

Multivariate Genetic Analysis

Boulder Workshop 2014

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Multivariate Questions

- Univariate Analysis: What are the contributions of additive genetic, dominance/ shared environmental and unique environmental factors to the variance?
- Multivariate Analysis: What are the contributions of genetic and environmental factors to the covariance between two or more traits?

Multivariate Models

- Saturated Model
 - equality of means/variances
- Genetic Models (ACE)
 - Cholesky Decomposition
 - Independent Pathway
 - Common Pathway

Scientific Questions

- Are these measures influenced by the same genes (single common factor)?
- Is there more than one factor (overall well being / happy / sad)?
- What is the structure of C and E?
- Contribution of A, C, E factors to covariance between traits

Saturated Model



function to assign values to diagonal of matrix

function to assign values to diagonal and off-diagonal elements of matrix

```
# Set Starting Values
svMe      <- c(5,5,1,1,1)      # start value for means
svVa      <- valDiag(ntv,1.0)  # start values for variances
lbVa      <- valODiag(ntv,.0001,-10) # lower bounds for covariances

# Algebra for expected Mean Matrices in MZ & DZ twins
meanMZ    <- mxMatrix( type="Full", nrow=1, ncol=ntv, free=TRUE,
                       values=svMe, labels=labFull("meMZ",1,ntv), name="expMeanMZ" )
meanDZ    <- mxMatrix( type="Full", nrow=1, ncol=ntv, free=TRUE,
                       values=svMe, labels=labFull("meDZ",1,ntv), name="expMeanDZ" )

# Algebra for expected Variance/Covariance Matrices in MZ & DZ twins
covMZ     <- mxMatrix( type="Symm", nrow=ntv, ncol=ntv, free=TRUE,
                       values=svVa, lbound=lbVa, labels=labSymm("vaMZ",ntv), name="expCovMZ" )
covDZ     <- mxMatrix( type="Symm", nrow=ntv, ncol=ntv, free=TRUE,
                       values=svVa, lbound=lbVa, labels=labSymm("vaDZ",ntv), name="expCovDZ" )
```

functions to assign labels to Full or Symmetric matrices

Functions

```
source("myFunctions.R")
source("GenEpiHelperFunctions.R")
```



```
# Functions to assign labels
labSymm    <- function(lab,nv) {
  paste(lab,rev(nv+1-sequence(1:nv)),rep(1:nv,nv:1),sep="_")
}
labFull    <- function(lab,nr,nc) {
  paste(lab,1:nr,rep(1:nc,each=nr),sep="_")
}

# Functions to assign values
valDiag    <- function(dim, valD) {
valF      <- diag(valD,dim,dim)      # values for diagonal of covariance matrix
valF
}
valODiag   <- function(dim, valD, valOD) {
valF      <- diag(valD,dim,dim)      # values for diagonal of covariance matrix
valF[lower.tri(valF)] <- valOD      # values for below diagonal elements
valF[upper.tri(valF)] <- valOD      # values for above diagonal elements
valF
}
```


Testing Equality of Means & Variances

change labels to
constrain parameters



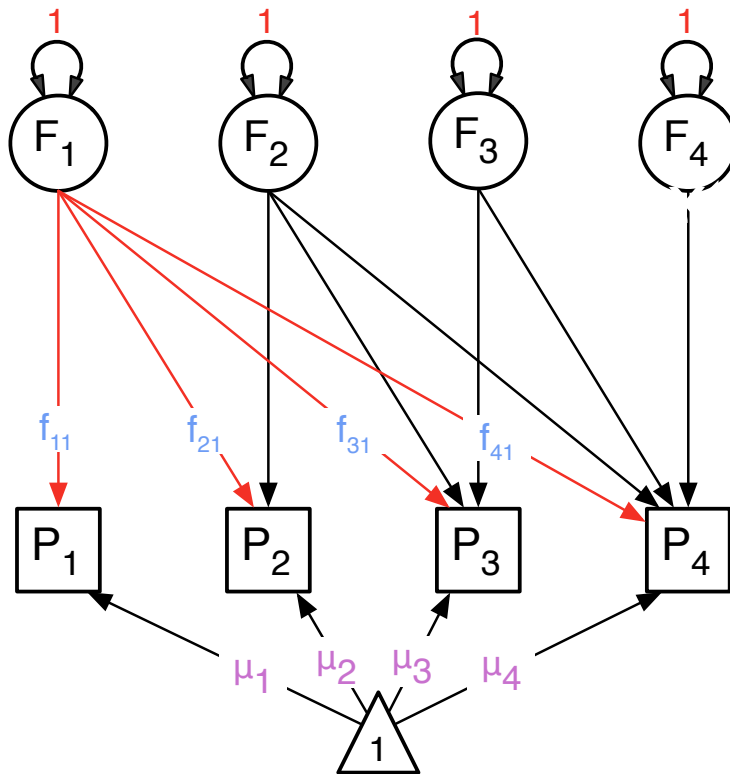
```
# Constrain expected Means and Variances to be equal across twin order
eqMeVaTwinModel <- mxModel( twinSatModel, name="eqM&Vtwins" )
eqMeVaTwinModel <- omxSetParameters( eqMeVaTwinModel, label=labFull("meMZ",1,ntv),
  free=TRUE, values=svMe, newLabels=labFull("meMZ",1,nv) )
eqMeVaTwinModel <- omxSetParameters( eqMeVaTwinModel, label=labFull("meDZ",1,ntv),
  free=TRUE, values=svMe, newLabels=labFull("meDZ",1,nv) )
eqMeVaTwinModel <- omxSetParameters( eqMeVaTwinModel, label=labDiag("vaMZ",ntv),
  free=TRUE, values=diag(svVa), newLabels=labDiag("vaMZ",nv) )
eqMeVaTwinModel <- omxSetParameters( eqMeVaTwinModel, label=labDiag("vaDZ",ntv),
  free=TRUE, values=diag(svVa), newLabels=labDiag("vaDZ",nv) )

# Constrain expected Means and Variances to be equal across twin order and zygosity
eqMeVaZygModel <- mxModel( eqMeVaTwinModel, name="eqM&Vzyg" )
eqMeVaZygModel <- omxSetParameters( eqMeVaZygModel,
  labels=c(labFull("meMZ",1,nv),labFull("meDZ",1,nv)),
  free=TRUE, values=svMe, newLabels=labFull("me",1,nv) )
eqMeVaZygModel <- omxSetParameters( eqMeVaZygModel,
  labels=c(labDiag("vaMZ",nv),labDiag("vaDZ",nv)),
  free=TRUE, values=diag(svVa), newLabels=labDiag("va",nv) )
```


Testing Assumptions

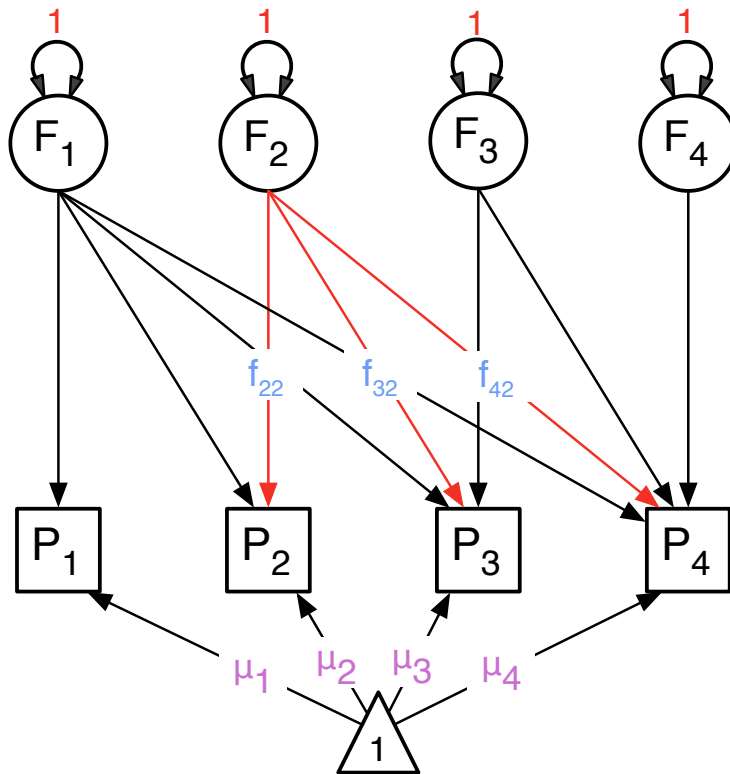
	ep	-2ll	df	AIC	chi	df	p
Saturated	180	14182.17	1895	10392			
EqMeVaTwin	156	14199.65	1919	10361	17.48	24	0.82
EqMeVaZyg	144	14216.14	1931	10354	33.96	36	0.56

Cholesky Decomposition



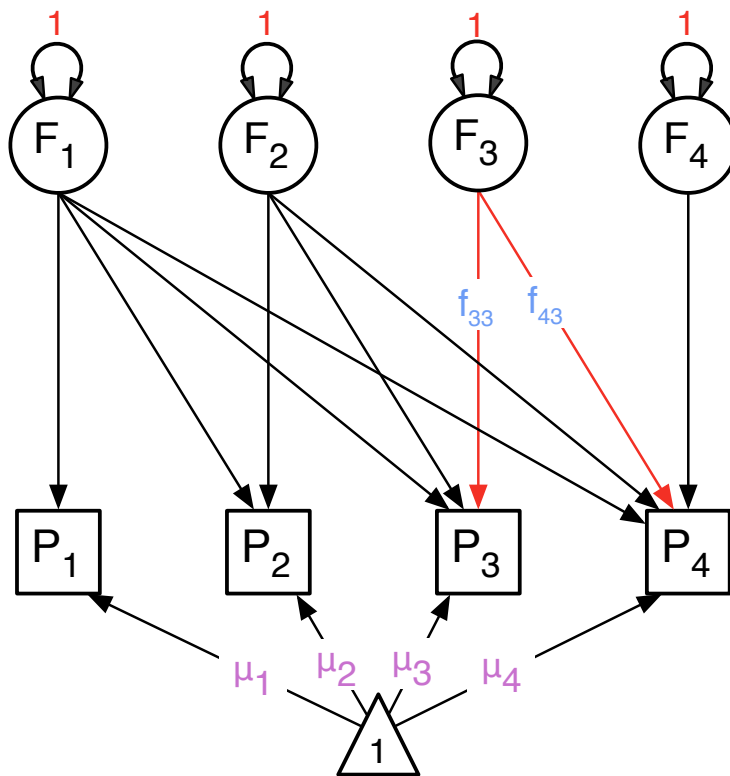
	F1	F2	F3	F4
P1	f_{11}			
P2	f_{21}			
P3	f_{31}			
P4	f_{41}			

Second Factor loads on all Variables but First



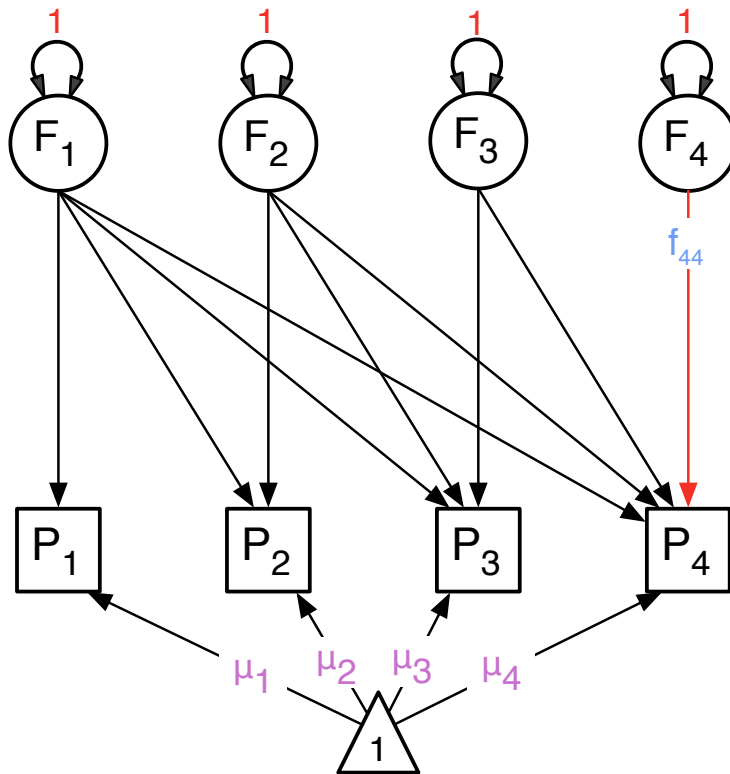
	F1	F2	F3	F4
P1	f_{11}	0		
P2	f_{21}	f_{22}		
P3	f_{31}	f_{32}		
P4	f_{41}	f_{42}		

Third Factor loads on Variables but Previous



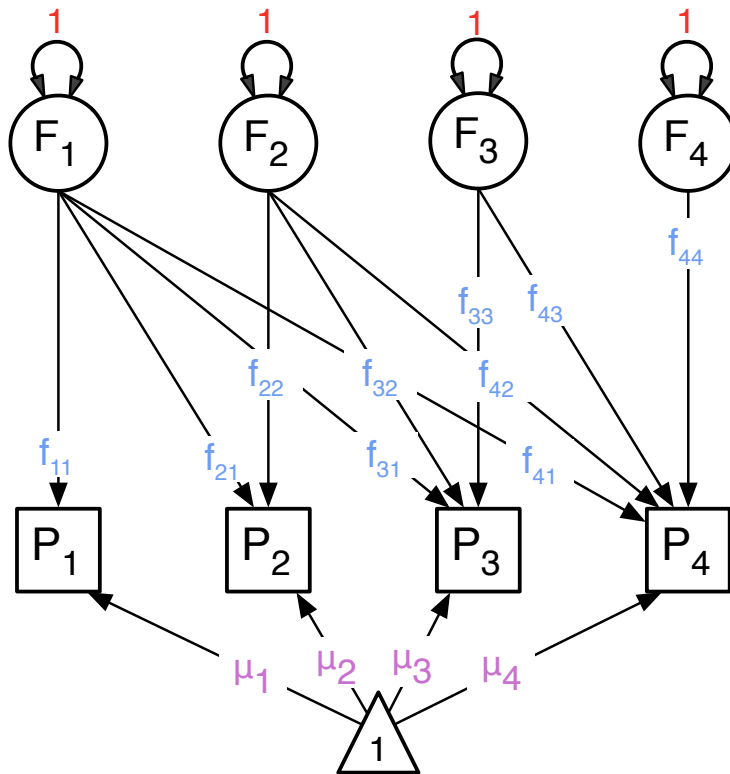
	F1	F2	F3	F4
P1	f_{11}	0	0	
P2	f_{21}	f_{22}	0	
P3	f_{31}	f_{32}	f_{33}	
P4	f_{41}	f_{42}	f_{43}	

Fourth Factor loads on Variables but Previous



	F1	F2	F3	F4
P1	f_{11}	0	0	0
P2	f_{21}	f_{22}	0	0
P3	f_{31}	f_{32}	f_{33}	0
P4	f_{41}	f_{42}	f_{43}	f_{44}

Phenotypic



Cholesky Decomposition

Estimate covariance matrix, fully saturated

$$\begin{array}{c} \mathbf{P1} \\ \mathbf{P2} \\ \mathbf{P3} \\ \mathbf{P4} \end{array} \begin{bmatrix} \mathbf{F1} & \mathbf{F2} & \mathbf{F3} & \mathbf{F4} \\ f_{11} & 0 & 0 & 0 \\ f_{21} & f_{22} & 0 & 0 \\ f_{31} & f_{32} & f_{33} & 0 \\ f_{41} & f_{42} & f_{43} & f_{44} \end{bmatrix}^*$$
$$\begin{array}{c} \mathbf{P1} \\ \mathbf{P2} \\ \mathbf{P3} \\ \mathbf{P4} \end{array} \begin{bmatrix} \mathbf{F1} & \mathbf{F2} & \mathbf{F3} & \mathbf{F4} \\ f_{11} & f_{21} & f_{31} & f_{41} \\ 0 & f_{22} & f_{32} & f_{42} \\ 0 & 0 & f_{33} & f_{43} \\ 0 & 0 & 0 & f_{44} \end{bmatrix}$$

\mathbf{F}

$\%*\%$

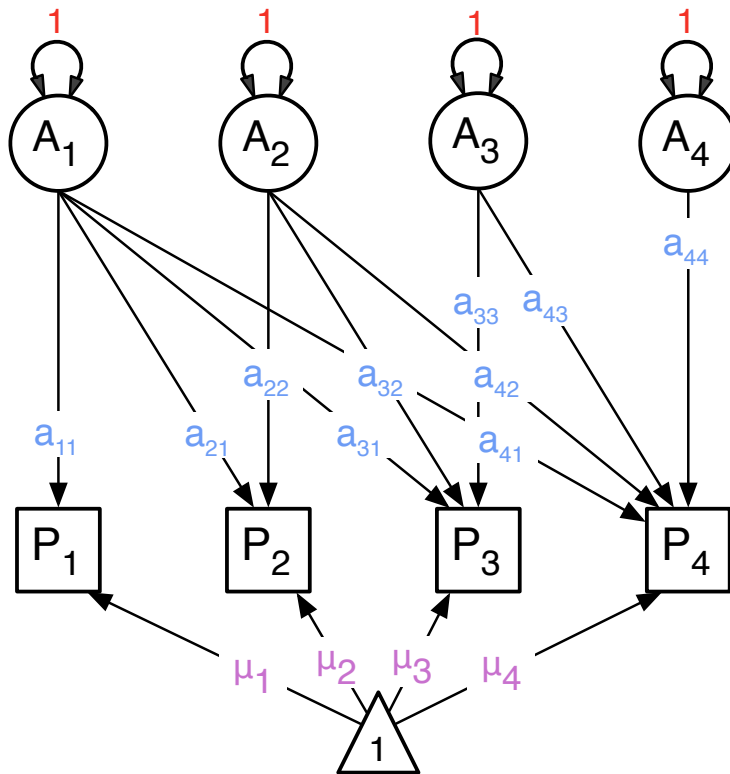
$\mathbf{t}(\mathbf{F})$

Cholesky Decomposition

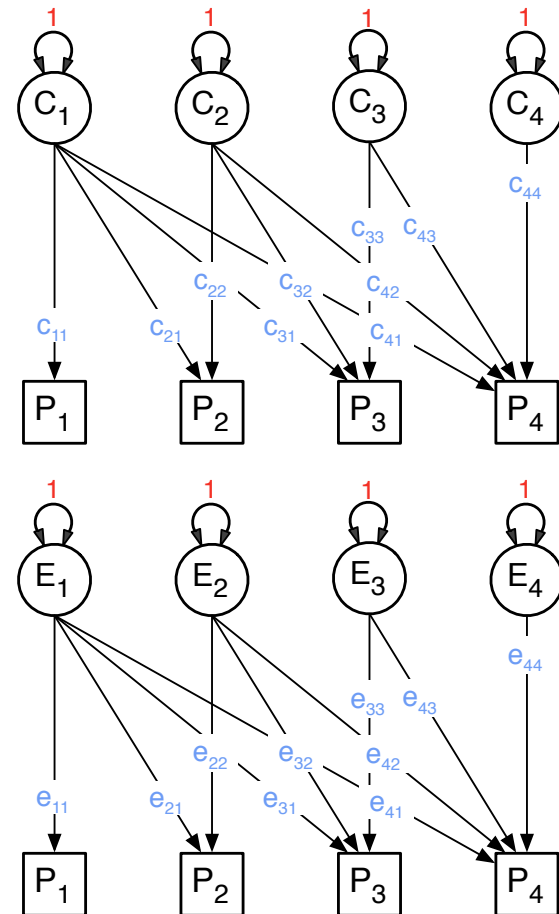
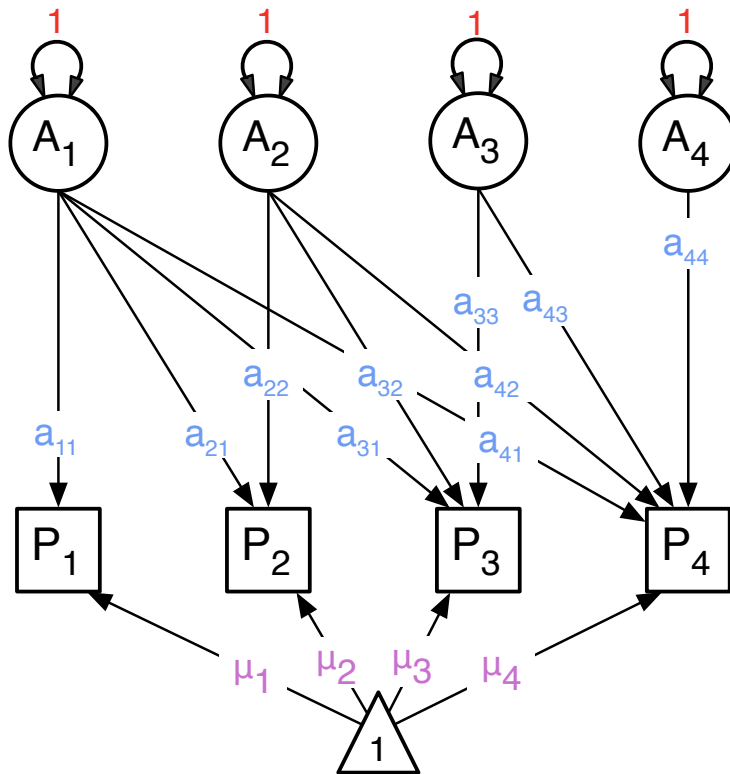
$$\begin{bmatrix} f_{11} & 0 & 0 & 0 \\ f_{21} & f_{22} & 0 & 0 \\ f_{31} & f_{32} & f_{33} & 0 \\ f_{41} & f_{42} & f_{43} & f_{44} \end{bmatrix} \times \begin{bmatrix} f_{11} & f_{21} & f_{31} & f_{41} \\ 0 & f_{22} & f_{32} & f_{42} \\ 0 & 0 & f_{33} & f_{43} \\ 0 & 0 & 0 & f_{44} \end{bmatrix}$$

$$\begin{bmatrix} f_{11}^2 & f_{11}f_{21} & f_{11}f_{31} & f_{11}f_{41} \\ f_{21}f_{11} & f_{21}^2 + f_{22}^2 & f_{22}f_{32} + f_{21}f_{31} & f_{22}f_{42} + f_{21}f_{41} \\ f_{31}f_{11} & f_{31}f_{21} + f_{32}f_{22} & f_{31}^2 + f_{32}^2 + f_{33}^2 & f_{33}f_{43} + f_{32}f_{42} + f_{31}f_{41} \\ f_{41}f_{11} & f_{41}f_{21} + f_{42}f_{22} & f_{41}f_{31} + f_{42}f_{32} + f_{43}f_{33} & f_{41}^2 + f_{42}^2 + f_{43}^2 + f_{44}^2 \end{bmatrix}$$

Genetic



& Environmental



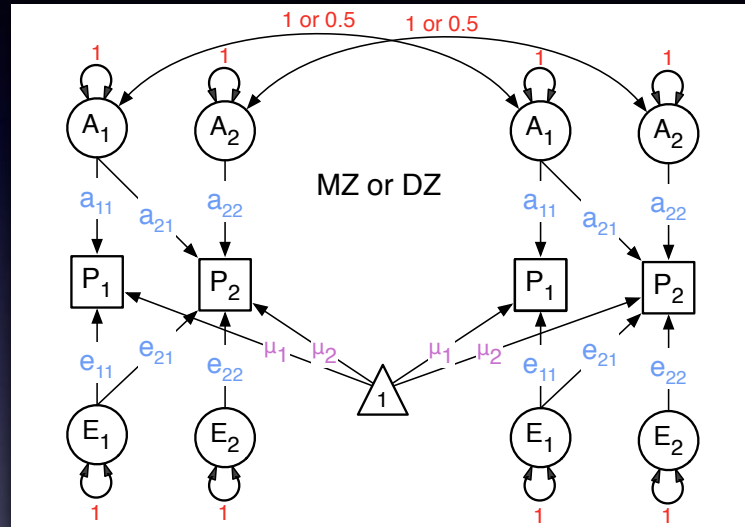
Cholesky Decomposition

$$\begin{bmatrix} a_{11} & 0 & 0 & 0 \\ a_{21} & a_{22} & 0 & 0 \\ a_{31} & a_{32} & a_{33} & 0 \\ a_{41} & a_{42} & a_{43} & a_{44} \end{bmatrix} \times \begin{bmatrix} a_{11} & a_{21} & a_{31} & a_{41} \\ 0 & a_{22} & a_{32} & a_{42} \\ 0 & 0 & a_{33} & a_{43} \\ 0 & 0 & 0 & a_{44} \end{bmatrix} = \begin{bmatrix} a_{11}^2 & a_{11}a_{21} & a_{11}a_{31} & a_{11}a_{41} \\ a_{21}a_{11} & a_{21}^2 + a_{22}^2 & a_{22}a_{32} + a_{21}a_{31} & a_{22}a_{42} + a_{21}a_{41} \\ a_{31}a_{11} & a_{31}a_{21} + a_{32}a_{22} & a_{31}^2 + a_{32}^2 + a_{33}^2 & a_{33}a_{43} + a_{32}a_{42} + a_{31}a_{41} \\ a_{41}a_{11} & a_{41}a_{21} + a_{42}a_{22} & a_{41}a_{31} + a_{42}a_{32} + a_{43}a_{33} & a_{41}^2 + a_{42}^2 + a_{43}^2 + a_{44}^2 \end{bmatrix}$$

$$\begin{bmatrix} c_{11} & 0 & 0 & 0 \\ c_{21} & c_{22} & 0 & 0 \\ c_{31} & c_{32} & c_{33} & 0 \\ c_{41} & c_{42} & c_{43} & c_{44} \end{bmatrix} \times \begin{bmatrix} c_{11} & c_{21} & c_{31} & c_{41} \\ 0 & c_{22} & c_{32} & c_{42} \\ 0 & 0 & c_{33} & c_{43} \\ 0 & 0 & 0 & c_{44} \end{bmatrix} = \begin{bmatrix} c_{11}^2 & c_{11}c_{21} & c_{11}c_{31} & c_{11}c_{41} \\ c_{21}c_{11} & c_{21}^2 + c_{22}^2 & c_{22}c_{32} + c_{21}c_{31} & c_{22}c_{42} + c_{21}c_{41} \\ c_{31}c_{11} & c_{31}c_{21} + c_{32}c_{22} & c_{31}^2 + c_{32}^2 + c_{33}^2 & c_{33}c_{43} + c_{32}c_{42} + c_{31}c_{41} \\ c_{41}c_{11} & c_{41}c_{21} + c_{42}c_{22} & c_{41}c_{31} + c_{42}c_{32} + c_{43}c_{33} & c_{41}^2 + c_{42}^2 + c_{43}^2 + c_{44}^2 \end{bmatrix}$$

$$\begin{bmatrix} e_{11} & 0 & 0 & 0 \\ e_{21} & e_{22} & 0 & 0 \\ e_{31} & e_{32} & e_{33} & 0 \\ e_{41} & e_{42} & e_{43} & e_{44} \end{bmatrix} \times \begin{bmatrix} e_{11} & e_{21} & e_{31} & e_{41} \\ 0 & e_{22} & e_{32} & e_{42} \\ 0 & 0 & e_{33} & e_{43} \\ 0 & 0 & 0 & e_{44} \end{bmatrix} = \begin{bmatrix} e_{11}^2 & e_{11}e_{21} & e_{11}e_{31} & e_{11}e_{41} \\ e_{21}e_{11} & e_{21}^2 + e_{22}^2 & e_{22}e_{32} + e_{21}e_{31} & e_{22}e_{42} + e_{21}e_{41} \\ e_{31}e_{11} & e_{31}e_{21} + e_{32}e_{22} & e_{31}^2 + e_{32}^2 + e_{33}^2 & e_{33}e_{43} + e_{32}e_{42} + e_{31}e_{41} \\ e_{41}e_{11} & e_{41}e_{21} + e_{42}e_{22} & e_{41}e_{31} + e_{42}e_{32} + e_{43}e_{33} & e_{41}^2 + e_{42}^2 + e_{43}^2 + e_{44}^2 \end{bmatrix}$$

OpenMx Specification



	X_1	Y_1	X_2	Y_2
X_1	V_{X1}	C_{X1Y1}	C_{X1X2}	C_{X1Y2}
Y_1	C_{Y1X1}	V_{Y1}	C_{Y1X2}	C_{Y1Y2}
X_2	C_{X2X1}	C_{X2Y1}	V_{X2}	C_{X2Y2}
Y_2	C_{Y2X1}	C_{Y2Y1}	C_{Y2X2}	V_{Y2}



OpenMx script

Cholesky Decomposition

```
object: pathA  
matrix name: a
```

$$\begin{bmatrix} a_{11} & 0 & 0 & 0 \\ a_{21} & a_{22} & 0 & 0 \\ a_{31} & a_{32} & a_{33} & 0 \\ a_{41} & a_{42} & a_{43} & a_{44} \end{bmatrix} \times \begin{bmatrix} a_{11} & a_{21} & a_{31} & a_{41} \\ 0 & a_{22} & a_{32} & a_{42} \\ 0 & 0 & a_{33} & a_{43} \\ 0 & 0 & 0 & a_{44} \end{bmatrix} = \begin{bmatrix} a_{11}^2 & a_{11}a_{21} & a_{11}a_{31} & a_{11}a_{41} \\ a_{21}a_{11} & a_{21}^2 + a_{22}^2 & a_{22}a_{32} + a_{21}a_{31} & a_{22}a_{42} + a_{21}a_{41} \\ a_{31}a_{11} & a_{31}a_{21} + a_{32}a_{22} & a_{31}^2 + a_{32}^2 + a_{33}^2 & a_{33}a_{43} + a_{32}a_{42} + a_{31}a_{41} \\ a_{41}a_{11} & a_{41}a_{21} + a_{42}a_{22} & a_{41}a_{31} + a_{42}a_{32} + a_{43}a_{33} & a_{41}^2 + a_{42}^2 + a_{43}^2 + a_{44}^2 \end{bmatrix}$$

```
object: covA  
matrix name: A
```

```
pathA <- mxMatrix( type="Lower", nrow=nv, ncol=nv, free=TRUE, values=svPa,  
labels=labLower("a",nv), lbound=lbPa, name="a" )
```

```
covA <- mxAlgebra( expression=a %**% t(a), name="A" )
```

Key Model Statements



```
# Matrices declared to store a, c, and e Path Coefficients
pathA <- mxMatrix( type="Lower", nrow=nv, ncol=nv, free=TRUE, values=svPa,
labels=labLower("a",nv), lbound=lbPa, name="a" )
pathC <- mxMatrix( type="Lower", nrow=nv, ncol=nv, free=TRUE, values=svPa,
labels=labLower("c",nv), lbound=lbPa, name="c" )
pathE <- mxMatrix( type="Lower", nrow=nv, ncol=nv, free=TRUE, values=svPe,
labels=labLower("e",nv), lbound=lbPa, name="e" )

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

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

lower triangular matrices

Standard Code



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

# Data objects for Multiple Groups
dataMZ     <- mxData( observed=mzData, type="row" )
dataDZ     <- mxData( observed=dzData, type="row" )

# Objective objects for Multiple Groups
objMZ      <- mxFIMLObjective( covariance="expCovMZ", means="expMean", dimnames=selVars )
objDZ      <- mxFIMLObjective( covariance="expCovDZ", means="expMean", dimnames=selVars )

# Combine Groups
pars       <- list( pathA, pathC, pathE, covA, covC, covE, covP, matI, invSD, meanG )
modelMZ    <- mxModel( pars, covMZ, dataMZ, objMZ, name="MZ" )
modelDZ    <- mxModel( pars, covDZ, dataDZ, objDZ, name="DZ" )
minus2ll   <- mxAlgebra( expression=MZ.objective + DZ.objective, name="m2LL" )
obj        <- mxAlgebraObjective( "m2LL" )
CholAceModel <- mxModel( "CholACE", pars, modelMZ, modelDZ, minus2ll, obj )
```

standard expectations

Model Fitting



```
# -----  
# RUN GENETIC MODEL  
  
# Run Cholesky Decomposition ACE model  
CholAceFit    <- mxRun(CholAceModel)  
CholAceSumm   <- summary(CholAceFit)  
CholAceSumm$pa  
round(CholAceFit@output$estimate,4)  
CholAceFit@objective@result  
CholAceFit    <- mxRun(CholAceFit)  
CholAceFit@objective@result
```

rerun model from solution

FormatOutputMatrices



```
# Generate List of Parameter Estimates and Derived Quantities using formatOutputMatrices
# ACE Path Coefficients & Standardized Path Coefficients (pre-multiplied by inverse of st devs)
CholACEpathMatrices <- c("iSD %%% a", "iSD %%% c", "iSD %%% e")
CholACEpathLabels <- c("stPathA", "stPathC", "stPathE")
formatOutputMatrices(CholAceFit, CholACEpathMatrices, CholACEpathLabels, Vars, 4)

# ACE Squared Standardized Path Coefficients
ACEpathMatrices <- c("(iSD%% a)*(iSD%% a)", "(iSD%% c)*(iSD%% c)", "(iSD%% e)*(iSD%% e)")
ACEpathLabels <- c("stPathA^2", "stPathC^2", "stPathE^2")
formatOutputMatrices(CholAceFit, ACEpathMatrices, ACEpathLabels, Vars, 4)

# ACE Covariance Matrices & Proportions of Variance Matrices
ACEcovMatrices <- c("A", "C", "E", "V", "A/V", "C/V", "E/V")
ACEcovLabels <- c("covA", "covC", "covE", "Var", "stCovA", "stCovC", "stCovE")
formatOutputMatrices(CholAceFit, ACEcovMatrices, ACEcovLabels, Vars, 4)

# ACE Correlation Matrices
ACEcorMatrices <- c("solve(sqrt(I*A)) %%% A", "solve(sqrt(I*C)) %%% C", "solve(sqrt(I*E)) %%% E")
ACEcorLabels <- c("corA", "corC", "corE")
formatOutputMatrices(CholAceFit, ACEcorMatrices, ACEcorLabels, Vars, 4)
```

squared

standardized path coefficients

correlations

proportions of variance & covariance

Cholesky

model:CholACE, matrix:a

```
      [,1]      [,2]      [,3]      [,4]      [,5]      [,6]
[1,] [a_1_1] 0          0          0          0          0
[2,] [a_2_1] [a_2_2] 0          0          0          0
[3,] [a_3_1] [a_3_2] [a_3_3] 0          0          0
[4,] [a_4_1] [a_4_2] [a_4_3] [a_4_4] 0          0
[5,] [a_5_1] [a_5_2] [a_5_3] [a_5_4] [a_5_5] 0
[6,] [a_6_1] [a_6_2] [a_6_3] [a_6_4] [a_6_5] [a_6_6]
```

model:CholACE, matrix:c

```
      [,1]      [,2]      [,3]      [,4]      [,5]      [,6]
[1,] [c_1_1] 0          0          0          0          0
[2,] [c_2_1] [c_2_2] 0          0          0          0
[3,] [c_3_1] [c_3_2] [c_3_3] 0          0          0
[4,] [c_4_1] [c_4_2] [c_4_3] [c_4_4] 0          0
[5,] [c_5_1] [c_5_2] [c_5_3] [c_5_4] [c_5_5] 0
[6,] [c_6_1] [c_6_2] [c_6_3] [c_6_4] [c_6_5] [c_6_6]
```

model:CholACE, matrix:e

```
      [,1]      [,2]      [,3]      [,4]      [,5]      [,6]
[1,] [e_1_1] 0          0          0          0          0
[2,] [e_2_1] [e_2_2] 0          0          0          0
[3,] [e_3_1] [e_3_2] [e_3_3] 0          0          0
[4,] [e_4_1] [e_4_2] [e_4_3] [e_4_4] 0          0
[5,] [e_5_1] [e_5_2] [e_5_3] [e_5_4] [e_5_5] 0
[6,] [e_6_1] [e_6_2] [e_6_3] [e_6_4] [e_6_5] [e_6_6]
```

model:CholACE, matrix:Mean

```
      [,1]      [,2]      [,3]      [,4]      [,5]      [,6]
[1,] [me_1_1] [me_1_2] [me_1_3] [me_1_4] [me_1_5] [me_1_6]
```

Testing Assumptions

	ep	-2ll	df	AIC	chi	df	p
Saturated	180	14182.17	1895	10392			
EqMeVaTwin	156	14199.65	1919	10361	17.48	24	0.82
EqMeVaZyg	144	14216.14	1931	10354	33.96	36	0.56
CholAce	69	14362.14	2006	10350	179.9	111	0
EqMeVaZyg	144	14216.14	1931	10354			
CholAce	69	14362.14	2006	10350	146.0	75	0

Standardized Path Coefficients

Cholesky

[1] "Matrix iSD %*% a"

	stPathA1	stPathA2	stPathA3	stPathA4	stPathA5	stPathA6
family	0.6126	0.0000	0.0000	0.0000	0.0000	0.0000
happy	0.3796	0.4009	0.0000	0.0000	0.0000	0.0000
life	0.3438	0.2414	0.1798	0.0000	0.0000	0.0000
anxdep	-0.2460	-0.4120	-0.0279	0.1307	0.0000	0.0000
somatic	-0.2514	-0.2657	-0.1271	0.3125	0.1110	0.0000
social	-0.1885	-0.2243	0.4444	-0.0054	0.1168	0.0001

[1] "Matrix iSD %*% c"

	stPathC1	stPathC2	stPathC3	stPathC4	stPathC5	stPathC6
family	0.4236	0.0000	0.0000	0.0000	0.0000	0.0000
happy	0.2580	0.1519	0.0000	0.0000	0.0000	0.0000
life	0.3508	0.1150	0.1504	0.0000	0.0000	0.0000
anxdep	-0.3040	-0.0634	-0.1613	0.3641	0.0000	0.0000
somatic	-0.1479	0.0509	-0.4462	0.0582	0.0001	0.0000
social	-0.2685	-0.0325	-0.2260	0.2428	0.0001	0.0001

[1] "Matrix iSD %*% e"

	stPathE1	stPathE2	stPathE3	stPathE4	stPathE5	stPathE6
family	0.6673	0.0000	0.0000	0.0000	0.0000	0.0000
happy	0.1296	0.7673	0.0000	0.0000	0.0000	0.0000
life	0.0879	0.5241	0.5915	0.0000	0.0000	0.0000
anxdep	-0.0419	-0.2804	-0.0644	0.6421	0.0000	0.0000
somatic	-0.0067	-0.0448	0.0253	0.2766	0.6587	0.0000
social	-0.0410	-0.0672	-0.0944	0.1590	0.0450	0.6909

Squared Standardized Path Coefficients

[1] "Matrix (iSD%% a)*(iSD%% a)"

	stPathA^21	stPathA^22	stPathA^23	stPathA^24	stPathA^25	stPathA^26
family	0.3753	0.0000	0.0000	0.0000	0.0000	0.0000
happy	0.1441	0.1607	0.0000	0.0000	0.0000	0.0000
life	0.1182	0.0583	0.0323	0.0000	0.0000	0.0000
anxdep	0.0605	0.1698	0.0008	0.0171	0.0000	0.0000
somatic	0.0632	0.0706	0.0162	0.0977	0.0123	0.0000
social	0.0355	0.0503	0.1975	0.0000	0.0136	0.0000

[1] "Matrix (iSD%% c)*(iSD%% c)"

	stPathC^21	stPathC^22	stPathC^23	stPathC^24	stPathC^25	stPathC^26
family	0.1794	0.0000	0.0000	0.0000	0.0000	0.0000
happy	0.0665	0.0231	0.0000	0.0000	0.0000	0.0000
life	0.1231	0.0132	0.0226	0.0000	0.0000	0.0000
anxdep	0.0924	0.0040	0.0260	0.1326	0.0000	0.0000
somatic	0.0219	0.0026	0.1991	0.0034	0.0000	0.0000
social	0.0721	0.0011	0.0511	0.0589	0.0000	0.0000

[1] "Matrix (iSD%% e)*(iSD%% e)"

	stPathE^21	stPathE^22	stPathE^23	stPathE^24	stPathE^25	stPathE^26
family	0.4453	0.0000	0.0000	0.0000	0.0000	0.0000
happy	0.0168	0.5888	0.0000	0.0000	0.0000	0.0000
life	0.0077	0.2747	0.3499	0.0000	0.0000	0.0000
anxdep	0.0018	0.0786	0.0041	0.4123	0.0000	0.0000
somatic	0.0000	0.0020	0.0006	0.0765	0.4338	0.0000
social	0.0017	0.0045	0.0089	0.0253	0.0020	0.4774

Proportions of (co)Variance

[1] "Matrix A/V"

	stCovA1	stCovA2	stCovA3	stCovA4	stCovA5	stCovA6
family	0.3753	0.5430	0.5041	0.4902	0.6965	0.4500
happy	0.5430	0.3048	0.3035	0.4558	0.7546	0.5520
life	0.5041	0.3035	0.2088	0.3664	0.5865	0.1471
anxdep	0.4902	0.4558	0.3664	0.2481	0.3999	0.2715
somatic	0.6965	0.7546	0.5865	0.3999	0.2600	0.2135
social	0.4500	0.5520	0.1471	0.2715	0.2135	0.2970

[1] "Matrix C/V"

	stCovC1	stCovC2	stCovC3	stCovC4	stCovC5	stCovC6
family	0.1794	0.2551	0.3556	0.4188	0.2832	0.4433
happy	0.2551	0.0896	0.1442	0.1552	0.1137	0.2537
life	0.3556	0.1442	0.1589	0.2678	0.3827	0.4967
anxdep	0.4188	0.1552	0.2678	0.2550	0.2500	0.4504
somatic	0.2832	0.1137	0.3827	0.2500	0.2270	0.5289
social	0.4433	0.2537	0.4967	0.4504	0.5289	0.1832

[1] "Matrix E/V"

	stCovE1	stCovE2	stCovE3	stCovE4	stCovE5	stCovE6
family	0.4453	0.2019	0.1403	0.0910	0.0202	0.1067
happy	0.2019	0.6056	0.5523	0.3889	0.1317	0.1943
life	0.1403	0.5523	0.6323	0.3658	0.0308	0.3562
anxdep	0.0910	0.3889	0.3658	0.4968	0.3501	0.2781
somatic	0.0202	0.1317	0.0308	0.3501	0.5131	0.2576
social	0.1067	0.1943	0.3562	0.2781	0.2576	0.5198

Genetic Correlations

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

	corA1	corA2	corA3	corA4	corA5	corA6
family	1.0000	0.6876	0.7524	-0.4938	-0.4931	-0.3459
happy	0.6876	1.0000	0.9010	-0.9401	-0.7174	-0.5367
life	0.7524	0.9010	1.0000	-0.8305	-0.7444	-0.1569
anxdep	-0.4938	-0.9401	-0.8305	1.0000	0.8493	0.4630
somatic	-0.4931	-0.7174	-0.7444	0.8493	1.0000	0.2223
social	-0.3459	-0.5367	-0.1569	0.4630	0.2223	1.0000

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

	corC1	corC2	corC3	corC4	corC5	corC6
family	1.0000	0.8618	0.8800	-0.6019	-0.3104	-0.6274
happy	0.8618	1.0000	0.9047	-0.5823	-0.2133	-0.5791
life	0.8800	0.9047	1.0000	-0.6864	-0.5958	-0.7733
anxdep	-0.6019	-0.5823	-0.6864	1.0000	0.5607	0.9648
somatic	-0.3104	-0.2133	-0.5958	0.5607	1.0000	0.7505
social	-0.6274	-0.5791	-0.7733	0.9648	0.7505	1.0000

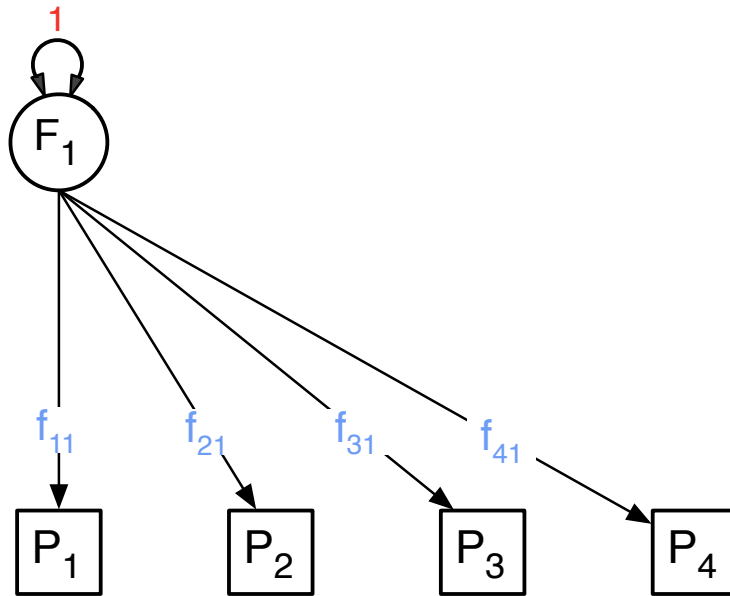
```
[1] "Matrix solve(sqrt(I*E)) %&% E"
```

	corE1	corE2	corE3	corE4	corE5	corE6
family	1.0000	0.1665	0.1105	-0.0594	-0.0094	-0.0569
happy	0.1665	1.0000	0.6683	-0.4022	-0.0632	-0.1013
life	0.1105	0.6683	1.0000	-0.3367	-0.0160	-0.1651
anxdep	-0.0594	-0.4022	-0.3367	1.0000	0.3740	0.2533
somatic	-0.0094	-0.0632	-0.0160	0.3740	1.0000	0.1443
social	-0.0569	-0.1013	-0.1651	0.2533	0.1443	1.0000

Theoretical Models

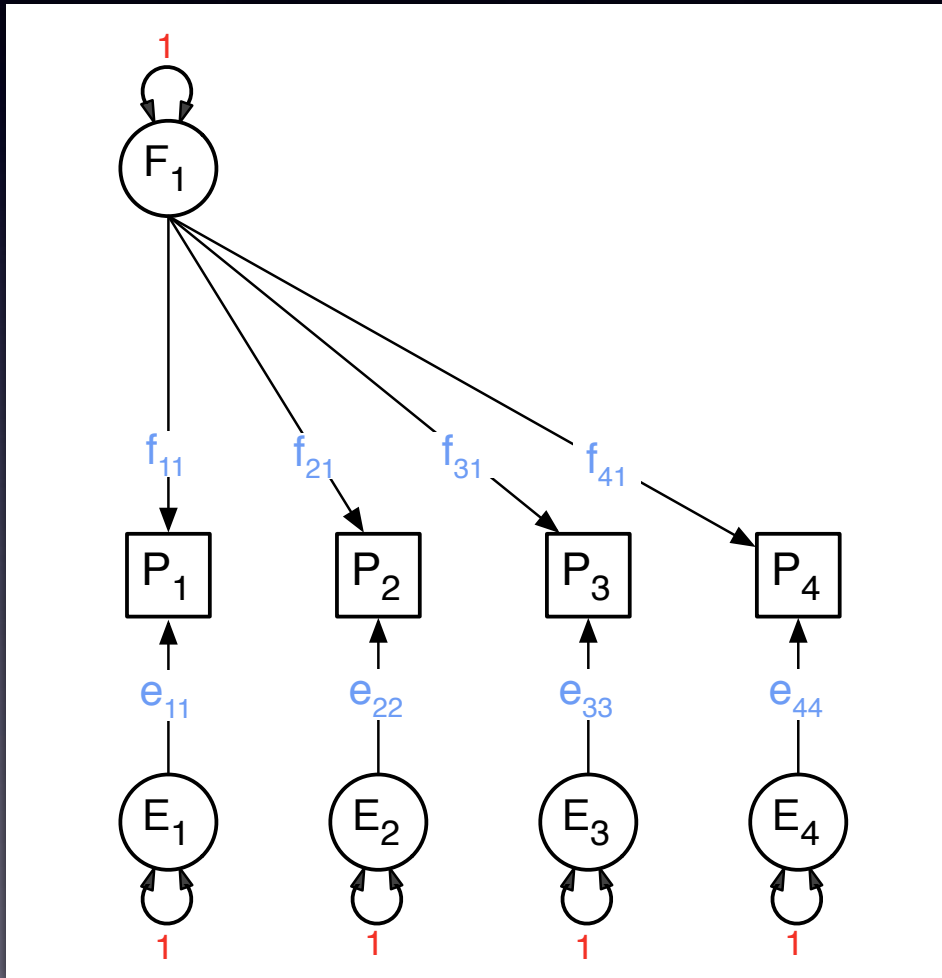
- Independent Pathway
- Common Pathway

Common Factor



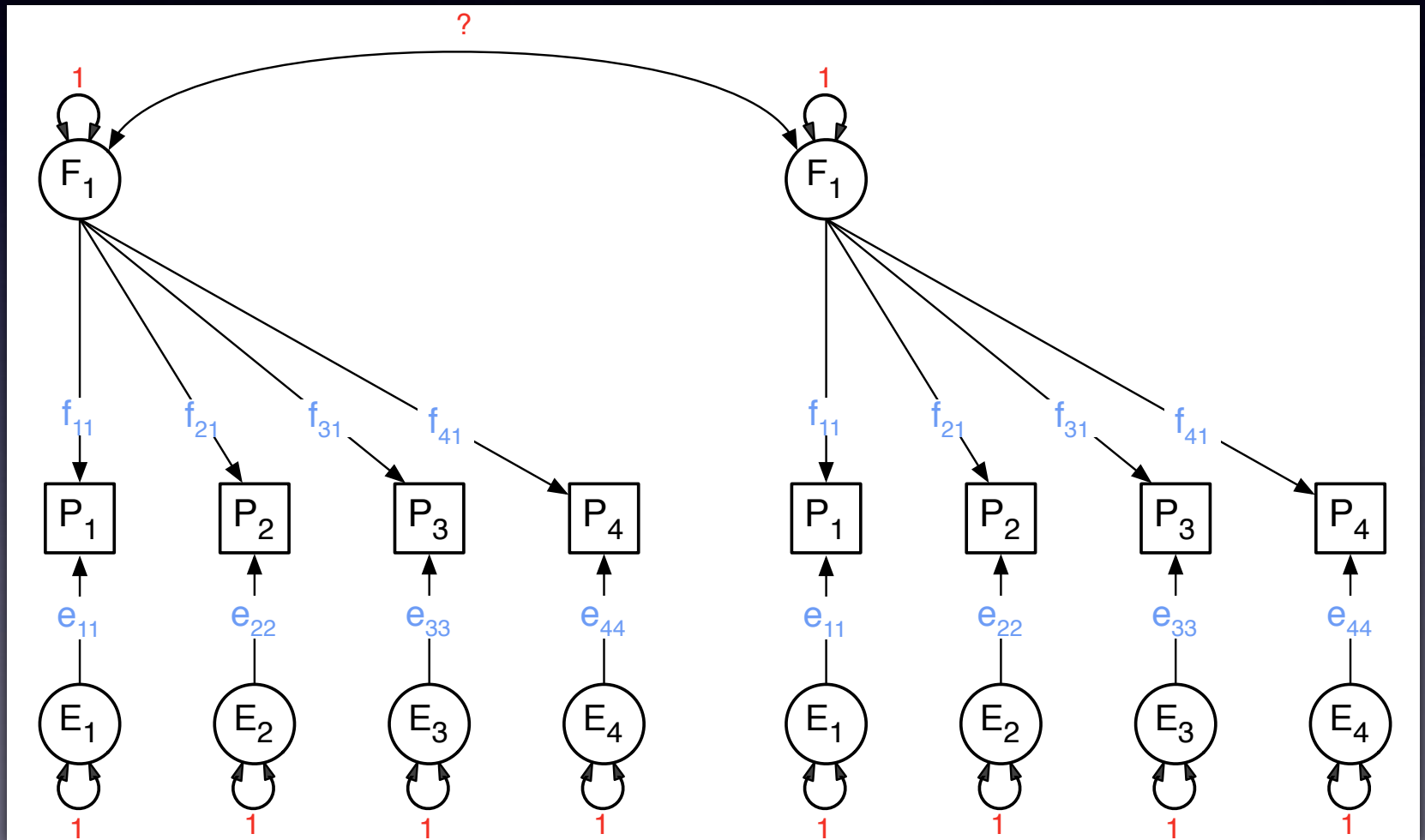
	FI
P1	f_{11}
P2	f_{21}
P3	f_{31}
P4	f_{41}

Residuals



	E1	E2	E3	E4
P1	e_{11}	0	0	0
P2	0	e_{22}	0	0
P3	0	0	e_{33}	0
P4	0	0	0	e_{44}

What about Twins



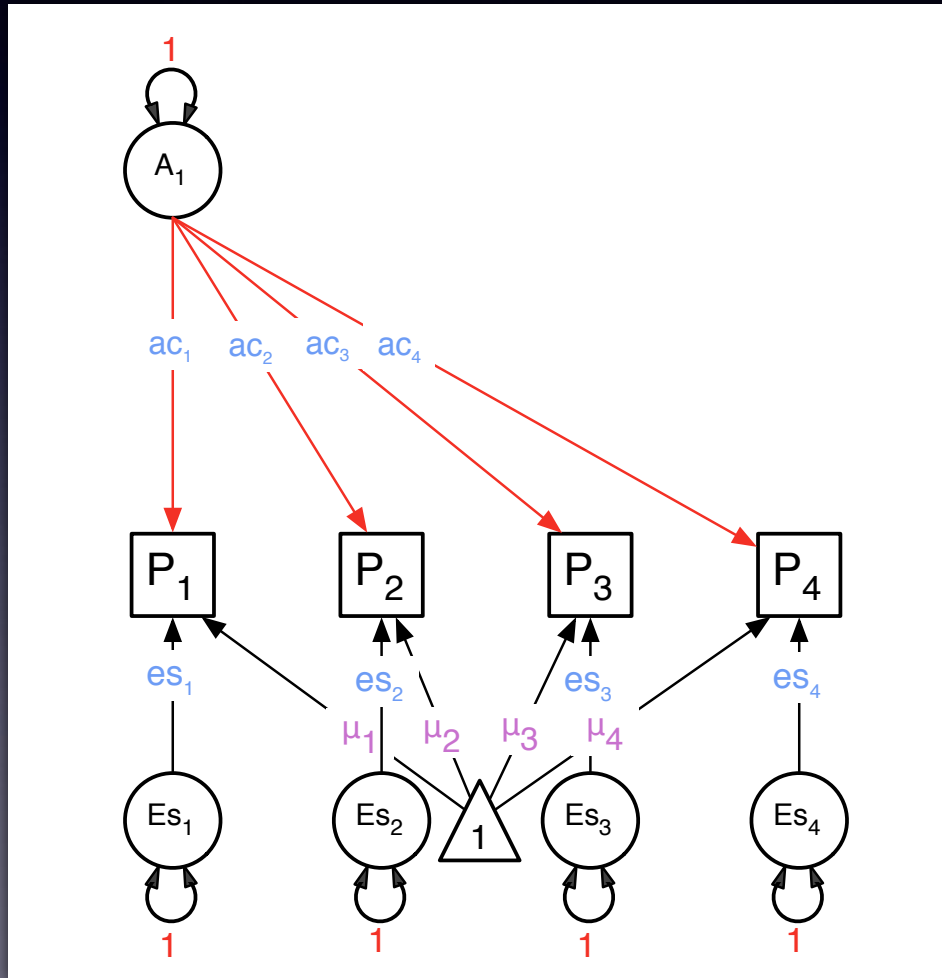
Common Factors

Specifics

$$\begin{bmatrix} f_{11} \\ f_{21} \\ f_{31} \\ f_{41} \end{bmatrix} \times \begin{bmatrix} f_{11} & f_{21} & f_{31} & f_{41} \end{bmatrix} = \begin{bmatrix} f_{11}^2 & f_{11}f_{21} & f_{11}f_{31} & f_{11}f_{41} \\ f_{21}f_{11} & f_{21}^2 & f_{21}f_{31} & f_{21}f_{41} \\ f_{31}f_{11} & f_{31}f_{21} & f_{31}^2 & f_{31}f_{41} \\ f_{41}f_{11} & f_{41}f_{21} & f_{41}f_{31} & f_{41}^2 \end{bmatrix}$$

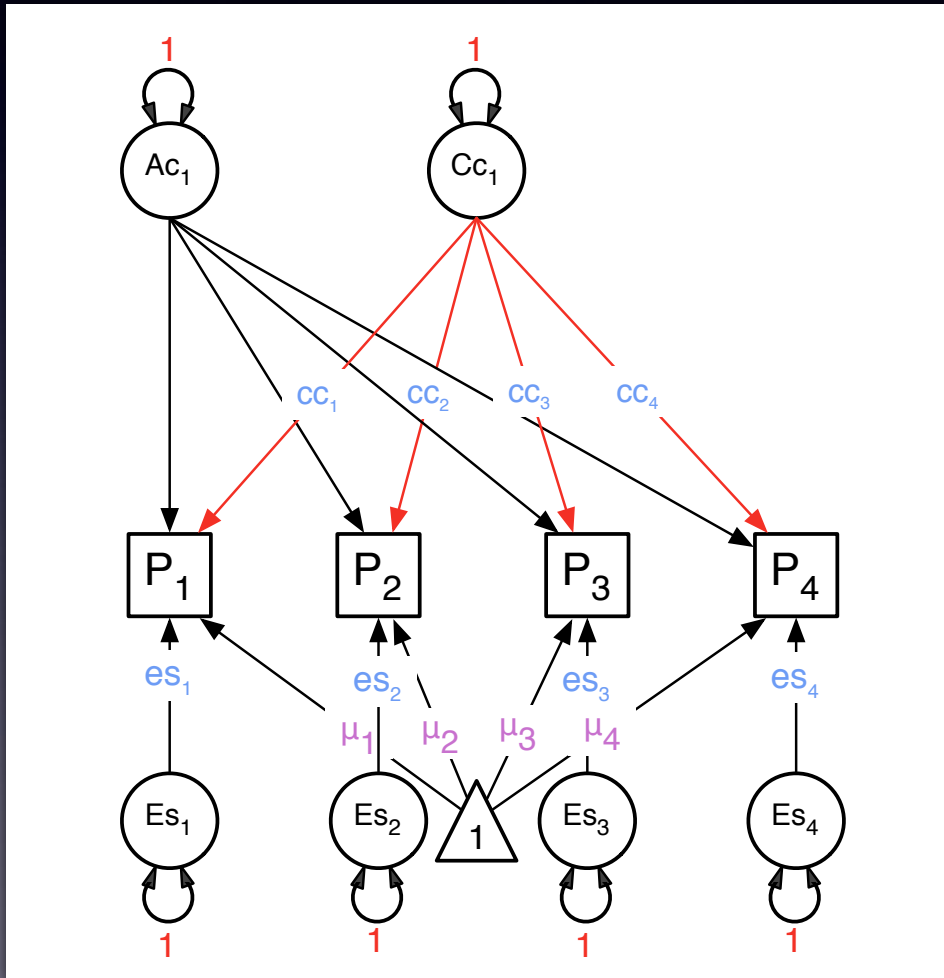
$$\begin{bmatrix} e_{11} & 0 & 0 & 0 \\ 0 & e_{22} & 0 & 0 \\ 0 & 0 & e_{33} & 0 \\ 0 & 0 & 0 & e_{44} \end{bmatrix} \times \begin{bmatrix} e_{11} & 0 & 0 & 0 \\ 0 & e_{22} & 0 & 0 \\ 0 & 0 & e_{33} & 0 \\ 0 & 0 & 0 & e_{44} \end{bmatrix} = \begin{bmatrix} e_{11}^2 & 0 & 0 & 0 \\ 0 & e_{22}^2 & 0 & 0 \\ 0 & 0 & e_{33}^2 & 0 \\ 0 & 0 & 0 & e_{44}^2 \end{bmatrix}$$

Common A Factor



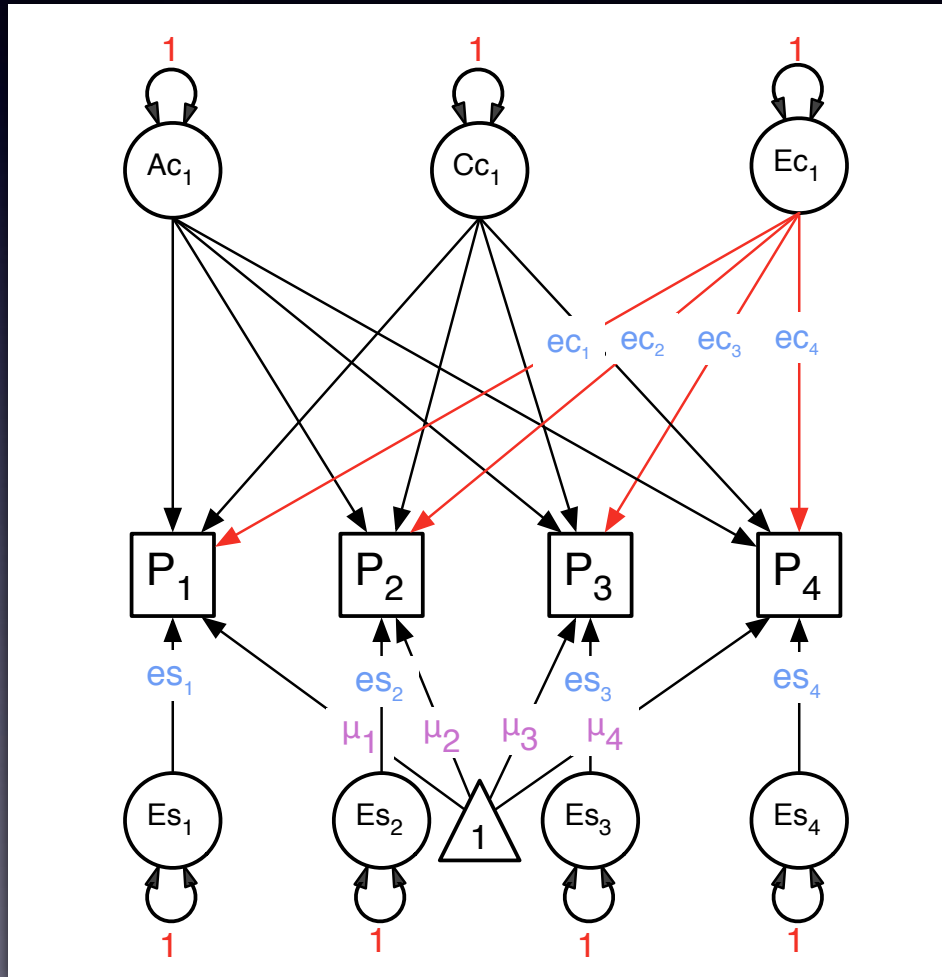
$$\begin{matrix} P1 \\ P2 \\ P3 \\ P4 \end{matrix} \begin{bmatrix} A1 \\ ac_{11} \\ ac_{21} \\ ac_{31} \\ ac_{41} \end{bmatrix}$$

Common C Factor



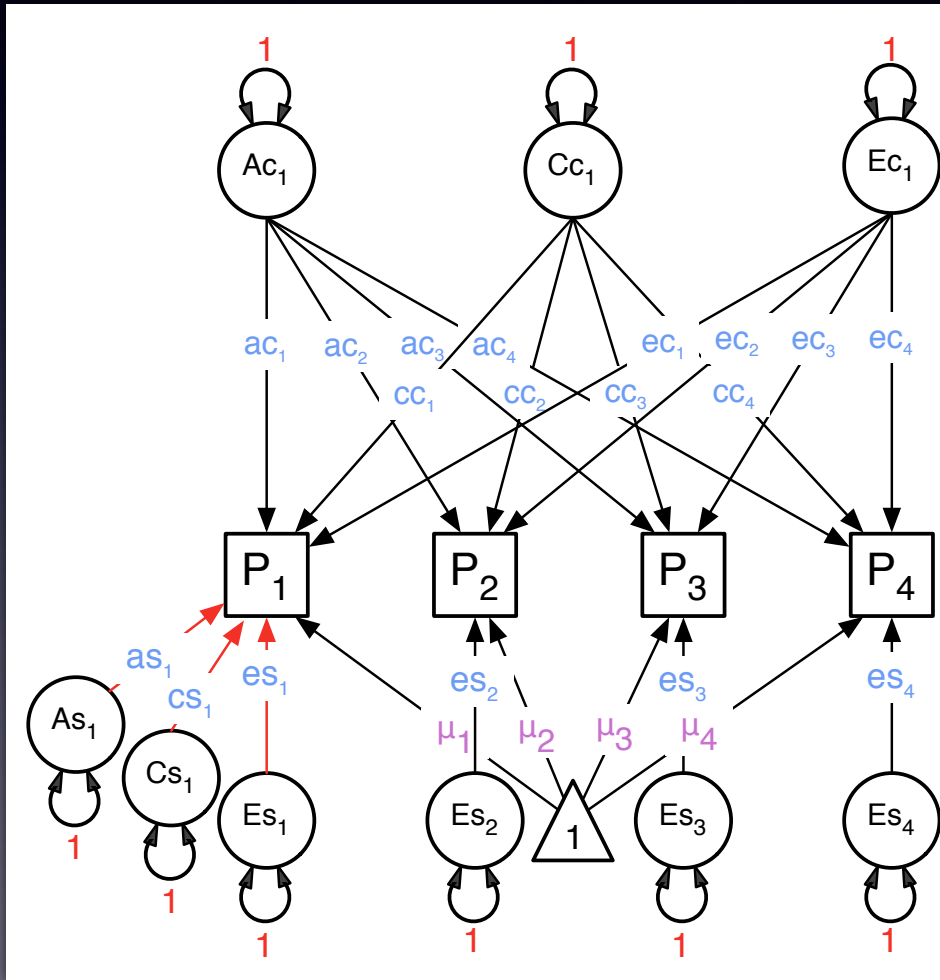
	CI
P1	cc_{11}
P2	cc_{21}
P3	cc_{31}
P4	cc_{41}

Common E Factor



	EI
P1	ec_{11}
P2	ec_{21}
P3	ec_{31}
P4	ec_{41}

ACE Specifics



$$\begin{matrix}
 P1 \\
 P2 \\
 P3 \\
 P4
 \end{matrix}
 \begin{bmatrix}
 EI & E2 & E3 & E4 \\
 es_{11} & 0 & 0 & 0 \\
 0 & es_{22} & 0 & 0 \\
 0 & 0 & es_{33} & 0 \\
 0 & 0 & 0 & es_{44}
 \end{bmatrix}$$

$$\begin{bmatrix}
 as_{11} & 0 & 0 & 0 \\
 0 & as_{22} & 0 & 0 \\
 0 & 0 & as_{33} & 0 \\
 0 & 0 & 0 & as_{44} \\
 cs_{11} & 0 & 0 & 0 \\
 0 & cs_{22} & 0 & 0 \\
 0 & 0 & cs_{33} & 0 \\
 0 & 0 & 0 & cs_{44}
 \end{bmatrix}$$

Independent Pathway Model

- Biometric model
- Different covariance structure for A, C and E

Common A Factors

Specific A Factors

object: pathAc
matrix name:
ac

$$\begin{bmatrix} ac_{11} \\ ac_{21} \\ ac_{31} \\ ac_{41} \end{bmatrix} \times \begin{bmatrix} ac_{11} & ac_{21} & ac_{31} & ac_{41} \end{bmatrix} = \begin{bmatrix} ac_{11}^2 & ac_{11}ac_{21} & ac_{11}ac_{31} & ac_{11}ac_{41} \\ ac_{21}ac_{11} & ac_{21}^2 & ac_{21}ac_{31} & ac_{21}ac_{41} \\ ac_{31}ac_{11} & ac_{31}ac_{21} & ac_{31}^2 & ac_{31}ac_{41} \\ ac_{41}ac_{11} & ac_{41}ac_{21} & ac_{41}ac_{31} & ac_{41}^2 \end{bmatrix}$$

$$\begin{bmatrix} as_{11} & 0 & 0 & 0 \\ 0 & as_{22} & 0 & 0 \\ 0 & 0 & as_{33} & 0 \\ 0 & 0 & 0 & as_{44} \end{bmatrix} \times \begin{bmatrix} as_{11} & 0 & 0 & 0 \\ 0 & as_{22} & 0 & 0 \\ 0 & 0 & as_{33} & 0 \\ 0 & 0 & 0 & as_{44} \end{bmatrix} = \begin{bmatrix} as_{11}^2 & 0 & 0 & 0 \\ 0 & as_{22}^2 & 0 & 0 \\ 0 & 0 & as_{33}^2 & 0 \\ 0 & 0 & 0 & as_{44}^2 \end{bmatrix}$$

object: pathAs
matrix name: as

```
pathAc    <- mxMatrix( type="Full", nrow=nv, ncol=nf, free=TRUE, values=.6,
labels=labFull("ac",nv, nf), lbound=lbPa, name="ac" )
pathAs    <- mxMatrix( type="Diag", nrow=nv, ncol=nv, free=TRUE, values=.5,
labels=labDiag("as",nv), lbound=.00001, name="as" )
```

Predicted A Covariance Common+Specific

`ac %**% t(ac)`

$$\begin{bmatrix} ac_{11}^2 & ac_{11}ac_{21} & ac_{11}ac_{31} & ac_{11}ac_{41} \\ ac_{21}ac_{11} & ac_{21}^2 & ac_{21}ac_{31} & ac_{21}ac_{41} \\ ac_{31}ac_{11} & ac_{31}ac_{21} & ac_{31}^2 & ac_{31}ac_{41} \\ ac_{41}ac_{11} & ac_{41}ac_{21} & ac_{41}ac_{31} & ac_{41}^2 \end{bmatrix}$$

$$+$$

$$\begin{bmatrix} as_{11}^2 & 0 & 0 & 0 \\ 0 & as_{22}^2 & 0 & 0 \\ 0 & 0 & as_{33}^2 & 0 \\ 0 & 0 & 0 & as_{44}^2 \end{bmatrix}$$

`as %**% t(as)`

$$=$$

$$\begin{bmatrix} ac_{11}^2 + as_{11}^2 & ac_{11}ac_{21} & ac_{11}ac_{31} & ac_{11}ac_{41} \\ ac_{21}ac_{11} & ac_{21}^2 + as_{22}^2 & ac_{21}ac_{31} & ac_{21}ac_{41} \\ ac_{31}ac_{11} & ac_{31}ac_{21} & ac_{31}^2 + as_{33}^2 & ac_{31}ac_{41} \\ ac_{41}ac_{11} & ac_{41}ac_{21} & ac_{41}ac_{31} & ac_{41}^2 + as_{44}^2 \end{bmatrix}$$

object: CovA
matrix name:A

```
covA <- mxAlgebra( expression=ac %**% t(ac) + as %**% t(as), name="A" )
```

Independent Pathways



```
# -----  
# FIT GENETIC SUBMODELS  
  
# -----  
# Fit Independent Pathway ACE Model  
# -----  
nf <- 1 # number of factors
```

specific number of independent
pathways by source of variance

Ind Common Factors Residuals



common factors of size $nv \times nf$ (full matrices)

```
# Matrices ac, cc, and ec to store a, c, and e path coefficients for common factors
pathAc  <- mxMatrix( type="Full", nrow=nv, ncol=nf, free=TRUE, values=.6,
labels=labFull("ac",nv,nf), name="ac" )
pathCc  <- mxMatrix( type="Full", nrow=nv, ncol=nf, free=TRUE, values=.6,
labels=labFull("cc",nv,nf), name="cc" )
pathEc  <- mxMatrix( type="Full", nrow=nv, ncol=nf, free=TRUE, values=.6,
labels=labFull("ec",nv,nf), name="ec" )

# Matrices as, cs, and es to store a, c, and e path coefficients for specific factors
pathAs  <- mxMatrix( type="Diag", nrow=nv, ncol=nv, free=T, values=4,
labels=labDiag("as",nv), lbound=.00001, name="as" )
pathCs  <- mxMatrix( type="Diag", nrow=nv, ncol=nv, free=T, values=4,
labels=labDiag("cs",nv), lbound=.00001, name="cs" )
pathEs  <- mxMatrix( type="Diag", nrow=nv, ncol=nv, free=T, values=5,
labels=labDiag("es",nv), lbound=.00001, name="es" )

# Matrices A, C, and E compute variance components
covA    <- mxAlgebra( expression=ac %*% t(ac) + as %*% t(as), name="A" )
covC    <- mxAlgebra( expression=cc %*% t(cc) + cs %*% t(cs), name="C" )
covE    <- mxAlgebra( expression=ec %*% t(ec) + es %*% t(es), name="E" )
```

specific factors of size $nv \times nv$
(diagonal only)

common factors + specifics

Fitting IP Model



```
# Combine Groups
pars      <- list( pathAc, pathCc, pathEc, pathAs, pathCs, pathEs, covA, covC, covE, covP,
matI, invSD, meanG, meanT )
modelMZ   <- mxModel( pars, covMZ, dataMZ, objMZ, name="MZ" )
modelDZ   <- mxModel( pars, covDZ, dataDZ, objDZ, name="DZ" )
minus2ll  <- mxAlgebra( expression=MZ.objective + DZ.objective, name="m2LL" )
obj       <- mxAlgebraObjective( "m2LL" )
IndAceModel <- mxModel( "IndACE", pars, modelMZ, modelDZ, minus2ll, obj )

# Run IndACE model
IndAceFit  <- mxRun(IndAceModel)
IndAceSumm <- summary(IndAceFit)
IndAceSumm$pa
round(IndAceFit@output$estimate,4)
```

include all relevant matrices

Create Relevant Output

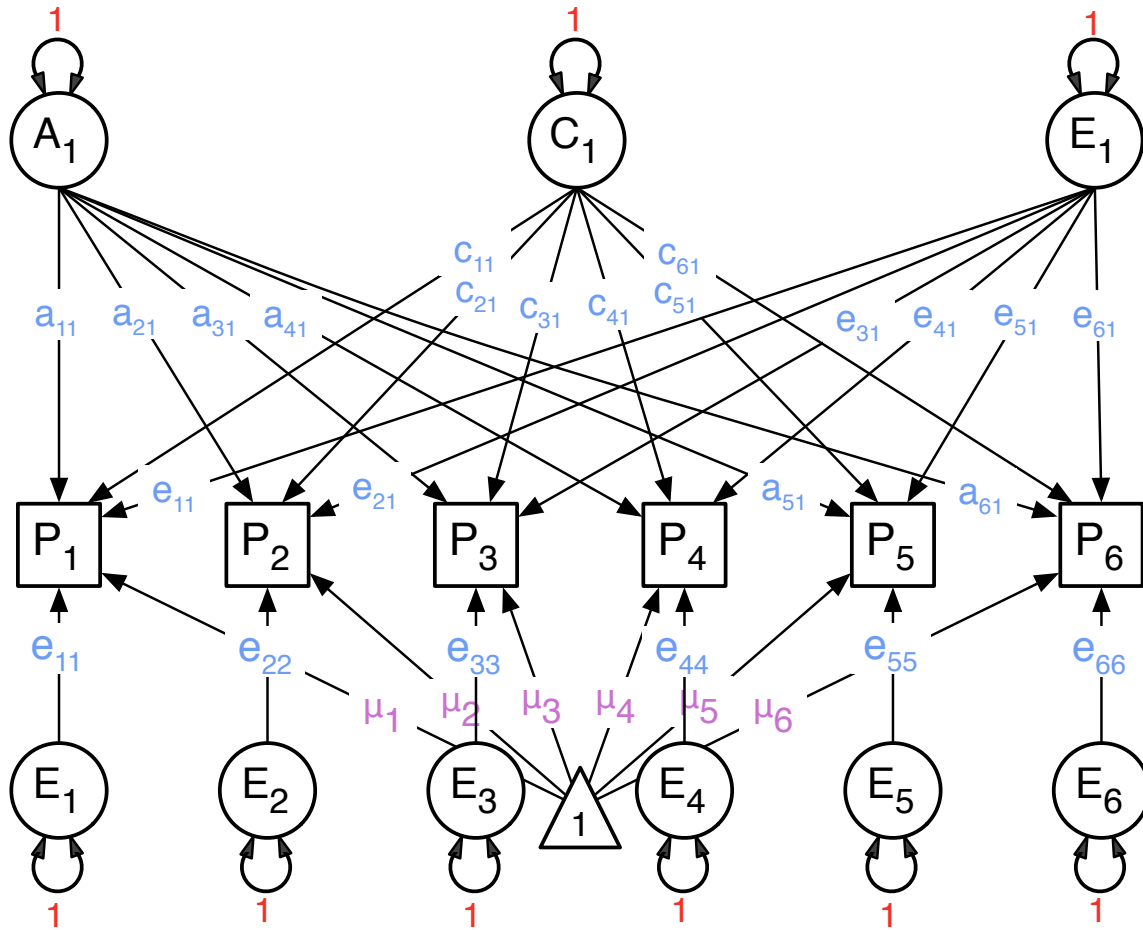


```
# Generate Independent Pathway ACE Output
parameterSpecifications(IndAceFit)
mxCompare(CholAceFit,IndAceFit)

# Generate List of Parameter Estimates and Derived Quantities using formatOutputMatrices
IndACEpathMatrices <- c("iSD %**% ac","iSD %**% cc","iSD %**% ec",
                        "iSD %**% as","iSD %**% cs","iSD %**% es")
IndACEpathLabels <- c("stPathAc","stPathCc","stPathEc","stPathAs","stPathCs","stPathEs")
formatOutputMatrices(IndAceFit,IndACEpathMatrices,IndACEpathLabels,Vars,4)
```

fitted model, list of matrices (in quotes), list of labels
(also in quotes), list of variable names, rounding value

IP Model



Independent Pathway

Variance Component	a^2	c^2	e^2
Common Factors	ac $nv \times 1$	cc $nv \times 1$	ec $nv \times 1$
Residual Factors	as $nv \times nv$	cs $nv \times nv$	es $nv \times nv$

Parameters

Independent Pathway

model:IndACE, matrix:ac

```
[ ,1]
[1,] [ac_1_1]
[2,] [ac_2_1]
[3,] [ac_3_1]
[4,] [ac_4_1]
[5,] [ac_5_1]
[6,] [ac_6_1]
```

model:IndACE, matrix:as

```
[ ,1] [ ,2] [ ,3] [ ,4] [ ,5] [ ,6]
[1,] [as_1_1] 0 0 0 0 0
[2,] 0 [as_2_2] 0 0 0 0
[3,] 0 0 [as_3_3] 0 0 0
[4,] 0 0 0 [as_4_4] 0 0
[5,] 0 0 0 0 [as_5_5] 0
[6,] 0 0 0 0 0 [as_6_6]
```

model:IndACE, matrix:cc

```
[ ,1]
[1,] [cc_1_1]
[2,] [cc_2_1]
[3,] [cc_3_1]
[4,] [cc_4_1]
[5,] [cc_5_1]
[6,] [cc_6_1]
```

model:IndACE, matrix:cs

```
[ ,1] [ ,2] [ ,3] [ ,4] [ ,5] [ ,6]
[1,] [cs_1_1] 0 0 0 0 0
[2,] 0 [cs_2_2] 0 0 0 0
[3,] 0 0 [cs_3_3] 0 0 0
[4,] 0 0 0 [cs_4_4] 0 0
[5,] 0 0 0 0 [cs_5_5] 0
[6,] 0 0 0 0 0 [cs_6_6]
```

model:IndACE, matrix:ec

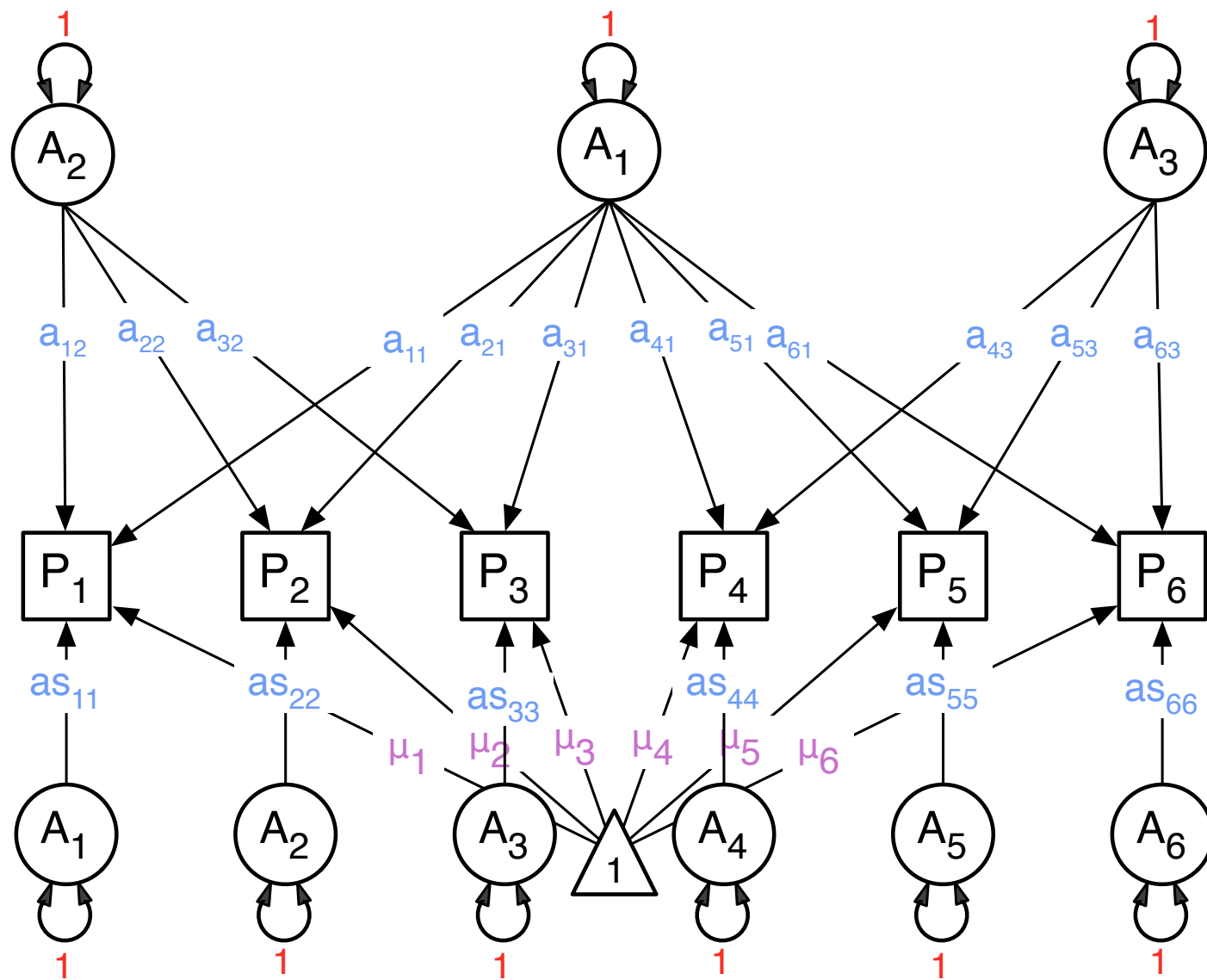
```
[ ,1]
[1,] [ec_1_1]
[2,] [ec_2_1]
[3,] [ec_3_1]
[4,] [ec_4_1]
[5,] [ec_5_1]
[6,] [ec_6_1]
```

model:IndACE, matrix:es

```
[ ,1] [ ,2] [ ,3] [ ,4] [ ,5] [ ,6]
[1,] [es_1_1] 0 0 0 0 0
[2,] 0 [es_2_2] 0 0 0 0
[3,] 0 0 [es_3_3] 0 0 0
[4,] 0 0 0 [es_4_4] 0 0
[5,] 0 0 0 0 [es_5_5] 0
[6,] 0 0 0 0 0 [es_6_6]
```

model:IndACE, matrix:Mean

```
[ ,1] [ ,2] [ ,3] [ ,4] [ ,5] [ ,6]
[1,] [me_1_1] [me_1_2] [me_1_3] [me_1_4] [me_1_5] [me_1_6]
```

Additional A Factors

changing one matrix



```
# -----  
# Fit 3A (1C 1E) Factor - Independent Pathway Model  
# -----  
  
# Change Dimension of Additive Genetic Factor Matrix Ac  
# Create Free and Values for 2 Additive Genetic Factors  
#           free           values  
#           A1  A2  A3           A1  A2  A3  
# P1  T   T   F   P1  .5  .5  0  
# P2  T   T   F   P2  .5  .5  0  
# P3  T   T   F   P3  .5  .5  0  
# P4  T   F   T   P4  .5  0  .5  
# P5  T   F   T   P4  .5  0  .5  
# P6  T   F   T   P4  .5  0  .5  
nfA      <- 3  
frAc3    <- c(T,T,T,T,T,T, T,T,T,F,F,F, F,F,F,T,T,T)  
svAc3    <- c(rep(.5,nv),rep(.5,3),rep(0,3),rep(0,3),rep(.5,3))  
pathAc   <- mxMatrix( type="Full", nrow=nv, ncol=nfA, free=frAc3, values=svAc3,  
labels=labFull("ac",nv,nfA), name="ac" )
```

Fitting New Model



```
# Rebuild & Run Model
pars      <- list(pathAc, pathCc, pathEc, pathAs, pathCs, pathEs,
                  covA, covC, covE, covP, matI, invSD, meanG )
modelMZ   <- mxModel( pars, covMZ, dataMZ, objMZ, name="MZ" )
modelDZ   <- mxModel( pars, covDZ, dataDZ, objDZ, name="DZ" )

Ind_3A_1C_1E_Model <- mxModel( "Ind3ACE", pars, modelMZ, modelDZ, minus2ll, obj )

# Run New Model
Ind_3A_1C_1E_Fit    <- mxRun(Ind_3A_1C_1E_Model)
IndNested <- list(IndAceFit, Ind_3A_1C_1E_Fit)
mxCompare(CholAceFit, IndNested)

formatOutputMatrices(Ind_3A_1C_1E_Fit, IndACEpathMatrices, IndACEpathLabels, Vars, 4)
```

matrix changed, thus models need to be rebuilt

Identification

- Be careful when adding common factors: total parameters per source of variance can not exceed $(nv*(nv+1))/2$
- For a common factor with only 2 indicators the two factor loadings on the latent factor need to be equated OR instead a correlation could be estimated between the residual factors (of the same source of variance) on the two indicators.

Model Fitting Results

	ep	-2ll	df	AIC	chi2	df	p
CholAce	69	14362.14	2006	10350			
CholAe	48	14379.03	2027	10325	16.88	21	0.72
IndAce	42	14449.87	2033	10383	87.73	27	0
IndAe	30	14499.02	2045	10409	136.88	39	0
Ind3Ace	48	14423.01	2027	10369	60.87	21	0
Ind3Ae	36	14439.73	2039	10361	77.59	33	0

Model Fitting Results

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Ind3Ace	48	14423.01	2027	10369	60.87	21	0
Ind3Ae	36	14439.73	2039	10361	77.59	33	0
Ind3Ac3e	48	14382.58	2027	10328	20.45	21	0.49

Standardized Path Coefficients

Independent Pathway 3A3E

[1] "Matrix iSD %*% ac"

	stPathAc1	stPathAc2	stPathAc3	stPathAs1	stPathAs2	stPathAs3	stPathAs4	stPathAs5	stPathAs6
family	0.4194	-0.5762	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
happy	0.4698	-0.1603	0.0000	0.0000	0.2385	0.0000	0.0000	0.0000	0.0000
life	0.5447	-0.1850	0.0000	0.0000	0.0000	0.0763	0.0000	0.0000	0.0000
anxdep	-0.4376	0.0000	0.2597	0.0000	0.0000	0.0000	0.2106	0.0000	0.0000
somatic	-0.4891	0.0000	0.5277	0.0000	0.0000	0.0000	0.0000	0.0003	0.0000
social	-0.2783	0.0000	0.1730	0.0000	0.0000	0.0000	0.0000	0.0000	0.4502

[1] "Matrix iSD %*% as"

[1] "Matrix iSD %*% cc"

	stPathCc1	stPathCs1	stPathCs2	stPathCs3	stPathCs4	stPathCs5	stPathCs6
family	-0.2456	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
happy	-0.2569	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
life	-0.1527	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
anxdep	0.4286	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
somatic	0.0225	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
social	0.4139	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000

[1] "Matrix iSD %*% cs"

[1] "Matrix iSD %*% ec"

	stPathEc1	stPathEc2	stPathEc3	stPathEs1	stPathEs2	stPathEs3	stPathEs4	stPathEs5	stPathEs6
family	-0.0489	0.1097	0.0000	0.6460	0.0000	0.0000	0.0000	0.0000	0.0000
happy	-0.6654	0.3787	0.0000	0.0000	0.2112	0.0000	0.0000	0.0000	0.0000
life	-0.5606	0.1313	0.0000	0.0000	0.0000	0.5554	0.0000	0.0000	0.0000
anxdep	0.3745	0.0000	0.5627	0.0000	0.0000	0.0000	0.2369	0.0000	0.0000
somatic	0.0426	0.0000	0.2840	0.0000	0.0000	0.0000	0.0000	0.6320	0.0000
social	0.0804	0.0000	0.1590	0.0000	0.0000	0.0000	0.0000	0.0000	0.6978

[1] "Matrix iSD %*% es"

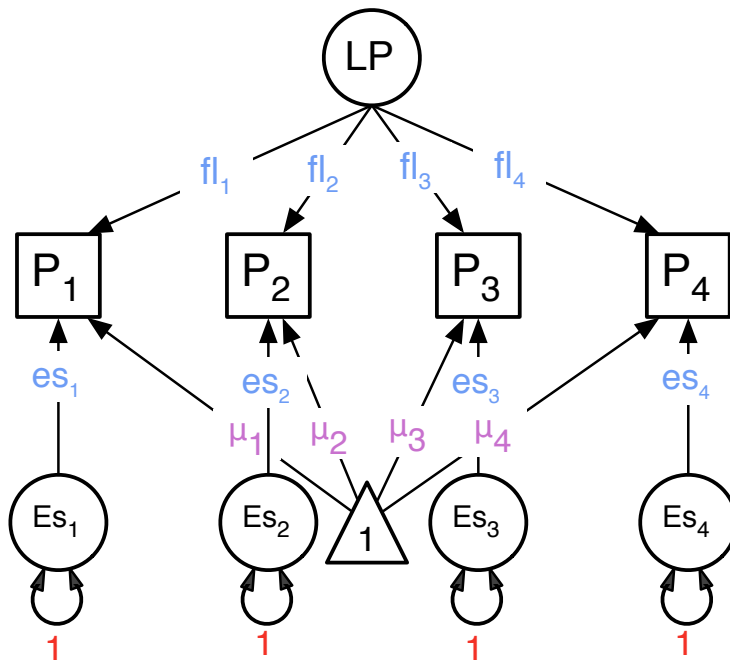
Alternative Common Factor Models for Multivariate Biometric Analyses

J. J. McArdle¹ and H. H. Goldsmith²

Received 4 Apr. 1988—Final 15 May 1990

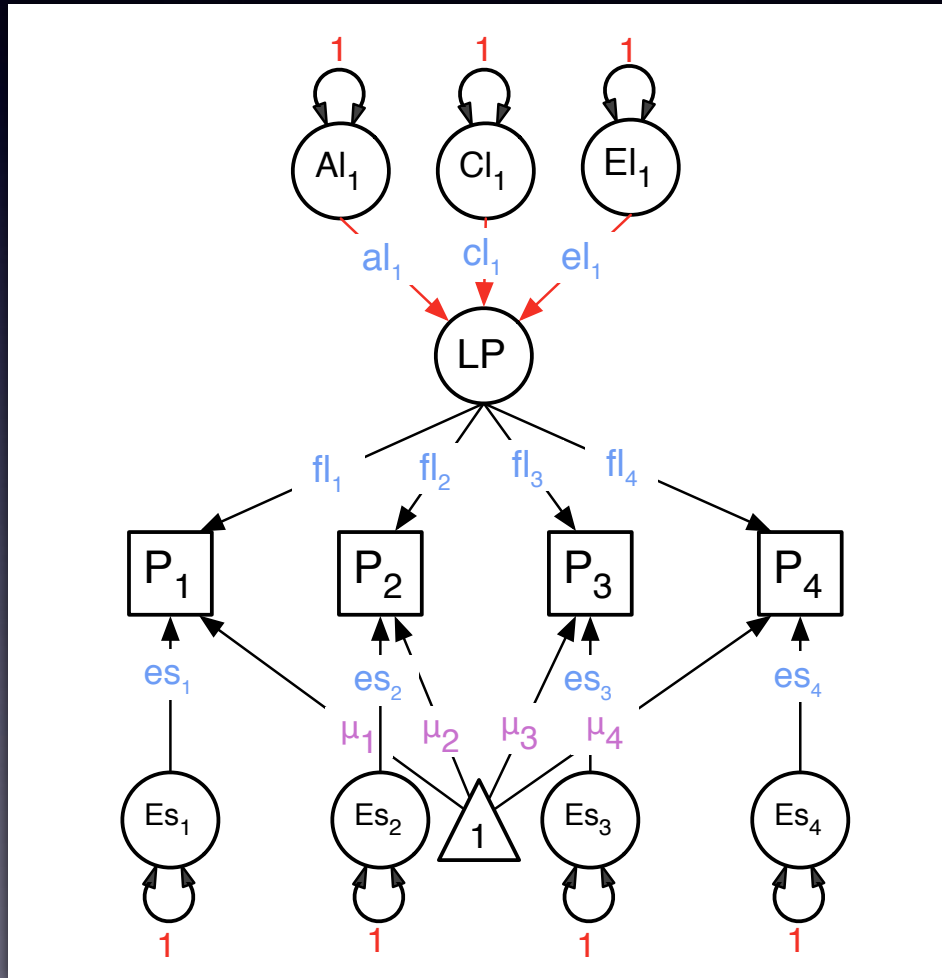
In prior research we have shown how linear structural equation models and computer programs (e.g., LISREL) may be simply and directly used to provide alternatives for the traditional biometric twin design. We use structural equations and path models to define biometric group differences, we write traditional common-factor models in the same way, and then we take a detailed look at some alternative multivariate and biometric models. We contrast the biometric-factors covariance structure approach used by Loehlin and Vandenberg (1968), Martin and Eaves (1977), and others with the psychometric-factors approach used by McArdle et al. (1980) and others. We use the multivariate primary mental abilities data on monozygotic (MZ) and dizygotic (DZ) twins from Loehlin and Vandenberg (1968) to detail fundamental differences in model specification and results. We extend both multivariate biometric approaches using exploratory and confirmatory multiple-factor models. These comparisons show that each alternative multivariate methodology has useful features for empirical applications.

Factor Loadings



	FI
P1	fl_{11}
P2	fl_{21}
P3	fl_{31}
P4	fl_{41}

Latent Phenotype ACE



AI
LP [al_{11}]

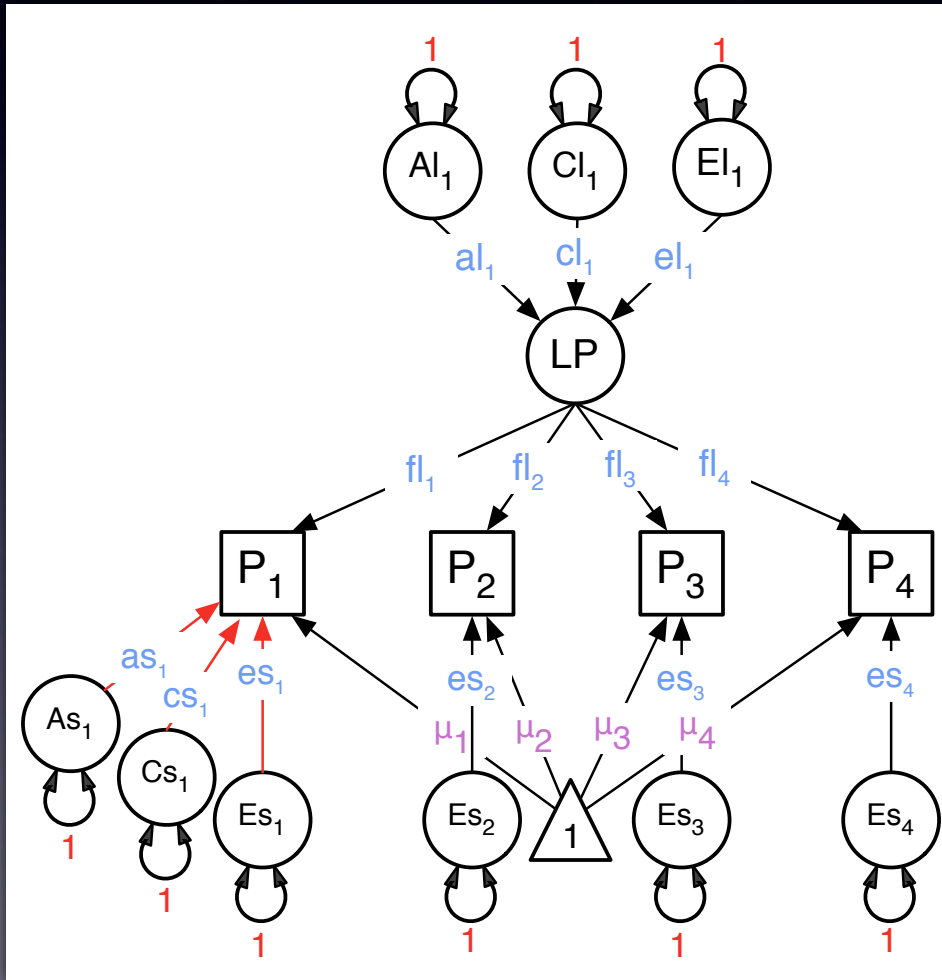
CI
LP [cl_{11}]

EI
LP [el_{11}]

P1
P2
P3
P4

LP
fl_{11}
fl_{21}
fl_{31}
fl_{41}

ACE Specifics



	E1	E2	E3	E4
P1	es_{11}	0	0	0
P2	0	es_{22}	0	0
P3	0	0	es_{33}	0
P4	0	0	0	es_{44}

as_{11}	0	0	0
0	as_{22}	0	0
0	0	as_{33}	0
0	0	0	as_{44}
cs_{11}	0	0	0
0	cs_{22}	0	0
0	0	cs_{33}	0
0	0	0	cs_{44}

Common Pathway Model

- Psychometric model
- Same covariance structure for A, C and E

Common A Factors

Specific A Factors

object: pathFl
matrix name: fl

object: pathAl
matrix name: al

$$\begin{bmatrix} fl_{11} \\ fl_{21} \\ fl_{31} \\ fl_{41} \end{bmatrix} \times [al_{11}] \times [al_{11}] \times \begin{bmatrix} fl_{11} & fl_{21} & fl_{31} & fl_{41} \end{bmatrix} = \begin{bmatrix} fl_{11}^2 al_{11}^2 & fl_{11} fl_{21} al_{11}^2 & fl_{11} fl_{31} al_{11}^2 & fl_{11} fl_{41} al_{11}^2 \\ fl_{21} fl_{11} al_{11}^2 & fl_{21}^2 al_{11}^2 & fl_{21} fl_{31} al_{11}^2 & fl_{21} fl_{41} al_{11}^2 \\ fl_{31} fl_{11} al_{11}^2 & fl_{31} fl_{21} al_{11}^2 & fl_{31}^2 al_{11}^2 & fl_{31} fl_{41} al_{11}^2 \\ fl_{41} fl_{11} al_{11}^2 & fl_{41} fl_{21} al_{11}^2 & fl_{41} fl_{31} al_{11}^2 & fl_{41}^2 al_{11}^2 \end{bmatrix}$$

$$\begin{bmatrix} as_{11} & 0 & 0 & 0 \\ 0 & as_{22} & 0 & 0 \\ 0 & 0 & as_{33} & 0 \\ 0 & 0 & 0 & as_{44} \end{bmatrix} \times \begin{bmatrix} as_{11} & 0 & 0 & 0 \\ 0 & as_{22} & 0 & 0 \\ 0 & 0 & as_{33} & 0 \\ 0 & 0 & 0 & as_{44} \end{bmatrix} = \begin{bmatrix} as_{11}^2 & 0 & 0 & 0 \\ 0 & as_{22}^2 & 0 & 0 \\ 0 & 0 & as_{33}^2 & 0 \\ 0 & 0 & 0 & as_{44}^2 \end{bmatrix}$$

object: pathAs
matrix name: as

```

pathFl    <- mxMatrix( type="Full", nrow=nv, ncol=nl, free=TRUE, values=.2,
                        labels=labFull("fl",nv,nl), name="fl" )
pathAl    <- mxMatrix( type="Lower", nrow=nl, ncol=nl, free=TRUE, values=.6,
                        labels=labLower("al",nl), lbound=.00001, name="al" )
pathAs    <- mxMatrix( type="Diag", nrow=nv, ncol=nv, free=TRUE, values=.5,
                        labels=labDiag("as",nv), lbound=.00001, name="as" )
    
```

Predicted A Covariance Common+Specific

`fl %&% (al %*% t(al))`

$$\begin{bmatrix} fl_{11}^2 al_{11}^2 & fl_{11} fl_{21} al_{11}^2 & fl_{11} fl_{31} al_{11}^2 & fl_{11} fl_{41} al_{11}^2 \\ fl_{21} fl_{11} al_{11}^2 & fl_{21}^2 al_{11}^2 & fl_{21} fl_{31} al_{11}^2 & fl_{21} fl_{41} al_{11}^2 \\ fl_{31} fl_{11} al_{11}^2 & fl_{31} fl_{21} al_{11}^2 & fl_{31}^2 al_{11}^2 & fl_{31} fl_{41} al_{11}^2 \\ fl_{41} fl_{11} al_{11}^2 & fl_{41} fl_{21} al_{11}^2 & fl_{41} fl_{31} al_{11}^2 & fl_{41}^2 al_{11}^2 \end{bmatrix}$$

$$+ \begin{bmatrix} as_{11}^2 & 0 & 0 & 0 \\ 0 & as_{22}^2 & 0 & 0 \\ 0 & 0 & as_{33}^2 & 0 \\ 0 & 0 & 0 & as_{44}^2 \end{bmatrix}$$

`as %*% t(as)`

$$= \begin{bmatrix} fl_{11}^2 al_{11}^2 + as_{11}^2 & fl_{11} fl_{21} al_{11}^2 & fl_{11} fl_{31} al_{11}^2 & fl_{11} fl_{41} al_{11}^2 \\ fl_{21} fl_{11} al_{11}^2 & fl_{21}^2 al_{11}^2 + as_{22}^2 & fl_{21} fl_{31} al_{11}^2 & fl_{21} fl_{41} al_{11}^2 \\ fl_{31} fl_{11} al_{11}^2 & fl_{31} fl_{21} al_{11}^2 & fl_{31}^2 al_{11}^2 + as_{33}^2 & fl_{31} fl_{41} al_{11}^2 \\ fl_{41} fl_{11} al_{11}^2 & fl_{41} fl_{21} al_{11}^2 & fl_{41} fl_{31} al_{11}^2 & fl_{41}^2 al_{11}^2 + as_{44}^2 \end{bmatrix}$$

object: CovA
matrix name:A

```
covA <- mxAlgebra( expression=fl %&% (al %*% t(al)) + as %*% t(as),
```

Constraint on Variance of Latent Phenotype



```
# -----  
# Fit Common Pathway ACE Model  
# -----  
n1      <- 1  
  
# Matrices ac, cc, and ec to store a, c, and e path coefficients for latent phenotype(s)  
pathA1  <- mxMatrix( type="Lower", nrow=n1, ncol=n1, free=T, values=.6, labels="a1_1_1",  
lbound=.00001, name="a1" )  
pathC1  <- mxMatrix( type="Lower", nrow=n1, ncol=n1, free=T, values=.6, labels="c1_1_1",  
lbound=.00001, name="c1" )  
pathE1  <- mxMatrix( type="Lower", nrow=n1, ncol=n1, free=T, values=.6, labels="e1_1_1",  
lbound=.00001, name="e1" )  
  
# Matrix and Algebra for constraint on variance of latent phenotype  
covarLP <- mxAlgebra( expression= a1 %**% t(a1) + c1 %**% t(c1) + e1 %**% t(e1),  
name="CovarLP" )  
varLP   <- mxAlgebra( expression= diag2vec(CovarLP), name="VarLP" )  
unit    <- mxMatrix( type="Unit", nrow=n1, ncol=1, name="Unit" )  
varLP1  <- mxConstraint( expression=VarLP == Unit, name="varLP1")
```

latent phenotype $n1 \times n1$

$$a^2 + c^2 + e^2 = 1$$

Factor Loadings Specifics



factor loadings

```
# Matrix f for factor loadings on latent phenotype
pathFl <- mxMatrix( type="Full", nrow=nv, ncol=nl, free=TRUE, values=.2, labels=laFl,
name="fl" )

# Matrices as, cs, and es to store a, c, and e path coefficients for specific factors
pathAs <- mxMatrix( type="Diag", nrow=nv, ncol=nv, free=TRUE, values=.5, labels=laAs,
lbound=.00001, name="as" )
pathCs <- mxMatrix( type="Diag", nrow=nv, ncol=nv, free=TRUE, values=.5, labels=laCs,
lbound=.00001, name="cs" )
pathEs <- mxMatrix( type="Diag", nrow=nv, ncol=nv, free=TRUE, values=.5, labels=laEs,
lbound=.00001, name="es" )

# Matrices A, C, and E compute variance components
covA <- mxAlgebra( expression=fl %&% (al %*% t(al)) + as %*% t(as), name="A" )
covC <- mxAlgebra( expression=fl %&% (cl %*% t(cl)) + cs %*% t(cs), name="C" )
covE <- mxAlgebra( expression=fl %&% (el %*% t(el)) + es %*% t(es), name="E" )
```

specifics similar to IP

factor loadings x ace on LP
+ specifics

Fitting CP Model



```
# Combine Groups
pars      <- list( pathA1, pathC1, pathE1, covarLP, varLP, unit, pathF1,
  pathAs, pathCs, pathEs, covA, covC, covE, covP, matI, invSD, meanG, meanT )
modelMZ   <- mxModel( pars, covMZ, dataMZ, objMZ, name="MZ" )
modelDZ   <- mxModel( pars, covDZ, dataDZ, objDZ, name="DZ" )
minus2ll  <- mxAlgebra( expression=MZ.objective + DZ.objective, name="m2LL" )
obj        <- mxAlgebraObjective( "m2LL" )
ComAceModel <- mxModel( "ComACE", pars, varLP1, modelMZ, modelDZ, minus2ll, obj )

# Run CholACE model
ComAceFit   <- mxRun(ComAceModel)
ComAceSumm  <- summary(ComAceFit)
ComAceSumm$pa
round(ComAceFit@output$estimate,4)
```

constraint object in combined model only

new objects

Read in and Transform Variable(s)

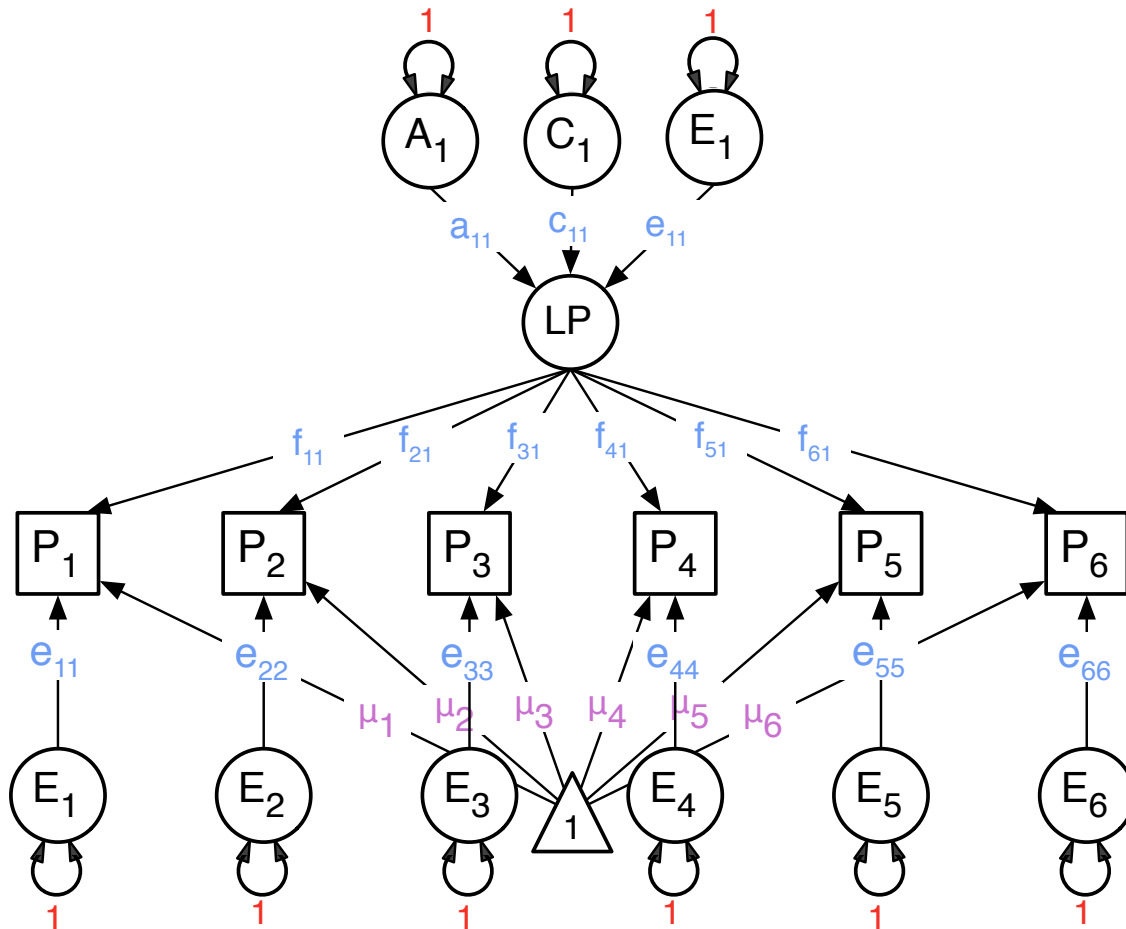


```
# Generate Common Pathway ACE Output  
parameterSpecifications(ComAceFit)  
tableFitStatistics(ComAceFit)
```

```
ACEpathMatricesLP <- c("al", "cl", "el", "iSD %% fl", "iSD %% as", "iSD %% cs", "iSD %% es")  
ACEpathLabelsLP <- c("stPathAl", "stPathCl", "stPathEl", "stPathFl", "stPathAs", "stPathCs", "stPathEs")  
formatOutputMatrices(ComAceFit, ComACEpathMatrices, ComACEpathLabels, Vars, 4)
```

already standardized

CP Model



Common Pathway

Variance Component	a^2	c^2	e^2	
Common Factors	a 1×1	c 1×1	e 1×1	f $nv \times 1$
Residual Factors	a_s $nv \times nv$	c_s $nv \times nv$	e_s $nv \times nv$	

Parameters

Common Pathway

```
model:ComACE, matrix:al
      [,1]
[1,] [al_1_1]
```

```
model:ComACE, matrix:cl
      [,1]
[1,] [cl_1_1]
```

```
model:ComACE, matrix:el
      [,1]
[1,] [el_1_1]
```

```
model:ComACE, matrix:fl
      [,1]
[1,] [fl_1_1]
[2,] [fl_2_1]
[3,] [fl_3_1]
[4,] [fl_4_1]
[5,] [fl_5_1]
[6,] [fl_6_1]
```

```
model:ComACE, matrix:as
      [,1] [,2] [,3] [,4] [,5] [,6]
[1,] [as_1_1] 0    0    0    0    0
[2,] 0        [as_2_2] 0    0    0    0
[3,] 0        0    [as_3_3] 0    0    0
[4,] 0        0    0    [as_4_4] 0    0
[5,] 0        0    0    0    [as_5_5] 0
[6,] 0        0    0    0    0    [as_6_6]
```

```
model:ComACE, matrix:cs
      [,1] [,2] [,3] [,4] [,5] [,6]
[1,] [cs_1_1] 0    0    0    0    0
[2,] 0        [cs_2_2] 0    0    0    0
[3,] 0        0    [cs_3_3] 0    0    0
[4,] 0        0    0    [cs_4_4] 0    0
[5,] 0        0    0    0    [cs_5_5] 0
[6,] 0        0    0    0    0    [cs_6_6]
```

```
model:ComACE, matrix:es
      [,1] [,2] [,3] [,4] [,5] [,6]
[1,] [es_1_1] 0    0    0    0    0
[2,] 0        [es_2_2] 0    0    0    0
[3,] 0        0    [es_3_3] 0    0    0
[4,] 0        0    0    [es_4_4] 0    0
[5,] 0        0    0    0    [es_5_5] 0
[6,] 0        0    0    0    0    [es_6_6]
```

```
model:ComACE, matrix:Mean
      [,1] [,2] [,3] [,4] [,5] [,6]
[1,] [me_1_1] [me_1_2] [me_1_3] [me_1_4] [me_1_5] [me_1_6]
```

Model Fitting Results

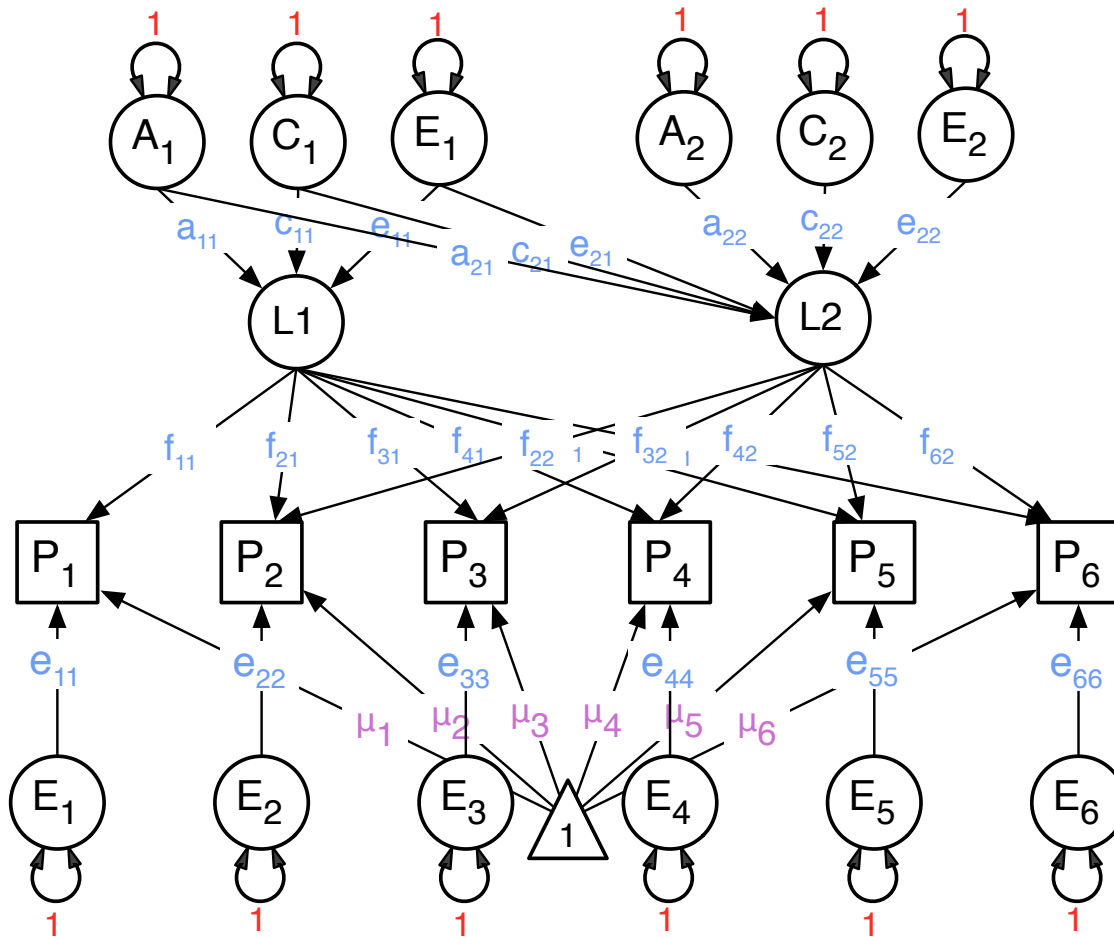
	ep	-2ll	df	AIC	chi2	df	p
CholAce	69	14362.14	2006	10350			
CholAe	48	14379.03	2027	10325	16.88	21	0.72
IndAce	42	14449.87	2033	10383	87.73	27	0
IndAe	30	14499.02	2045	10409	136.88	39	0
Ind3Ace	48	14423.01	2027	10369	60.87	21	0
Ind3Ae	36	14439.73	2039	10361	77.59	33	0
Ind3Ac3e	48	14382.58	2027	10328	20.45	21	0.49
ComAce	33	14713.00	2043	10627	350.86	37	0

Standardized Path Coefficients

Common Pathway

[1] "Matrix al"	[1] "Matrix iSD %*% as"
stPathAl1	stPathAs1 stPathAs2 stPathAs3 stPathAs4 stPathAs5 stPathAs6
LP1 0.7208	family 0.5565 0.0000 0.0000 0.0000 0.0000 0.0000
	happy 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000
[1] "Matrix cl"	life 0.0000 0.0000 0.1387 0.0000 0.0000 0.0000
stPathCl1	anxdep 0.0000 0.0000 0.0000 0.1707 0.0000 0.0000
LP1 0.3267	somatic 0.0000 0.0000 0.0000 0.0000 0.5050 0.0000
	social 0.0000 0.0000 0.0000 0.0000 0.0000 0.5837
[1] "Matrix el"	[1] "Matrix iSD %*% cs"
stPathEl1	stPathCs1 stPathCs2 stPathCs3 stPathCs4 stPathCs5 stPathCs6
LP1 0.6113	family 0.1541 0.0000 0.0000 0.0000 0.0000 0.0000
	happy 0.0000 0.1247 0.0000 0.0000 0.0000 0.0000
[1] "Matrix iSD %*% fl"	life 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000
stPathFl1	anxdep 0.0000 0.0000 0.0000 0.3818 0.0000 0.0000
family 0.4768	somatic 0.0000 0.0000 0.0000 0.0000 0.3064 0.0000
happy 0.8582	social 0.0000 0.0000 0.0000 0.0000 0.0000 0.1828
life 0.8228	
anxdep -0.6811	[1] "Matrix iSD %*% es"
somatic -0.4018	stPathEs1 stPathEs2 stPathEs3 stPathEs4 stPathEs5 stPathEs6
social -0.3843	family 0.6627 0.0000 0.0000 0.0000 0.0000 0.0000
	happy 0.0000 0.4979 0.0000 0.0000 0.0000 0.0000
	life 0.0000 0.0000 0.5511 0.0000 0.0000 0.0000
	anxdep 0.0000 0.0000 0.0000 0.6010 0.0000 0.0000
	somatic 0.0000 0.0000 0.0000 0.0000 0.6997 0.0000
	social 0.0000 0.0000 0.0000 0.0000 0.0000 0.6915

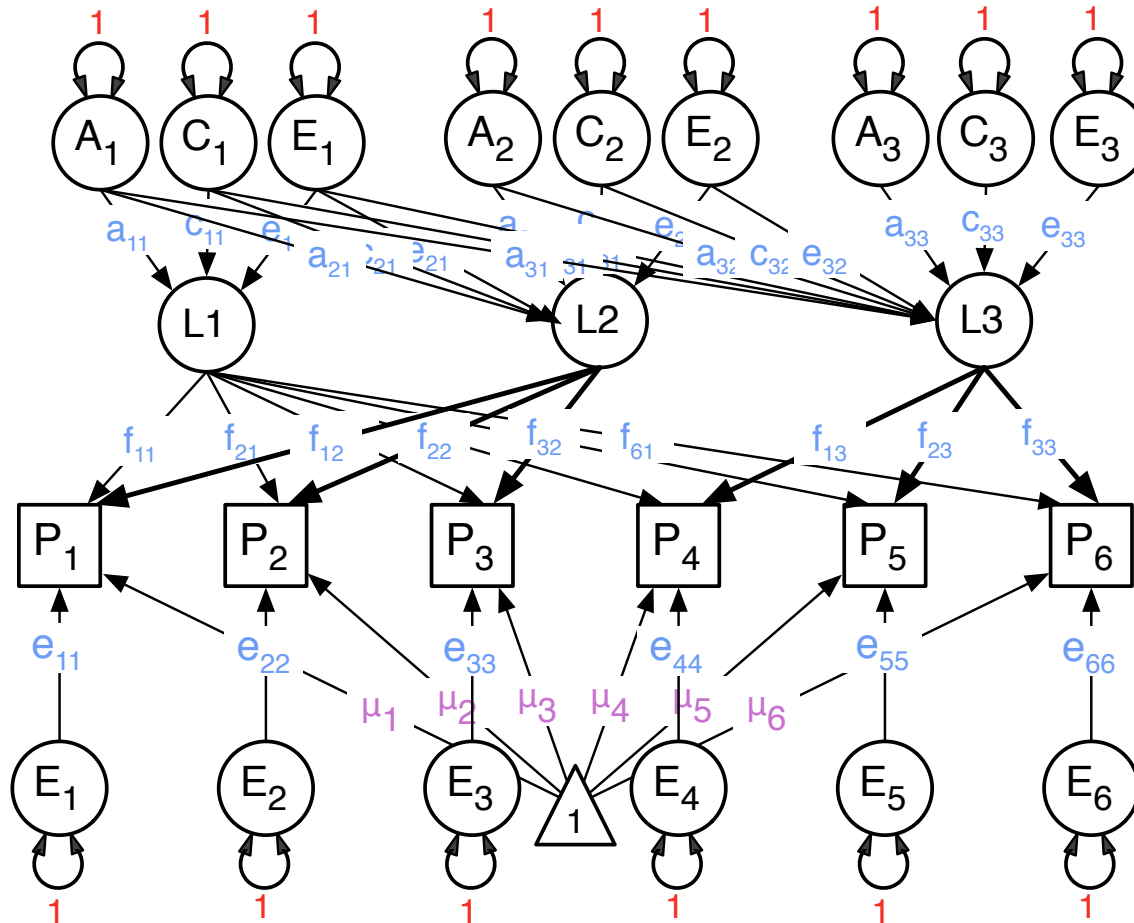
2 Latent Phenotypes



Model Fitting Results

	ep	-2ll	df	AIC	chi2	df	p
CholAce	69	14362.14	2006	10350			
CholAe	48	14379.03	2027	10325	16.88	21	0.72
IndAce	42	14449.87	2033	10383	87.73	27	0
IndAe	30	14499.02	2045	10409	136.88	39	0
Ind3Ace	48	14423.01	2027	10369	60.87	21	0
Ind3Ae	36	14439.73	2039	10361	77.59	33	0
Ind3Ac3e	48	14382.58	2027	10328	20.45	21	0.49
ComAce	33	14713.00	2043	10627	350.86	37	0
ComAce2L	44	14435.88	2033	10369	73.74	27	0

3 Latent Phenotypes



Model Fitting Results

	ep	-2ll	df	AIC	chi2	df	p
CholAce	69	14362.14	2006	10350			
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Ind3Ae	36	14439.73	2039	10361	77.59	33	0
Ind3Ac3e	48	14382.58	2027	10328	20.45	21	0.49
ComAce	33	14713.00	2043	10627	350.86	37	0
ComAce2L	44	14435.88	2033	10369	73.74	27	0
ComAce3L	54	14404.09	2024	10356	42.35	18	0

Thank you!

