Introduction to Multivariate Genetic Analysis

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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)

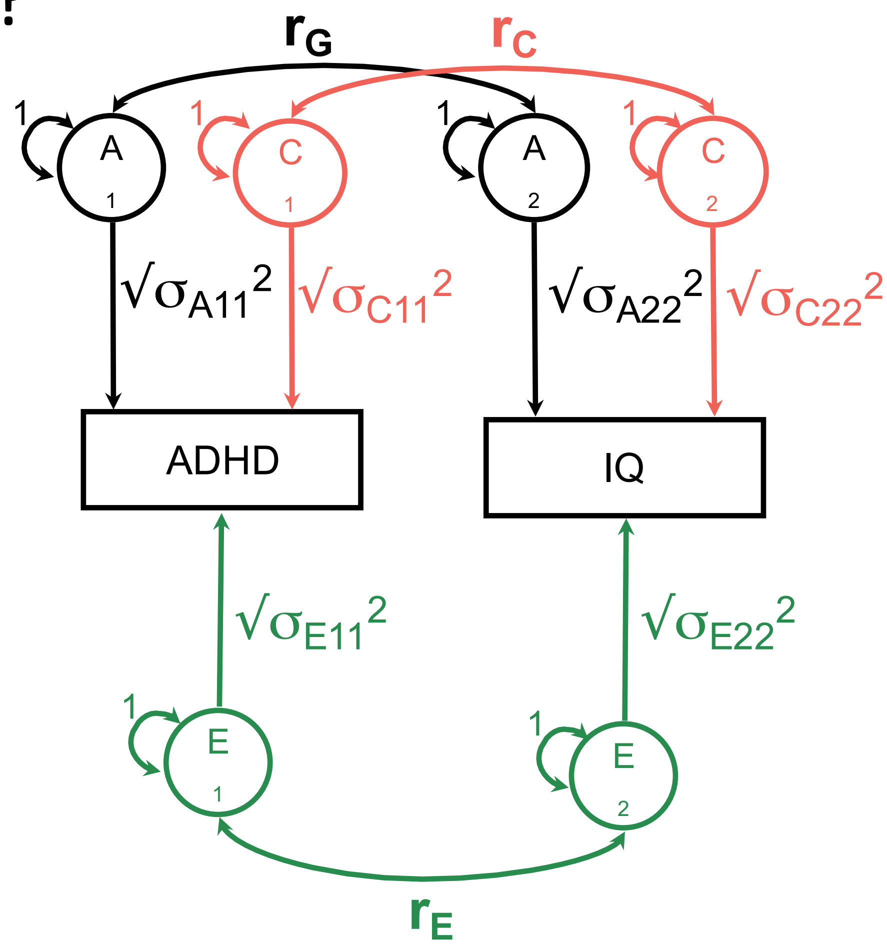
Can use information on multiple traits from twin pairs to partition covariation into genetic and environmental components

Example 1

Why do traits correlate/covary?

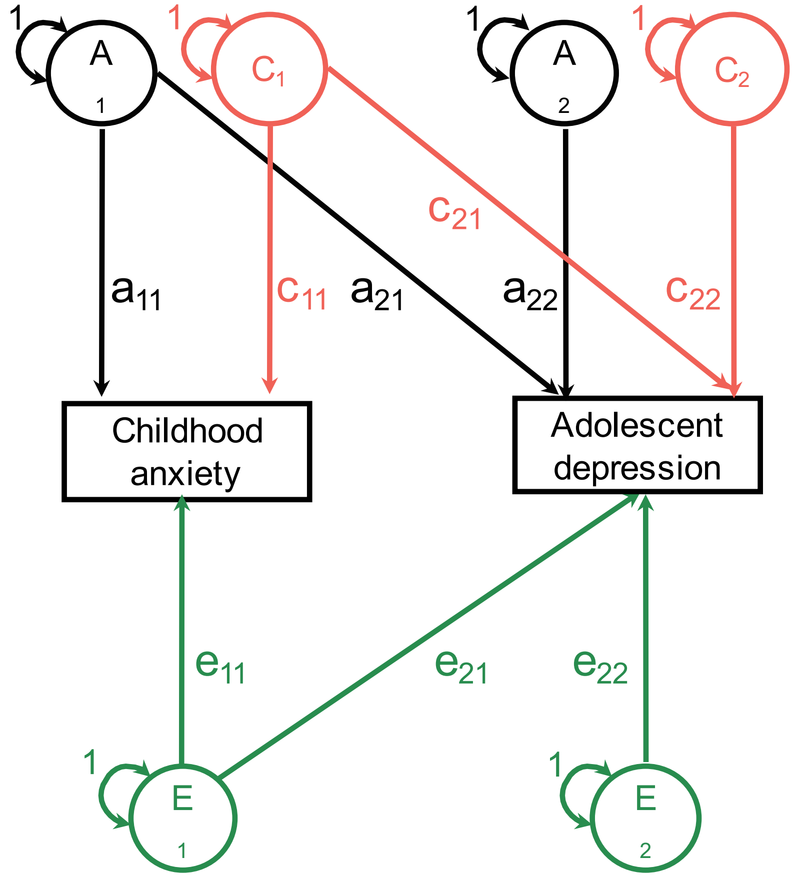
How can we explain the association?

- 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

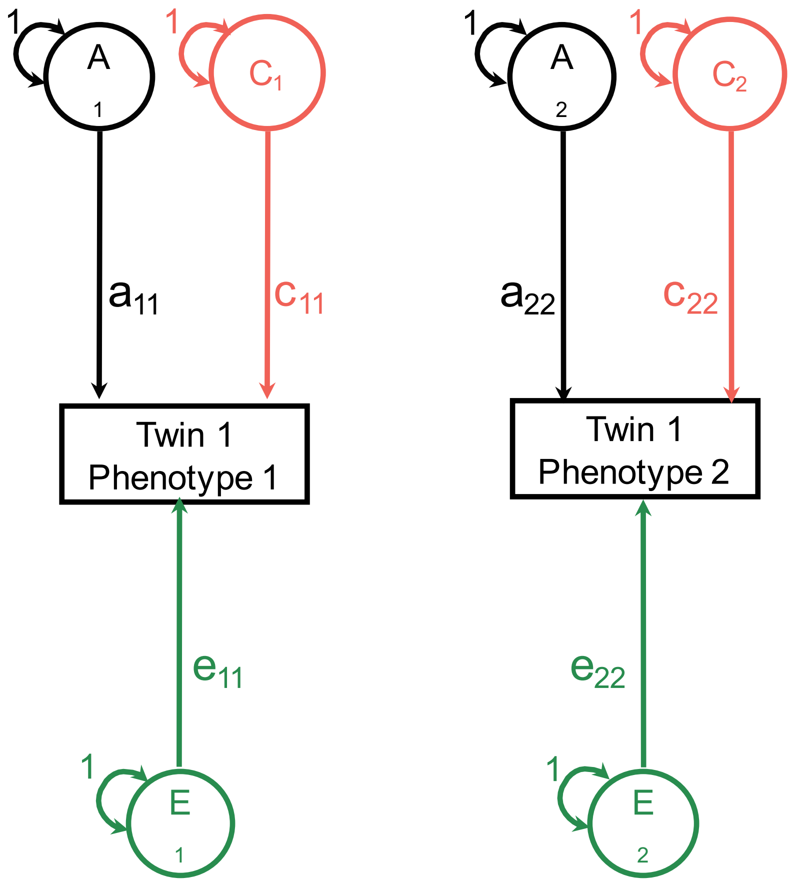
Observed Covariance Matrix

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

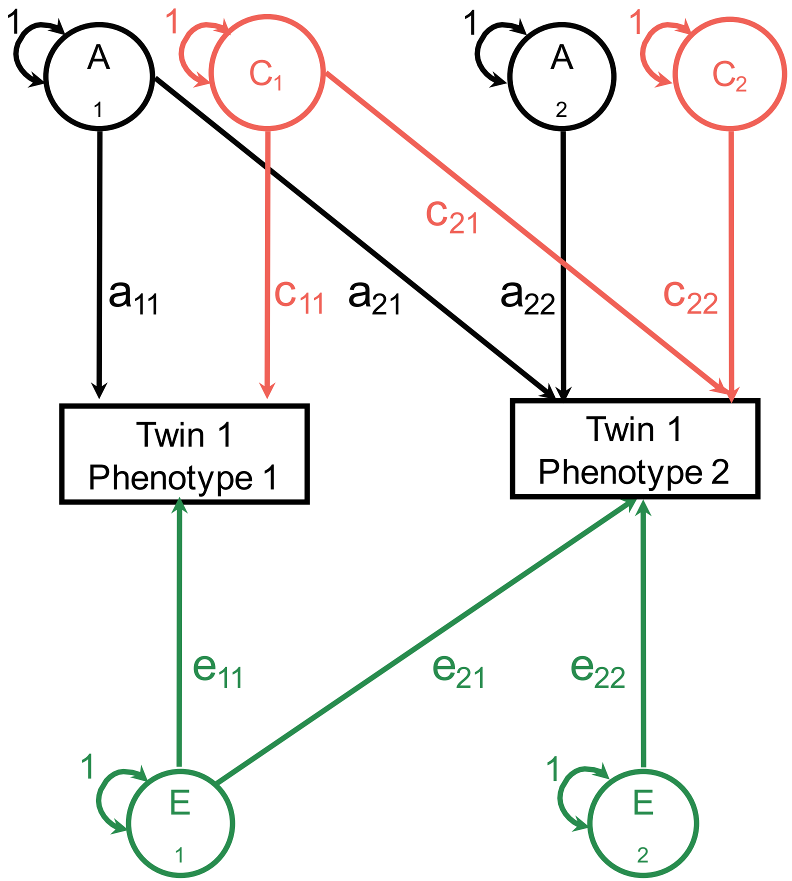
Observed Covariance Matrix

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

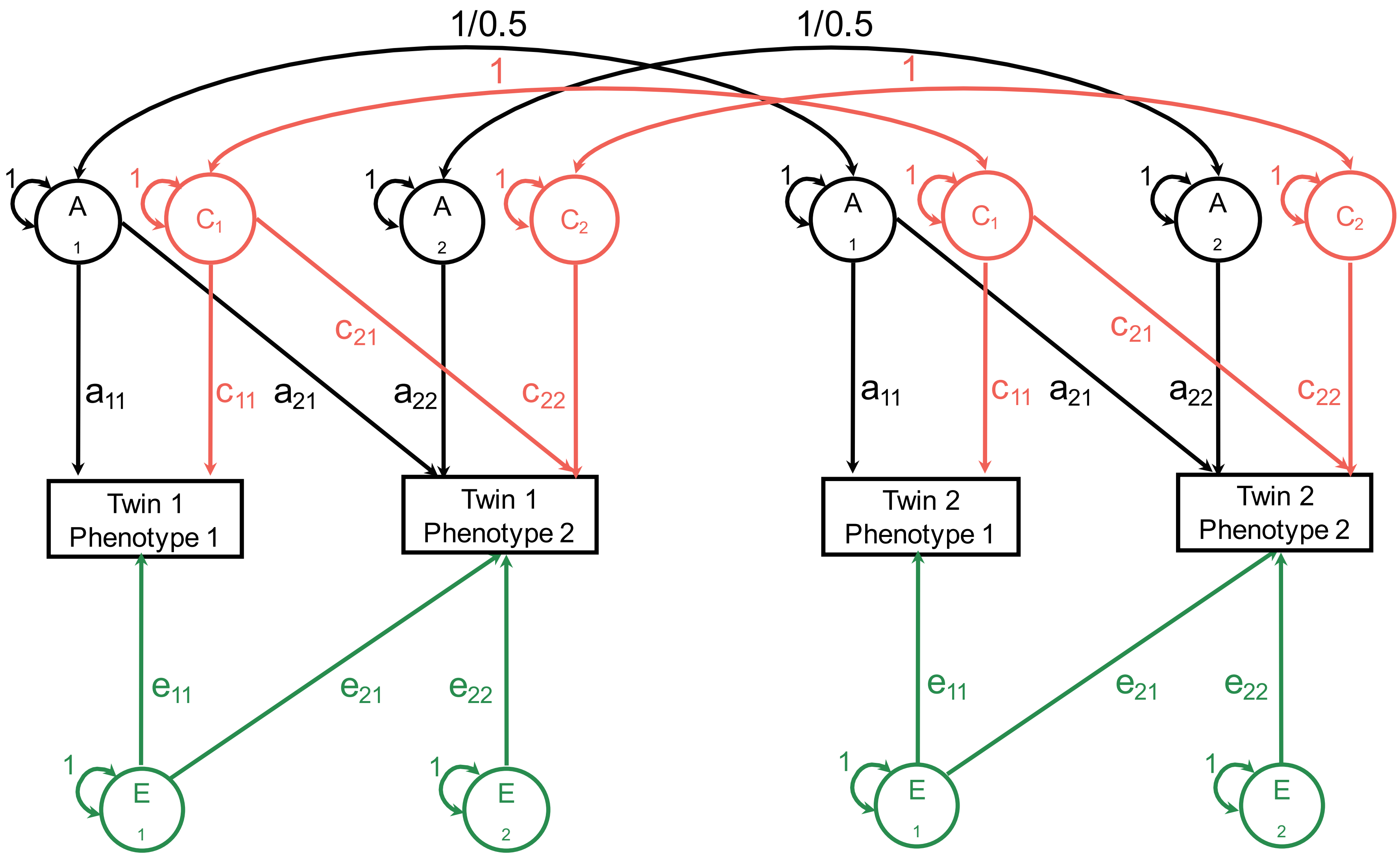
SEM: Cholesky Decomposition



SEM: Cholesky Decomposition



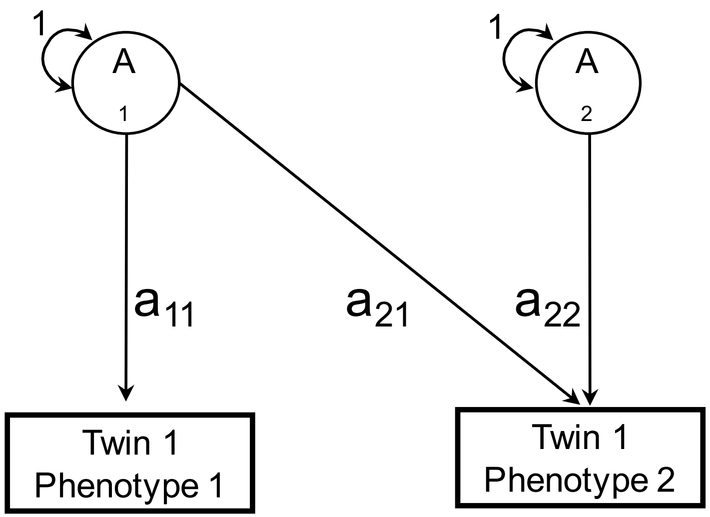
SEM: Cholesky Decomposition



Cholesky Decomposition

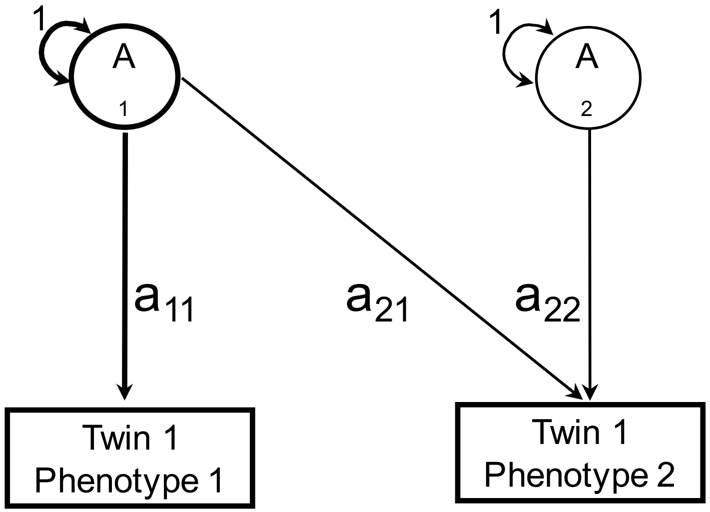
Path Tracing

Within-Twin Covariances (A)



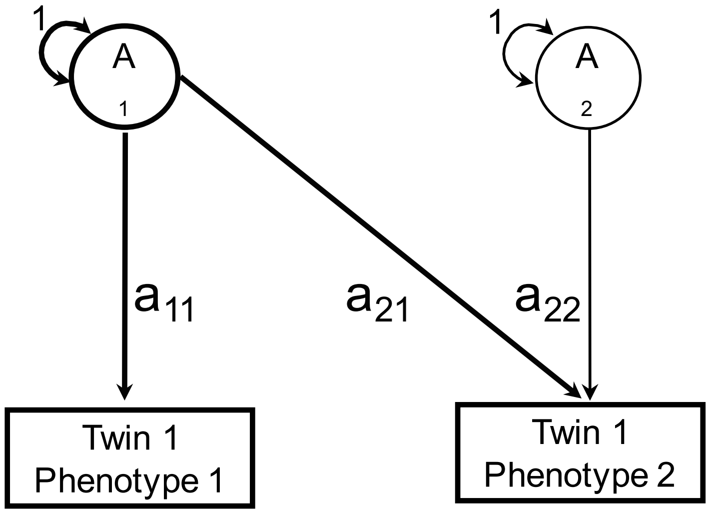
		Twin 1	
		Phenotype 1	Phenotype 2
Twin 1	Phenotype 1		
	Phenotype 2		

Within-Twin Covariances (A)



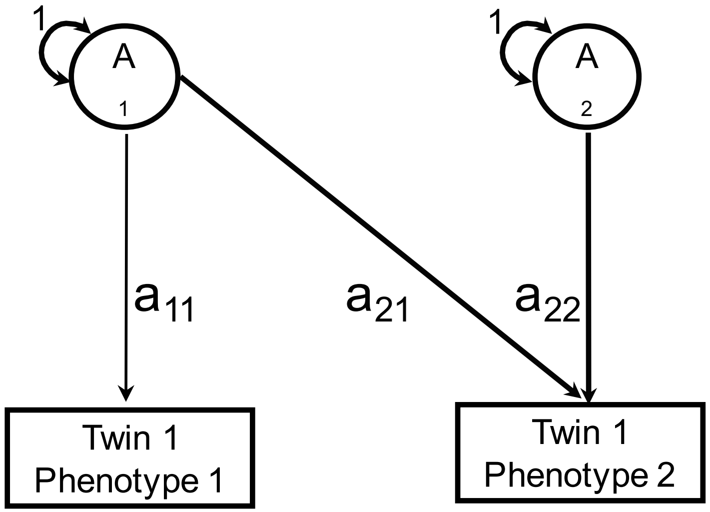
		Twin 1	
		Phenotype 1	Phenotype 2
Twin 1	Phenotype 1	a_{11}^2	
	Phenotype 2		

Within-Twin Covariances (A)



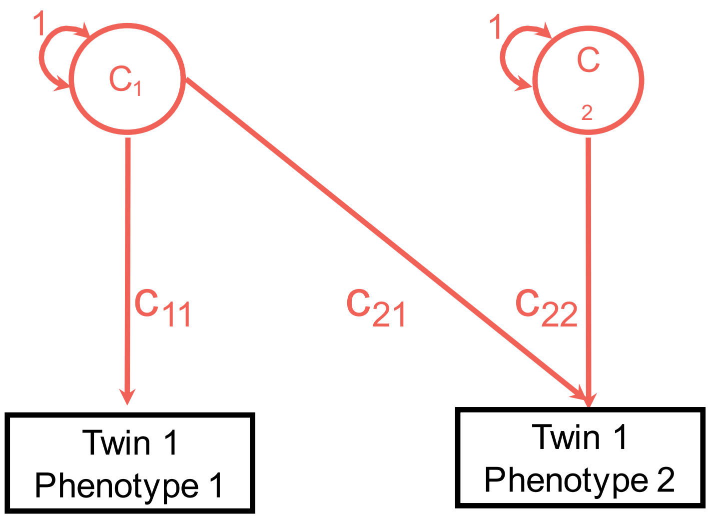
		Twin 1	
		Phenotype 1	Phenotype 2
Twin 1	Phenotype 1	a_{11}^2	
	Phenotype 2	$a_{11}a_{21}$	

Within-Twin Covariances (A)



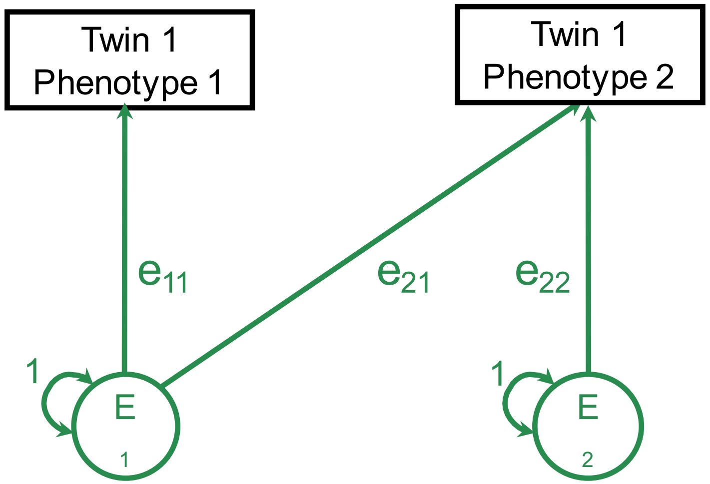
		Twin 1	
		Phenotype 1	Phenotype 2
Twin 1	Phenotype 1	a_{11}^2	
	Phenotype 2	$a_{11}a_{21}$	$a_{22}^2+a_{21}^2$

Within-Twin Covariances (C)



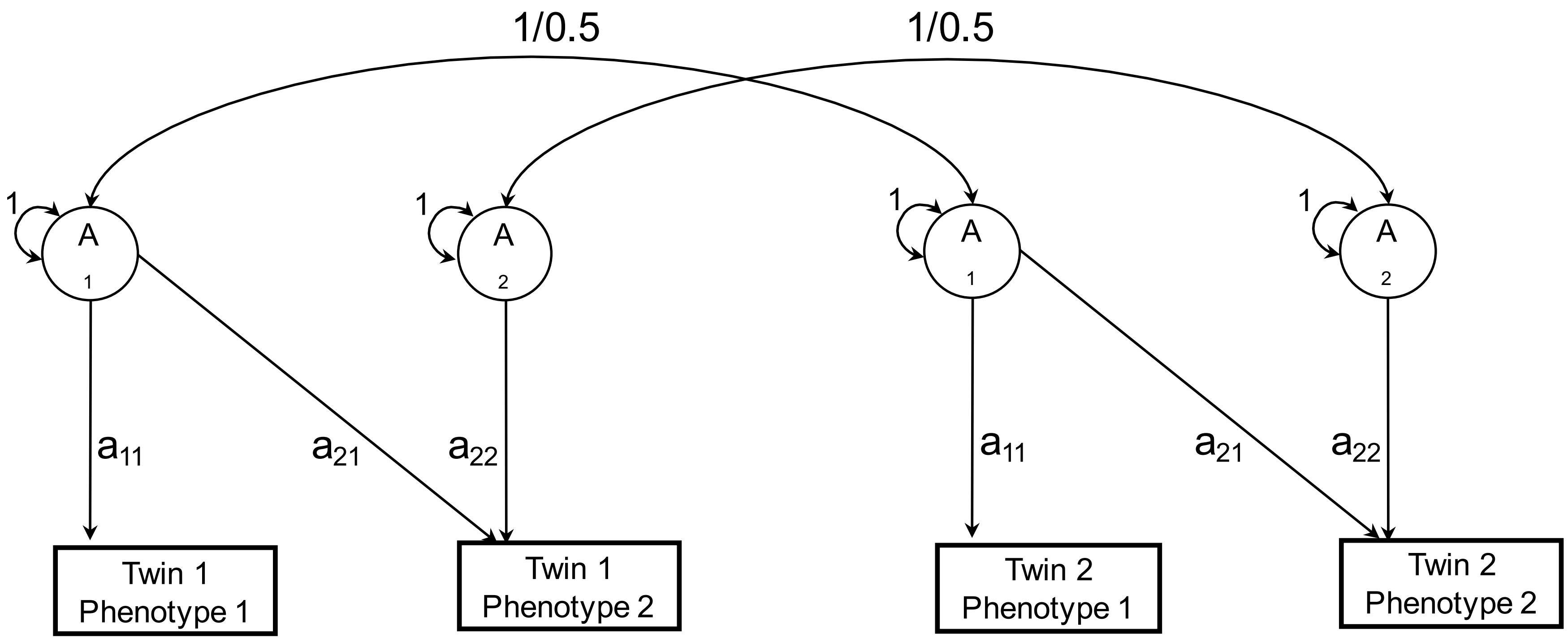
		Twin 1	
		Phenotype 1	Phenotype 2
Twin 1	Phenotype 1	$a_{11}^2+c_{11}^2$	
	Phenotype 2	$a_{11}a_{21}+c_{11}c_{21}$	$a_{22}^2+a_{21}^2+c_{22}^2+c_{21}^2$

Within-Twin Covariances (E)



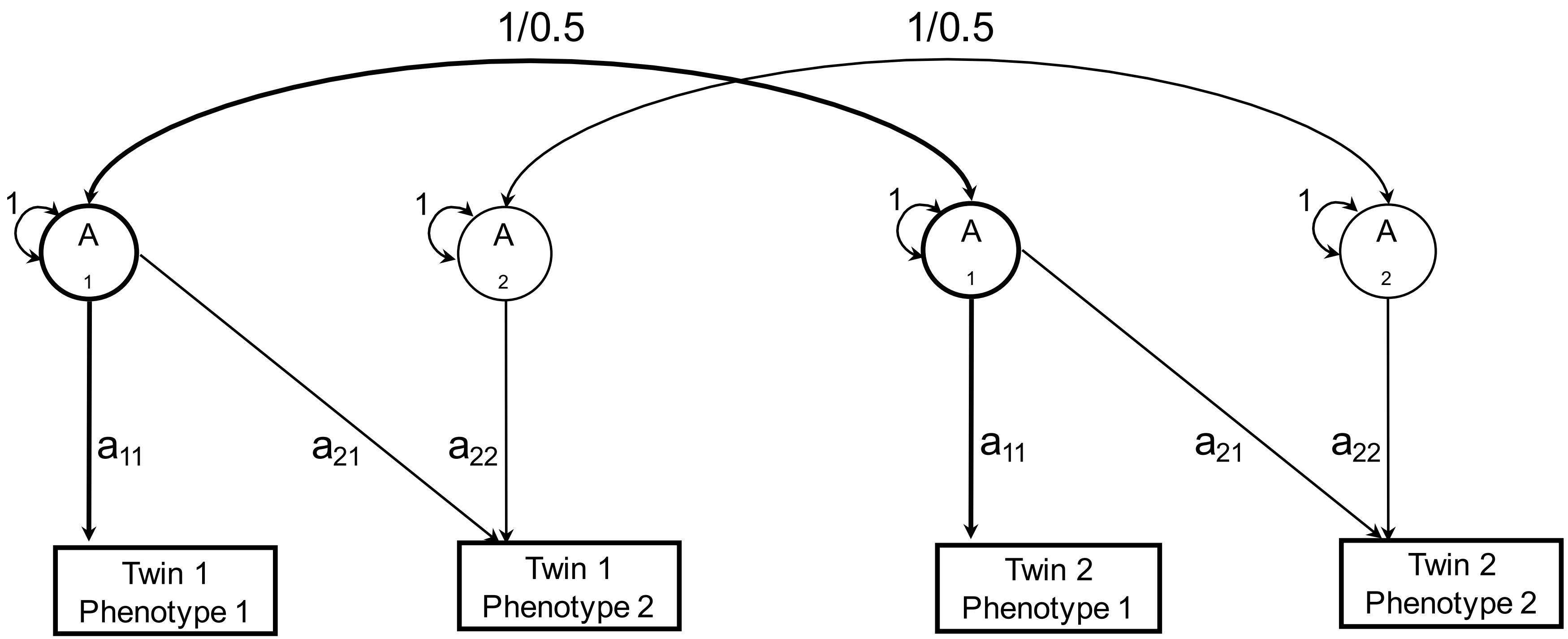
Twin 1		Twin 1 Phenotype 1	Twin 1 Phenotype 2
Twin 1	Phenotype 1	$a_{11}^2+c_{11}^2+e_{11}^2$	
Twin 1	Phenotype 2	$a_{11}a_{21}+c_{11}c_{21}+e_{11}e_{21}$	$a_{22}^2+a_{21}^2+c_{22}^2+c_{21}^2+e_{22}^2+e_{21}^2$

Cross-Twin Covariances (A)



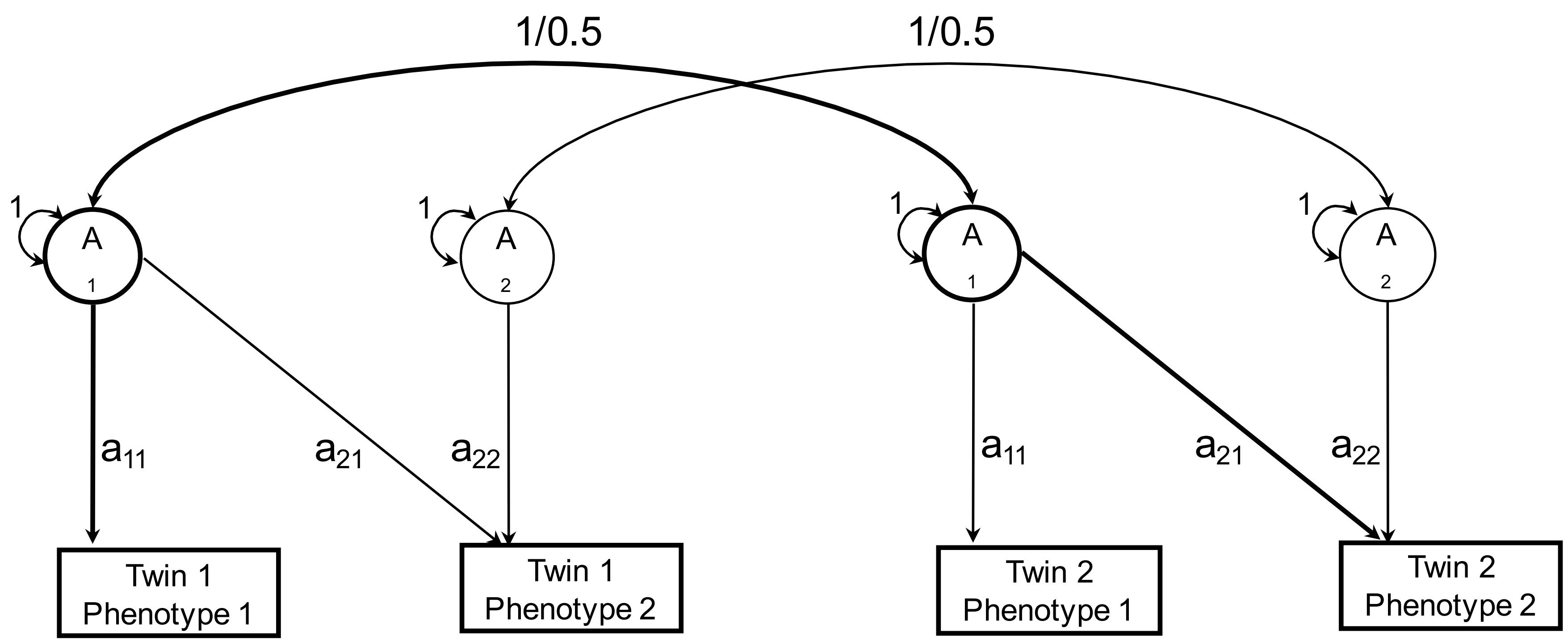
		Twin 1	
		Phenotype 1	Phenotype 2
Twin 2	Phenotype 1		
	Phenotype 2		

Cross-Twin Covariances (A)



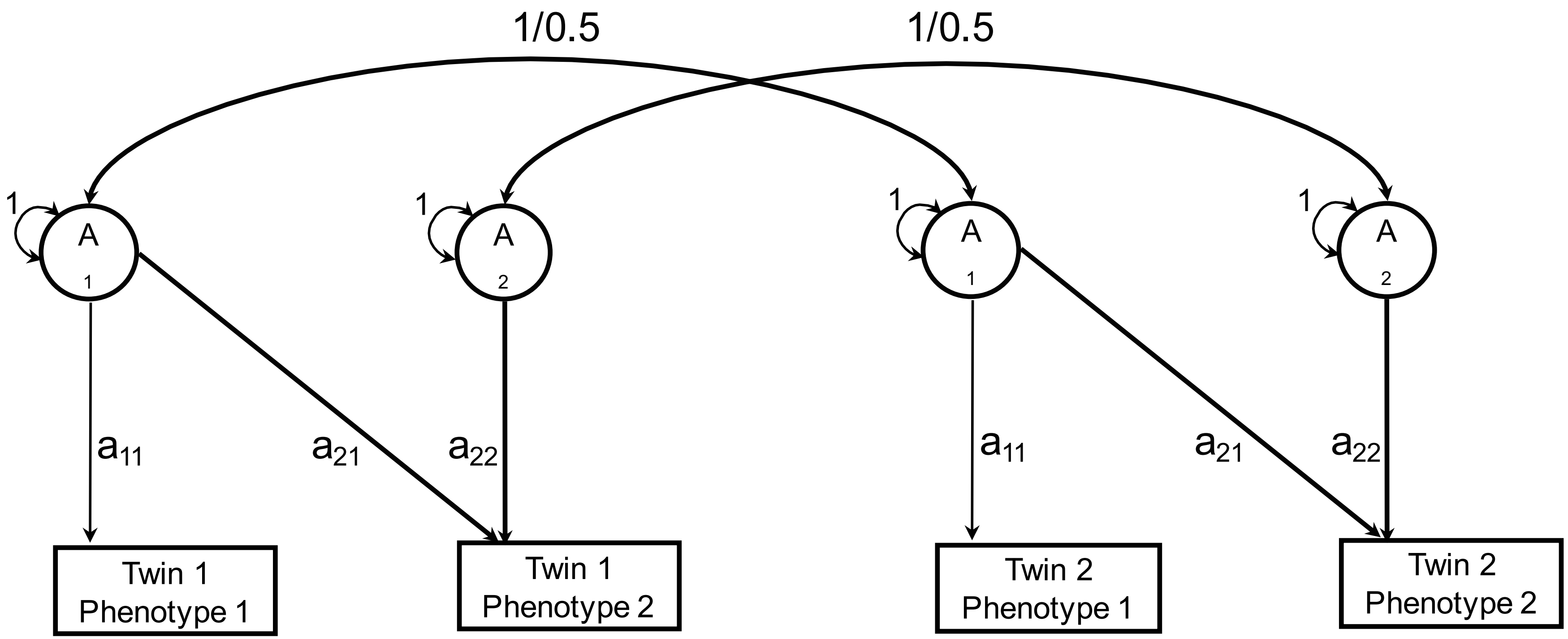
	Twin 1: Phenotype 1	Twin 1: Phenotype 2
Twin 2: Phenotype 1	$1/0.5 a_{11}^2$	
Twin 2: Phenotype 2		

Cross-Twin Covariances (A)



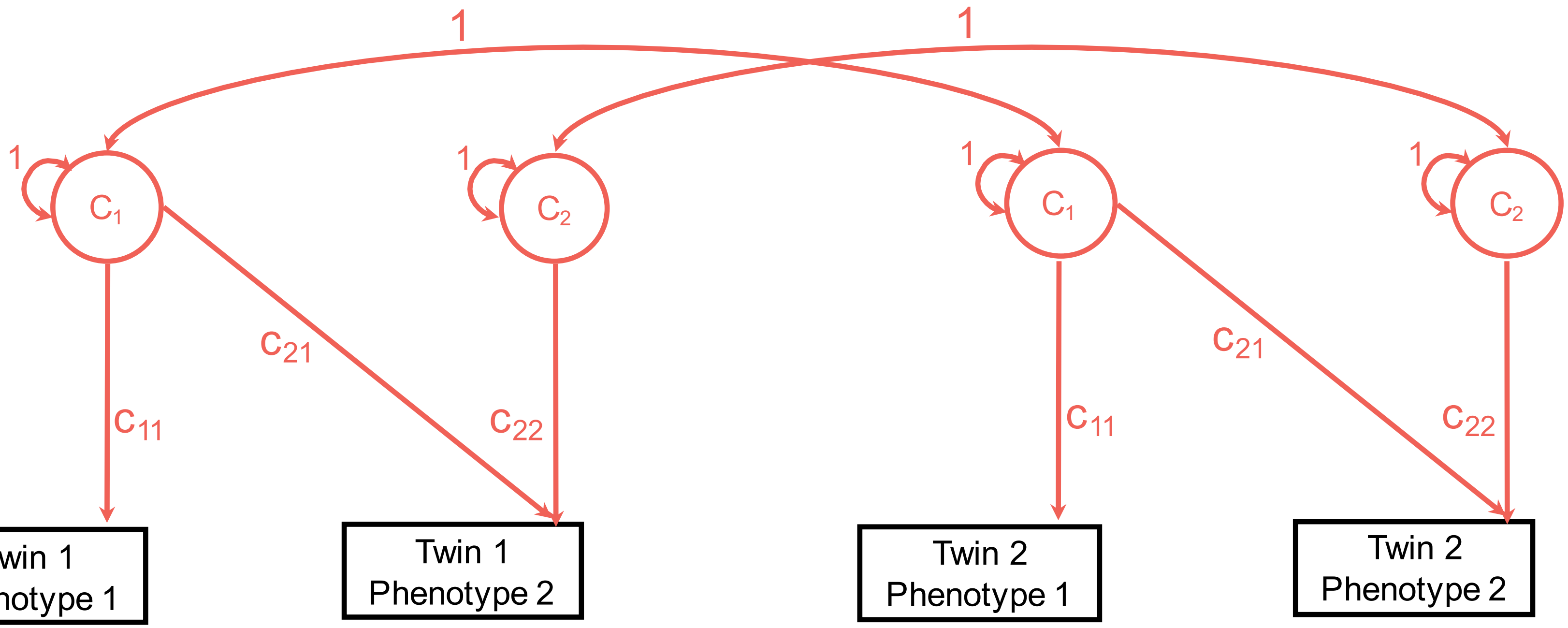
		Twin 1	
		Phenotype 1	Phenotype 2
Twin 2	Phenotype 1	$1/0.5a_{11}^2$	
	Phenotype 2	$1/0.5a_{11}a_{21}$	

Cross-Twin Covariances (A)



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

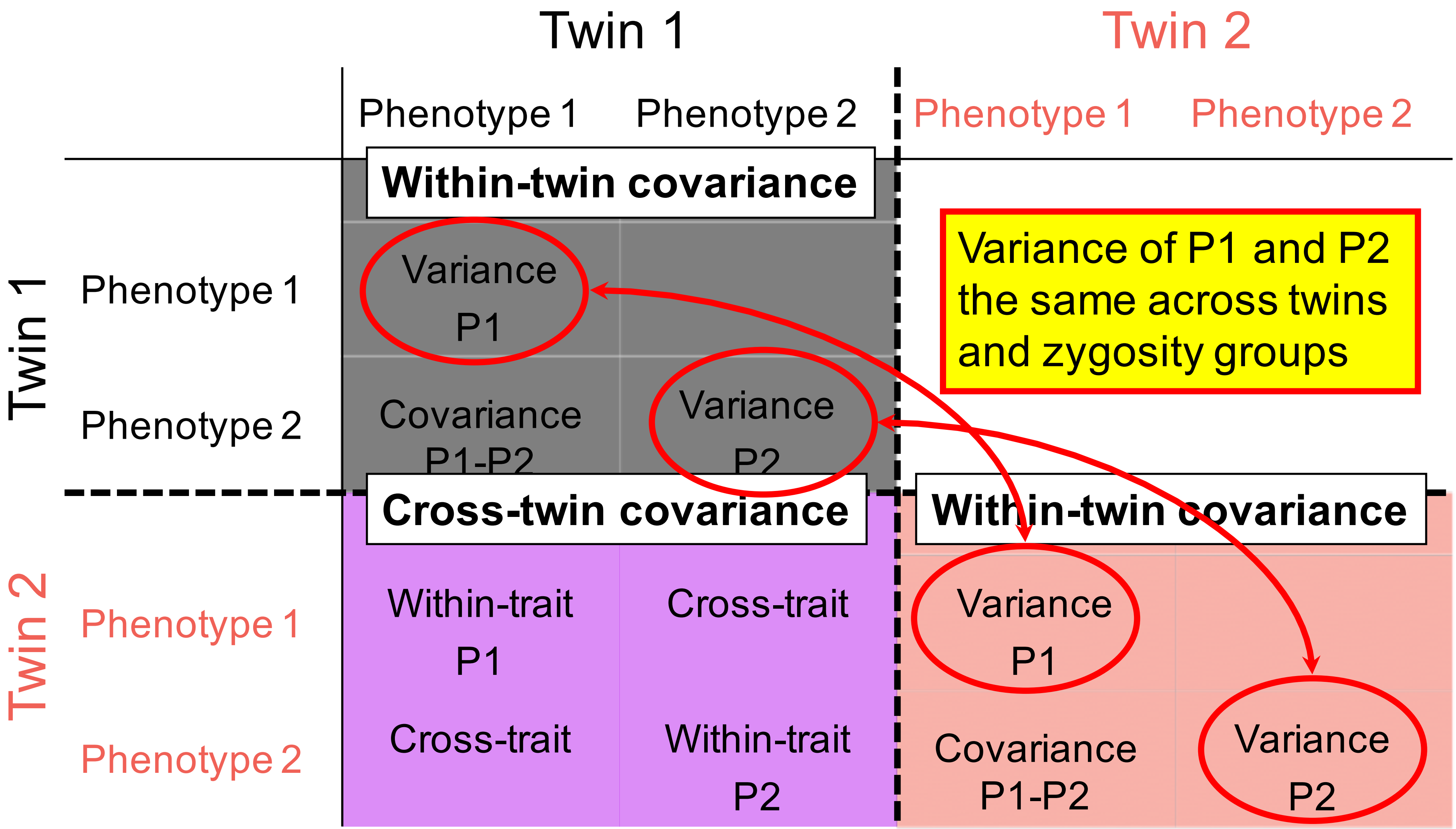
Predicted Model

		Twin 1		Twin 2	
		Phenotype 1	Phenotype 2	Phenotype 1	Phenotype 2
		Within-twin covariance			
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 covariance		**Within-twin covariance**	
Twin 2	Phenotype 1	$1/.5a_{11}^2+c_{11}^2$		$a_{11}^2+c_{11}^2+e_{11}^2$	
	Phenotype 2	$1/.5a_{11}a_{21}+c_{11}c_{21}$	$1/.5a_{22}^2+1/.5a_{21}^2+c_{22}^2+c_{21}^2$	$a_{11}a_{21}+c_{11}c_{21}+e_{11}e_{21}$	$a_{22}^2+a_{21}^2+c_{22}^2+c_{21}^2+e_{22}^2+e_{21}^2$

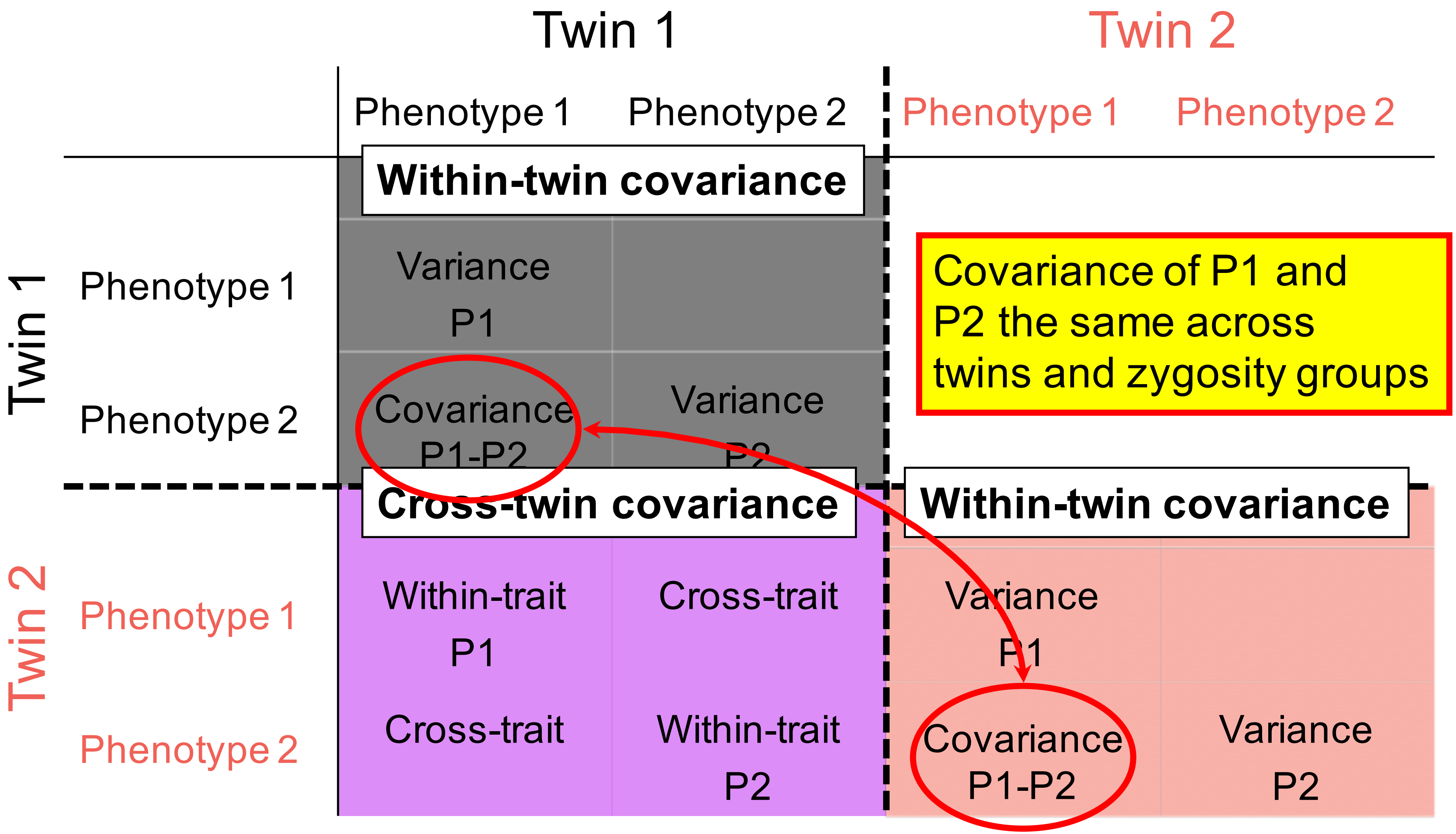
Predicted Model

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

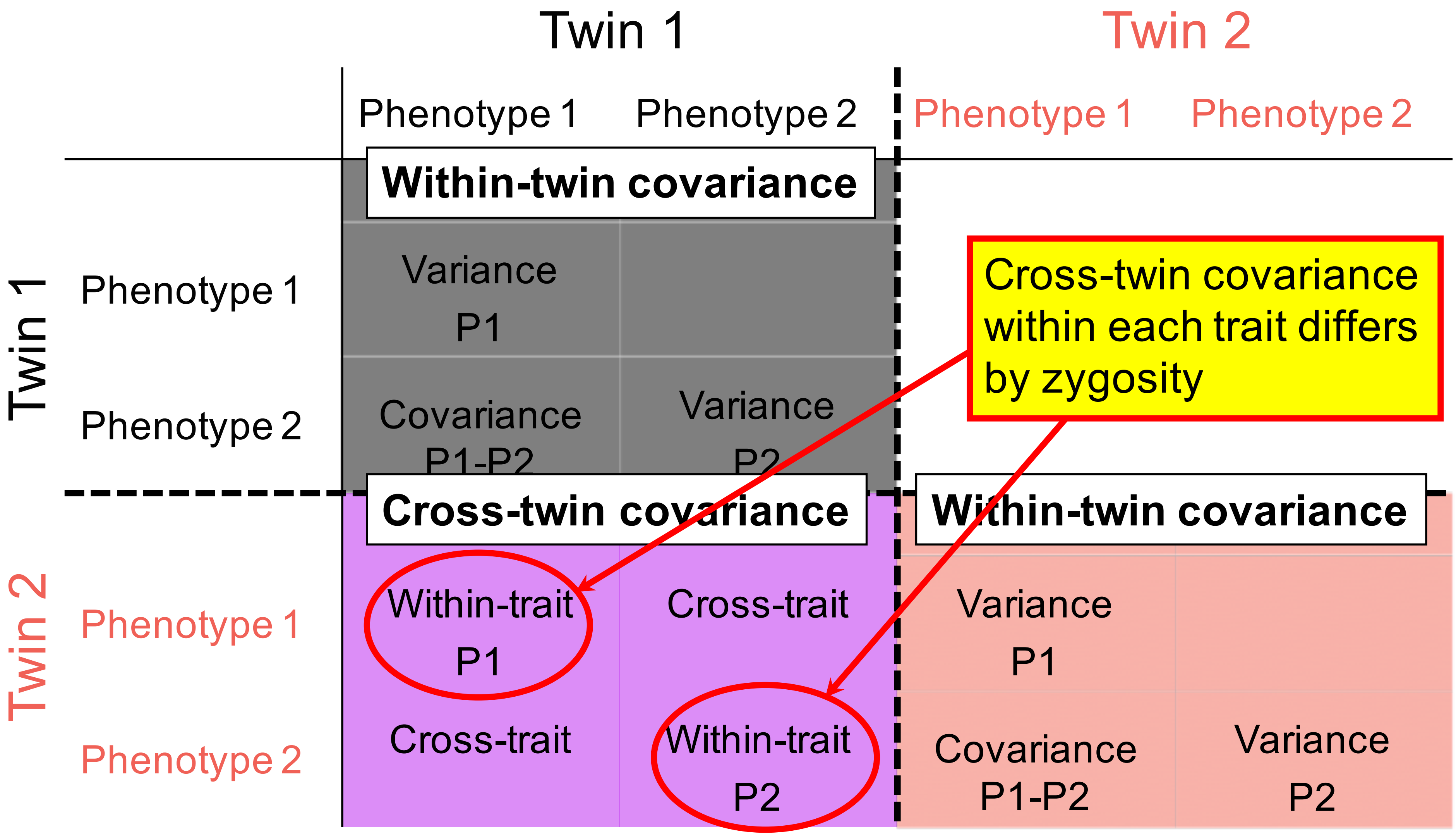
Predicted Model



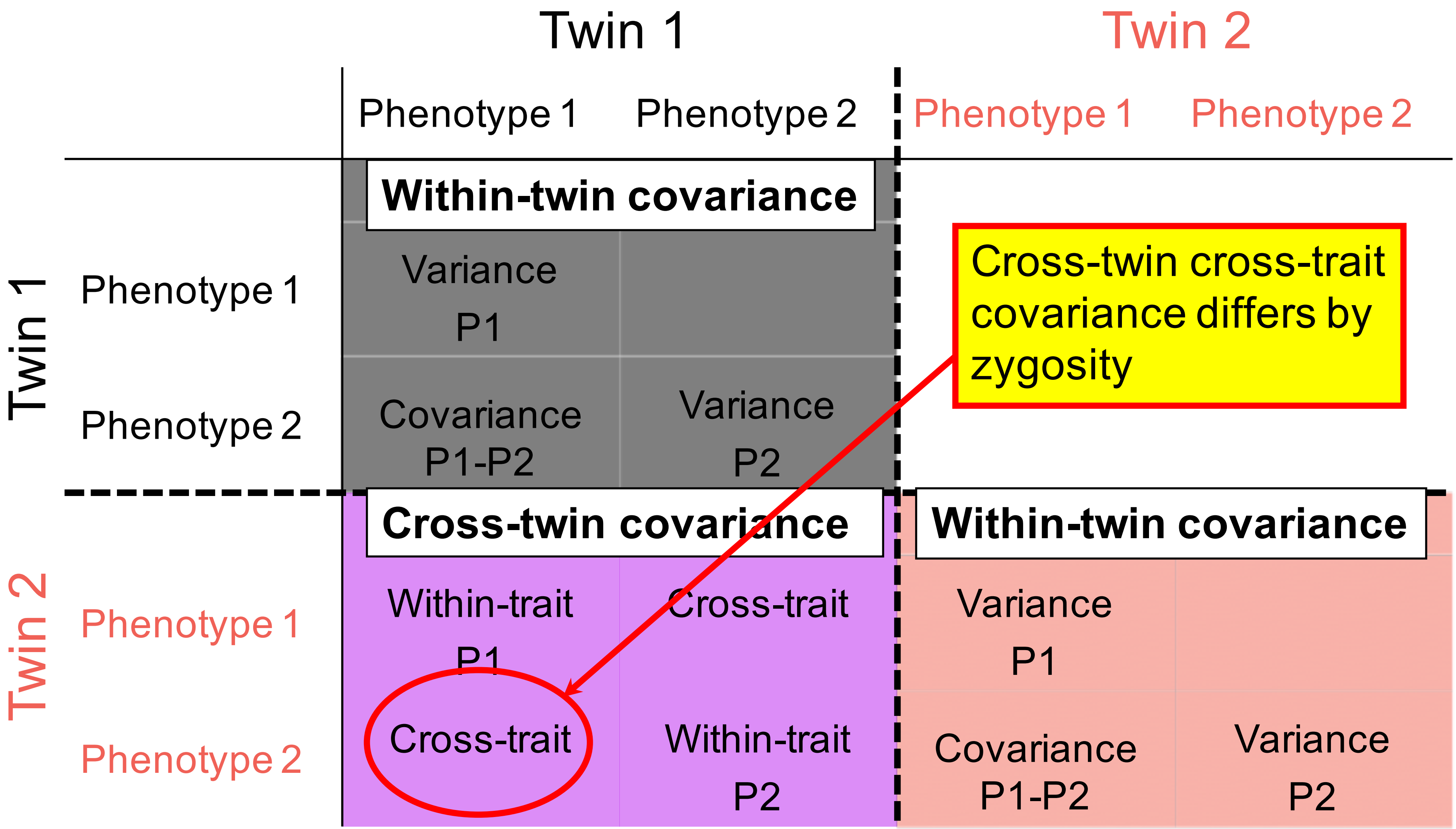
Predicted Model



Predicted Model



Predicted Model



Example Covariance Matrix

MZ

Within-twin covariance (Twin 1) · Cross-twin covariance · Within-twin covariance (Twin 2)

		Twin 1		Twin 2	
				P1	P2
Twin 1	P1	1			
	P2				
Twin 2	P1	0.79	0.49	1	
	P2	0.50	0.59	0.29	1

DZ

Within-twin covariance (Twin 1) · Cross-twin covariance · Within-twin covariance (Twin 2)

		Twin 1		Twin 2	
				P1	P2
Twin 1	P1	1			
	P2				
Twin 2	P1	0.39	0.25	1	
	P2	0.24	0.43	0.31	1

Example Covariance Matrix

MZ

Within-twin covariance (Twin 1) · Cross-twin covariance · Within-twin covariance (Twin 2)

		Twin 1 P1	Twin 1 P2	Twin 2 P1	Twin 2 P2
Twin 1	P1	1			
	P2				
Twin 2	P1	0.79	0.49	1	
	P2	0.50	0.59	0.29	1

DZ

Within-twin covariance (Twin 1) · Cross-twin covariance · Within-twin covariance (Twin 2)

		Twin 1 P1	Twin 1 P2	Twin 2 P1	Twin 2 P2
Twin 1	P1	1			
	P2				
Twin 2	P1	0.39	0.25	1	
	P2	0.24	0.43	0.31	1

Example Covariance Matrix

MZ

Within-twin covariance · Cross-twin covariance · Within-twin covariance

		Twin 1 P1	Twin 1 P2	Twin 2 P1	Twin 2 P2
Twin 1	P1	1			
Twin 1	P2				
Twin 2	P1	0.79	0.49	1	
Twin 2	P2	0.50	0.59	0.29	1

DZ

Within-twin covariance · Cross-twin covariance · Within-twin covariance

		Twin 1 P1	Twin 1 P2	Twin 2 P1	Twin 2 P2
Twin 1	P1	1			
Twin 1	P2				
Twin 2	P1	0.39	0.25	1	
Twin 2	P2	0.24	0.43	0.31	1

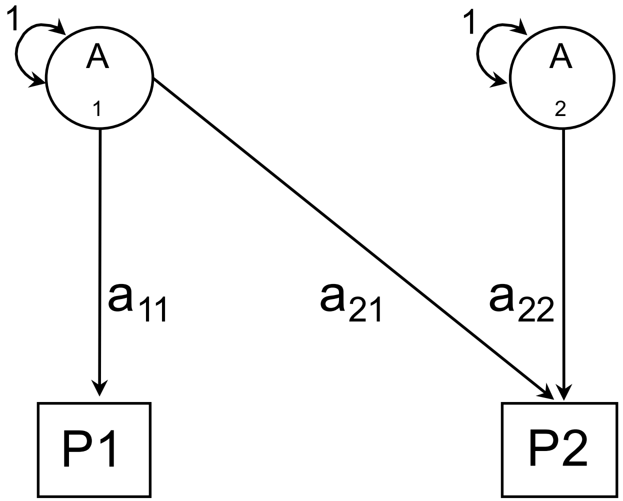
Summary

- 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

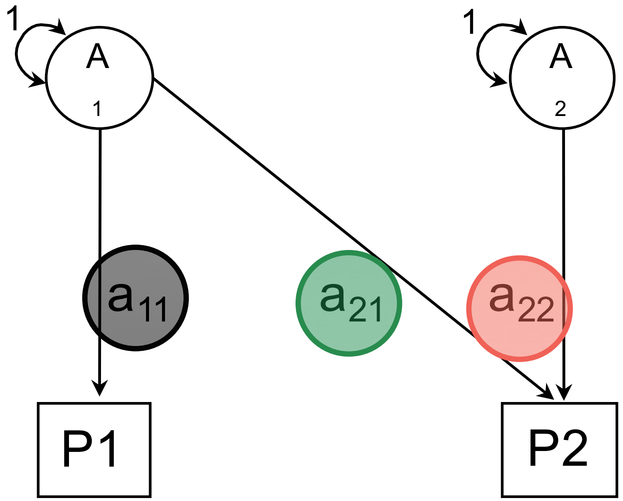
Within-Twin Covariance



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:

	a1	a2
P1	a_{11}	0
P2	a_{21}	a_{22}

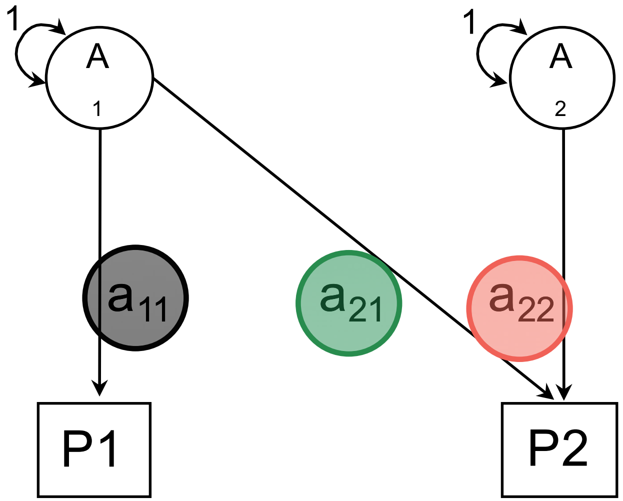
Starting values and labels

```
# Set Starting Values
svMe     <- c(15,5)       # start value for means
laMe     <- paste(selVars,"Mean",sep="_")
svPa     <- .6            # start value for parameters
svPas    <- diag(svPa,nv,nv)
laA      <- paste("a",rev(nv+1-sequence(1:nv)),rep(1:nv,nv:1),sep="")    # c("a11","a21","a22")
laD      <- paste("d",rev(nv+1-sequence(1:nv)),rep(1:nv,nv:1),sep="")
laC      <- paste("c",rev(nv+1-sequence(1:nv)),rep(1:nv,nv:1),sep="")
laE      <- paste("e",rev(nv+1-sequence(1:nv)),rep(1:nv,nv:1),sep="")
```

create numbered labels to fill the lower triangular matrices with the first number corresponding to the variable being pointed to and the second number corresponding to the factor

```
> nv <- 2
>
> rev(nv+1-sequence(1:nv))
[1] 1 2 2
>
> rep(1:nv,nv:1)
[1] 1 1 2
>
> paste("a",rep(1:nv,1:nv),rep(1:nv,nv:1),sep="")
[1] "a11" "a21" "a22"
```

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:

	a1	a2
P1	a_{11}	0
P2	a_{21}	a_{22}

$\Sigma_A = a * a^T$

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

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

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

Within-Twin Covariance

$$\Sigma_A = a * a^T$$

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

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

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

Total Within-Twin Covar.

$$\Sigma_A = a \%*\% \, t(a) = \begin{bmatrix} a_{11}^2 & a_{11}a_{21} \\ a_{21}a_{11} & a_{21}^2 + a_{22}^2 \end{bmatrix}$$

$$\Sigma_C = c \%*\% \, t(c) = \begin{bmatrix} c_{11}^2 & c_{11}c_{21} \\ c_{21}c_{11} & c_{21}^2 + c_{22}^2 \end{bmatrix}$$

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

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

$$\Sigma_V = \Sigma_A + \Sigma_C + \Sigma_E$$

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

OpenMx Matrices & Algebra

```
# Matrices declared to store a, c, and e Path Coefficients
pathA     <- mxMatrix( type="Lower", nrow=nv, ncol=nv, free=TRUE, values=svPas, label=laA, name="a" )
pathD     <- mxMatrix( type="Lower", nrow=nv, ncol=nv, free=TRUE, values=svPas, label=laD, name="d" )
pathC     <- mxMatrix( type="Lower", nrow=nv, ncol=nv, free=FALSE, values=0, label=laC, name="c" )
pathE     <- mxMatrix( type="Lower", nrow=nv, ncol=nv, free=TRUE, values=svPas, label=laE, name="e" )

# Matrices generated to hold A, C, and E computed Variance Components
covA      <- mxAlgebra( expression=a %*% t(a), name="A" )
covD      <- mxAlgebra( expression=d %*% t(d), name="D" )
covC      <- mxAlgebra( expression=c %*% t(c), name="C" )
covE      <- mxAlgebra( expression=e %*% t(e), name="E" )
```

	A1	A2
P1	a_{11}	0
P2	a_{21}	a_{22}

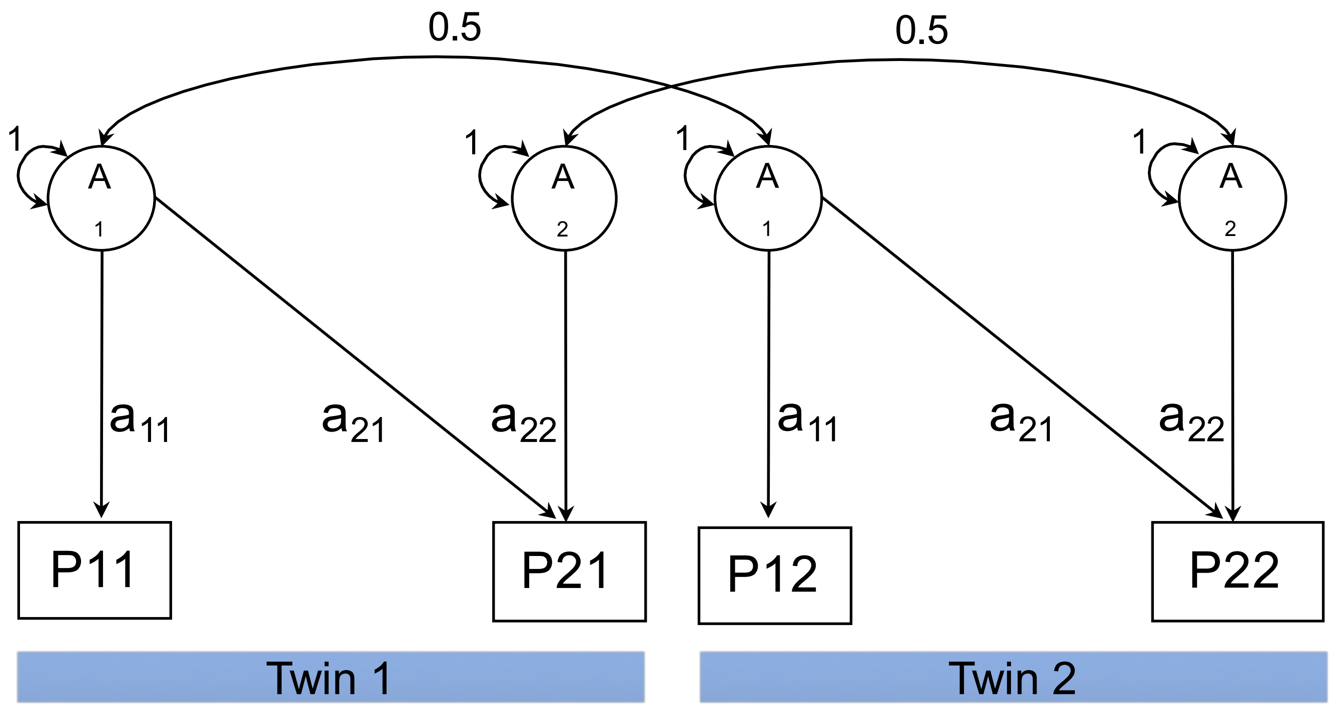
$$a = \begin{bmatrix} a_{11} & 0 \\ a_{21} & a_{22} \end{bmatrix}$$

$$\sum_A = a * a^T$$

a %*% t(a)

regular multiplication of lower triangular matrix and its transpose

Additive Genetic Cross-Twin Covariance (DZ)



Path Tracing:

Within-traits

P11-P12 = $0.5a_{11}^2$

P21-P22 = $0.5a_{22}^2 + 0.5a_{21}^2$

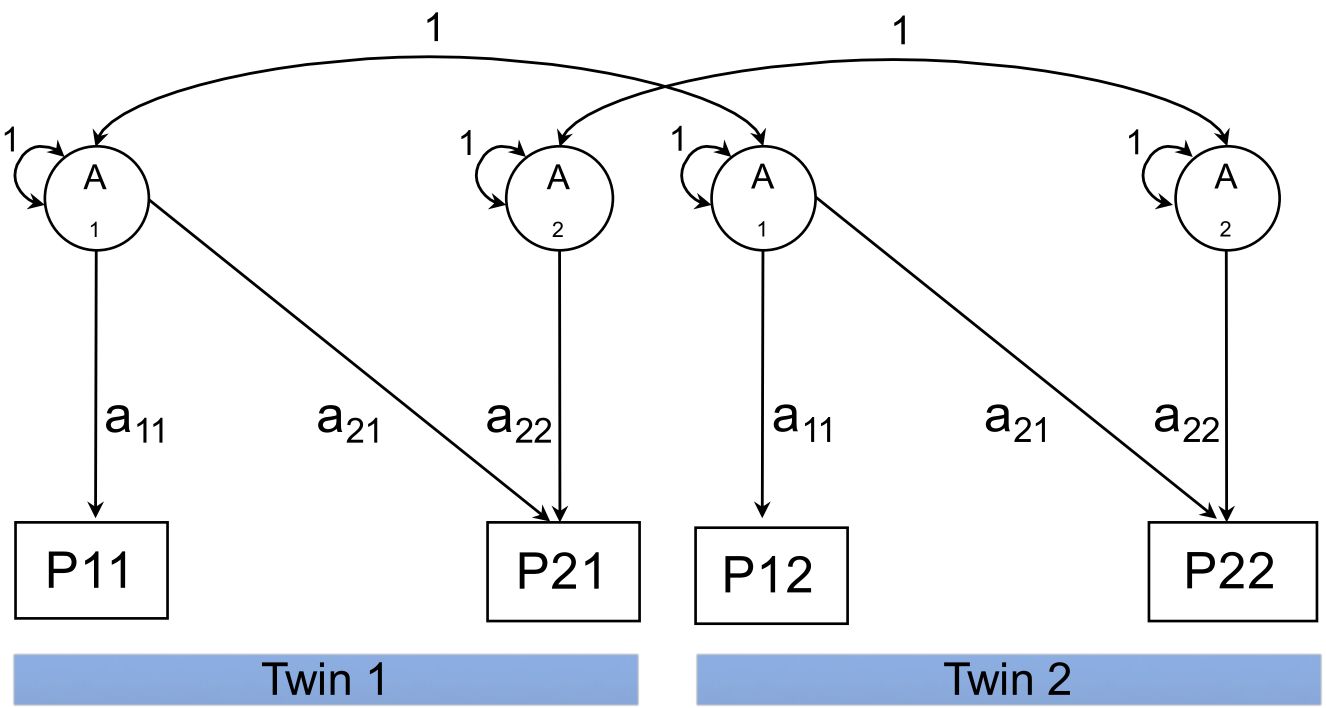
Cross-traits

P11-P22 = $0.5a_{11}a_{21}$

P21-P12 = $0.5a_{21}a_{11}$

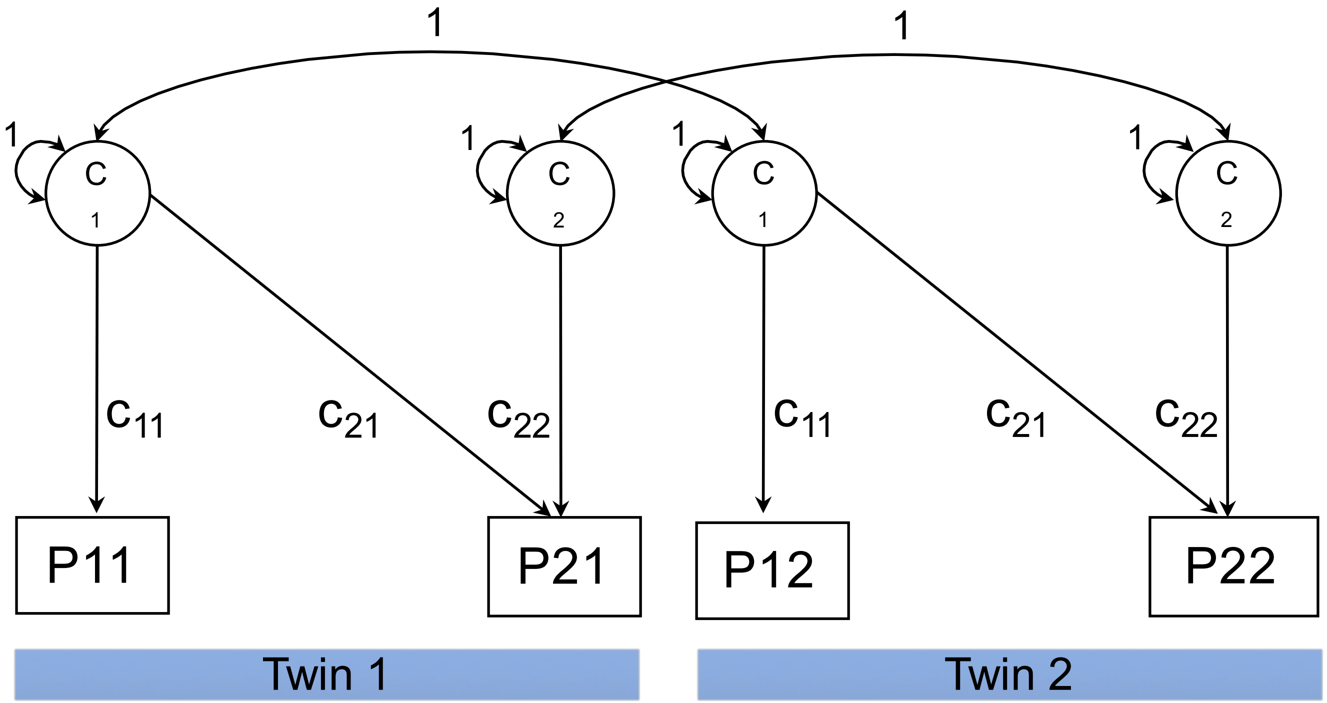
$$0.5 \otimes \Sigma_A = 0.5\%x\%(a\%*\%t(a)) = \begin{bmatrix} 0.5a_{11}^2 & 0.5a_{11}a_{21} \\ 0.5a_{21}a_{11} & 0.5(a_{21}^2 + a_{22}^2) \end{bmatrix}$$

Additive Genetic Cross-Twin Covariance (MZ)



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

Common Environment Cross-Twin Covariance



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

Covariance Model for Twin Pairs

```
# Algebra for expected Mean and Variance/Covariance Matrices in MZ & DZ twins
meanG     <- mxMatrix( type="Full", nrow=1, ncol=nv, free=TRUE, values=svMe, labels=laMe, name="Mean" )
meanT     <- mxAlgebra( expression= cbind(Mean,Mean), name="expMean" )
covMZ     <- mxAlgebra( expression= rbind( cbind(V, A+D+C), cbind(A+D+C, V)), name="expCovMZ" )
covDZ     <- mxAlgebra( expression= rbind( cbind(V, 0.5%x%A+0.25%x%D+C), cbind(0.5%x%A+0.25%x%D+C ,V)),
 name="expCovDZ" )
```

cbind creates two nv x ntv row matrices
rbind turns them into to ntv x ntv matrix

$$\Sigma_{MZ} = \begin{bmatrix} \Sigma_A+\Sigma_D+\Sigma_C+\Sigma_E & \Sigma_A+\Sigma_D+\Sigma_C \\ \Sigma_A+\Sigma_D+\Sigma_C & \Sigma_A+\Sigma_D+\Sigma_C+\Sigma_E \end{bmatrix}$$

$$\Sigma_{DZ} = \begin{bmatrix} \Sigma_A+\Sigma_D+\Sigma_C+\Sigma_E & 0.5\Sigma_A+0.25\Sigma_D+\Sigma_C \\ 0.5\Sigma_A+0.25\Sigma_D+\Sigma_C & \Sigma_A+\Sigma_D+\Sigma_C+\Sigma_E \end{bmatrix}$$

Obtaining Standardized Estimates

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

# Algebras generated to hold Parameter Estimates and Derived Variance Components
rowVars  <- rep('vars',nv)
colVars  <- rep(c('A','D','C','E','SA','SD','SC','SE'),each=nv)
estVars  <- mxAlgebra( expression=cbind(A,D,C,E,A/V,D/V,C/V,E/V), name="Vars",
 dimnames=list(rowVars,colVars))
```

$$\Sigma_P = \Sigma_A + \Sigma_D + \Sigma_C + \Sigma_E$$

each of covariance matrices is of size nv x nv

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

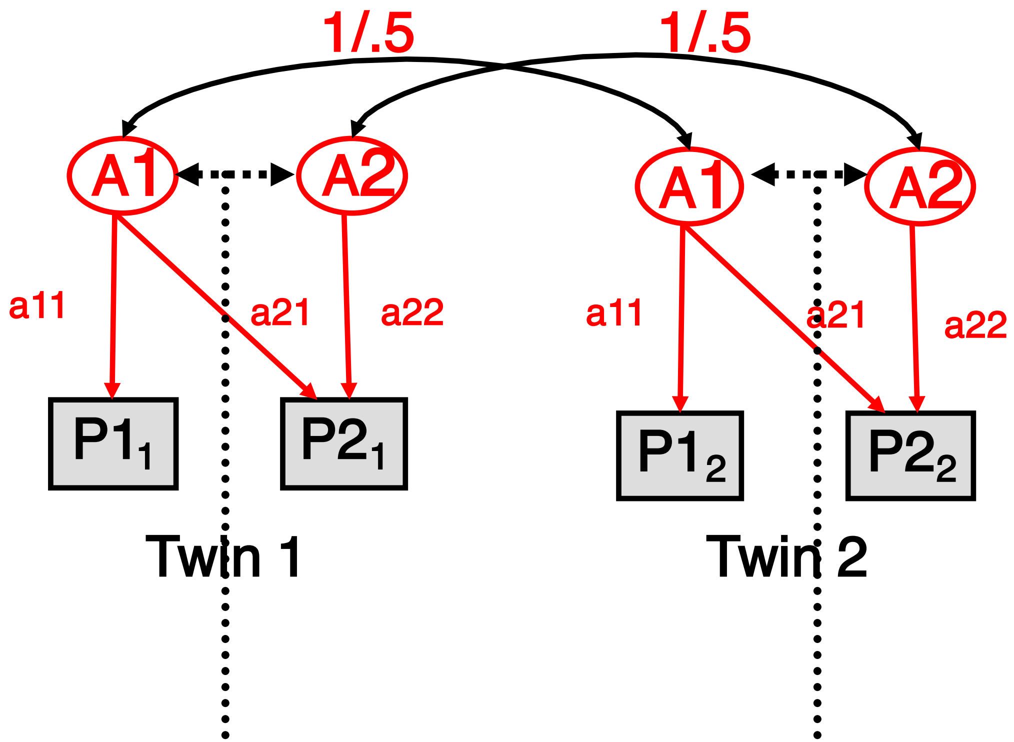
“is there a large overlap in gene/ environmental sets”

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

	A	A	C	C	E	E	SA	SA	SC	SC	SE	SE
VC	0.4885	0.3446	0.0934	0.0540	0.4340	0.0831	0.4809	0.7154	0.0919	0.1121	0.4272	0.1725
VC	0.3446	0.4984	0.0540	0.0312	0.0831	0.7180	0.7154	0.3995	0.1121	0.0250	0.1725	0.5755

Genetic correlation



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

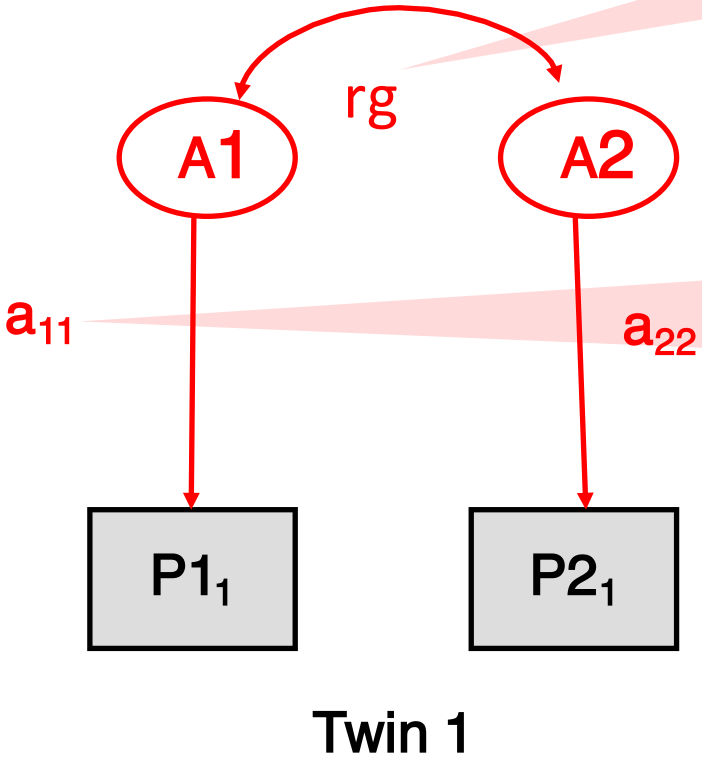
OpenMx Output

- fitACE$rA
- [,1] [,2]
- [1,] 1.00000000 0.69847252
- [2,] 0.69847252 1.00000000

- fitACE$rC
- [,1] [,2]
- [1,] 1.00000000 0.99999984
- [2,] 0.99999984 1.00000000

- fitACE$rE
- [,1] [,2]
- [1,] 1.00000000 0.14881543
- [2,] 0.14881543 1.00000000

Genetic correlation & contribution to observed correlation



If the rg = 1, the two sets of genes overlap completely

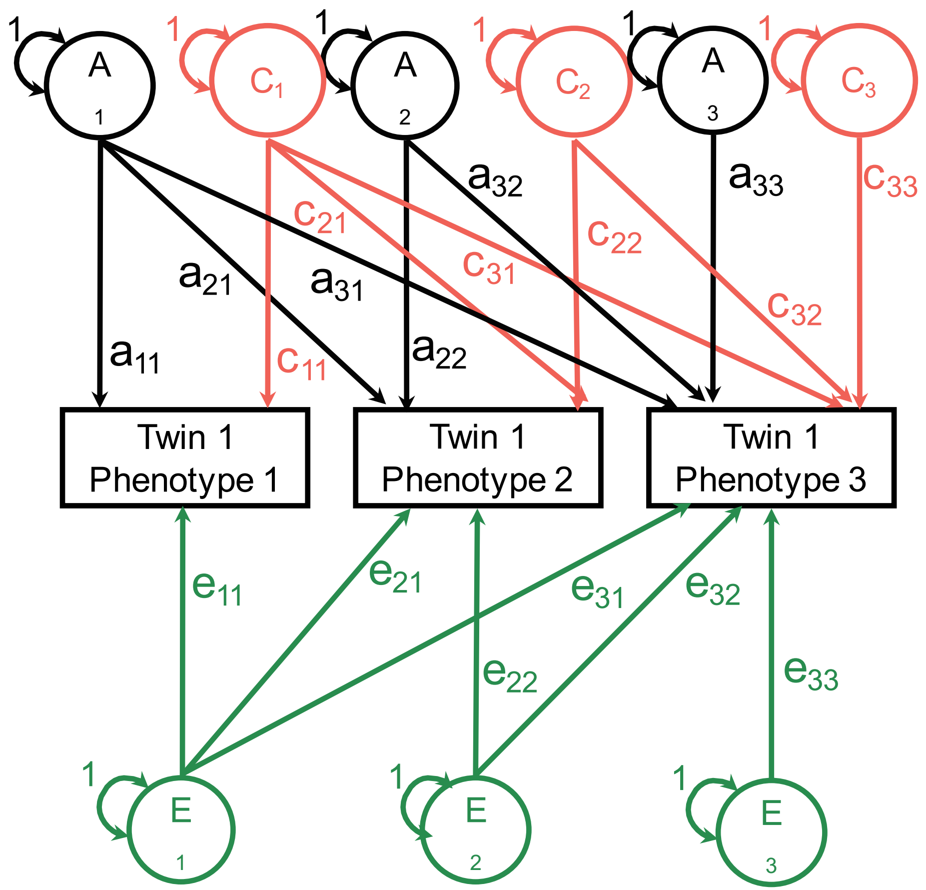
If however a11 and a22 are near to zero, genes do not contribute to the observed correlation

Interpreting Results

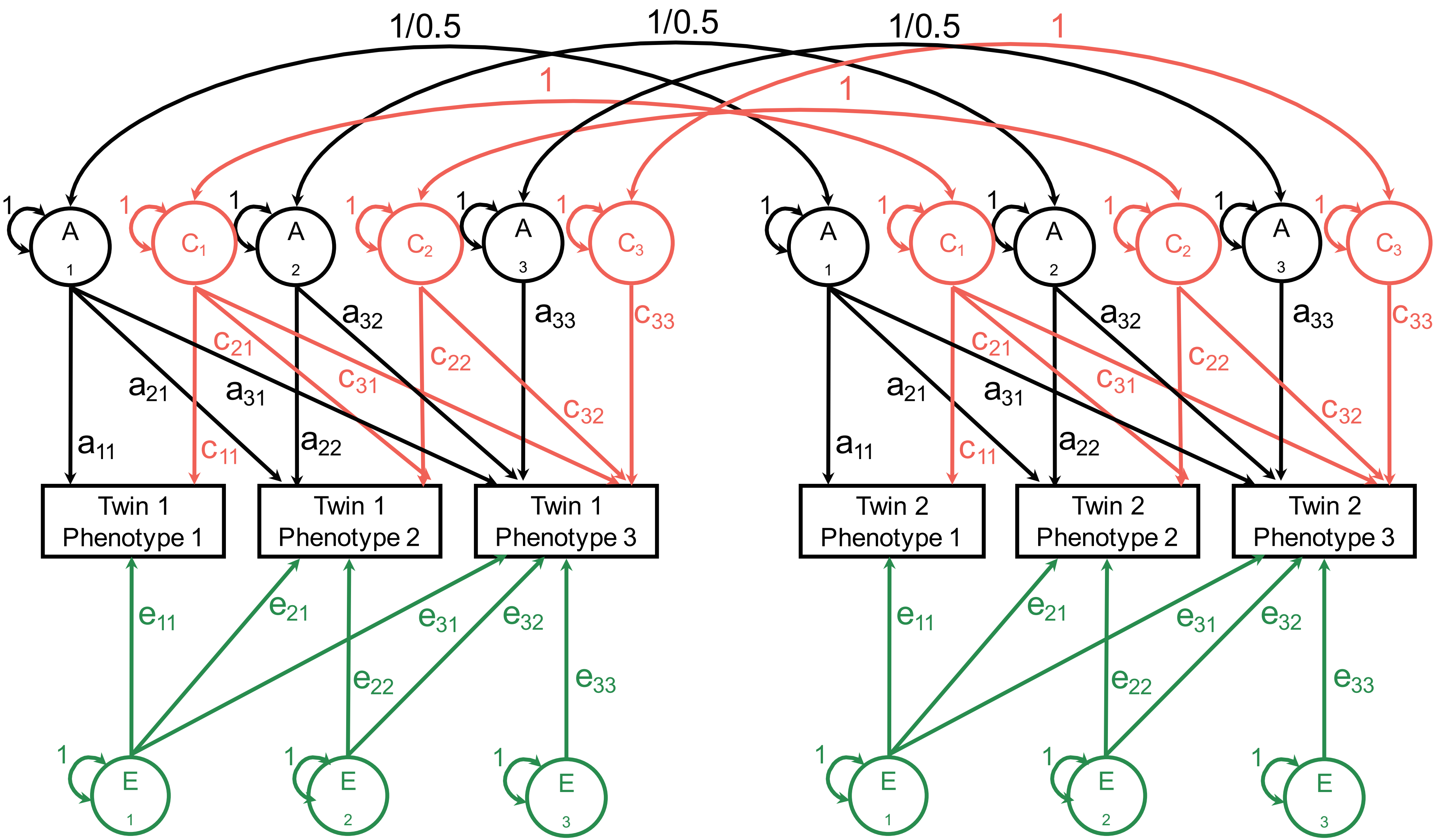
- High genetic correlation = large overlap in genetic effects on the two phenotypes

- 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

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
```

Practical

SCRIPT:

F:\meike\2016\Multivariate

DATA:

DHBQ_bs.dat

DATA

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

Observed Cross-twin Cross-trait Correlations

```
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	0.06
happy1	0.47	1.00	0.30	0.21
family2	0.30	0.30	1.00	0.37
happy2	0.06	0.21	0.37	1.00

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

	A	A	C	C	E	E	SA	SA	SC	SC	SE	SE
VC	0.4885	0.3446	0.0934	0.0540	0.4340	0.0831	0.4809	0.7154	0.0919	0.1121	0.4272	0.1725
VC	0.3446	0.4984	0.0540	0.0312	0.0831	0.7180	0.7154	0.3995	0.1121	0.0250	0.1725	0.5755

OpenMx Output

- fitACE$rA
- [,1] [,2]
- [1,] 1.00000000 0.69847252
- [2,] 0.69847252 1.00000000

- fitACE$rC
- [,1] [,2]
- [1,] 1.00000000 0.99999984
- [2,] 0.99999984 1.00000000

- fitACE$rE
- [,1] [,2]
- [1,] 1.00000000 0.14881543
- [2,] 0.14881543 1.00000000

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"

	Family	Happy	Life
Family	1.00	0.76	0.78
Happy	0.76	1.00	0.88
life	0.78	0.88	1.00

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

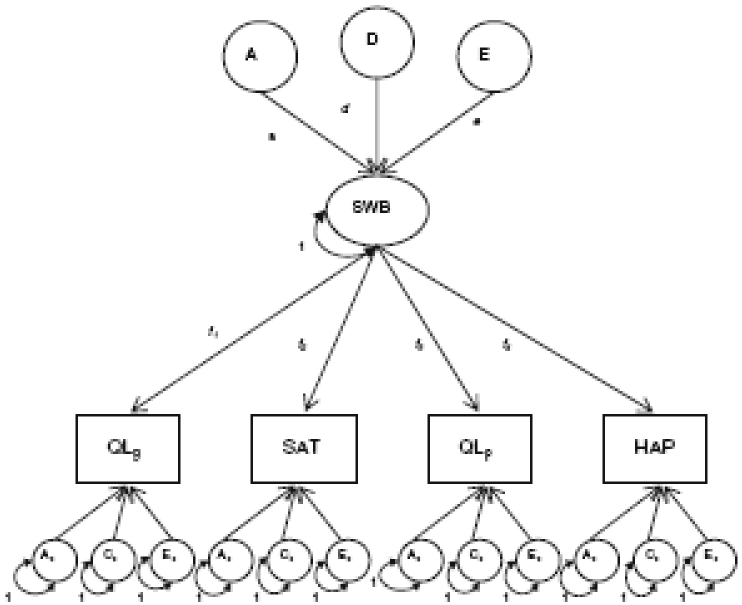
	Family	Happy	Life
Family	1.00	0.72	0.85
happy	0.72	1.00	0.97
life	0.85	0.97	1.00

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

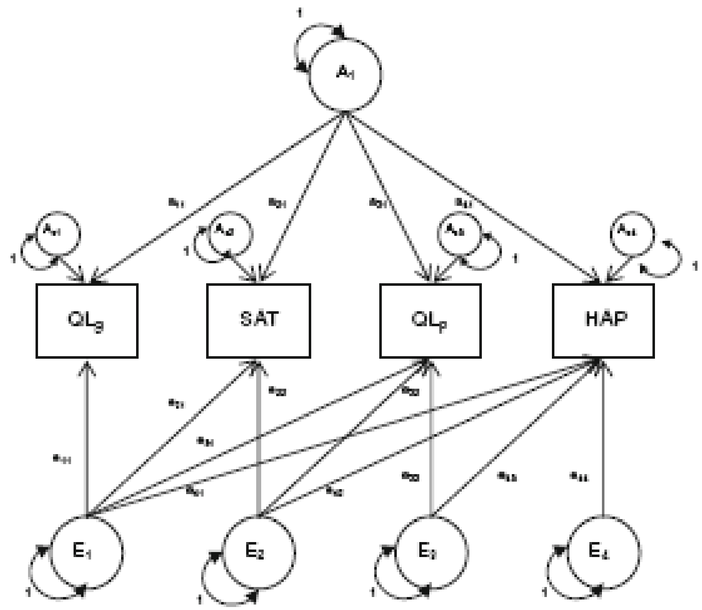
	Family	Happy	Life
Family	1.00	0.14	0.10
happy	0.14	1.00	0.66
life	0.10	0.66	1.00

Genetic Models

Genetic and environmental factor analysis examples



Common Pathway Model



Independent Pathway Model