2020 International Statistical Genetics Workshop

Introduction to Multivariate Genetic Analysis
PRACTICAL

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with thanks to Katrina Grasby, Jose Morosoli, Sarah Medland, and Dorret Boomsma

In \\workshop\Faculty\lucia\2020\Wednesday\twoACEvc_practical_2traits.R

The dataset: Simulated data

- Children age ~ 8 years old, 50 % females
- Phenotypes are scores on reading, grammar, writing, and math skills.
- Available both raw and scaled (mean 0, SD 1) – before restructuring the file to one row per family!
- Means and Variances could be equated across Twin Order and Zygosity
- No need of sex-limitation model
- Age and sex should be included as covariates

- We'll analyse "Read" and "Writ"

Three Concepts

1.- What is the variance due to genetic and (shared and unique) environmental contributions for each trait?
Variance Decomposition

2.- How much of the phenotypic correlation between the traits is accounted for by genetic and (shared and unique) environmental factors?
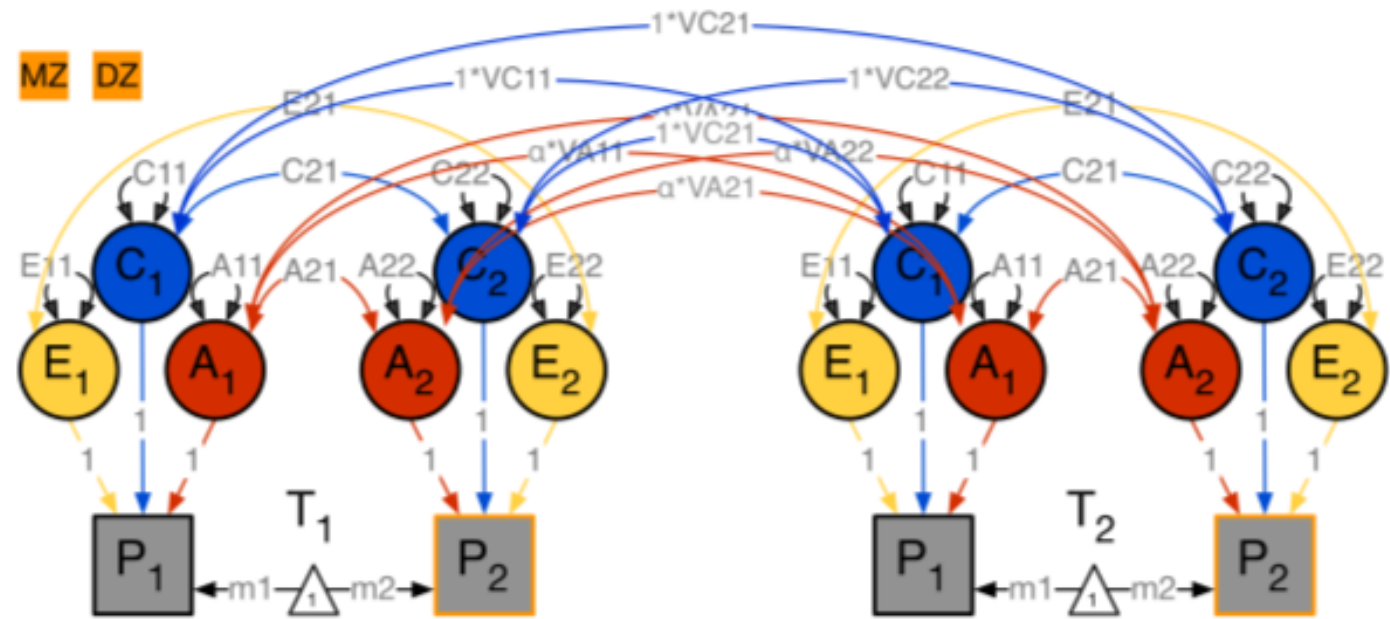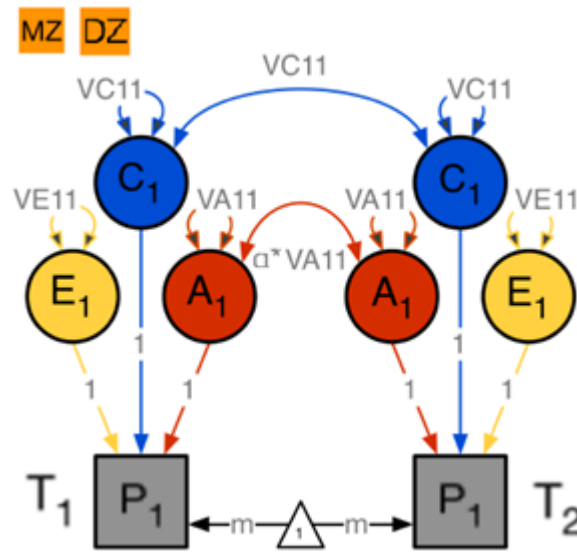*Covariance Decomposition*

3.- To what extent do the genetic factors underlying each trait overlap? And the (shared and unique) environmental factors?
Genetic and Environmental correlations

From

univariate

to

multivariate

α = assumed degree of genetic relatedness (1, 0.5)

Twin Covariances / Correlations

	twin 1		twin 2	
	$P1_{T1}$	$P2_{T1}$	$P1_{T2}$	$P2_{T2}$
$P1_{T1}$	$VP1_{T1}$	$CP1_{T1}P2_{T1}$	$CP1_{T1}P1_{T2}$	$CP1_{T1}P2_{T2}$
$P2_{T1}$	$CP1_{T1}P2_{T1}$	$VP2_{T1}$	$CP2_{T1}P1_{T2}$	$CP2_{T1}P2_{T2}$
$P1_{T2}$	$CP1_{T1}P1_{T2}$	$CP2_{T1}P1_{T2}$	$VP1_{T2}$	$CP1_{T2}P2_{T2}$
$P2_{T2}$	$CP1_{T1}P2_{T2}$	$CP2_{T1}P2_{T2}$	$CP1_{T2}P2_{T2}$	$VP2_{T2}$

Twin Covariances / Correlations

Variance/covariance matrices

MZ

		Twin 1		Twin 2	
		read_1	writ_1	read_2	writ_2
Twin 1	read_1	10.44	5.01	7.60	4.07
	writ_1	5.01	8.21	4.53	4.01
Twin 2	read_2	7.60	4.53	10.38	4.88
	writ_2	4.07	4.01	4.88	8.18

DZ

		Twin 1		Twin 2	
		read_1	writ_1	read_2	writ_2
Twin 1	read_1	9.75	4.33	4.21	2.27
	writ_1	4.33	7.66	2.97	2.71
Twin 2	read_2	4.21	2.97	9.78	5.13
	writ_2	2.27	2.71	5.13	7.68

Correlation matrices

MZ

		Twin 1		Twin 2	
		read_1	writ_1	read_2	writ_2
Twin 1	read_1	1.00	0.54	0.73	0.44
	writ_1	0.54	1.00	0.49	0.49
Twin 2	read_2	0.73	0.49	1.00	0.53
	writ_2	0.44	0.49	0.53	1.00

DZ

		Twin 1		Twin 2	
		read_1	writ_1	read_2	writ_2
Twin 1	read_1	1.00	0.50	0.43	0.26
	writ_1	0.50	1.00	0.34	0.35
Twin 2	read_2	0.43	0.34	1.00	0.59
	writ_2	0.26	0.35	0.59	1.00

Variance/covariance matrices

Correlation matrices

MZ

		Twin 1		Twin 2	
		read_1	writ_1	read_2	writ_2
Twin 1	read_1	10.44			
	writ_1	5.01	8.21		
Twin 2	read_2	7.60	4.53	10.38	
	writ_2	4.07	4.01	4.88	8.18

MZ

		Twin 1		Twin 2	
		read_1	writ_1	read_2	writ_2
Twin 1	read_1	1.00			
	writ_1	0.54	1.00		
Twin 2	read_2	0.73	0.49	1.00	
	writ_2	0.44	0.49	0.53	1.00

DZ

		Twin 1		Twin 2	
		read_1	writ_1	read_2	writ_2
Twin 1	read_1	9.75			
	writ_1	4.33	7.66		
Twin 2	read_2	4.21	2.97	9.78	
	writ_2	2.27	2.71	5.13	7.68

DZ

		Twin 1		Twin 2	
		read_1	writ_1	read_2	writ_2
Twin 1	read_1	1.00			
	writ_1	0.50	1.00		
Twin 2	read_2	0.43	0.34	1.00	
	writ_2	0.26	0.35	0.59	1.00

MZ

	Twin 1		Twin 2	
	read_1	writ_1	read_2	writ_2
Twin 1 read_1	1.00			
writ_1	0.54	1.00		
Twin 2 read_2	0.73	0.49	1.00	
writ_2	0.44	0.49	0.53	1.00

DZ

	Twin 1		Twin 2	
	read_1	writ_1	read_2	writ_2
Twin 1 read_1	1.00			
writ_1	0.50	1.00		
Twin 2 read_2	0.43	0.34	1.00	
writ_2	0.26	0.35	0.59	1.00

What are our initial expectations after looking at the covariance and correlation matrices by zygosity?

- Are there common etiological influences?

MZ

	Twin 1		Twin 2	
	read_1	writ_1	read_2	writ_2
Twin 1 read_1	1.00			
writ_1	0.54	1.00		
Twin 2 read_2	0.73	0.49	1.00	
writ_2	0.44	0.49	0.53	1.00

DZ

	Twin 1		Twin 2	
	read_1	writ_1	read_2	writ_2
Twin 1 read_1	1.00			
writ_1	0.50	1.00		
Twin 2 read_2	0.43	0.34	1.00	
writ_2	0.26	0.35	0.59	1.00

What are our initial expectations after looking at the covariance and correlation matrices by zygosity?

- Are there common etiological influences?
  Within-twin Cross-trait covariances

MZ

	Twin 1		Twin 2	
	read_1	writ_1	read_2	writ_2
Twin 1 read_1	1.00			
writ_1	0.54	1.00		
Twin 2 read_2	0.73	0.49	1.00	
writ_2	0.44	0.49	0.53	1.00

What are our initial expectations after looking at the covariance and correlation matrices by zygosity?

- Are there common etiological influences?
  Within-twin Cross-trait covariances

- Do familial common etiological influences contribute to the covariation?

DZ

	Twin 1		Twin 2	
	read_1	writ_1	read_2	writ_2
Twin 1 read_1	1.00			
writ_1	0.50	1.00		
Twin 2 read_2	0.43	0.34	1.00	
writ_2	0.26	0.35	0.59	1.00

MZ

	Twin 1		Twin 2	
	read_1	writ_1	read_2	writ_2
Twin 1 read_1	1.00			
writ_1	0.54	1.00		
Twin 2 read_2	0.73	0.49	1.00	
writ_2	0.44	0.49	0.53	1.00

DZ

	Twin 1		Twin 2	
	read_1	writ_1	read_2	writ_2
Twin 1 read_1	1.00			
writ_1	0.50	1.00		
Twin 2 read_2	0.43	0.34	1.00	
writ_2	0.26	0.35	0.59	1.00

What are our initial expectations after looking at the covariance and correlation matrices by zygosity?

- Are there common etiological influences?
  Within-twin Cross-trait covariances

- Do familial common etiological influences contribute to the covariation?
  Cross-twin Cross-trait covariances

MZ

	Twin 1		Twin 2	
	read_1	writ_1	read_2	writ_2
Twin 1 read_1	1.00			
writ_1	0.54	1.00		
Twin 2 read_2	0.73	0.49	1.00	
writ_2	0.44	0.49	0.53	1.00

DZ

	Twin 1		Twin 2	
	read_1	writ_1	read_2	writ_2
Twin 1 read_1	1.00			
writ_1	0.50	1.00		
Twin 2 read_2	0.43	0.34	1.00	
writ_2	0.26	0.35	0.59	1.00

What are our initial expectations after looking at the covariance and correlation matrices by zygosity?

- Are there common etiological influences?
  Within-twin Cross-trait covariances

- Do familial common etiological influences contribute to the covariation?
  Cross-twin Cross-trait covariances

- Are the common etiological influences genetic and/or environmental (A and/or C)?

MZ

	Twin 1		Twin 2	
	read_1	writ_1	read_2	writ_2
Twin 1 read_1	1.00			
writ_1	0.54	1.00		
Twin 2 read_2	0.73	0.49	1.00	
writ_2	0.44	0.49	0.53	1.00

DZ

	Twin 1		Twin 2	
	read_1	writ_1	read_2	writ_2
Twin 1 read_1	1.00			
writ_1	0.50	1.00		
Twin 2 read_2	0.43	0.34	1.00	
writ_2	0.26	0.35	0.59	1.00

What are our initial expectations after looking at the covariance and correlation matrices by zygosity?

- Are there common etiological influences?
  Within-twin Cross-trait covariances

- Do familial common etiological influences contribute to the covariation?
  Cross-twin Cross-trait covariances

- Are the common etiological influences genetic and/or environmental (A and/or C)?
  MZ/DZ ratio of Cross-twin Cross-trait covariances

MZ

	Twin 1		Twin 2	
	read_1	writ_1	read_2	writ_2
Twin 1 read_1	1.00			
writ_1	0.54	1.00		
Twin 2 read_2	0.73	0.49	1.00	
writ_2	0.44	0.49	0.53	1.00

DZ

	Twin 1		Twin 2	
	read_1	writ_1	read_2	writ_2
Twin 1 read_1	1.00			
writ_1	0.50	1.00		
Twin 2 read_2	0.43	0.34	1.00	
writ_2	0.26	0.35	0.59	1.00

What are our initial expectations after looking at the covariance and correlation matrices by zygosity?

- Are there common etiological influences?
  Within-twin Cross-trait covariances

- Do familial common etiological influences contribute to the covariation?
 Cross-twin Cross-trait covariances

- Are the common etiological influences genetic and/or environmental (A and/or C)?
  MZ/DZ ratio of Cross-twin Cross-trait covariances

- Is there evidence of covariation due to unique environment (E)?

MZ

		Twin 1		Twin 2	
		read_1	writ_1	read_2	writ_2
Twin 1	read_1	1.00			
	writ_1	0.54	1.00		
Twin 2	read_2	0.73	0.49	1.00	
	writ_2	0.44	0.49	0.53	1.00

DZ

		Twin 1		Twin 2	
		read_1	writ_1	read_2	writ_2
Twin 1	read_1	1.00			
	writ_1	0.50	1.00		
Twin 2	read_2	0.43	0.34	1.00	
	writ_2	0.26	0.35	0.59	1.00

What are our initial expectations after looking at the covariance and correlation matrices by zygosity?

- Are there common etiological influences?
  Within-twin Cross-trait covariances

- Do familial common etiological influences contribute to the covariation?
  Cross-twin Cross-trait covariances

- Are the common etiological influences genetic and/or environmental (A and/or C)?
  MZ/DZ ratio of Cross-twin Cross-trait covariances

- Is there evidence of covariation due to unique environment (E)?
  Ratio of cross-twin to within-twin cross-trait covariance

Variance Components
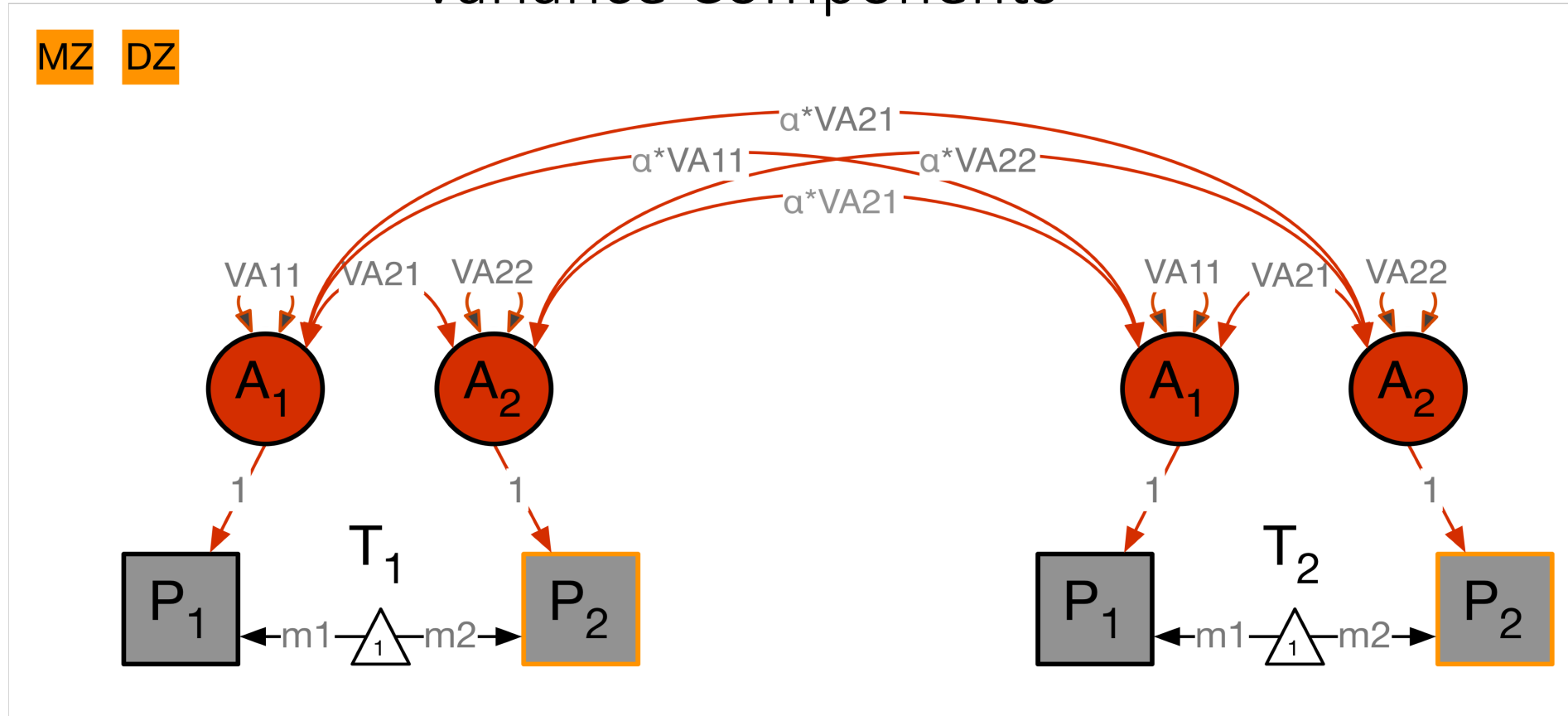

```
covA  <- mxMatrix( type="Symm", nrow=nv, ncol=nv, free=TRUE,
values=valDiag(svPa,nv), labels=labLower("VA",nv), name="VA" )
```

```
          [,1]    [,2]
[1,]  "VA11"  "VA21"
[2,]  "VA21"  "VA22"
```

α = assumed degree of genetic relatedness (1, 0.5)

Predicted MZ Twin Covariance

		twin 1		twin 2	
		$P1_{T1}$	$P2_{T1}$	$P1_{T2}$	$P2_{T2}$
twin 1	$P1_{T1}$	VA11 +VC11 +VE11	VA21 +VC21 +VE21	VA11 +VC11	VA21 +VC21
	$P2_{T1}$	VA21 +VC21 +VE21	VA22 +VC22 +VE22	VA21 +VC21	VA22 +VC22
twin 2	$P1_{T2}$	VA11 +VC11	VA21 +VC21	VA11 +VC11 +VE11	VA21 +VC21 +VE21
	$P2_{T2}$	VA21 +VC21	VA22 +VC22	VA21 +VC21 +VE21	VA22 +VC22 +VE22

Predicted DZ Twin Covariance

		twin 1		twin 2	
		$P1_{T1}$	$P2_{T1}$	$P1_{T2}$	$P2_{T2}$
twin 1	$P1_{T1}$	VA11 +VC11 +VE11	VA21 +VC21 +VE21	0.5 * VA11 +VC11	0.5 * VA21 +VC21
	$P2_{T1}$	VA21 +VC21 +VE21	VA22 +VC22 +VE22	0.5 * VA21 +VC21	0.5 *VA22 +VC22
twin 2	$P1_{T2}$	0.5 * VA11 +VC11	0.5 * VA21 +VC21	VA11 +VC11 +VE11	VA21 +VC21 +VE21
	$P2_{T2}$	0.5 * VA21 +VC21	0.5 *VA22 +VC22	VA21 +VC21 +VE21	VA22 +VC22 +VE22

```
## Create Algebra for expected Variance/Covariance Matrices in MZ & DZ twins

covP        <- mxAlgebra( expression= VA+VC+VE, name="V" )
covMZ       <- mxAlgebra( expression= VA+VC, name="cMZ" )
covDZ       <- mxAlgebra( expression= 0.5%x%VA+ VC, name="cDZ" )

expCovMZ  <- mxAlgebra( expression= rbind( cbind(V, cMZ),
                                           cbind(t(cMZ), V)), name="expCovMZ" )
expCovDZ  <- mxAlgebra( expression= rbind( cbind(V, cDZ),
                                           cbind(t(cDZ), V)), name="expCovDZ" )
```
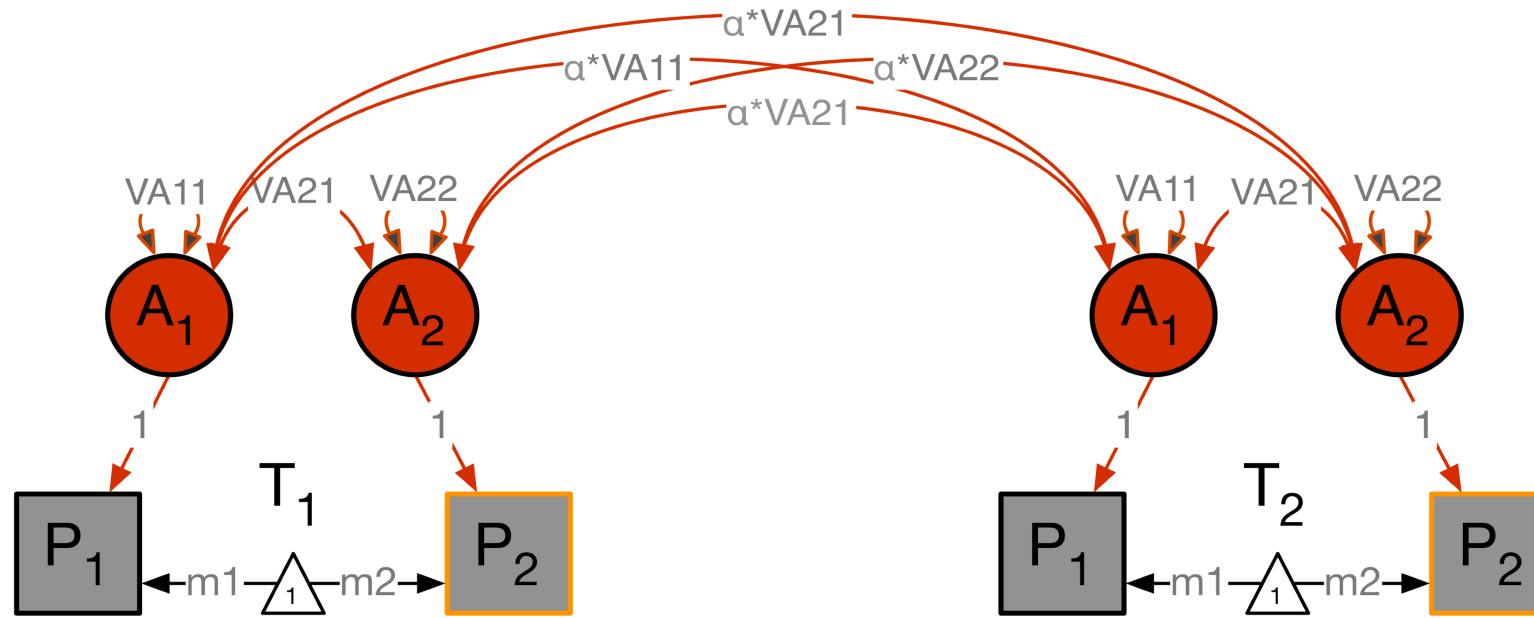
Correlations

corA   <- mxAlgebra(expression=solve(sqrt(I*VA))%&%VA, name ="rA")

$$r_g = \frac{VA_{12}}{\sqrt{VA_{11} * VA_{22})}}$$

$$\begin{bmatrix} 1 & r_g \\ r_g & 1 \end{bmatrix} = \begin{bmatrix} \frac{1}{\sqrt{\sigma^2_{A_{11}}}} & 0 \\ 0 & \frac{1}{\sqrt{\sigma^2_{A_{22}}}} \end{bmatrix} * \begin{bmatrix} \sigma^2_{A_{11}} & \sigma^2_{A_{12}} \\ \sigma^2_{A_{21}} & \sigma^2_{A_{22}} \end{bmatrix} * \begin{bmatrix} \frac{1}{\sqrt{\sigma^2_{A_{11}}}} & 0 \\ 0 & \frac{1}{\sqrt{\sigma^2_{A_{22}}}} \end{bmatrix}$$

Three Important Concepts

1.- What is the variance due to genetic and environmental contributions for each trait?
Variance Decomposition

2.- How much of the phenotypic correlation between the traits is accounted for by genetic and environmental factors?
Covariance Decomposition

3.- To what extent do the genetic factors underlying each trait overlap? And the environmental factors?
Genetic and Environmental correlations

	SA	SC	SE
Read			
Write			

```
> fitACE$algebras$SV
mxAlgebra 'SV'
$formula:  cbind(VA/V, VC/V, VE/V)
$result:
        SA          SA          SC          SC          SE          SE
SV 0.57018782 0.60226513 0.14994850 0.25553311 0.27986369 0.14220176
SV 0.60226513 0.25562130 0.25553311 0.22731236 0.14220176 0.51706634
```

	SA	SC	SE
Read			
Write			

```
> fitACE$algebras$SV
mxAlgebra 'SV'
$formula:  cbind(VA/V, VC/V, VE/V)
$result:
            SA           SA           SC           SC           SE         SE
SV 0.57018782  0.60226513  0.14994850  0.25553311  0.27986369  0.14220176
SV 0.60226513  0.25562130  0.25553311  0.22731236  0.14220176  0.51706634
```

	SA	SC	SE
Read	0.57 (0.44,0.70)	0.15 (0.03,0.26)	0.28 (0.24,0.32)
Write			

To retrieve the intervals, run: fitACE   <- mxRun(modelACE, intervals=T)

```
> fitACE$algebras$SV
mxAlgebra 'SV'
$formula:  cbind(VA/V, VC/V, VE/V)
$result:
            SA          SA          SC          SC          SE          SE
SV 0.57018782 0.60226513 0.14994850 0.25553311 0.27986369 0.14220176
SV 0.60226513 0.25562130 0.25553311 0.22731236 0.14220176 0.51706634
```

	SA	SC	SE
Read	0.57 (0.44,0.70)	0.15 (0.03,0.26)	0.28 (0.24,0.32)
Write	0.26 (0.08,0.42)	0.23 (0.09,0.36)	0.52 (0.45,0.59)

To retrieve the intervals, run: fitACE   <- mxRun(modelACE, intervals=T)

Three Important Concepts

1.- What is the variance due to genetic and (shared and unique) environmental contributions for each trait?
Variance Decomposition

Genetic, common environmental and unique genetic factors (including measurement error) contribute to 57%, 15%, and 28% of the individual differences in read, respectively.
Genetic, common environmental and unique genetic factors (including measurement error) contribute to 26%, 23%, and 52% of the individual differences in write, respectively.

Three Important Concepts

1.- What is the variance due to genetic and (shared and unique) environmental contributions for each trait?
Variance Decomposition

2.- How much of the phenotypic correlation between the traits is accounted for by genetic and (shared and unique) environmental factors?
Covariance Decomposition

3.- To what extent do the genetic factors underlying each trait overlap? And the (shared and unique) environmental factors?
Genetic and Environmental correlations

	SA12	SC12	SE12
Read-write			

```
> fitACE$algebras$SV
mxAlgebra 'SV'
$formula:  cbind(VA/V, VC/V, VE/V)
$result:
          SA          SA          SC          SC          SE          SE
SV 0.57018782 0.60226513 0.14994850 0.25553311 0.27986369 0.14220176
SV 0.60226513 0.25562130 0.25553311 0.22731236 0.14220176 0.51706634
```

	SA12	**SC12**	**SE12**
Read-write			

To retrieve the intervals, run: fitACE   <- mxRun(modelACE, intervals=T)

```
> fitACE$algebras$SV
mxAlgebra 'SV'
$formula:  cbind(VA/V, VC/V, VE/V)
$result:
           SA           SA           SC           SC           SE           SE
SV 0.57018782 0.60226513 0.14994850 0.25553311 0.27986369 0.14220176
SV 0.60226513 0.25562130 0.25553311 0.22731236 0.14220176 0.51706634
```

	SA12	SC12	SE12
Read-write	0.60 (0.40,0.81)	0.26 (0.08,0.42)	0.14 (0.08,0.21)

To retrieve the intervals, run: fitACE   <- mxRun(modelACE, intervals=T)

```
> fitACE$algebras$SV
mxAlgebra 'SV'
$formula:  cbind(VA/V, VC/V, VE/V)
$result:
           SA            SA            SC            SC            SE            SE
SV  0.57018782  0.60226513  0.14994850  0.25553311  0.27986369  0.14220176
SV  0.60226513  0.25562130  0.25553311  0.22731236  0.14220176  0.51706634
```

	SA12	SC12	SE12
Read-write	0.60 (0.40,0.81)	0.26 (0.08,0.42)	0.14 (0.08,0.21)

Remember the relative importance of the covariance of A, C, and E depends on the r_{ph}.
If r_{ph} is very low, a covariance of 0.60 due to genetic factors means nothing.

To retrieve the intervals, run: fitACE   <- mxRun(modelACE, intervals=T)

Three Important Concepts

2.- How much of the phenotypic correlation between the traits is accounted for by genetic and (shared and unique) environmental factors?
Covariance Decomposition

Genetic, common environmental and unique genetic factors contribute to 60%, 26%, and 14% of the covariance between read and write, respectively.

Three Important Concepts

1.- What is the variance due to genetic and (shared and unique) environmental contributions for each trait?
Variance Decomposition

2.- How much of the phenotypic correlation between the traits is accounted for by genetic and (shared and unique) environmental factors?
Covariance Decomposition

3.- To what extent do the genetic factors underlying each trait overlap? And the (shared and unique) environmental factors?
Genetic and Environmental correlations

	r_a	r_c	r_e	r_{ph}
Read-write				

```
> fitACE$algebras$corr
mxAlgebra 'corr'
$formula:  cbind(rA, rC, rE, rP)
$result:
          rA          rA          rC          rC          rE        rE        rP        rP
corr 1.00000000 0.85377382 1.00000000 0.74907828 1.00000000 0.20231178 1.000000 0.541206
corr 0.85377382 1.00000000 0.74907828 1.00000000 0.20231178 1.00000000 0.541206 1.000000
```

	r_a	r_c	r_e	r_{ph}
Read-write	0.85 (0.62,1)	0.75 (0.33,1)	0.20 (0.11,0.29)	0.54 (0.51,0.57)

Three Important Concepts

3.- To what extent do the genetic factors underlying each trait overlap? And the (shared and unique) environmental factors?
Genetic and Environmental correlations

The genetic and common shared environment correlations between read and write are large (r_a = .85 and r_c = .75); the unique environment correlation is low (r_e = .20).

85%, 75%, and 20% of the genetic factors, shared environmental factors, and unique environmental factors between read and write overlap.

Correlations. Interpreting Results

- High r_a = large overlap in genetic effects on the two traits
  - If r_a = 1, the two sets of genes influencing each trait overlap completely

- If there is a high r_a , does it mean that the phenotypic correlation between the traits is largely due to genetic effects?

  No: The contribution to r_{ph} is a function of both h^2 of the traits and r_a

  - i.e. the substantive importance of genetic effects depends on the value of the r_a and the heritability of each phenotype (h^2)

$$\text{Proportion of } r_{ph} \text{ due to A:} \quad \frac{\sqrt{h^2_{P1}} * r_g * \sqrt{h^2_{P2}}}{r_{ph}}$$

- Same for r_c and r_e

Consider write-read

$r_{ph} = 0.54$ and $r_a = 0.85$

$SA_{read} = 0.58$ and $SA_{write} = 0.26$

What is the contribution to phenotypic correlation attributable to additive genetic effects?

Proportion of r_{ph} due to A:
$$\frac{\sqrt{h^2_{P1}} * r_g * \sqrt{h^2_{P2}}}{r_{ph}}$$

- Same for r_c and r_e

Consider write-read

r_{ph} = 0.54 and r_a = 0.85

SA_{read}=0.58 and SA_{write}=0.26

What is the contribution to phenotypic correlation attributable to additive genetic effects?

Proportion of r_{ph} due to A: $$\frac{\sqrt{h^2_{P1}} * r_g * \sqrt{h^2_{P2}}}{r_{ph}}$$

- Same for r_c and r_e

Prop of r_{ph} due to A: (sqrt(0.58)*0.85*sqrt(0.26))/0.54 = 0.61 (61%)
Prop of r_{ph} due to C: (sqrt(0.15)*0.75*sqrt(0.23))/0.54 = 0.22 (26%)
Prop of r_{ph} due to E: (sqrt(0.28)*0.20*sqrt(0.52))/0.54 = 0.15 (15%)

Consider write-read

$r_{ph} = 0.54$ and $r_a = 0.85$

$SA_{read}=0.58$ and $SA_{write}=0.26$

What is the contribution to phenotypic correlation attributable to additive genetic effects?

Proportion of r_{ph} due to A: $\dfrac{\sqrt{h^2_{P1}} * r_g * \sqrt{h^2_{P2}}}{r_{ph}}$

- Same for r_c and r_e

Prop of r_{ph} due to A: (sqrt(0.58)*0.85*sqrt(0.26))/0.54 = 0.61 (61%)
Prop of r_{ph} due to C: (sqrt(0.15)*0.75*sqrt(0.23))/0.54 = 0.22 (26%)
Prop of r_{ph} due to E: (sqrt(0.28)*0.20*sqrt(0.52))/0.54 = 0.15 (15%)

	SA12	SC12	SE12
Read-write	0.60 (0.40,0.81)	0.26 (0.08,0.42)	0.14 (0.08,0.21)

Consider write-read

r_{ph} = 0.54 and r_a = 0.85

SA_{read}=0.58 and SA_{write}=0.26

This only makes sense if all the covariances have the same sign

What is the contribution to phenotypic correlation attributable to additive genetic effects?

Proportion of r_{ph} due to A: $$\frac{\sqrt{h^2_{P1}} * r_g * \sqrt{h^2_{P2}}}{r_{ph}}$$

- Same for r_c and r_e

Prop of r_{ph} due to A: (sqrt(0.58)*0.85*sqrt(0.26))/0.54 = 0.61 (61%)
Prop of r_{ph} due to C: (sqrt(0.15)*0.75*sqrt(0.23))/0.54 = 0.22 (26%)
Prop of r_{ph} due to E: (sqrt(0.28)*0.20*sqrt(0.52))/0.54 = 0.15 (15%)

	SA12	SC12	SE12
Read-write	0.60 (0.40,0.81)	0.26 (0.08,0.42)	0.14 (0.08,0.21)

Consider other variables with

$r_{ph} = 0.54$ and $r_a = 0.85$

$SA_{P1} = 0.10$ and $SA_{P2} = 0.15$

What is the contribution to phenotypic correlation attributable to additive genetic effects?

Proportion of r_{ph} due to A: $\dfrac{\sqrt{h^2_{P1}} * r_g * \sqrt{h^2_{P2}}}{r_{ph}}$

- Same for r_c and r_e

Prop of r_{ph} due to A: (sqrt(0.10)*0.85*sqrt(0.15))/0.54 = 0.20 (20%)

What's the best fitting model?

- Check submodels

Now let's add more variables!

In \\workshop\Faculty\lucia\2020\Wednesday\twoACEvc_practical_3traits.R

	SA			SC			SE		
	Read	Write	Math_R	Read	Write	Math_R	Read	Write	Math_R
Read									
Write									
Math_R									

	r_a			r_c			r_e			r_{ph}		
	Read	Write	Math_R	Read	Write	Math_R	Read	Write	Math_R	Write	Read	Math_R
Read												
Write												
Math_R												

	SA			SC			SE		
	Read	Write	Math_R	Read	Write	Math_R	Read	Write	Math_R
Read	0.58			0.15			0.28		
Write	0.62	0.27		0.24	0.22		0.14	0.51	
Math_R	0.69	0.60	0.58	0.22	0.31	0.15	0.09	0.08	0.27

	r_a			r_c			r_e			r_{ph}		
	Read	Write	Math_R	Read	Write	Math_R	Read	Write	Math_R	Write	Read	Math_R
Read	1			1			1			1		
Write	0.85	1		0.74	1		0.19	1		0.54	1	
Math_R	0.79	0.80	1	0.98	0.86	1	0.22	0.12	1	0.66	0.51	1