/2$  implies  
(*at least in part* different genes).

Nesting ACE model (cov structure, discarding the means)

**non-scalar qualitative**

7 parameters:  $\sigma^2_{Am}$   $\sigma^2_{Af}$   $\sigma^2_{Cm}$   $\sigma^2_{Cf}$   $\sigma^2_{Ef}$   $\sigma^2_{Ef}$   $r_{DZOS}$

fix  $r_{DZOS} = 1/2$  (1 df): **non-scalar quantitative** (omnibus: 3 differences)

6 parameters:  $\sigma^2_{Am}$   $\sigma^2_{Af}$   $\sigma^2_{Cm}$   $\sigma^2_{Cf}$   $\sigma^2_{Em}$   $\sigma^2_{Ef}$

proportionality constraint (2df): **scalar**

4 parameters:  $\sigma^2_{Cf}$   $\sigma^2_{Ef}$   $\sigma^2_{Ef}$   $k$

set  $k=1$  (1 df): **homogeneity**

3 parameters  $\sigma^2_{Cf}$   $\sigma^2_{Ef}$   $\sigma^2_{Ef}$

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# Alternate Parameterization for Scalar and Non-scalar Sex-limitation Models in Mx

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Sarah E. Medland<sup>1,2</sup>

Twin Research Volume 7 Number 3 pp. 299–308

# Caveat: Tests of moderation (interaction) are scale dependent.

*Br. J. math. statist. Psychol.* (1977), 30, 1–42 Printed in Great Britain

1

**A progressive approach to non-additivity and genotype–environmental covariance in the analysis of human differences.**

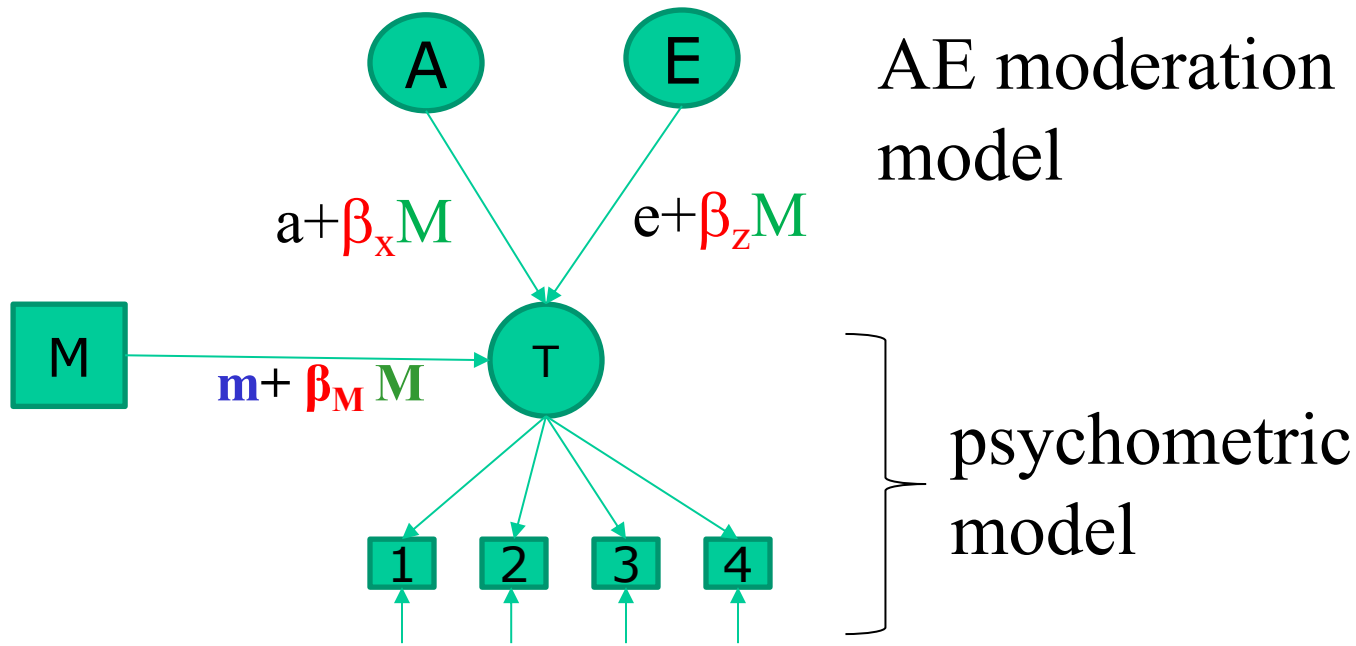
**L. J. Eaves, Krystyna Last, N. G. Martin and J. L. Jinks**

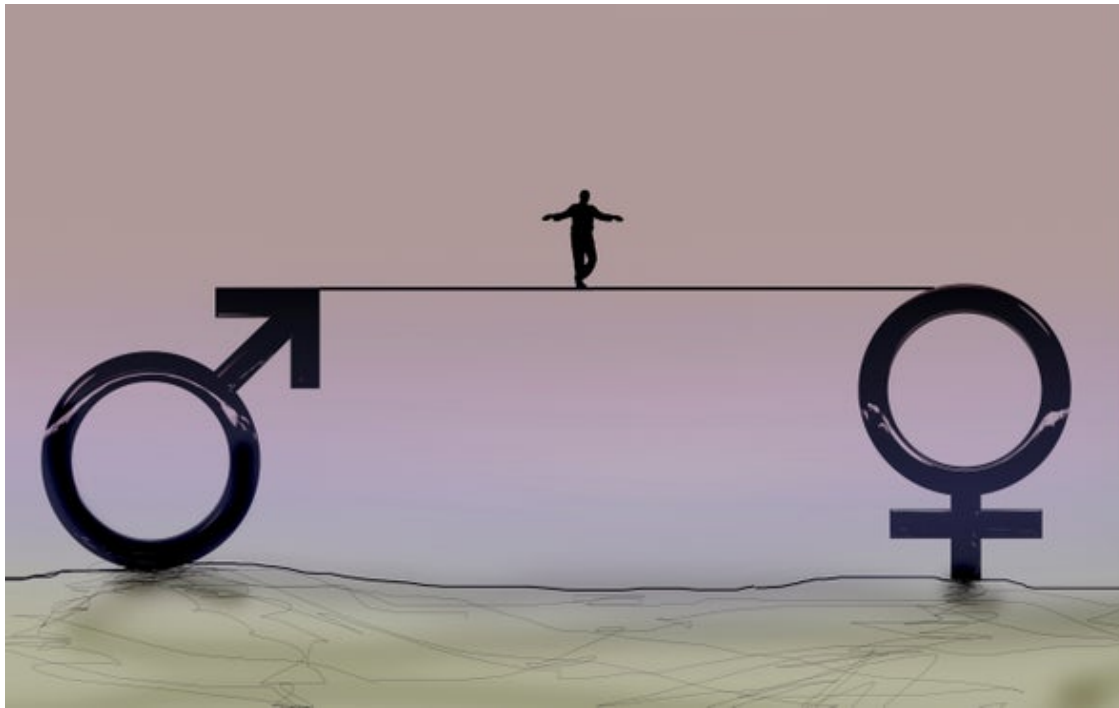
*Memory & Cognition*  
1978, Vol. 6 (3), 312-319

## On interpretation of interactions

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**Solution???:** Common pathway model with appropriate psychometric model (IRT model or a common factor model) & Define moderation at the level of the latent phenotype (Nathan Friday)





How would you revise the sex limitations model if you had a dimensional measure of sex?