

# **Introduction to Multivariate Genetic Analysis**

**Meike Bartels, Hermine Maes, Elizabeth  
Prom-Wormley and Michel Nivard**

# Aim and Rationale

---

Aim: to examine the source of factors that make traits correlate or co-vary

Rationale: Traits may be correlated due to shared genetic factors (A) or shared environmental factors (C or E)

Can use information on multiple traits from twin pairs to partition covariation into genetic and environmental components

# Example 1

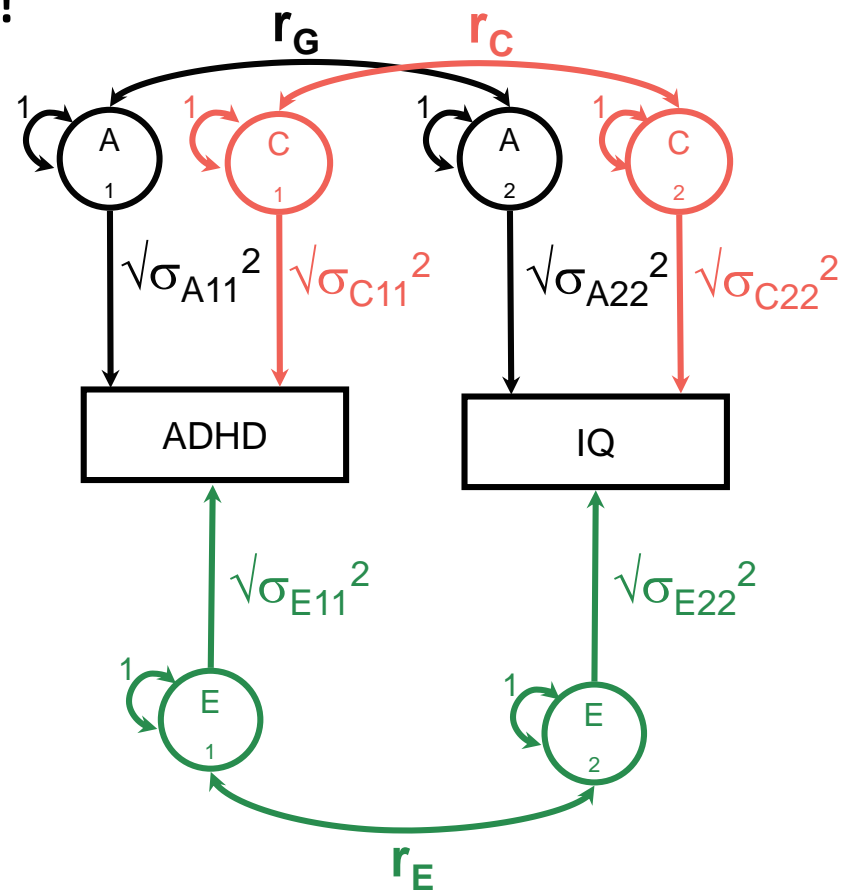
Why do traits correlate/covary?

How can we explain the association?

Additive genetic factors ( $r_G$ )

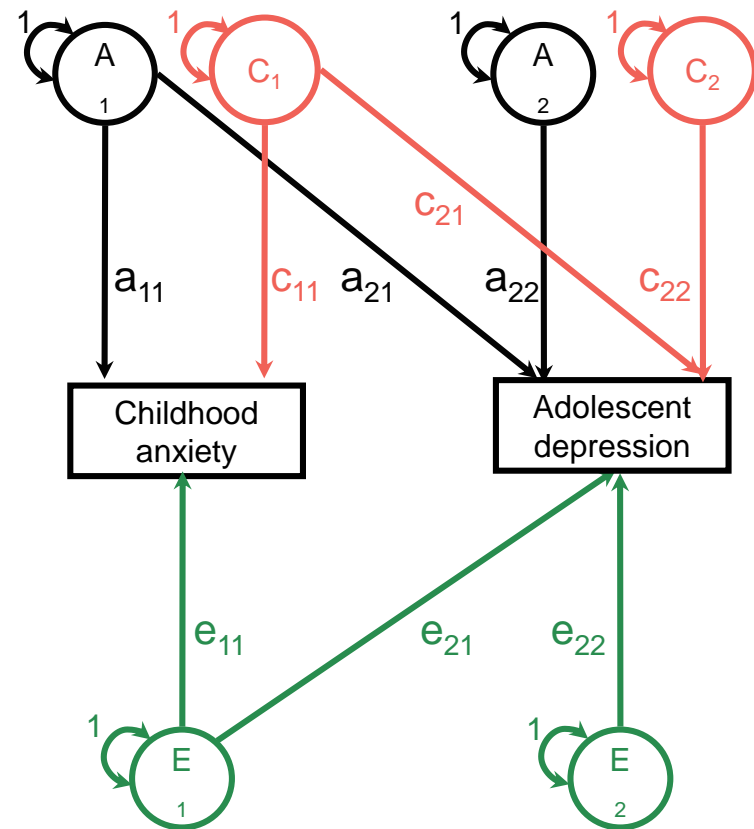
Shared environment ( $r_C$ )

Non-shared environment ( $r_E$ )



# Example 2

- Associations between phenotypes over time
  - ◆ Does anxiety in childhood lead to depression in adolescence?
- How can we explain the association?
  - ◆ Additive genetic factors ( $a_{21}$ )
  - ◆ Shared environment ( $c_{21}$ )
  - ◆ Non-shared environment ( $e_{21}$ )
  - ◆ How much is not explained by prior anxiety?



# Sources of Information

---

- For example: two traits measured in twin pairs
- Interested in:
  - ◆ Cross-trait covariance *within* individuals
  - ◆ Cross-trait covariance *between* twins
  - ◆ MZ:DZ ratio of cross-trait covariance between twins

# Observed Covariance Matrix

		Twin 1		Twin 2	
		Phenotype 1	Phenotype 2	Phenotype 1	Phenotype 2
Twin 1	Phenotype 1	Variance P1			
	Phenotype 2	Covariance P1-P2	Variance P2		
Twin 2	Phenotype 1	Within-trait P1	Cross-trait	Variance P1	
	Phenotype 2	Cross-trait	Within-trait P2	Covariance P1-P2	Variance P2

# Observed Covariance Matrix

		Twin 1		Twin 2	
		Phenotype 1	Phenotype 2	Phenotype 1	Phenotype 2
Twin 1		<b>Within-twin covariance</b>			
	Phenotype 1	Variance P1			
	Phenotype 2	Covariance P1-P2	Variance P2		
Twin 2				<b>Within-twin covariance</b>	
	Phenotype 1	Within-trait P1	Cross-trait	Variance P1	
	Phenotype 2	Cross-trait	Within-trait P2	Covariance P1-P2	Variance P2

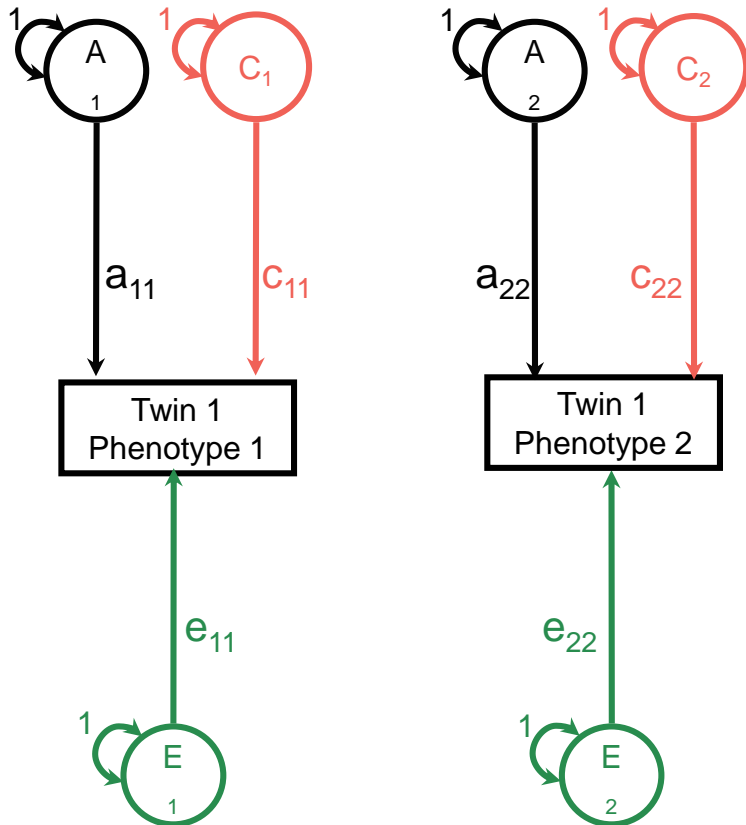
# Observed Covariance Matrix

		Twin 1		Twin 2	
		Phenotype 1	Phenotype 2	Phenotype 1	Phenotype 2
Twin 1		<b>Within-twin covariance</b>			
	Phenotype 1	Variance P1			
	Phenotype 2	Covariance P1-P2	Variance P2		
Twin 2		<b>Cross-twin covariance</b>		<b>Within-twin covariance</b>	
	Phenotype 1	Within-trait P1	Cross-trait	Variance P1	
	Phenotype 2	Cross-trait	Within-trait P2	Covariance P1-P2	Variance P2



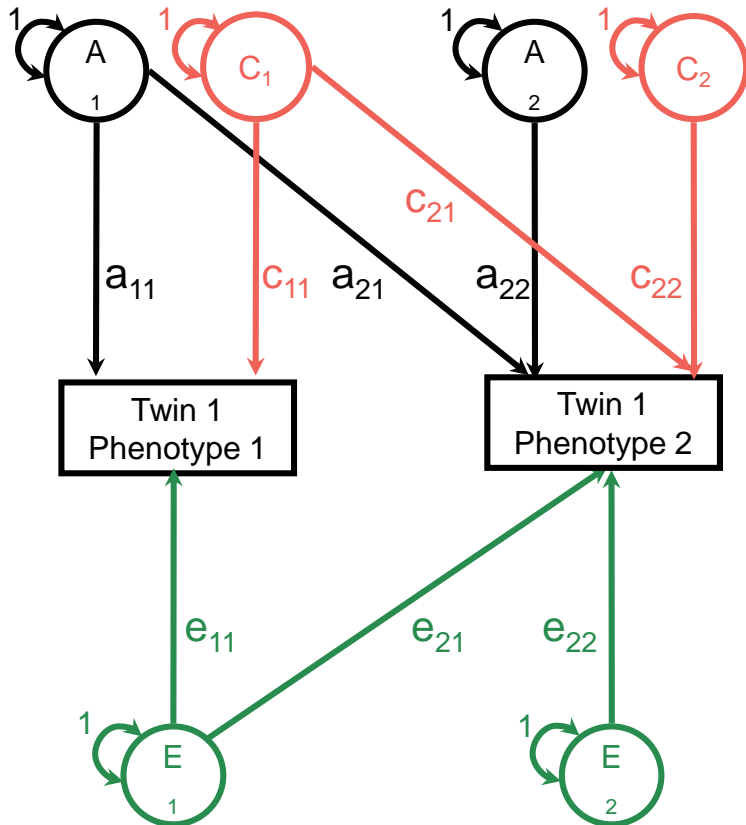
# SEM: Cholesky Decomposition

---

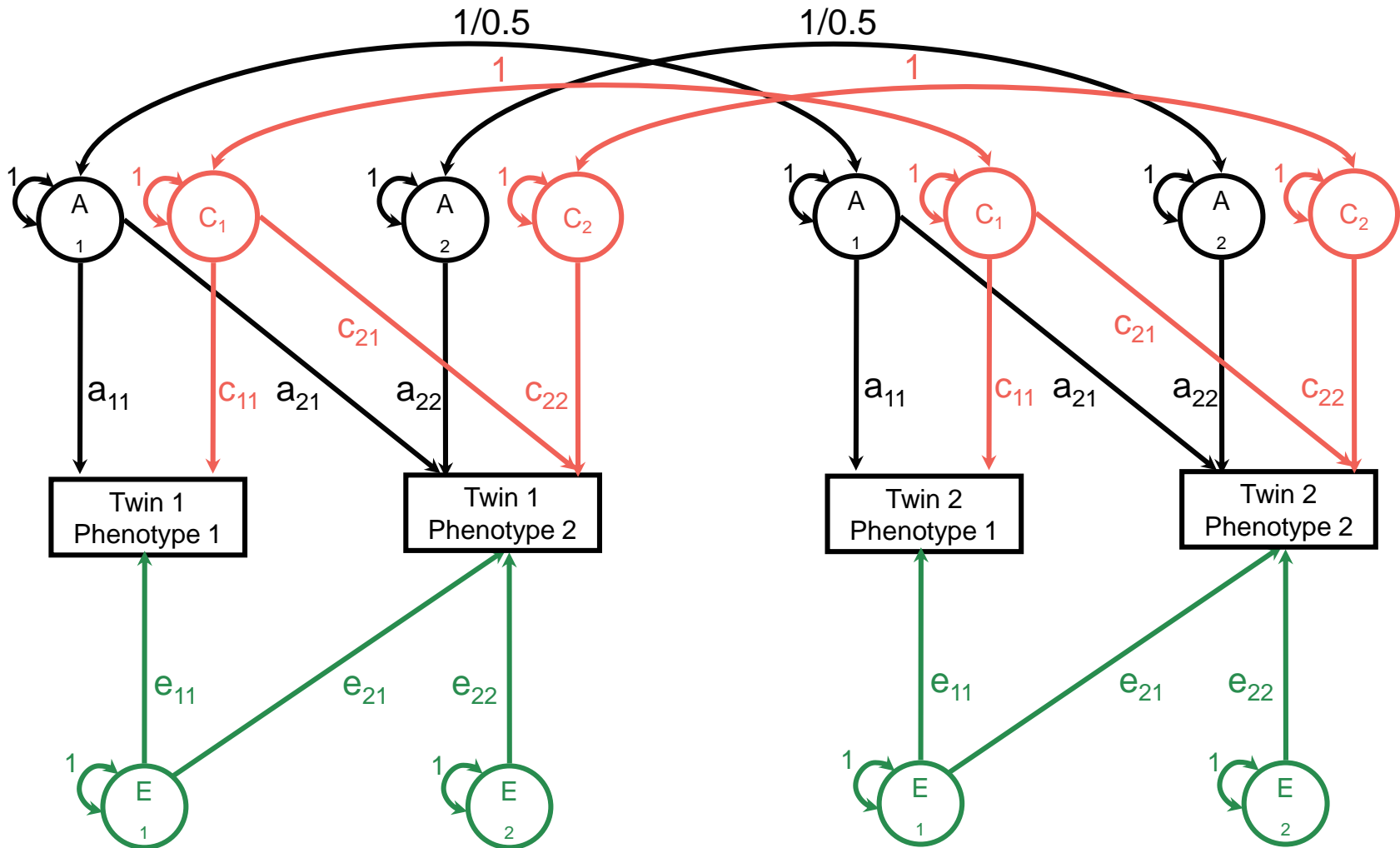


# SEM: Cholesky Decomposition

---



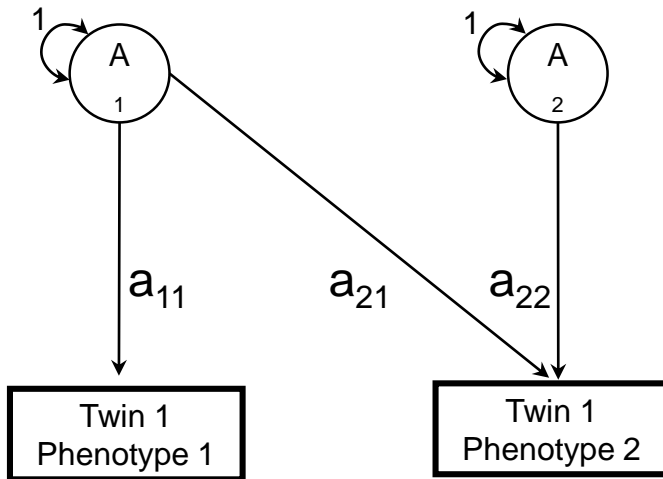
# SEM: Cholesky Decomposition



# **Cholesky Decomposition**

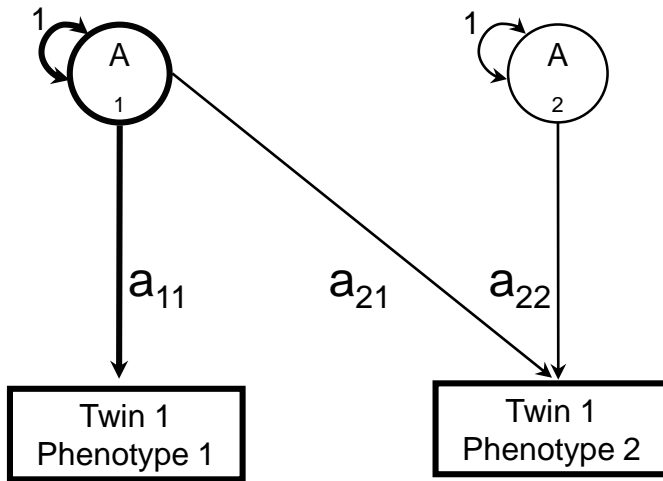
## **Path Tracing**

# Within-Twin Covariances (A)



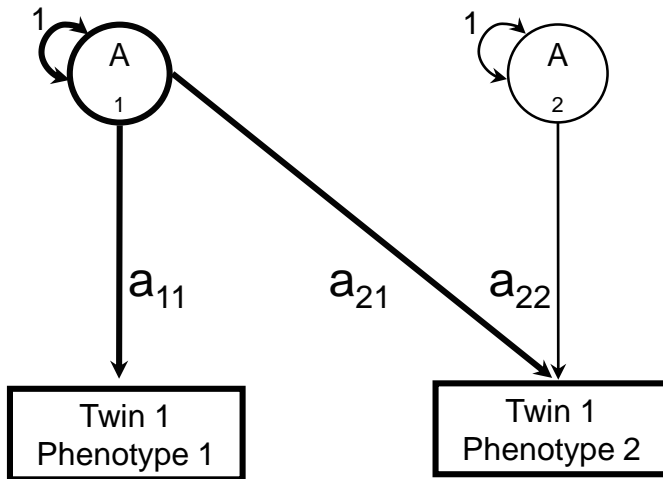
		Twin 1	
		Phenotype 1	Phenotype 2
Twin 1	Phenotype 1		
	Phenotype 2		

# Within-Twin Covariances (A)



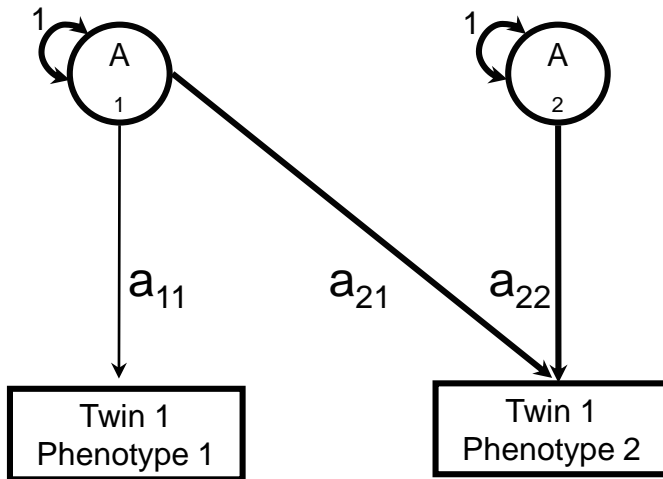
		Twin 1	
		Phenotype 1	Phenotype 2
Twin 1	Phenotype 1	$a_{11}^2$	
	Phenotype 2		

# Within-Twin Covariances (A)



		Twin 1	
		Phenotype 1	Phenotype 2
Twin 1	Phenotype 1	$a_{11}^2$	
	Phenotype 2	$a_{11}a_{21}$	

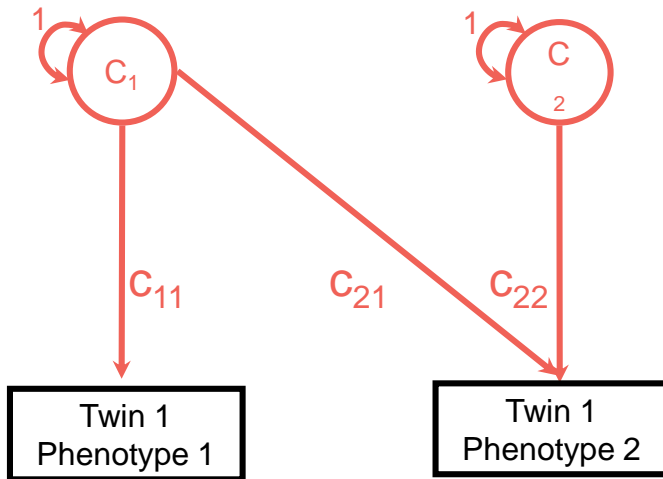
# Within-Twin Covariances (A)



		Twin 1	
		Phenotype 1	Phenotype 2
Twin 1	Phenotype 1	$a_{11}^2$	
	Phenotype 2	$a_{11}a_{21}$	$a_{22}^2 + a_{21}^2$

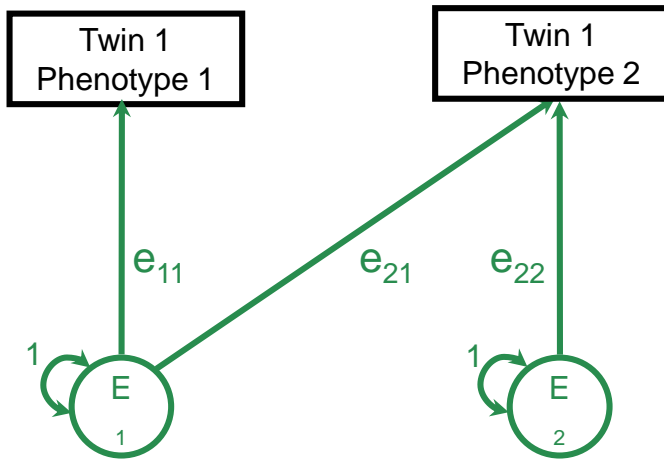


# Within-Twin Covariances (C)



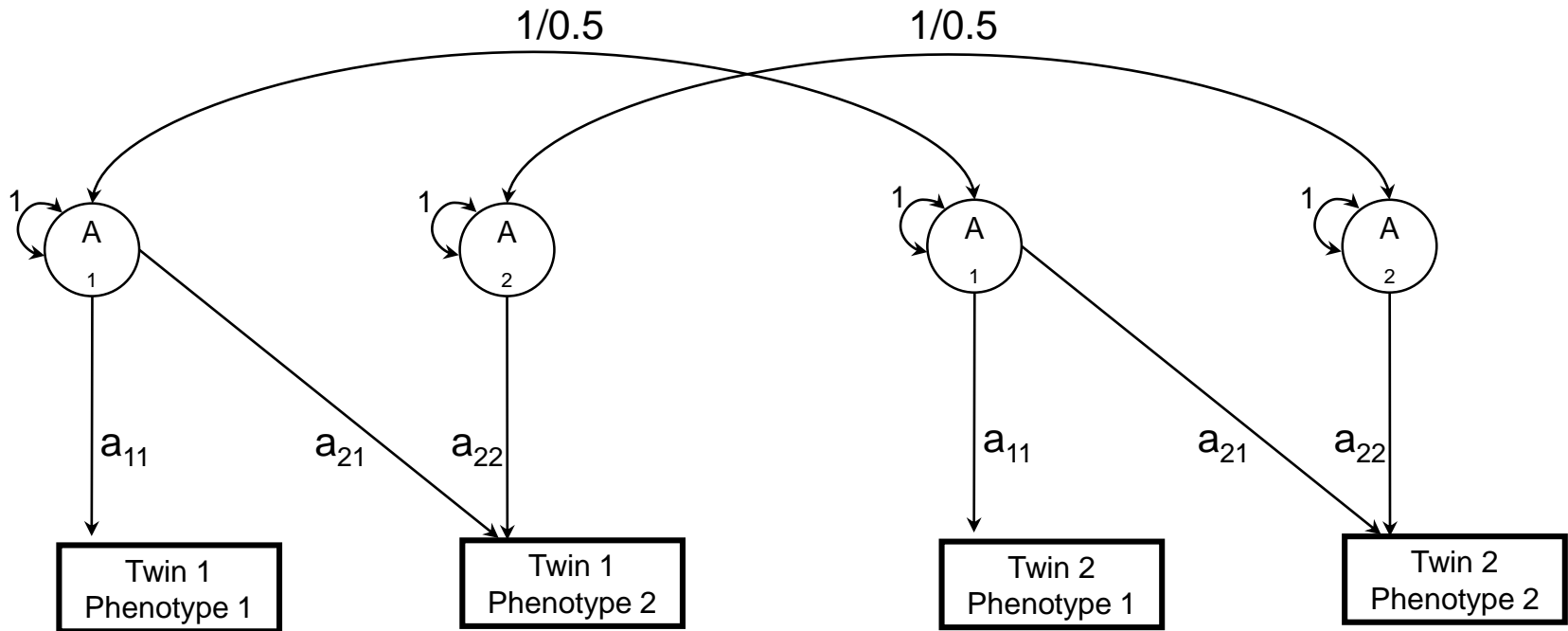
		Twin 1	
		Phenotype 1	Phenotype 2
Twin 1	Phenotype 1	$a_{11}^2 + c_{11}^2$	
	Phenotype 2	$a_{11}a_{21} + c_{11}c_{21}$	$a_{22}^2 + a_{21}^2 + c_{22}^2 + c_{21}^2$

# Within-Twin Covariances (E)



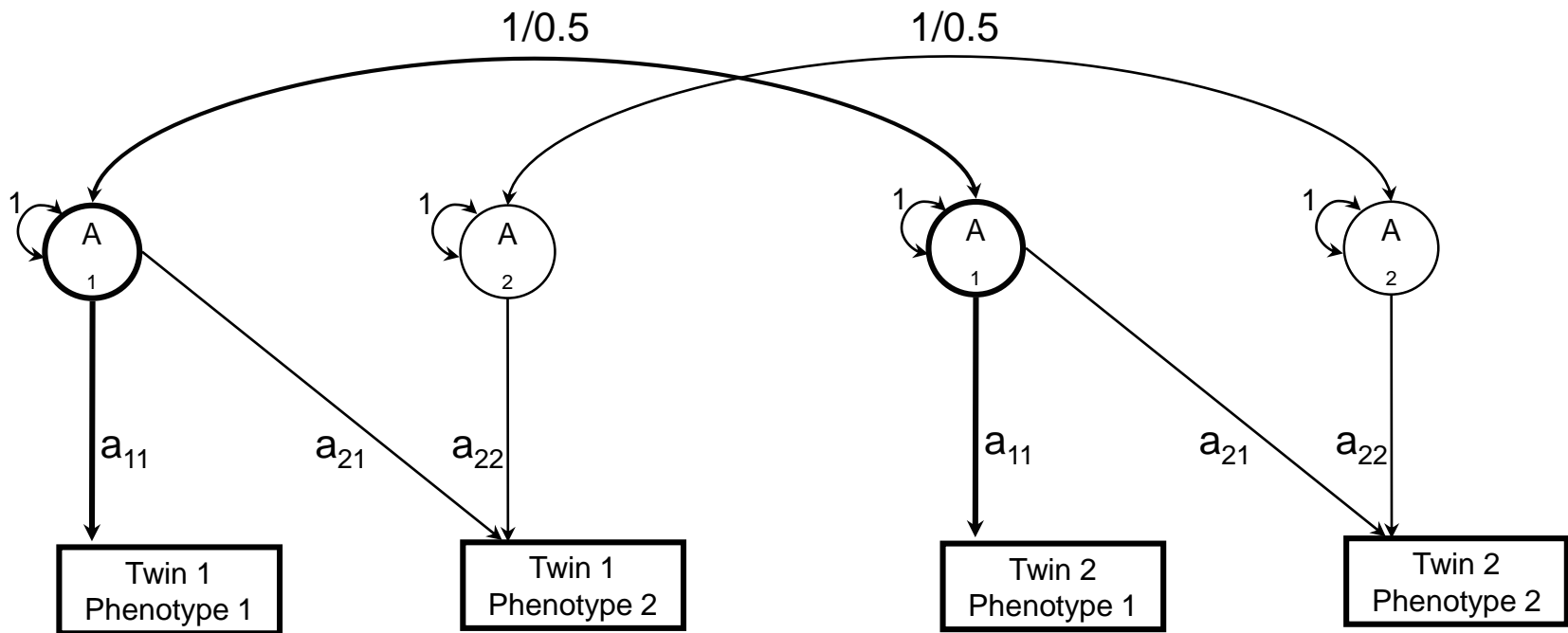
		Twin 1	
		Phenotype 1	Phenotype 2
Twin 1	Phenotype 1	$a_{11}^2 + c_{11}^2 + e_{11}^2$	
	Phenotype 2	$a_{11}a_{21} + c_{11}c_{21} + e_{11}e_{21}$	$a_{22}^2 + a_{21}^2 + c_{22}^2 + c_{21}^2 + e_{22}^2 + e_{21}^2$

# Cross-Twin Covariances (A)



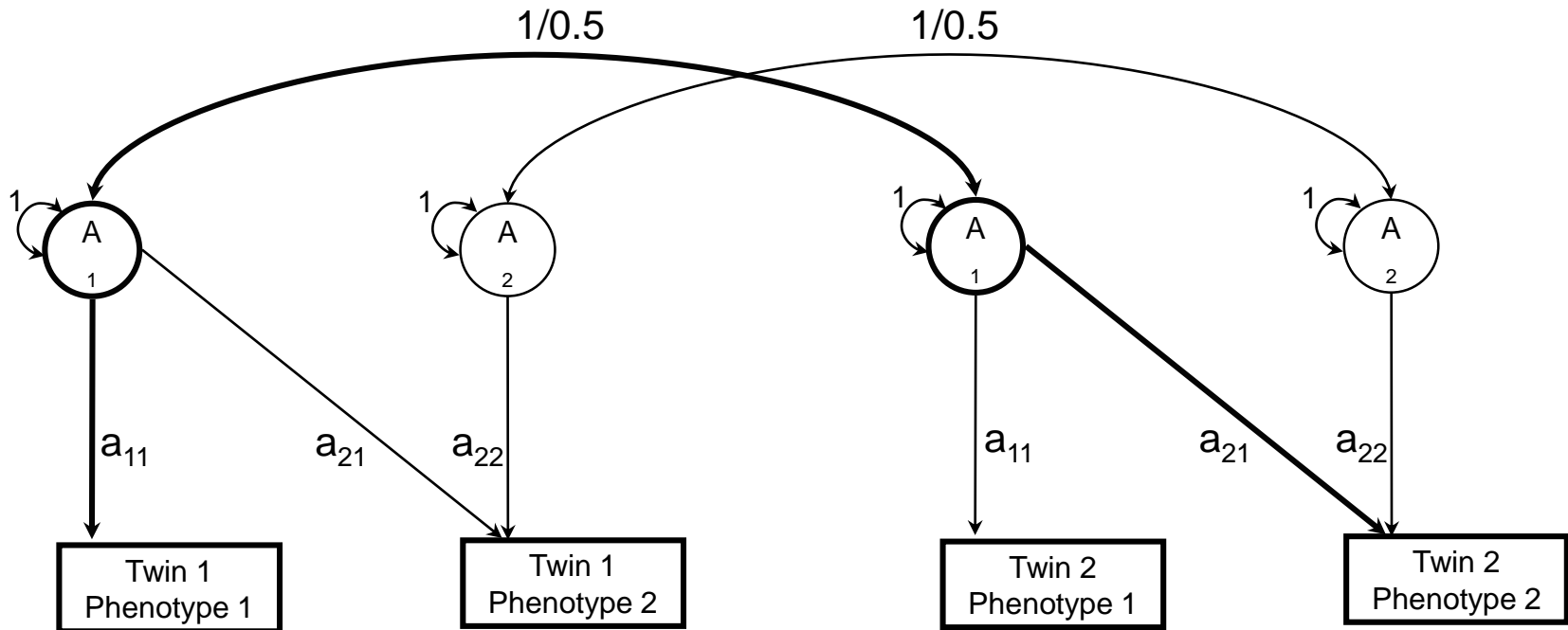
		Twin 1		
		Phenotype 1		Phenotype 2
Twin 2	Phenotype 1			
	Phenotype 2			

# Cross-Twin Covariances (A)



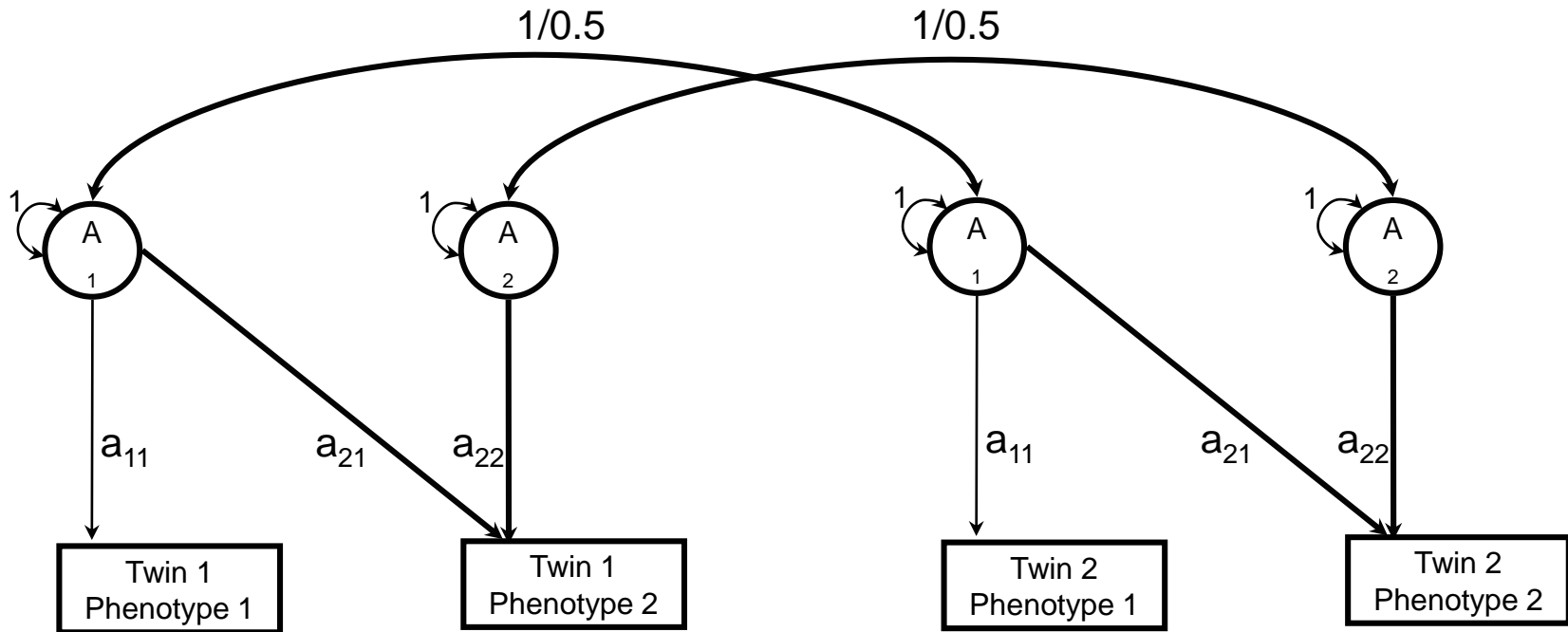
		Twin 1	
		Phenotype 1	Phenotype 2
Twin 2	Phenotype 1	$1/0.5a_{11}^2$	
	Phenotype 2		

# Cross-Twin Covariances (A)



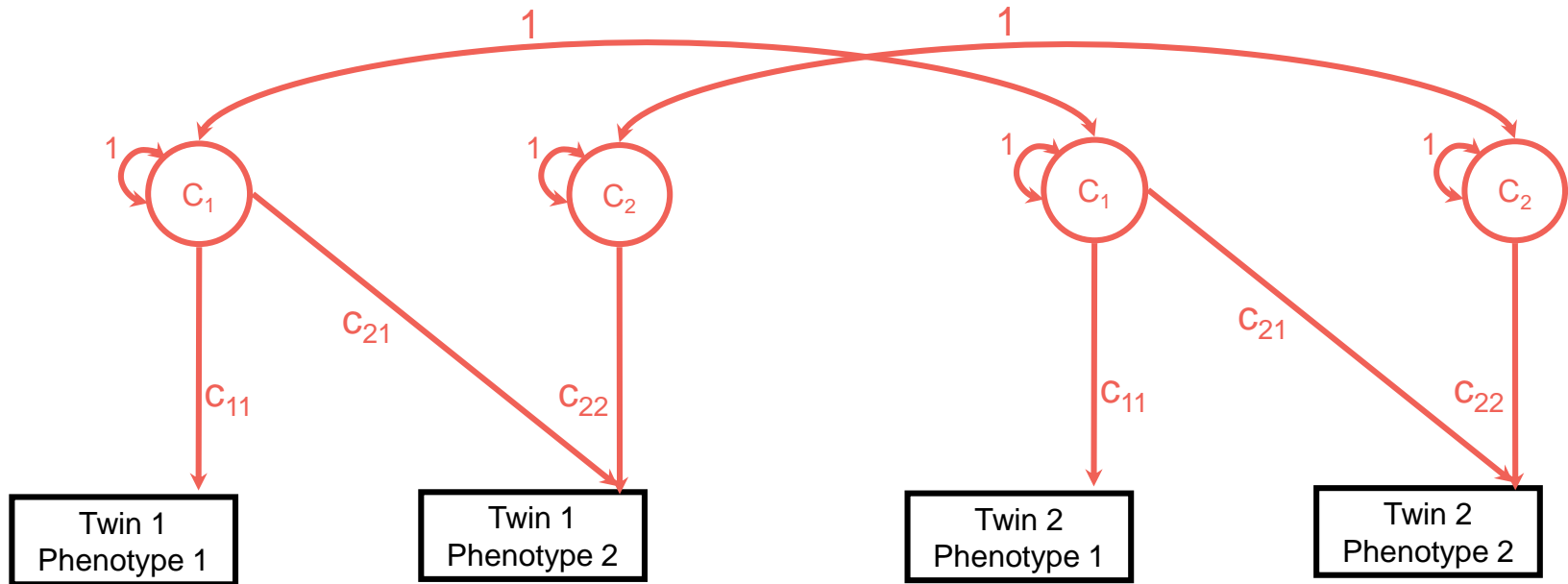
		Twin 1	
		Phenotype 1	Phenotype 2
Twin 2	Phenotype 1	$1/0.5 a_{11}^2$	
	Phenotype 2	$1/0.5 a_{11} a_{21}$	

# Cross-Twin Covariances (A)



		Twin 1	
		Phenotype 1	Phenotype 2
Twin 2	Phenotype 1	$1/0.5a_{11}^2$	
	Phenotype 2	$1/0.5a_{11}a_{21}$	$1/0.5a_{22}^2 + 1/0.5a_{21}^2$

# Cross-Twin Covariances (C)



		Twin 1	
		Phenotype 1	Phenotype 2
Twin 2	Phenotype 1	$1/0.5a_{11}^2 + c_{11}^2$	
	Phenotype 2	$1/0.5a_{11}a_{21} + c_{11}c_{21}$	$1/0.5a_{22}^2 + 1/0.5a_{21}^2 + c_{22}^2 + c_{21}^2$

# Predicted Model

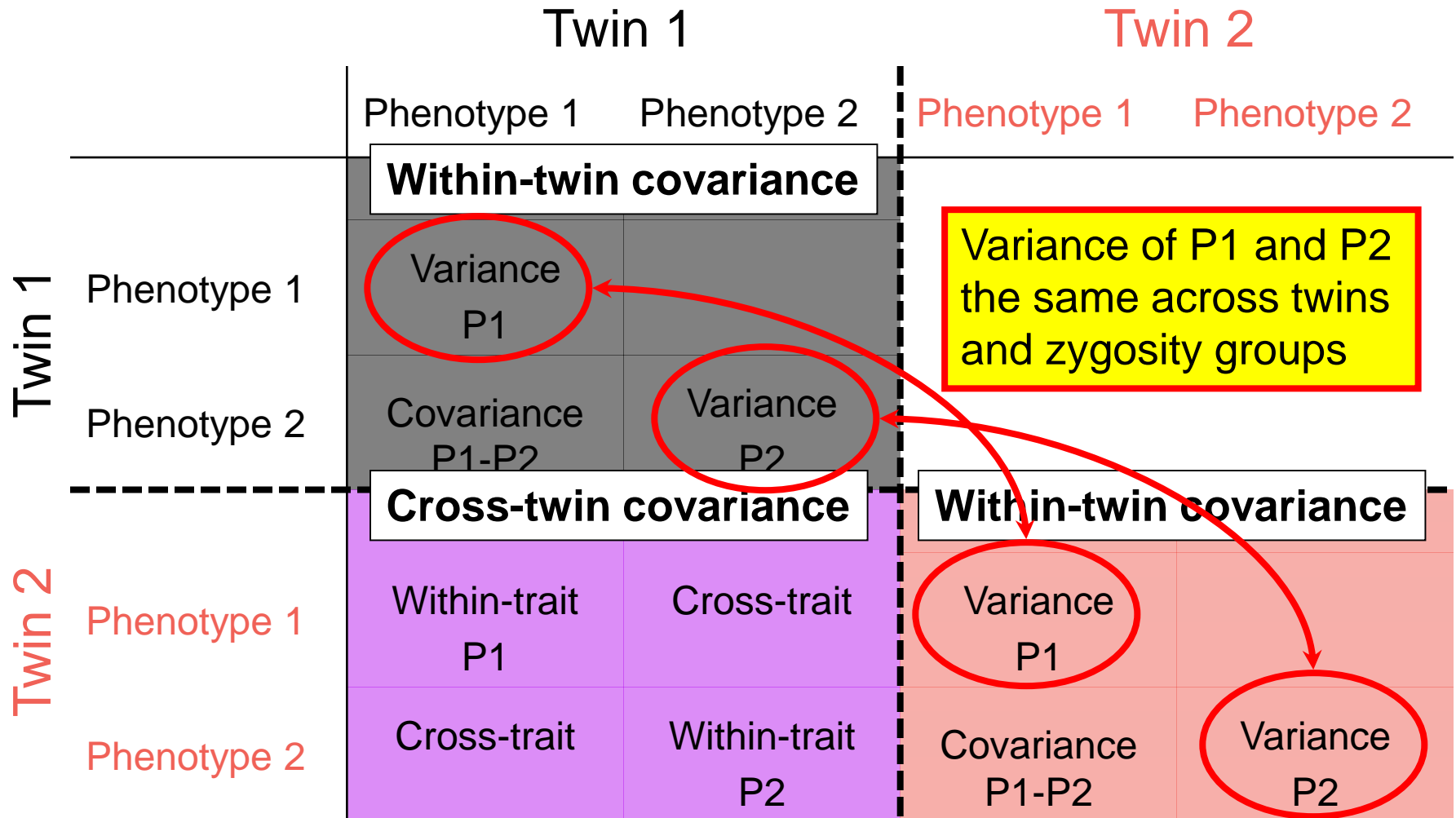
		Twin 1		Twin 2	
		Phenotype 1	Phenotype 2	Phenotype 1	Phenotype 2
Twin 1		<b>Within-twin covariance</b>			
	Phenotype 1	$a_{11}^2 + c_{11}^2 + e_{11}^2$			
	Phenotype 2	$a_{11}a_{21} + c_{11}c_{21} + e_{11}e_{21}$	$a_{22}^2 + a_{21}^2 + c_{22}^2 + c_{21}^2 + e_{22}^2 + e_{21}^2$		
Twin 2		<b>Cross-twin covariance</b>		<b>Within-twin covariance</b>	
	Phenotype 1	$1/5a_{11}^2 + c_{11}^2$		$a_{11}^2 + c_{11}^2 + e_{11}^2$	
	Phenotype 2	$1/5a_{11}a_{21} + c_{11}c_{21}$	$1/5a_{22}^2 + 1/5a_{21}^2 + c_{22}^2 + c_{21}^2$	$a_{11}a_{21} + c_{11}c_{21} + e_{11}e_{21}$	$a_{22}^2 + a_{21}^2 + c_{22}^2 + c_{21}^2 + e_{22}^2 + e_{21}^2$



# Predicted Model

		Twin 1		Twin 2	
		Phenotype 1	Phenotype 2	Phenotype 1	Phenotype 2
		<b>Within-twin covariance</b>			
Twin 1	Phenotype 1	Variance P1			
	Phenotype 2	Covariance P1-P2	Variance P2		
		<b>Cross-twin covariance</b>		<b>Within-twin covariance</b>	
Twin 2	Phenotype 1	Within-trait P1	Cross-trait	Variance P1	
	Phenotype 2	Cross-trait	Within-trait P2	Covariance P1-P2	Variance P2

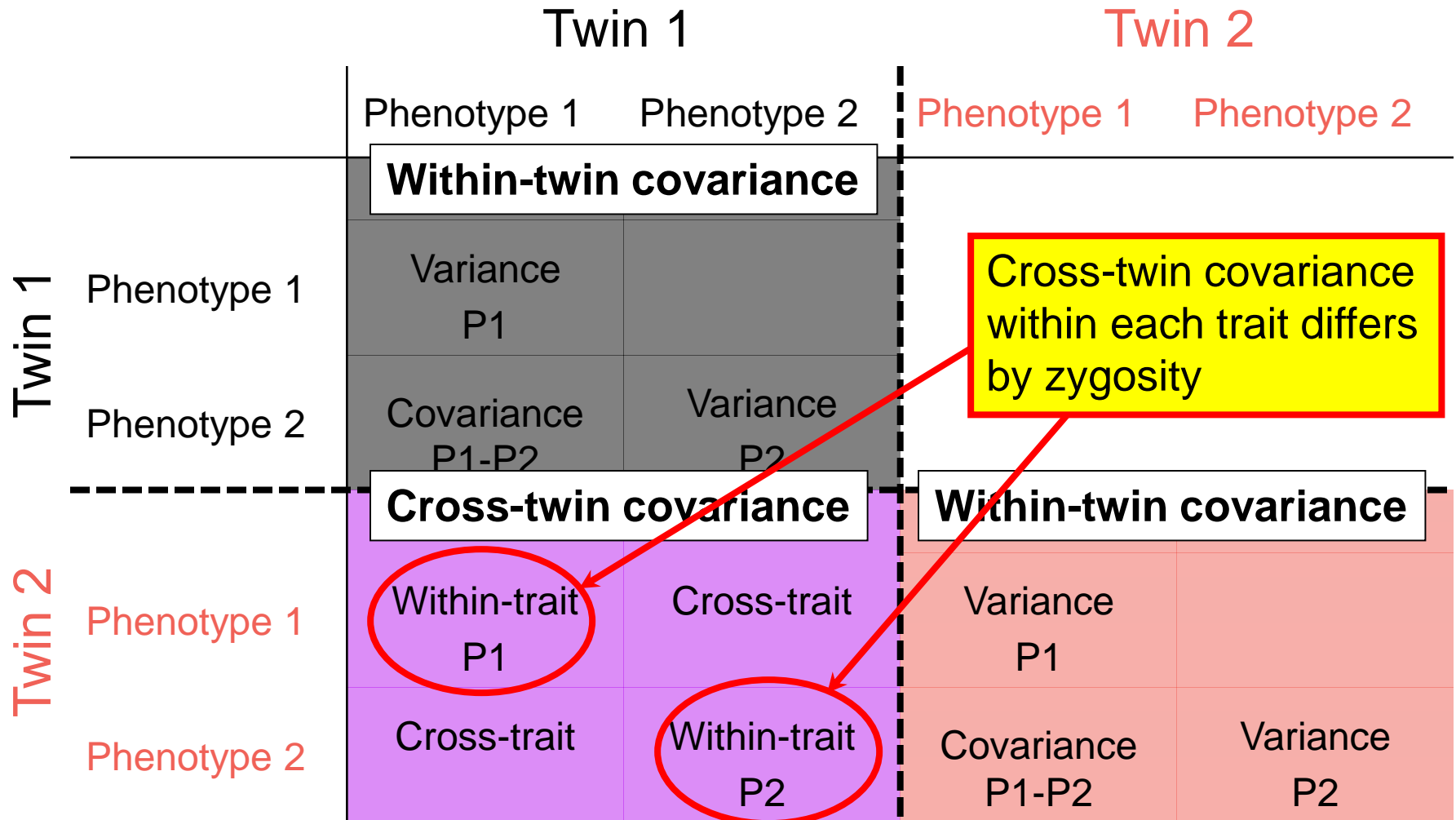
# Predicted Model



# Predicted Model

		Twin 1		Twin 2	
		Phenotype 1	Phenotype 2	Phenotype 1	Phenotype 2
		<b>Within-twin covariance</b>			
Twin 1	Phenotype 1	Variance P1		Covariance of P1 and P2 the same across twins and zygosity groups	
	Phenotype 2	Covariance P1-P2	Variance P2		
		<b>Cross-twin covariance</b>		<b>Within-twin covariance</b>	
Twin 2	Phenotype 1	Within-trait P1	Cross-trait	Variance P1	
	Phenotype 2	Cross-trait	Within-trait P2	Covariance P1-P2	Variance P2

# Predicted Model



# Predicted Model

		Twin 1		Twin 2	
		Phenotype 1	Phenotype 2	Phenotype 1	Phenotype 2
Twin 1	<b>Within-twin covariance</b>				
	Phenotype 1	Variance P1			
	Phenotype 2	Covariance P1-P2	Variance P2		
Twin 2	<b>Cross-twin covariance</b>		<b>Within-twin covariance</b>		
	Phenotype 1	Within-trait P1	Cross-trait	Variance P1	
	Phenotype 2	Cross-trait	Within-trait P2	Covariance P1-P2	Variance P2

Cross-twin cross-trait covariance differs by zygosity

# Example Covariance Matrix

**MZ**

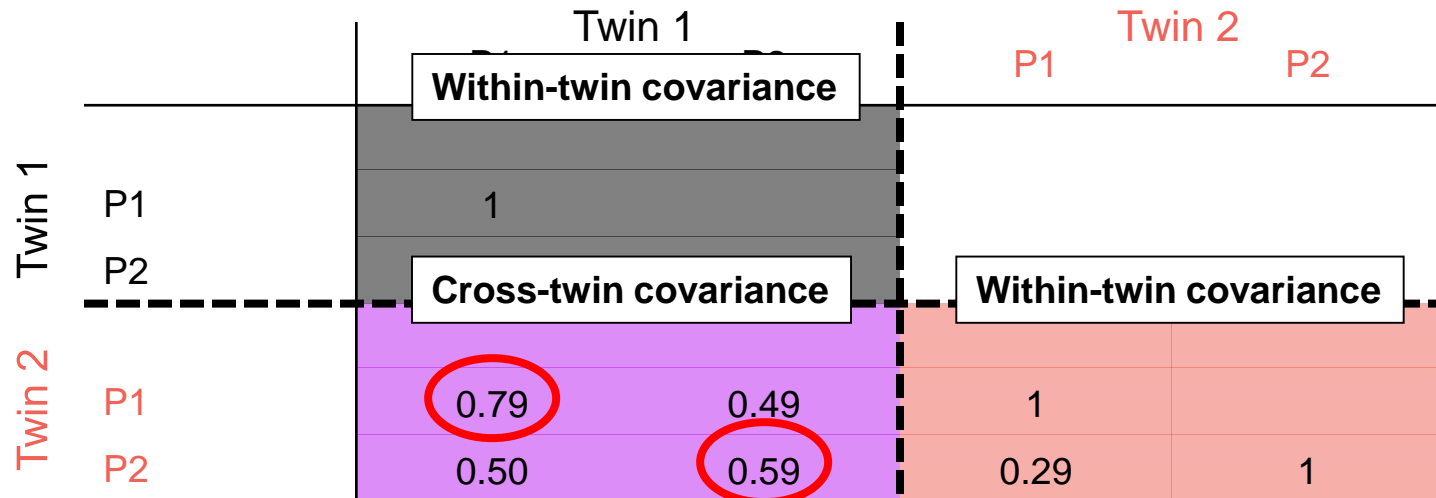
		Twin 1		Twin 2	
		P1	P2	P1	P2
Twin 1	P1	Within-twin covariance			
	P2	1			
Twin 2	P1	Cross-twin covariance		Within-twin covariance	
	P2	0.79	0.49	1	
		0.50	0.59	0.29	1

**DZ**

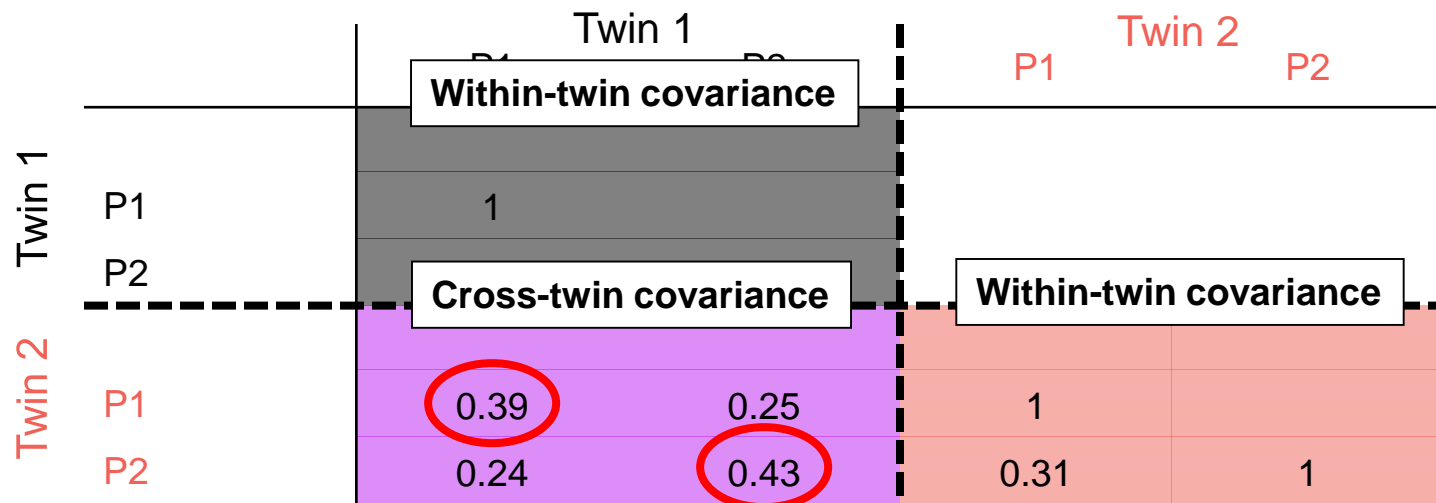
		Twin 1		Twin 2	
		P1	P2	P1	P2
Twin 1	P1	Within-twin covariance			
	P2	1			
Twin 2	P1	Cross-twin covariance		Within-twin covariance	
	P2	0.39	0.25	1	
		0.24	0.43	0.31	1

# Example Covariance Matrix

**MZ**

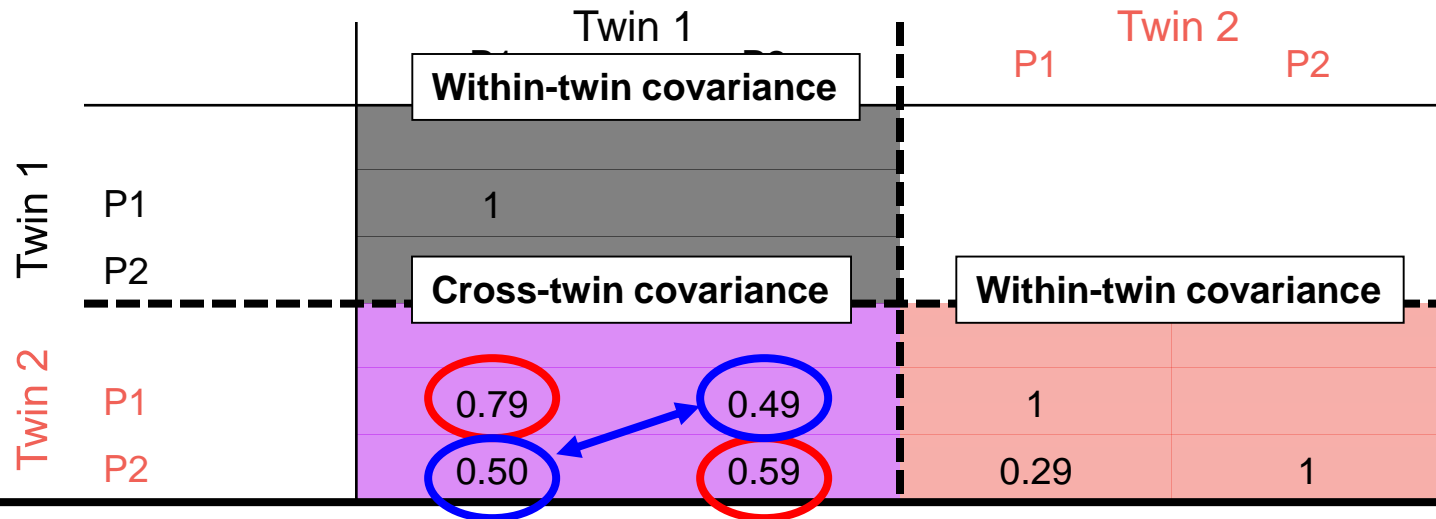


**DZ**

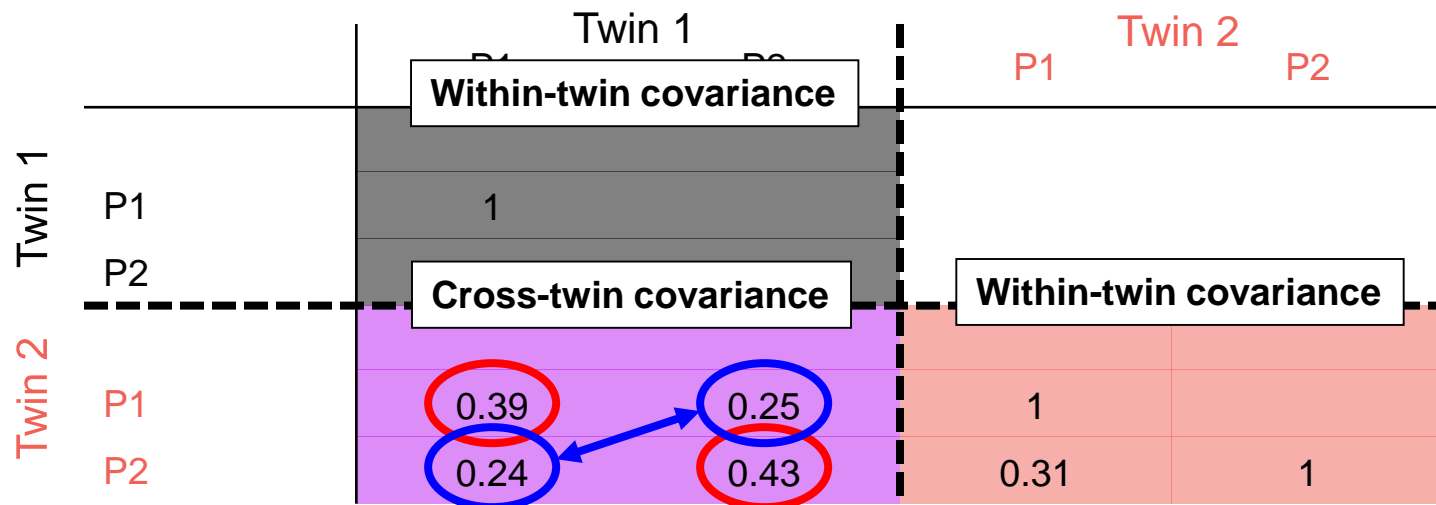


# Example Covariance Matrix

**MZ**



**DZ**





# Summary

---

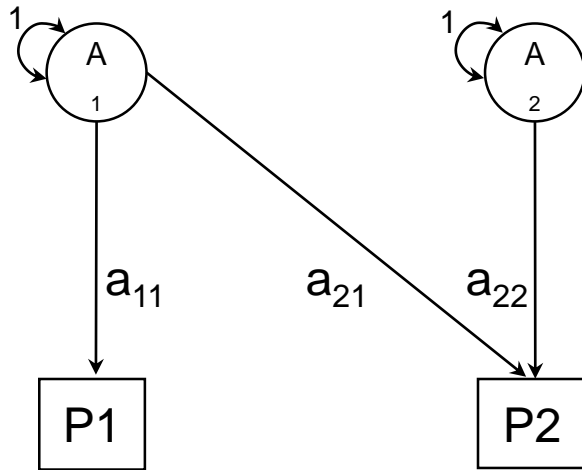
- Within-individual cross-trait covariance implies common aetiological influences
- Cross-twin cross-trait covariance implies common aetiological influences are familial
- Whether familial influences genetic or environmental shown by MZ:DZ ratio of cross-twin cross-trait covariances

# **Cholesky Decomposition Bivariate Genetic analyses**

## **Specification in OpenMx**

# Within-Twin Covariance

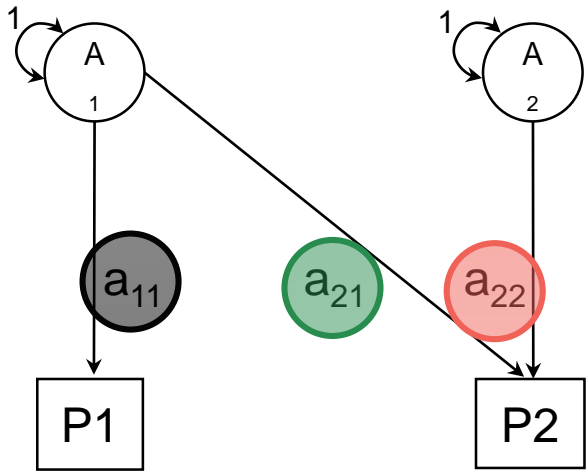
---



Path Tracing:

$$\Sigma_A = \begin{bmatrix} a_{11}^2 & a_{11}a_{21} \\ a_{21}a_{11} & a_{21}^2 + a_{22}^2 \end{bmatrix}$$

# Within-Twin Covariance



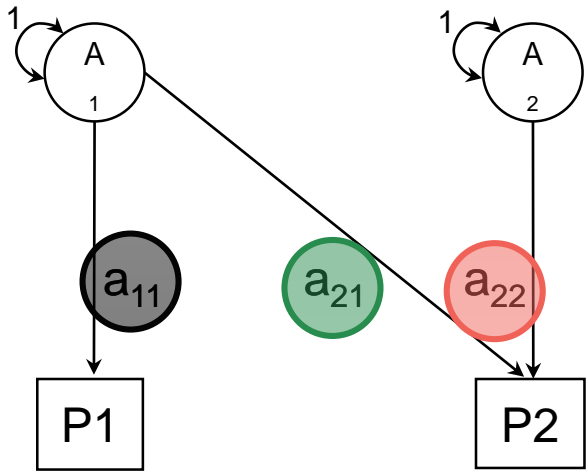
Path Tracing:

$$\Sigma_A = \begin{bmatrix} a_{11}^2 & a_{11}a_{21} \\ a_{21}a_{11} & a_{21}^2 + a_{22}^2 \end{bmatrix}$$

a Lower 2 x 2:

$$\begin{matrix} & a_1 & a_2 \\ \text{P1} & \begin{bmatrix} a_{11} & 0 \end{bmatrix} \\ \text{P2} & \begin{bmatrix} a_{21} & a_{22} \end{bmatrix} \end{matrix}$$

# Within-Twin Covariance



Path Tracing:

$$\Sigma_A = \begin{bmatrix} a_{11}^2 & a_{11}a_{21} \\ a_{21}a_{11} & a_{21}^2 + a_{22}^2 \end{bmatrix}$$

a Lower 2 x 2:

$$\begin{matrix} & a_1 & a_2 \\ \text{P1} & \begin{bmatrix} a_{11} & 0 \end{bmatrix} \\ \text{P2} & \begin{bmatrix} a_{21} & a_{22} \end{bmatrix} \end{matrix}$$

$$S_A = a * a^T$$

$$S_A = a \% * \% t(a)$$

$$= \begin{bmatrix} a_{11} & 0 \\ a_{21} & a_{22} \end{bmatrix} * \begin{bmatrix} a_{11} & a_{21} \\ 0 & a_{22} \end{bmatrix}$$

$$= \begin{bmatrix} a_{11}^2 + 0 \times 0 & a_{11}a_{21} + 0 \times a_{22} \\ a_{21}a_{11} + 0 \times a_{22} & a_{21}^2 + a_{22}^2 \end{bmatrix}$$

# Within-Twin Covariance

$$\begin{aligned} S_A &= a * a^T \\ S_A &= a \% * \% t(a) \end{aligned} = \begin{bmatrix} a_{11} & 0 \\ a_{21} & a_{22} \end{bmatrix} * \begin{bmatrix} a_{11} & a_{21} \\ 0 & a_{22} \end{bmatrix}$$
$$= \begin{bmatrix} a_{11}^2 + 0 \times 0 & a_{11}a_{21} + 0 \times a_{22} \\ a_{21}a_{11} + 0 \times a_{22} & a_{21}^2 + a_{22}^2 \end{bmatrix}$$

```
nv <- 2
```

```
..
```

```
mxMatrix ( type="Lower", nrow=nv, ncol=nv, free=TRUE, values=.6, name="a" ),  
mxAlgebra( expression=a %*% t(a), name="A" ),
```

OpenMx

OpenMx

# Total Within-Twin Covar.

---

$$S_A = a \% \% t(a) = \begin{bmatrix} a_{11}^2 & a_{11}a_{21} \\ a_{21}a_{11} & a_{21}^2 + a_{22}^2 \end{bmatrix} \quad S_C = c \% \% t(c) = \begin{bmatrix} c_{11}^2 & c_{11}c_{21} \\ c_{21}c_{11} & c_{21}^2 + c_{22}^2 \end{bmatrix}$$

$$S_E = e \% \% t(e) = \begin{bmatrix} e_{11}^2 & e_{11}e_{21} \\ e_{21}e_{11} & e_{21}^2 + e_{22}^2 \end{bmatrix}$$

Using matrix addition, the total within-twin covariance for the phenotypes is defined as:

$$S_V = \Sigma_A + \Sigma_C + \Sigma_E$$

$$S_V = \begin{bmatrix} a_{11}^2 + c_{11}^2 + e_{11}^2 & a_{11}a_{21} + c_{11}c_{21} + e_{11}e_{21} \\ a_{21}a_{11} + c_{21}c_{11} + e_{11}e_{21} & a_{21}^2 + a_{22}^2 + c_{21}^2 + c_{22}^2 + e_{21}^2 + e_{22}^2 \end{bmatrix}$$

# OpenMx Matrices & Algebra

## OpenMx

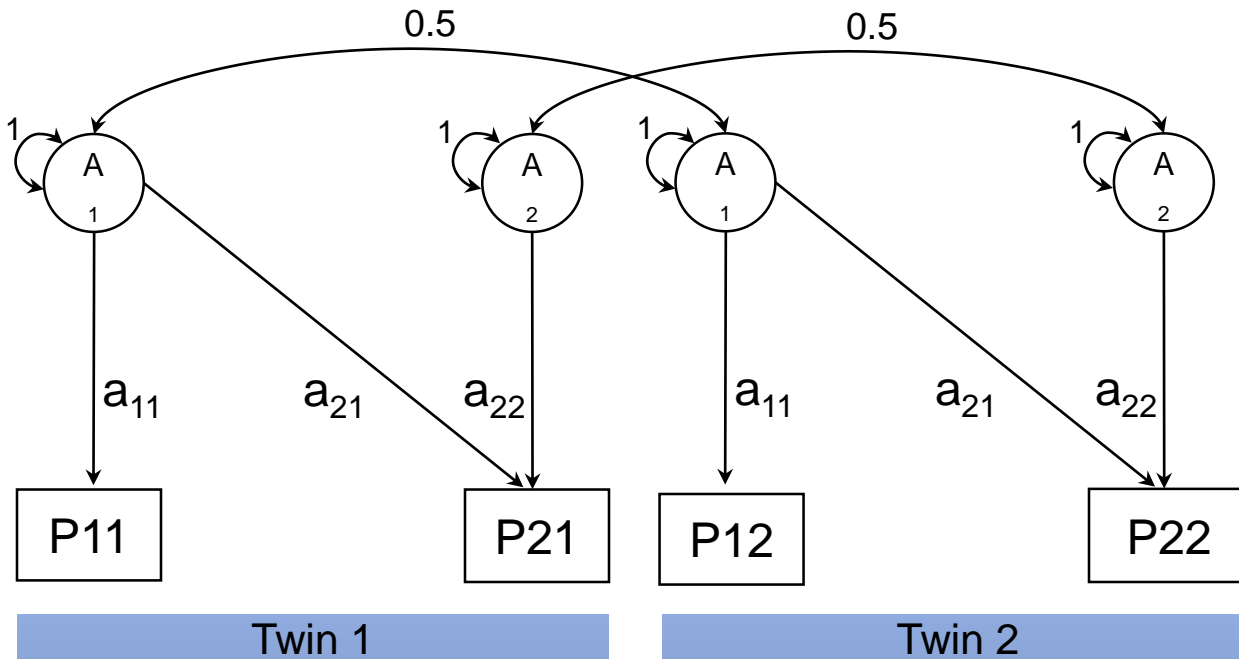
```
multACEModel <- mxModel("multACE", mxModel("ACE",
# Matrices a, c, and e to store a, c, and e path coefficients
mxMatrix( type="Lower", nrow=nv, ncol=nv, free=TRUE, values=.6, name="a" ), mxMatrix(
type="Lower", nrow=nv, ncol=nv, free=TRUE, values=.6, name="c" ), mxMatrix( type="Lower",
nrow=nv, ncol=nv, free=TRUE, values=.6, name="e" ),

# Matrices A, C, and E compute variance components mxAlgebra( expression=a %*% t(a),
name="A" ),
mxAlgebra( expression=c %*% t(c), name="C" ),
mxAlgebra( expression=e %*% t(e), name="E" ),

# Algebra to compute total variances and standard deviations (diagonal only) mxAlgebra(
expression=A+C+E, name="V" ),
mxMatrix( type="Iden", nrow=nv, ncol=nv, name="I" ), mxAlgebra( expression=solve(sqrt(I*V)),
name="isd"),
```



# Additive Genetic Cross-Twin Covariance (DZ)



Path Tracing:

Within-traits

$$P_{11}-P_{12} = 0.5a_{11}^2$$

$$P_{21}-P_{22} = 0.5a_{22}^2 + 0.5a_{21}^2$$

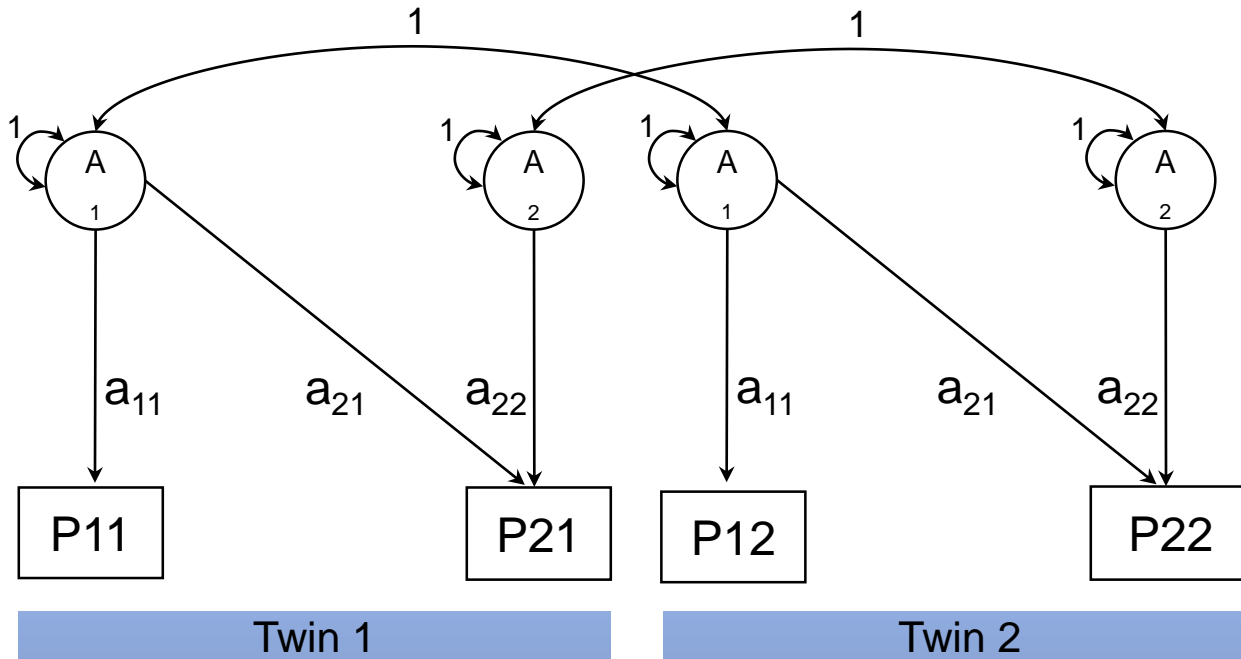
Cross-traits

$$P_{11}-P_{22} = 0.5a_{11}a_{21}$$

$$P_{21}-P_{12} = 0.5a_{21}a_{11}$$

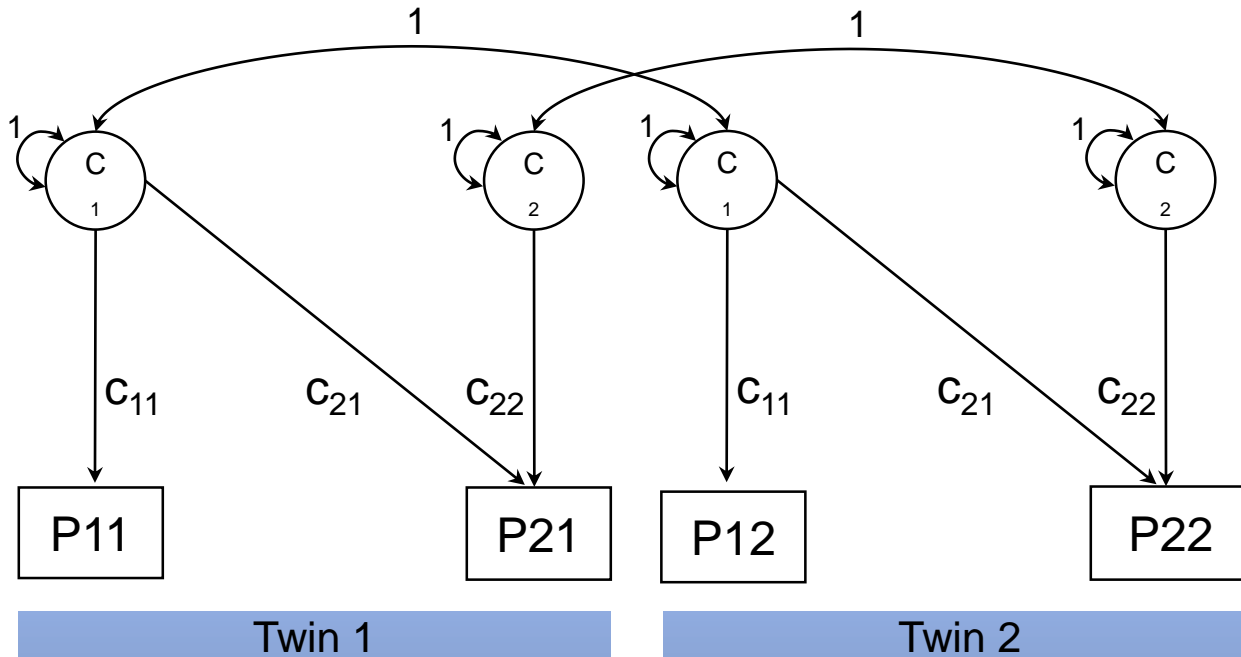
$$0.5 \ddot{A} S_A = 0.5 \begin{pmatrix} a_{11}^2 & a_{11}a_{21} \\ a_{21}a_{11} & a_{21}^2 + a_{22}^2 \end{pmatrix} = \begin{bmatrix} 0.5a_{11}^2 & 0.5a_{11}a_{21} \\ 0.5a_{21}a_{11} & 0.5(a_{21}^2 + a_{22}^2) \end{bmatrix}$$

# Additive Genetic Cross-Twin Covariance (MZ)



$$1 \ddot{A} S_A = 1 \% x \% (a \% * \% t(a)) = \begin{bmatrix} a_{11}^2 & a_{11} a_{21} \\ a_{21} a_{11} & (a_{21}^2 + a_{22}^2) \end{bmatrix}$$

# Common Environment Cross-Twin Covariance



$$1 \text{ \AA } S_C = 1 \% x \% (c \% * \% t(c)) = \begin{bmatrix} c_{11}^2 & c_{11}c_{21} \\ c_{21}c_{11} & (c_{21}^2 + c_{22}^2) \end{bmatrix}$$

# Covariance Model for Twin Pairs

---

OpenMx

```
# Algebra for expected variance/covariance matrix in MZ
cbind(A+C+E , A+C),
A+C+E)),
mxAlgebra( expression= rbind (
                                cbind(A+C ,
                                name="expCovMZ" ),
```

```
# Algebra for expected variance/covariance matrix in DZ, note use of 0.5, converted to 1*1 matrix
mxAlgebra( expression= rbind ( cbind(A+C+E , 0.5%x%A+C),
                                cbind(0.5%x%A+C , A+C+E)),
                                name="expCovDZ" ) ),
```

# **Obtaining Standardised Estimates**

# Three Important Results

1. Variance Decomposition -> Heritability, (Shared) environmental influences
2. Covariance Decomposition -> The influences of genes and environment on the covariance between the two variables

“how much of the phenotypic correlation is accounted for by genetic and environmental influences”

3. Genetic and Environmental correlations -> the overlap in genes and environmental effects

“is there a large overlap in gene/ environmental sets”

# OpenMx Output

1. Variance Decomposition -> Heritability, (Shared) environmental influences
2. Covariance Decomposition -> The influences of genes and environment on the covariance between the two variables

```
[1] "Matrix A/V"
```

```
stCovA1 stCovA2
```

```
family 0.4809 0.7154
```

```
happy 0.7154 0.3995
```

```
[1] "Matrix C/V"
```

```
stCovC1 stCovC2
```

```
family 0.0919 0.1121
```

```
happy 0.1121 0.0250
```

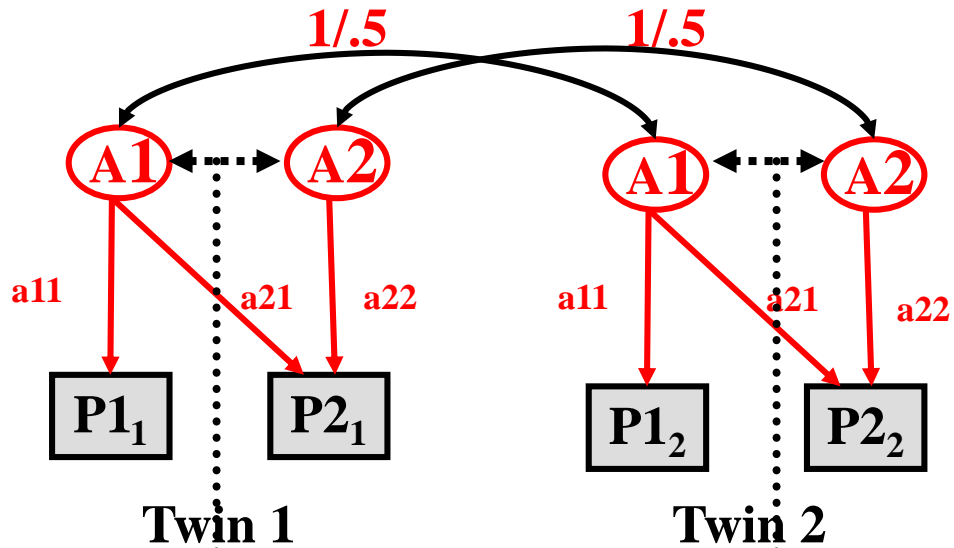
```
[1] "Matrix E/V"
```

```
stCovE1 stCovE2
```

```
family 0.4272 0.1725
```

```
happy 0.1725 0.5755
```

# Genetic correlation



$$r_g = \frac{a_{21}a_{11}}{\sqrt{a_{11}^2 * (a_{21}^2 + a_{22}^2)}}$$



# OpenMx Output

```
[1] "Matrix solve(sqrt(I*A)) %&% A"
```

```
corA1 corA2
```

```
family 1.0000 0.6985
```

```
happy 0.6985 1.0000
```

```
[1] "Matrix solve(sqrt(I*C)) %&% C"
```

```
corC1 corC2
```

```
family 1.0000 1.0000
```

```
happy 1.0000 1.0000
```

```
[1] "Matrix solve(sqrt(I*E)) %&% E"
```

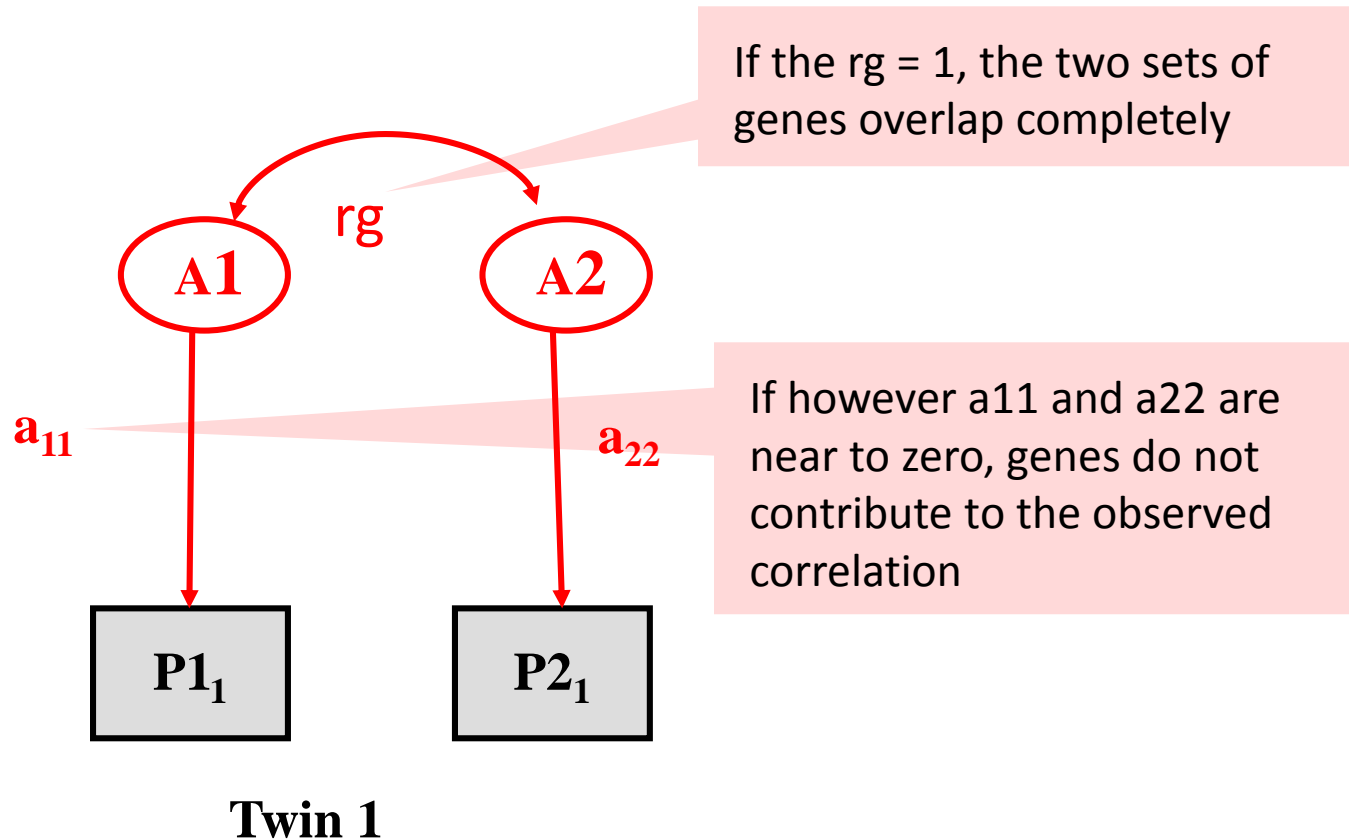
```
corE1 corE2
```

```
family 1.0000 0.1488
```

```
happy 0.1488 1.0000
```

# Genetic correlation & contribution to observed correlation

---

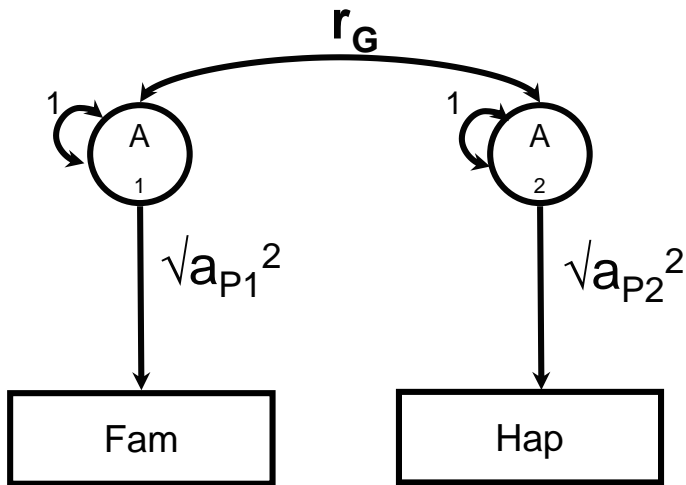


# Interpreting Results

---

- High genetic correlation = large overlap in genetic effects on the two phenotypes
- Does it mean that the phenotypic correlation between the traits is largely due to genetic effects?
  - ◆ **No:** the substantive importance of a particular  $r_G$  depends the value of the correlation **and** the value of the  $\sqrt{\sigma_A^2}$  paths i.e. importance is also determined by the heritability of each phenotype

# Example



Proportion of  $r_P$  due to additive genetic factors:

$$\frac{\left( \sqrt{a_x^2} * r_g * \sqrt{a_y^2} \right)}{r_p}$$

Heritability of Fam	Genetic correlation between Fam and Hap	Heritability of Hap	Phenotypic corr. Fam & Hap	Proportion of pheno.corr. Due to genetic factors
$\sqrt{.48}$	$.69$	$\sqrt{.39}$	$.42$	$.71$

$\sqrt{.48} * .69 * \sqrt{.39} / .42 = .71$

# Interpretation of Correlations

---

Consider two traits with a phenotypic correlation of 0.40 :

$$h^2_{P1} = 0.7 \text{ and } h^2_{P2} = 0.6 \text{ with } r_G = .3$$

- Correlation due to additive genetic effects = ?
- Proportion of phenotypic correlation attributable to additive genetic effects = ?

$$h^2_{P1} = 0.2 \text{ and } h^2_{P2} = 0.3 \text{ with } r_G = 0.8$$

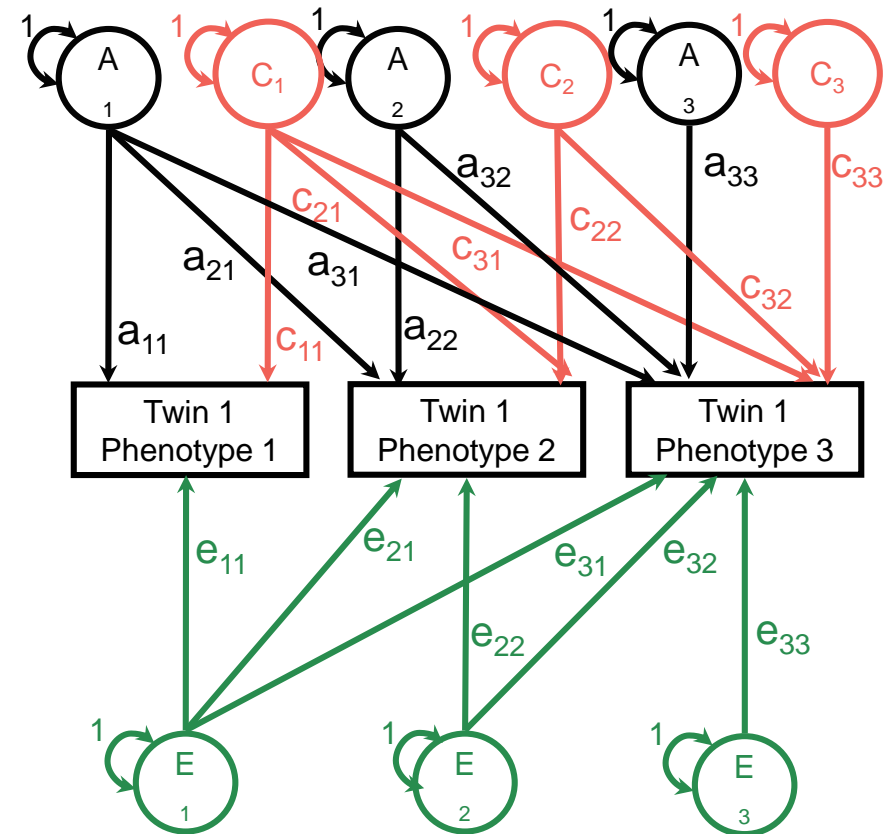
- Correlation due to additive genetic effects = ?
- Proportion of phenotypic correlation attributable to additive genetic effects = ?

Correlation due to A:  $\sqrt{h^2_{P1}} * r_G * \sqrt{h^2_{P2}}$

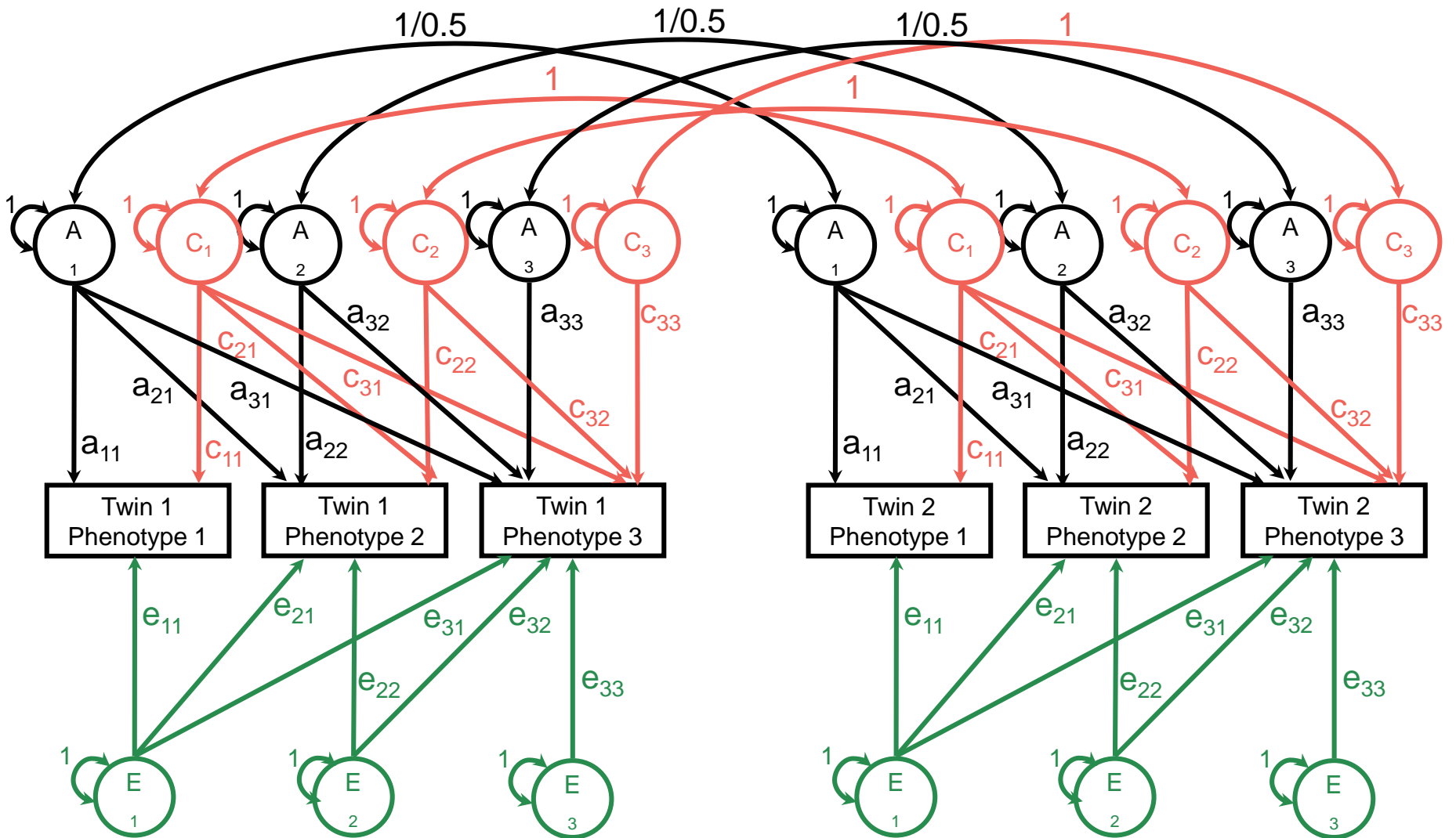
Divide by  $r_P$  to find proportion of phenotypic correlation.

# More Variables...

---





# More Variables...




# Expanded Matrices

---

a Lower 3 x 3  
$$\begin{bmatrix} a_{11} & 0 & 0 \\ a_{21} & a_{22} & 0 \\ a_{31} & a_{32} & a_{33} \end{bmatrix}$$

c Lower 3 x 3  
$$\begin{bmatrix} c_{11} & 0 & 0 \\ c_{21} & c_{22} & 0 \\ c_{31} & c_{32} & c_{33} \end{bmatrix}$$

e Lower 3 x 3  
$$\begin{bmatrix} e_{11} & 0 & 0 \\ e_{21} & e_{22} & 0 \\ e_{31} & e_{32} & e_{33} \end{bmatrix}$$



# OpenMx Parameter Matrices

---

OpenMx

```
Vars <- c('varx', 'vary', 'varz')
```

```
nv <- 3
```

```
multACEModel <- mxModel("multACE", mxModel("ACE",  
# Matrices a, c, and e to store a, c, and e path coefficients  
mxMatrix( type="Lower", nrow=nv, ncol=nv, free=TRUE, values=.6, name="a" ), mxMatrix(  
type="Lower", nrow=nv, ncol=nv, free=TRUE, values=.6, name="c" ), mxMatrix( type="Lower",  
nrow=nv, ncol=nv, free=TRUE, values=.6, name="e" ),
```

# Practical

## SCRIPT:

F:\meike\2014\Multivariate\Bivariate

## DATA:

DHBQ\_bs.dat

# DATA

- General Family Functioning, Subjective Happiness
- T1, T2, brother, sister
- missing -999



# Observed Cross-twin Cross-trait Correlations

```
describe(mzData, skew=F)
```

```
describe(dzData, skew=F)
```

```
dim(mzData)
```

```
dim(dzData)
```

```
colMeans(mzData,na.rm=TRUE)
```

```
colMeans(dzData,na.rm=TRUE)
```

```
cov(mzData,use="complete")
```

```
cov(dzData,use="complete")
```

```
cor(mzData,use="complete")
```

```
cor(dzData,use="complete")
```

# Observed Cross-twin Cross-trait Correlations

```
> cor(mzData,use="complete")
```

	family1	happy1	family2	happy2
family1	1.00	0.40	0.58	0.37
happy1	0.40	1.00	0.35	0.46
family2	0.58	0.35	1.00	0.41
happy2	0.37	0.46	0.41	1.00

```
> cor(dzData,use="complete")
```

	family1	happy1	family2	happy2
family1	1.00	0.47	0.30	0.061
happy1	0.47	1.00	0.30	0.217
family2	0.30	0.30	1.00	0.379
happy2	0.06	0.21	0.37	1.000

# PRAC I.

## The ACE model and its estimates

1. Run the ACE model
2. What is the heritability of FAM and HAP?
3. What is the genetic influence on the covariance?
4. What is the genetic correlation?

# OpenMx Output

1. Variance Decomposition -> Heritability, (Shared) environmental influences
2. Covariance Decomposition -> The influences of genes and environment on the covariance between the two variables

```
[1] "Matrix A/V"
```

```
stCovA1 stCovA2
```

```
family 0.4809 0.7154
```

```
happy 0.7154 0.3995
```

```
[1] "Matrix C/V"
```

```
stCovC1 stCovC2
```

```
family 0.0919 0.1121
```

```
happy 0.1121 0.0250
```

```
[1] "Matrix E/V"
```

```
stCovE1 stCovE2
```

```
family 0.4272 0.1725
```

```
happy 0.1725 0.5755
```

# OpenMx Output

```
[1] "Matrix solve(sqrt(I*A)) %&% A"
```

```
corA1 corA2
```

```
family 1.0000 0.6985
```

```
happy 0.6985 1.0000
```

```
[1] "Matrix solve(sqrt(I*C)) %&% C"
```

```
corC1 corC2
```

```
family 1.0000 1.0000
```

```
happy 1.0000 1.0000
```

```
[1] "Matrix solve(sqrt(I*E)) %&% E"
```

```
corE1 corE2
```

```
family 1.0000 0.1488
```

```
happy 0.1488 1.0000
```



# PRAC II.

## Trivariate Model

1. Add a third variable (Satisfaction with Life) to the model
2. Run model
3. What are the parameter estimates?
4. What is the genetic correlation?

# Changes that had to be made

# Select Variables for Analysis

```
Vars <- c('family','happy','life')
```

```
nv <- 3 # number of variables
```

```
ntv <- nv*2 # number of total variables
```

```
selVars <- paste(Vars,c(rep(1,nv),rep(2,nv)),sep="")
```

```
svMe <- c(7,5,5)
```

# Genetic and Environmental Influences

[1] "Matrix A/V"

	stCovA1	stCovA2	stCovA3
family	0.4117	0.6549	0.5697
happy	0.6549	0.3297	0.3224
life	0.5697	0.3224	0.2246

[1] "Matrix C/V"

	stCovC1	stCovC2	stCovC3
Family	0.1517	0.1709	0.3004
happy	0.1709	0.0681	0.1275
life	0.3004	0.1275	0.1406

[1] "Matrix E/V"

	stCovE1	stCovE2	stCovE3
Family	0.4366	0.1742	0.1299
happy	0.1742	0.6022	0.5501
life	0.1299	0.5501	0.6348

# Genetic and Environmental Correlations

[1] "Matrix solve(sqrt(I\*A)) %&% A"

	corA1	corA2	corA3
Family	1.0000	0.7620	0.7817
Happy	0.7620	1.0000	0.8856
life	0.7817	0.8856	1.0000

[1] "Matrix solve(sqrt(I\*C)) %&% C"

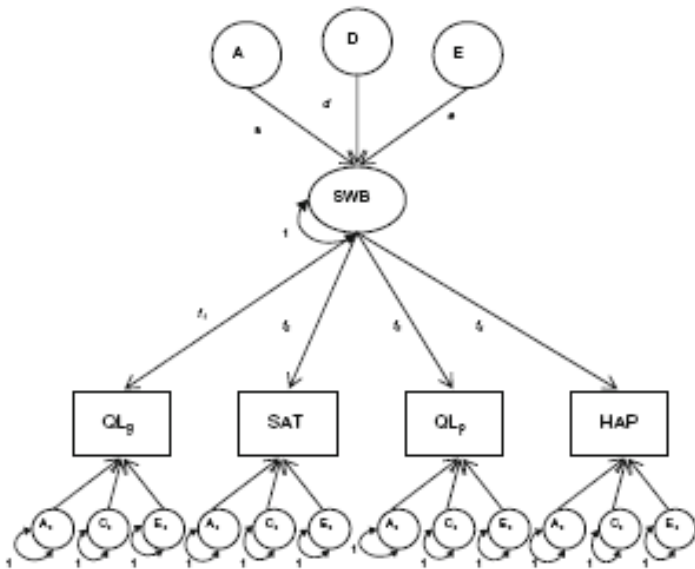
	corC1	corC2	corC3
Family	1.0000	0.7208	0.8585
happy	0.7208	1.0000	0.9743
life	0.8585	0.9743	1.0000

[1] "Matrix solve(sqrt(I\*E)) %&% E"

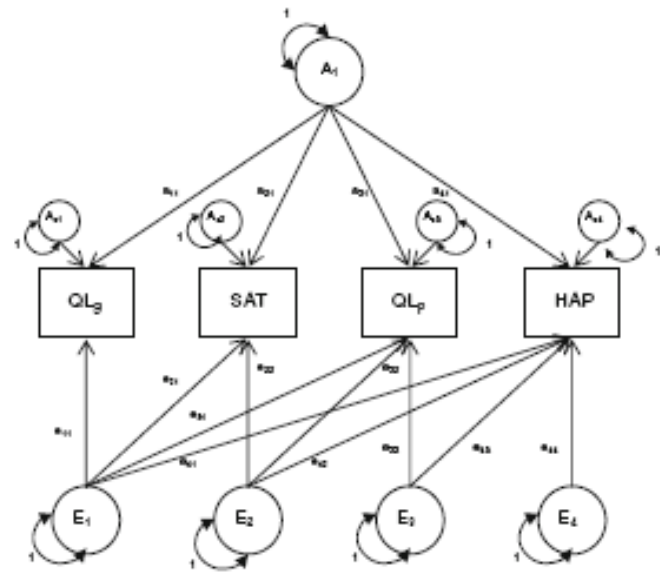
	corE1	corE2	corE3
Family	1.0000	0.1456	0.1029
happy	0.1456	1.0000	0.6651
life	0.1029	0.6651	1.0000

# Genetic Models

Genetic and environmental factor analysis examples



Common Pathway Model



Independent Pathway Model