Multivariate Genetic Analysis

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faculty/hmaes/2016/maes/MultivariateAnalysis

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)
  - multivariate -> Cholesky Decomposition
  - Independent Pathway
  - Common Pathway

Scientific Questions

- Are these measures influenced by the same genes
  - single common A factor?
- Is there more than one A factor
  - 3 factors: overall well being / happy / sad?
- What is the structure of C and E?

- Contribution of A, C, E factors to covariance between traits

Multivariate Saturated Model mulSATc2.R

```
# -----------------------------------------------------------------------------
# Program: mulSATc2.R
#  Author: Hermine Maes
#    Date: 02 25 2016
#
# Twin Multivariate Saturated model to estimate means and (co)variances across multiple groups
# Matrix style model - Raw data - Continuous data
# -------|---------|---------|---------|---------|---------|---------|---------|

# Load Libraries & Options
library(OpenMx)
library(psych)
source("miFunctions2.R")
```

my functions which you can edit as you like

```
# Create Output
filename    <- "mulSATc2"
sink(paste(filename,".Ro",sep=""), append=FALSE, split=TRUE)

# -----------------------------------------------------------------------------
# PREPARE DATA

# Load Data
nl <- read.table ("DHBQ_bs.dat", header=T, na=-999)
describe(nl, skew=F)

# Recode Data for Analysis - Rescale variables to have variances around 1.0
nl$family1  <- nl$gff1/5 ;    nl$family2  <- nl$gff2/5
nl$happy1   <- nl$hap1/4 ;    nl$happy2   <- nl$hap2/4
nl$life1    <- nl$sat1/5 ;    nl$life2    <- nl$sat2/5
nl$anxdep1  <- nl$AD1/4 ;     nl$anxdep2  <- nl$AD2/4
nl$somatic1 <- nl$SOMA1/2 ;   nl$somatic2 <- nl$SOMA2/2
nl$social1  <- nl$SOC1/1.5 ;  nl$social2  <- nl$SOC2/1.5
```

makes optimization easier

Multivariate Saturated Model mulSATc2.R

```
# Select Variables for Analysis
vars      <- c('family','happy','life','anxdep','somatic','social')
nv        <- 6        # number of variables
ntv       <- nv*2     # number of total variables
selVars   <- paste(vars,c(rep(1,nv),rep(2,nv)),sep="")

# Select Random Subset to reduce time to Fit Examples
testData  <- head(nl,n=500)

# Select Data for Analysis
mzData    <- subset(testData, zyg2==1, selVars)
dzData    <- subset(testData, zyg2==2, selVars)

# Generate Descriptive Statistics
round(colMeans(mzData,na.rm=TRUE),4)
round(colMeans(dzData,na.rm=TRUE),4)
round(cov(mzData,use="complete"),4)
round(cov(dzData,use="complete"),4)

# Set Starting Values
svMe      <- c(7,5,5,1,1,1)      # start value for means
svVa      <- 1                   # start value for variances
svVas     <- diag(svVa,ntv,ntv)  # assign start values to diagonal of matrix
lbVa      <- .0001               # start value for lower bounds
lbVas     <- diag(lbVa,ntv,ntv)  # assign lower bounds values to diagonal of matrix
lbVas[lower.tri(lbVas)] <- -10   # lower bounds for below diagonal elements
lbVas[upper.tri(lbVas)] <- NA    # lower bounds for above diagonal elements

# Create Labels
labMeMZ   <- paste("meanMZ",selVars,sep="_")
labMeDZ   <- paste("meanDZ",selVars,sep="_")
labMeZ    <- paste("meanZ",selVars,sep="_")  ….
```

6 variables

Cholesky decomposition to keep covariance matrices positive definite

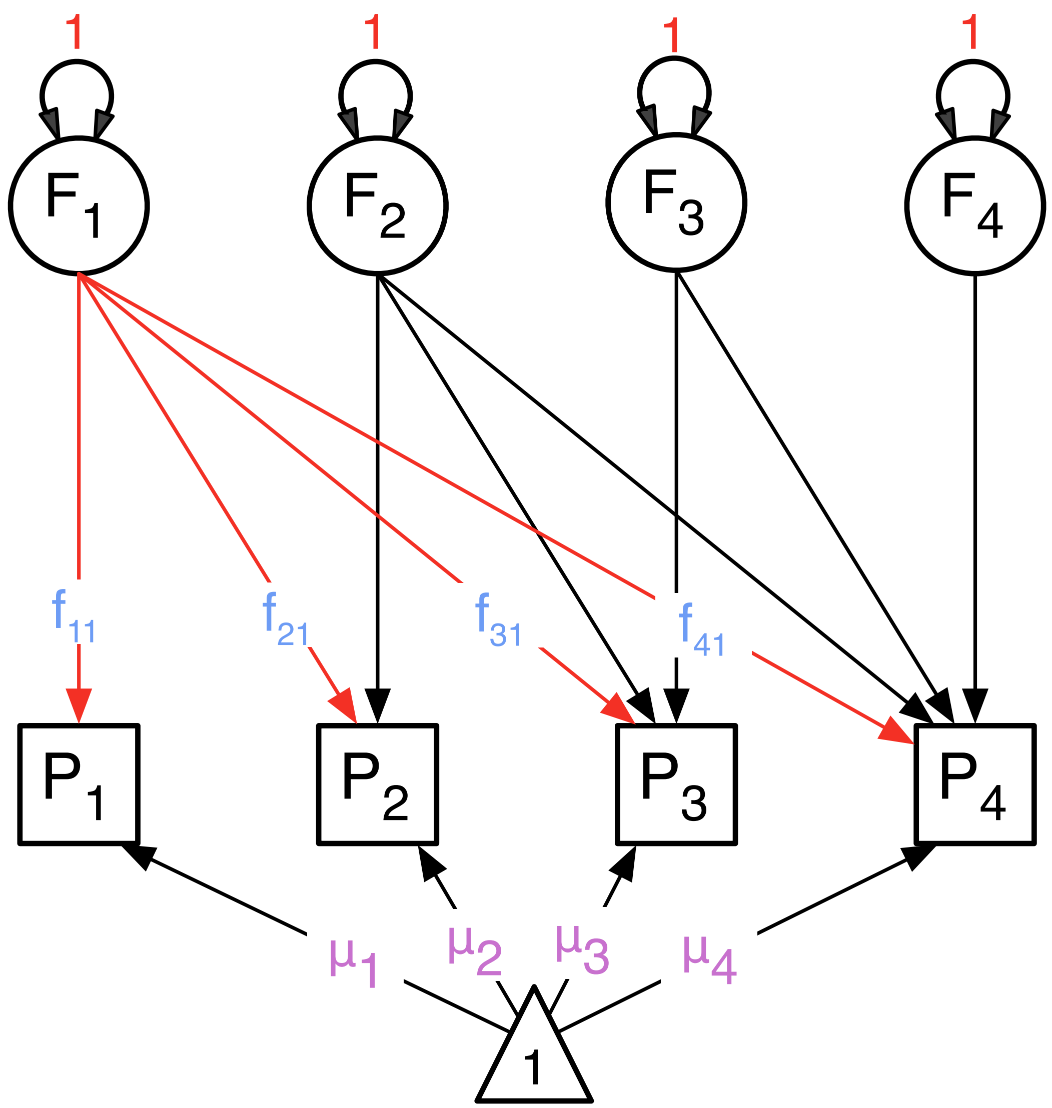
Multivariate Saturated Model mulSATc2.R

```
# ------------------------------------------------------------------------------
# PREPARE MODEL

# Saturated Model
# Create Algebra for expected Mean Matrices
meanMZ    <- mxMatrix( type="Full", nrow=1, ncol=ntv, free=TRUE, values=svMe, labels=labMeMZ, name="meanMZ" )
meanDZ    <- mxMatrix( type="Full", nrow=1, ncol=ntv, free=TRUE, values=svMe, labels=labMeDZ, name="meanDZ" )

# Create Algebra for expected Variance/Covariance Matrices
cholMZ    <- mxMatrix( type="Lower", nrow=ntv, ncol=ntv, free=TRUE, values=svVas, lbound=lbVas, labels=labCvMZ, name="cholMZ" )
cholDZ    <- mxMatrix( type="Lower", nrow=ntv, ncol=ntv, free=TRUE, values=svVas, lbound=lbVas, labels=labCvDZ, name="cholDZ" )
covMZ     <- mxAlgebra( expression=cholMZ %*% t(cholMZ), name="covMZ" )
covDZ     <- mxAlgebra( expression=cholDZ %*% t(cholDZ), name="covDZ" )

# Create Data Objects for Multiple Groups
dataMZ    <- mxData( observed=mzData, type="raw" )
dataDZ    <- mxData( observed=dzData, type="raw" )

# Create Expectation Objects for Multiple Groups
expMZ     <- mxExpectationNormal( covariance="covMZ", means="meanMZ", dimnames=selVars )
expDZ     <- mxExpectationNormal( covariance="covDZ", means="meanDZ", dimnames=selVars )
funML     <- mxFitFunctionML()

# Create Model Objects for Multiple Groups
modelMZ   <- mxModel( "MZ", meanMZ, cholMZ, covMZ, dataMZ, expMZ, funML )
modelDZ   <- mxModel( "DZ", meanDZ, cholDZ, covDZ, dataDZ, expDZ, funML )
multi     <- mxFitFunctionMultigroup( c("MZ","DZ") )

# Create Confidence Interval Objects
ciCov     <- mxCI( c('MZ.covMZ','DZ.covDZ') )
ciMean    <- mxCI( c('MZ.meanMZ','DZ.meanDZ') )
```

lower triangular matrices multiplied by their transpose

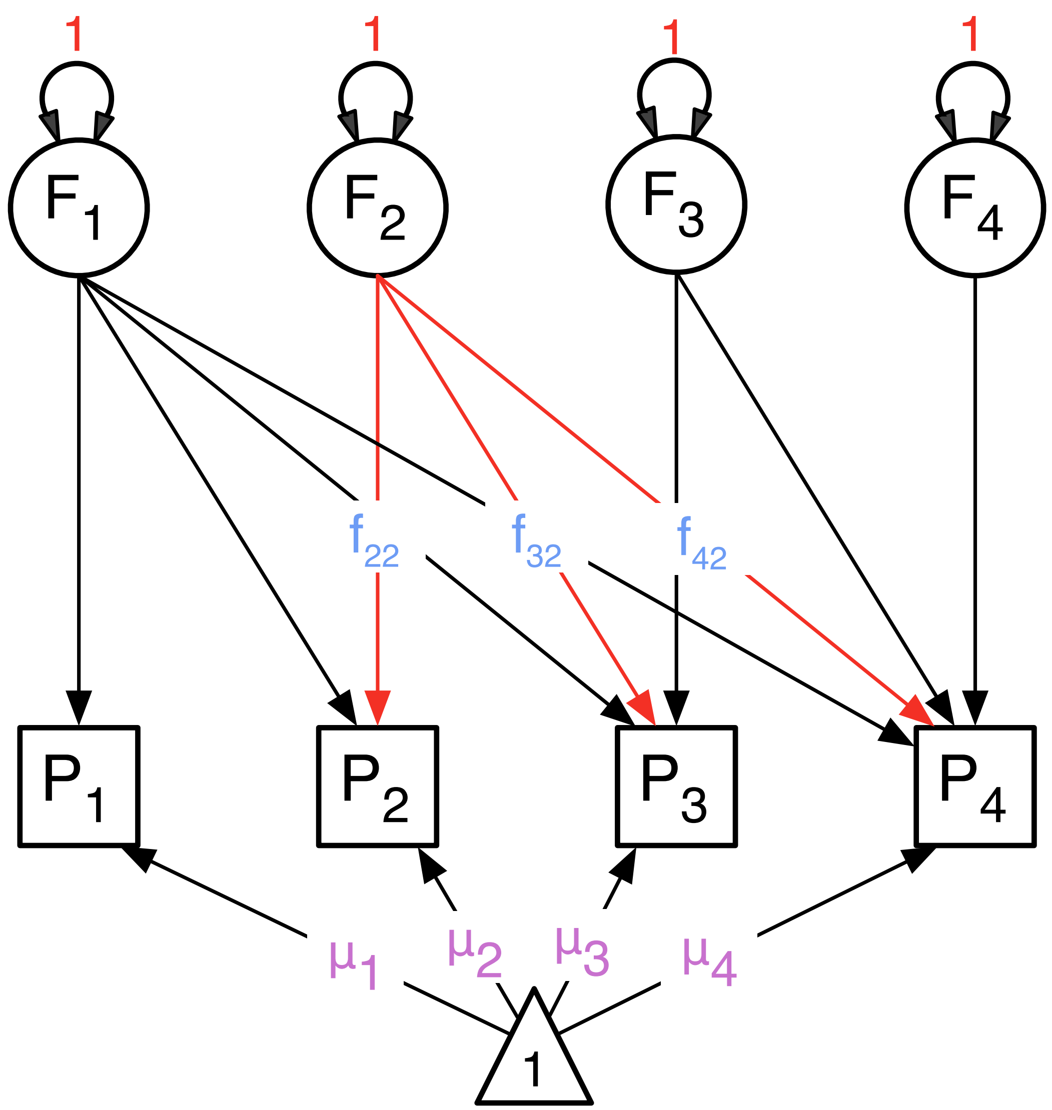
include relevant objects

Cholesky Decomposition



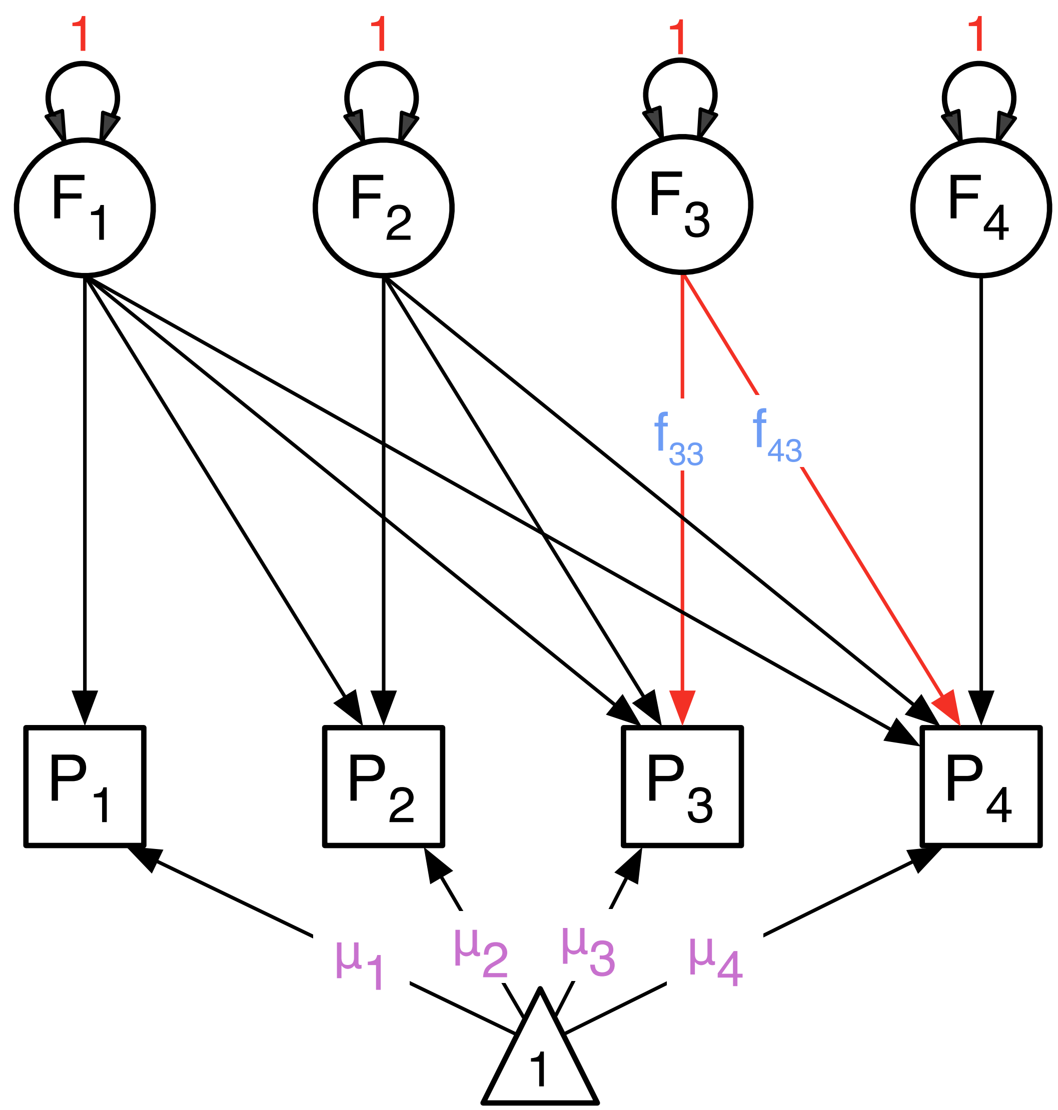
$$
\begin{array}{c} \\ P_1 \\ P_2 \\ P_3 \\ P_4 \end{array}
\begin{array}{c}
\begin{array}{cccc} F_1 & F_2 & F_3 & F_4 \end{array} \\
\left[\begin{array}{cccc}
f_{11} & & & \\
f_{21} & & & \\
f_{31} & & & \\
f_{41} & & &
\end{array}\right]
\end{array}
$$

Second Factor loads on all Variables but First



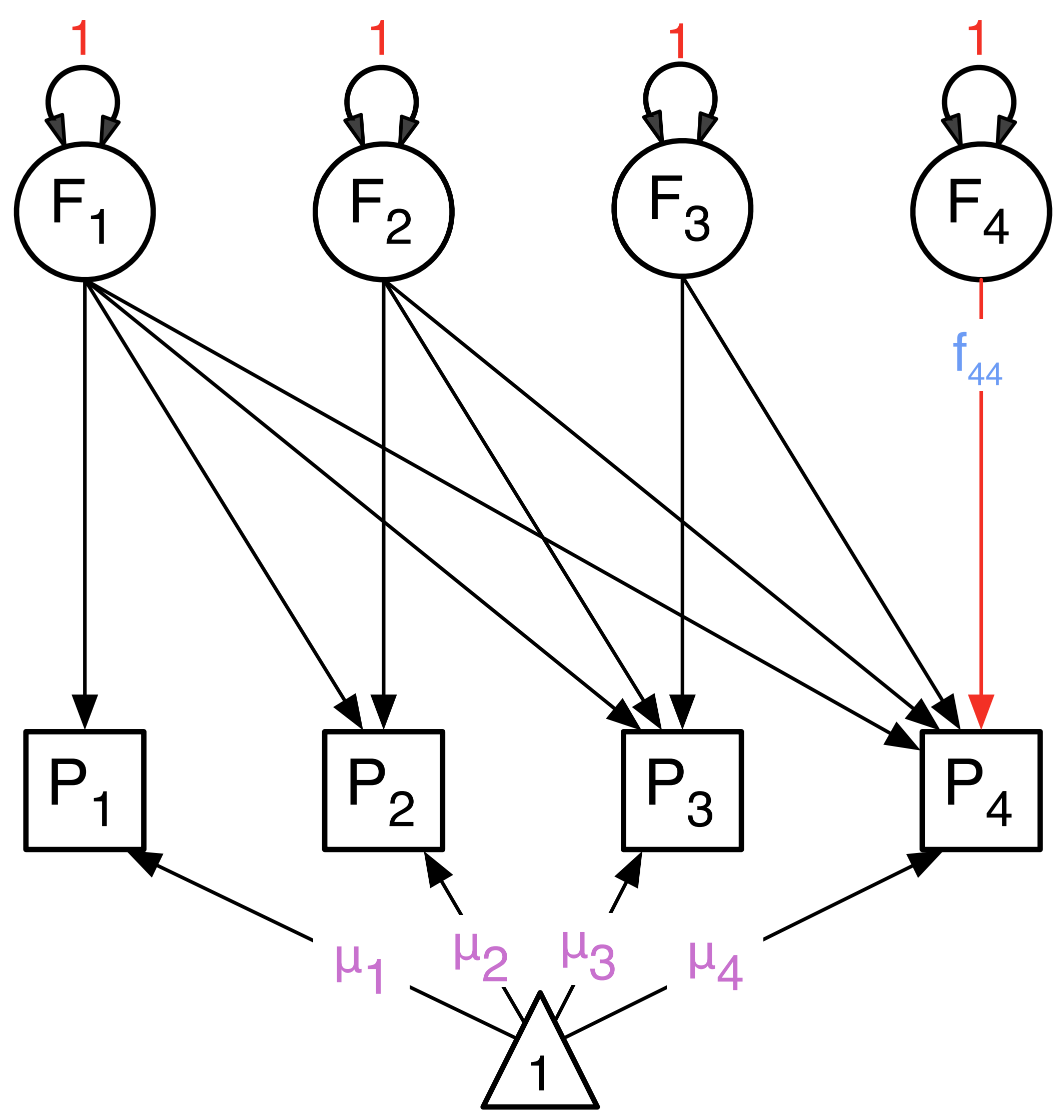
$$
\begin{array}{c c}
 & \begin{array}{cccc} F_1 & F_2 & F_3 & F_4 \end{array} \\
\begin{array}{c} P_1 \\ P_2 \\ P_3 \\ P_4 \end{array} &
\begin{bmatrix}
f_{11} & 0 & & \\
f_{21} & f_{22} & & \\
f_{31} & f_{32} & & \\
f_{41} & f_{42} & &
\end{bmatrix}
\end{array}
$$

Third Factor loads on Variables but Previous



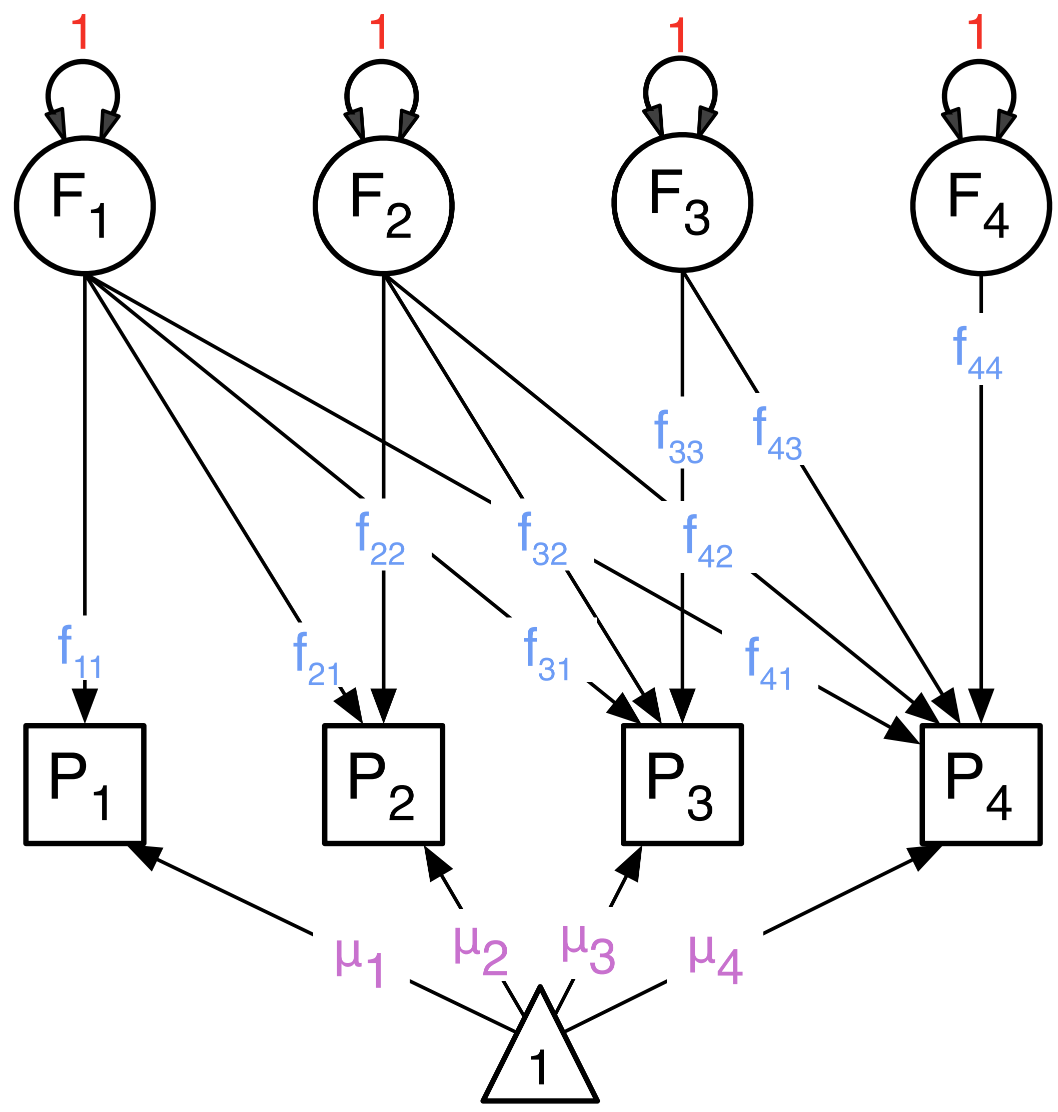
$$
\begin{array}{c|cccc}
 & F_1 & F_2 & F_3 & F_4 \\
\hline
P_1 & f_{11} & 0 & 0 & \\
P_2 & f_{21} & f_{22} & 0 & \\
P_3 & f_{31} & f_{32} & f_{33} & \\
P_4 & f_{41} & f_{42} & f_{43} &
\end{array}
$$

Fourth Factor loads on Variables but Previous



$$
\begin{array}{c c}
 & \begin{array}{cccc} F_1 & F_2 & F_3 & F_4 \end{array} \\
\begin{array}{c} P_1 \\ P_2 \\ P_3 \\ P_4 \end{array} &
\begin{bmatrix}
f_{11} & 0 & 0 & 0 \\
f_{21} & f_{22} & 0 & 0 \\
f_{31} & f_{32} & f_{33} & 0 \\
f_{41} & f_{42} & f_{43} & f_{44}
\end{bmatrix}
\end{array}
$$

Phenotypic



1
1
1
1
F1
F2
F3
F4
f44
f33
f43
f22
f32
f42
f11
f21
f31
f41
P1
P2
P3
P4
μ1
μ2
μ3
μ4
1

Cholesky Decomposition

Estimate covariance matrix, fully saturated

$$\begin{array}{c} \\ P_1 \\ P_2 \\ P_3 \\ P_4 \end{array}
\begin{array}{c} \begin{array}{cccc} F_1 & F_2 & F_3 & F_4 \end{array} \\ \begin{bmatrix} f_{11} & 0 & 0 & 0 \\ f_{21} & f_{22} & 0 & 0 \\ f_{31} & f_{32} & f_{33} & 0 \\ f_{41} & f_{42} & f_{43} & f_{44} \end{bmatrix} \end{array}
*
\begin{array}{c} \\ P_1 \\ P_2 \\ P_3 \\ P_4 \end{array}
\begin{array}{c} \begin{array}{cccc} F_1 & F_2 & F_3 & F_4 \end{array} \\ \begin{bmatrix} f_{11} & f_{21} & f_{31} & f_{41} \\ 0 & f_{22} & f_{32} & f_{42} \\ 0 & 0 & f_{33} & f_{43} \\ 0 & 0 & 0 & f_{44} \end{bmatrix} \end{array}$$

F %*% t(F)

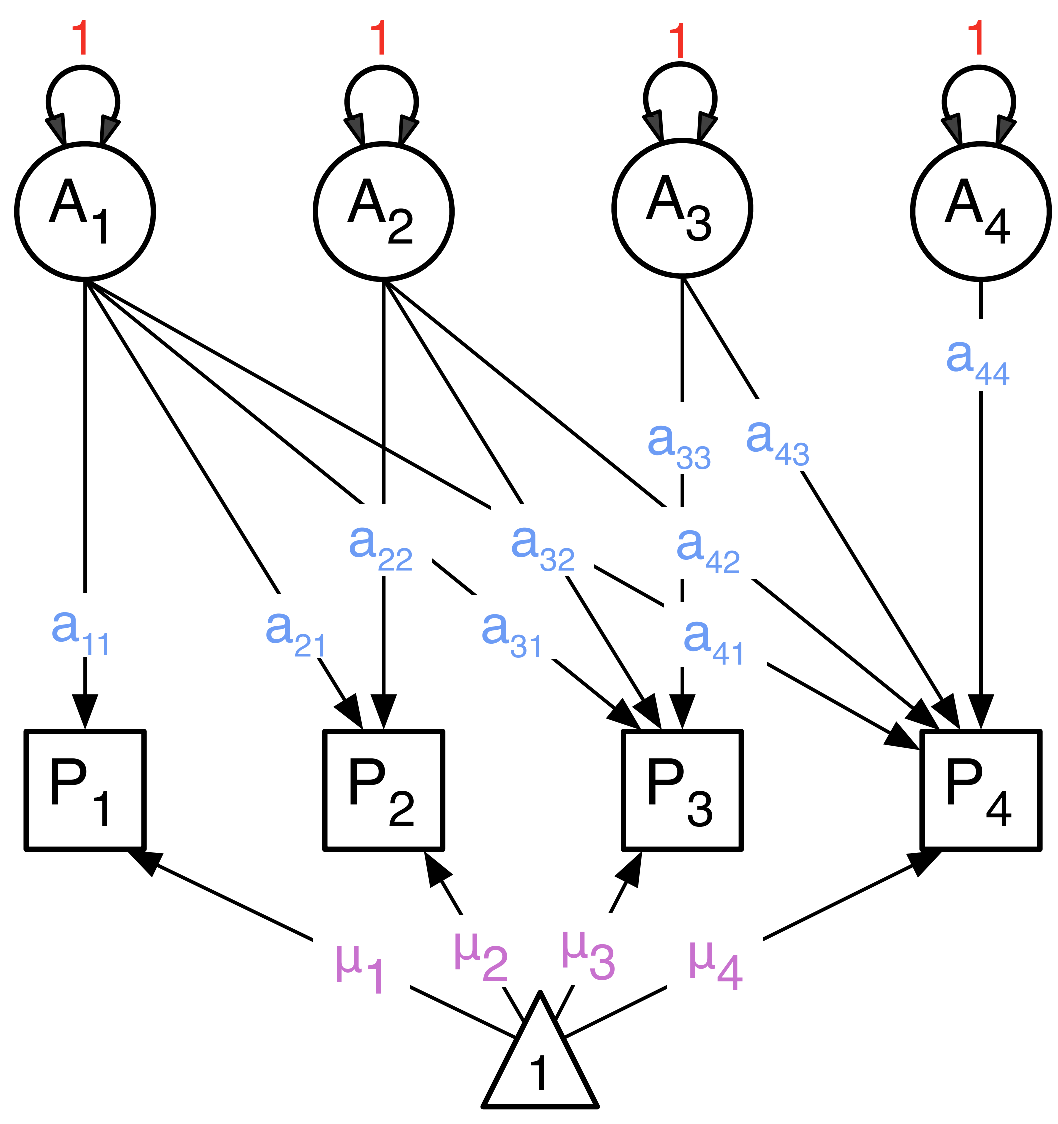
Cholesky Decomposition

‘Saturated’ Phenotypic Model

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

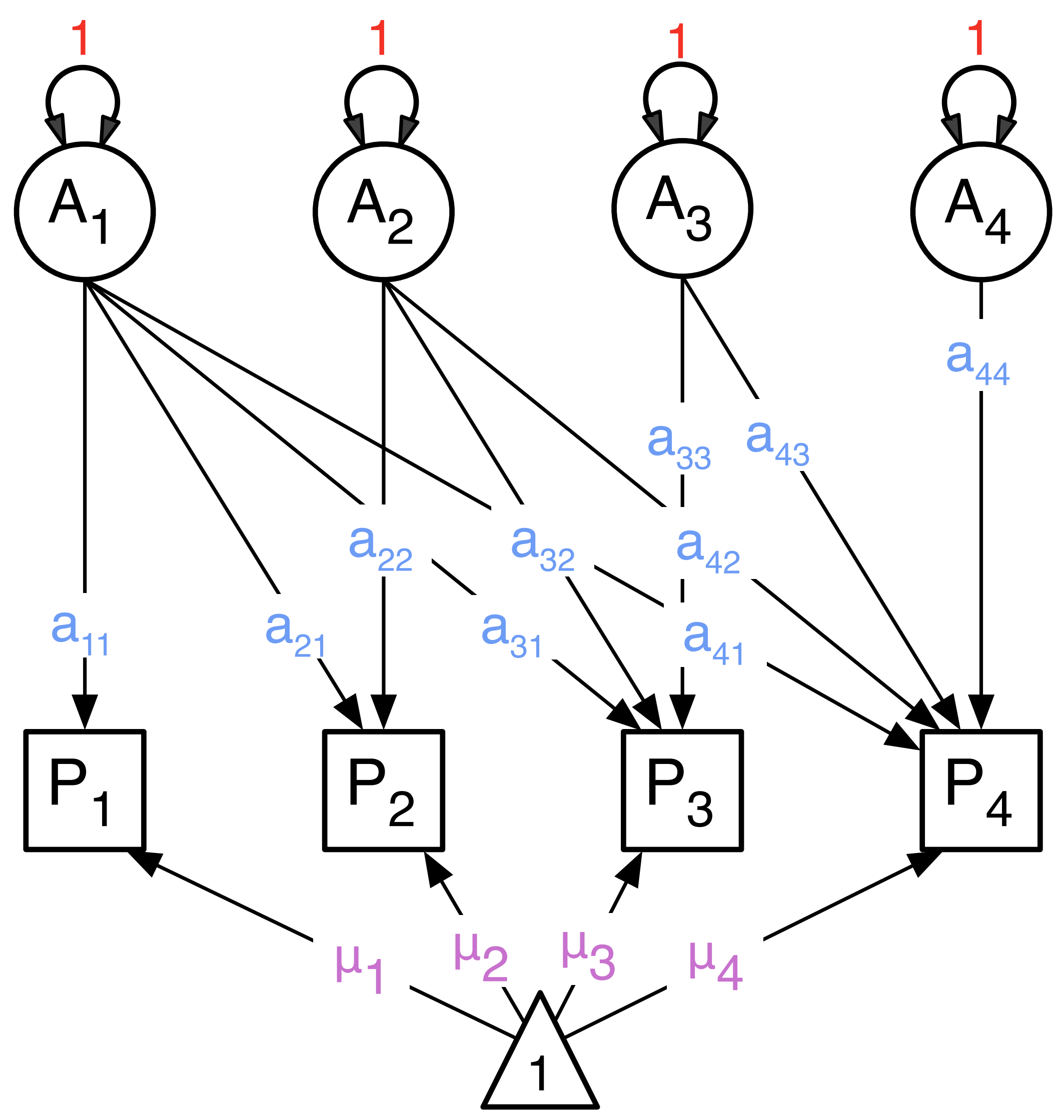
$$\begin{bmatrix} f_{11}^2 & f_{11}f_{21} & f_{11}f_{31} & f_{11}f_{41} \\ f_{21}f_{11} & f_{21}^2 + f_{22}^2 & f_{22}f_{32} + f_{21}f_{31} & f_{22}f_{42} + f_{21}f_{41} \\ f_{31}f_{11} & f_{31}f_{21} + f_{32}f_{22} & f_{31}^2 + f_{32}^2 + f_{33}^2 & f_{33}f_{43} + f_{32}f_{42} + f_{31}f_{41} \\ f_{41}f_{11}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

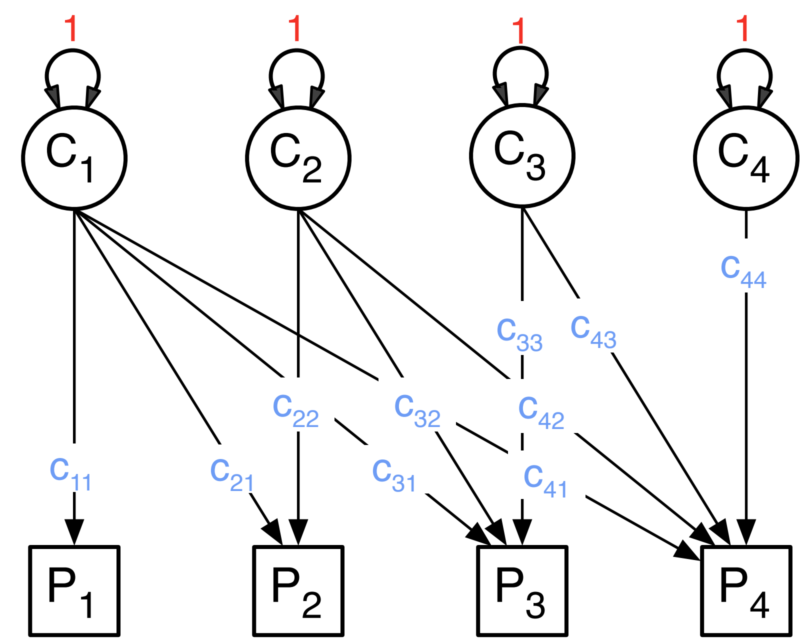
Genetic

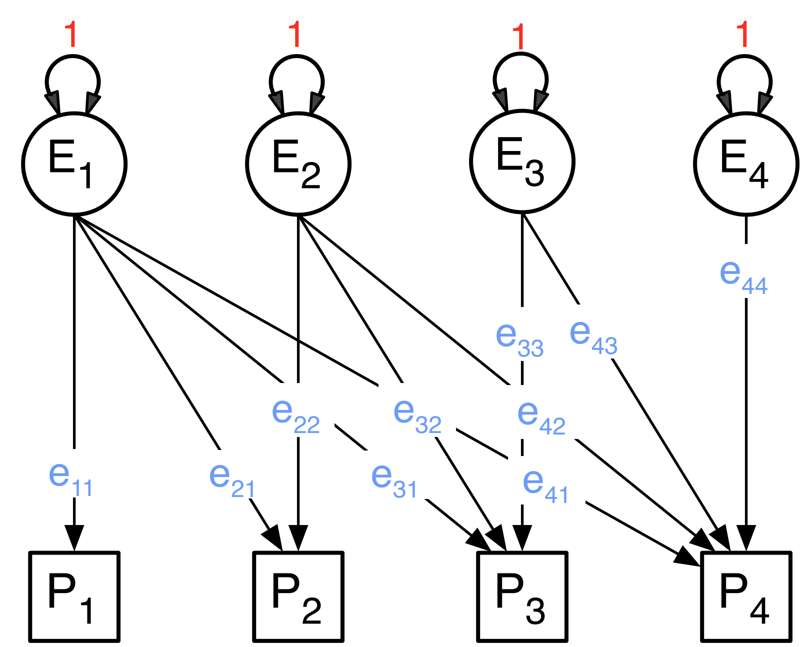


1
1
1
1
A1
A2
A3
A4
a44
a33
a43
a22
a32
a42
a11
a21
a31
a41
P1
P2
P3
P4
μ1
μ2
μ3
μ4
1

& Environmental







Cholesky Decomposition

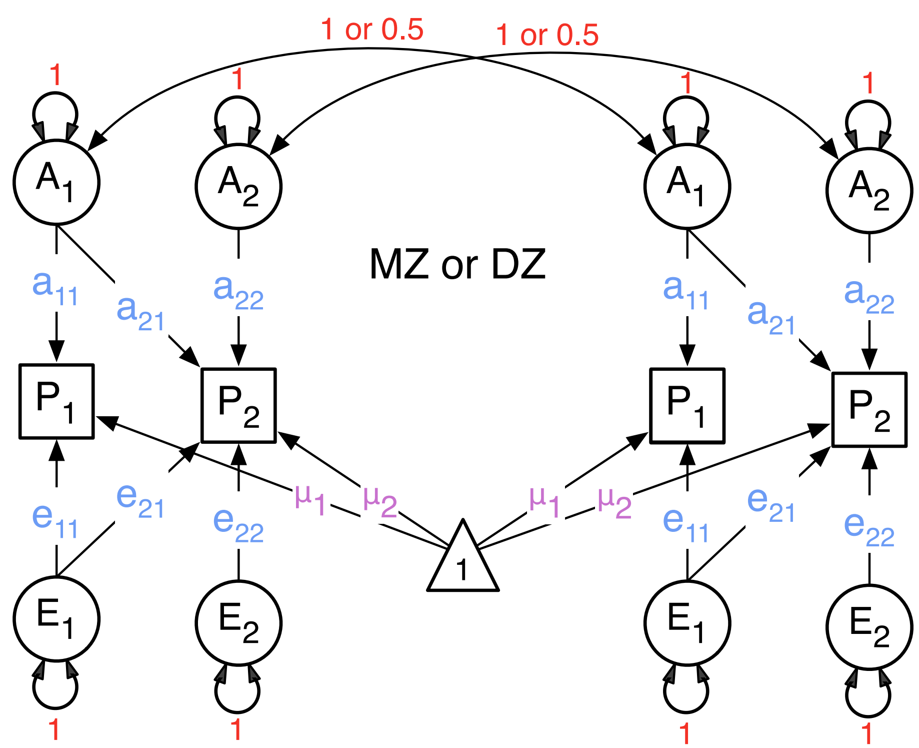
'Saturated' Genetic Model

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

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

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

OpenMx Specification



	X1	Y1	X2	Y2
X1	VX1	CX1Y1	CX1X2	CX1Y2
Y1	CY1X1	VY1	CY1X2	CY1Y2
X2	CX2X1	CX2Y1	VX2	CX2Y2
Y2	CY2X1	CY2Y1	CY2X2	VY2

OpenMx script

Key Data Statements mulACEc2.R

```
# Select Variables for Analysis
vars      <- c('family','happy','life','anxdep','somatic','social')
nv        <- 6        # number of variables
ntv       <- nv*2     # number of total variables
selVars   <- paste(vars,c(rep(1,nv),rep(2,nv)),sep="")

# Select Random Subset to reduce time to Fit Examples
testData  <- head(nl,n=500)

# Select Data for Analysis
mzData    <- subset(testData, zyg2==1, selVars)
dzData    <- subset(testData, zyg2==2, selVars)

# Generate Descriptive Statistics
round(colMeans(mzData,na.rm=TRUE),4)
round(colMeans(dzData,na.rm=TRUE),4)
round(cov(mzData,use="complete"),4)
round(cov(dzData,use="complete"),4)

# Set Starting Values
svMe      <- c(7,5,5,1,1,1)            # start value for means
svPa      <- .4                        # start value for path coefficient
svPaD     <- vech(diag(svPa,nv,nv))    # start values for diagonal of covariance matrix
svPe      <- .8                        # start value for path coefficient for e
svPeD     <- vech(diag(svPe,nv,nv))    # start values for diagonal of covariance matrix
lbPa      <- .0001                     # start value for lower bounds
lbPaD     <- diag(lbPa,nv,nv)          # lower bounds for diagonal of covariance matrix
lbPaD[lower.tri(lbPaD)] <- -10         # lower bounds for below diagonal elements
lbPaD[upper.tri(lbPaD)] <- NA          # lower bounds for above diagonal elements

# Create Labels
labMe     <- paste("mean",vars,sep="_")
```

start values for diagonals only

greater start values for E

lower bounds: .0001 on diagonal,
-10 below diagonal, NA above diagonal

Key Model Statements mulACEc2.R

lower triangular matrices

```
# -----------------------------------------------------------------------------
# PREPARE MODEL

# ACE Model
# Create Algebra for expected Mean Matrices
meanG     <- mxMatrix( type="Full", nrow=1, ncol=ntv, free=TRUE, values=svMe, labels=labMe, name="meanG" )

# Create Matrices for Path Coefficients
pathA     <- mxMatrix( type="Lower", nrow=nv, ncol=nv, free=TRUE, values=svPaD, label=labLower("a",nv), lbound=lbPaD, name="a" )
pathC     <- mxMatrix( type="Lower", nrow=nv, ncol=nv, free=TRUE, values=svPaD, label=labLower("c",nv), lbound=lbPaD, name="c" )
pathE     <- mxMatrix( type="Lower", nrow=nv, ncol=nv, free=TRUE, values=svPeD, label=labLower("e",nv), lbound=lbPaD, name="e" )

# Create Algebra for 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" )

# Create Algebra for expected Variance/Covariance Matrices in MZ & DZ twins
covP      <- mxAlgebra( expression= A+C+E, name="V" )
covMZ     <- mxAlgebra( expression= A+C, name="cMZ" )
covDZ     <- mxAlgebra( expression= 0.5%x%A+ C, name="cDZ" )
expCovMZ  <- mxAlgebra( expression= rbind( cbind(V, cMZ), cbind(t(cMZ), V)), name="expCovMZ" )
expCovDZ  <- mxAlgebra( expression= rbind( cbind(V, cDZ), cbind(t(cDZ), V)), name="expCovDZ" )

# Create Algebra for Standardization
matI      <- mxMatrix( type="Iden", nrow=nv, ncol=nv, name="I")
invSD     <- mxAlgebra( expression=solve(sqrt(I*V)), name="iSD")

# Calculate genetic and environmental correlations
corA      <- mxAlgebra( expression=solve(sqrt(I*A))%&%A, name ="rA" ) #cov2cor()
corC      <- mxAlgebra( expression=solve(sqrt(I*C))%&%C, name ="rC" )
corE      <- mxAlgebra( expression=solve(sqrt(I*E))%&%E, name ="rE" )
```

pathA versus covA

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=svPaD, labels=labLower("a",nv), lbound=lbPaD, name="a" )


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

Model Fitting

mulACEc2.R

```
# Create Data Objects for Multiple Groups
dataMZ     <- mxData( observed=mzData, type="raw" )
dataDZ     <- mxData( observed=dzData, type="raw" )

# Create Expectation Objects for Multiple Groups
expMZ      <- mxExpectationNormal( covariance="expCovMZ", means="meanG", dimnames=selVars )
expDZ      <- mxExpectationNormal( covariance="expCovDZ", means="meanG", dimnames=selVars )
funML      <- mxFitFunctionML()

# Create Model Objects for Multiple Groups
pars       <- list(meanG, matI, invSD,
                   pathA, pathC, pathE, covA, covC, covE, covP, corA, corC, corE)
modelMZ    <- mxModel( name="MZ", pars, covMZ, expCovMZ, dataMZ, expMZ, funML )
modelDZ    <- mxModel( name="DZ", pars, covDZ, expCovDZ, dataDZ, expDZ, funML )
multi      <- mxFitFunctionMultigroup( c("MZ","DZ") )

# Create Algebra for Variance Components
colVC      <- vars
rowVC      <- rep(c('A','C','E','SA','SC','SE'),each=nv)
estVC      <- mxAlgebra( expression=rbind(A,C,E,A/V,C/V,E/V), name="VC", dimnames=list(rowVC,colVC))

# Build Model with Confidence Intervals
modelACE   <- mxModel( "mulACEc", pars, modelMZ, modelDZ, multi, estVC )

# ------------------------------------------------------------------------------
# RUN MODEL

# Run ACE Model
fitACE     <- mxRun( modelACE, intervals=F )
sumACE     <- summary( fitACE )

parameterSpecifications(fitACE)
```

standard expectations

useful check of free parameters

Fitting Submodels

```
# Compare with Saturated Model
#mxCompare( fit, fitACE )
lrtSAT(fitACE,14182.17,5283)

# Print Goodness-of-fit Statistics & Parameter Estimates
fitGofs(fitACE)
fitEst0(fitACE)

# ------------------------------------------------------------------------------
# RUN SUBMODELS

# Run AE model
modelAE    <- mxModel( fitACE, name="mulAEc" )
modelAE    <- omxSetParameters( modelAE, labels=labLower("c",nv), free=FALSE, values=0 )
fitAE      <- mxRun( modelAE, intervals=T )
mxCompare( fitACE, fitAE )
fitGofs(fitAE)

# Run CE model
modelCE    <- mxModel( fitACE, name="mulCEc" )
modelCE    <- omxSetParameters( modelCE, labels=labLower("a",nv), free=FALSE, values=0 )
fitCE      <- mxRun( modelCE, intervals=T )
mxCompare( fitACE, fitCE )
fitGofs(fitCE)

# Run E model
modelE     <- mxModel( fitAE, name="mulEc" )
modelE     <- omxSetParameters( modelE, labels=labLower("a",nv), free=FALSE, values=0 )
fitE       <- mxRun( modelE, intervals=T )
mxCompare( fitAE, fitE )
fitGofs(fitE)
```

Cholesky Specification

```
> parameterSpecifications(fitACE)
model:mulACEc, matrix:meanG
     [,1]          [,2]         [,3]        [,4]          [,5]           [,6]          [,7]          [,8]
[1,] [mean_family] [mean_happy] [mean_life] [mean_anxdep] [mean_somatic] [mean_social] [mean_family] [mean_happy]
     [,9]        [,10]         [,11]          [,12]
[1,] [mean_life] [mean_anxdep] [mean_somatic] [mean_social]

model:mulACEc, 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:mulACEc, 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:mulACEc, 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]
```

FormatOutputMatrices

```r
# Generate List of Parameter Estimates and Derived Quantities using formatOutputMatrices
# ACE  Estimated Path Coefficients
matACEepaths <- c("a","c","e","iSD")
labACEepaths <- c("PathA","PathC","PathE","iSD")
formatOutputMatrices(fitACE, matACEepaths, labACEepaths, vars,4)
```

standardized path coefficients

```r
# ACE  Standardized Path Coefficients (pre-multiplied by inverse of standard deviations)
matACEpaths <- c("iSD %*% a","iSD %*% c","iSD %*% e")
labACEpaths <- c("stPathA","stPathC","stPathE")
formatOutputMatrices(fitACE, matACEpaths, labACEpaths, vars,4)
```

squared

```r
# ACE Squared Standardized Path Coefficients
matACEpath2 <- c("(iSD%*% a)*(iSD%*% a)","(iSD%*% c)*(iSD%*% c)","(iSD%*% e)*(iSD%*% e)")
labACEpath2 <- c("stPathA^2","stPathC^2","stPathE^2")
formatOutputMatrices(fitACE, matACEpath2, labACEpath2, vars,4)

# ACE Covariance Matrices & Proportions of Variance Matrices
matACEcov   <- c("A","C","E","V","A/V","C/V","E/V")
labACEcov   <- c("covA","covC","covE","Var","stCovA","stCovC","stCovE")
formatOutputMatrices(fitACE, matACEcov, labACEcov, vars,4)
```

proportions of variance & covariance

```r
# ACE Correlation Matrices
matACEcor   <- c("solve(sqrt(I*A)) %&% A","solve(sqrt(I*C)) %&% C","solve(sqrt(I*E)) %&% E")
labACEcor   <- c("corA","corC","corE")
formatOutputMatrices(fitACE, matACEcor, labACEcor, vars, 4)
```

correlations

ACE Path Coefficients & Standardized Path Coefficients (pre-multiplied by inverse of standard deviations)

```
> formatOutputMatrices(fitACE, matACEepaths, labACEepaths, vars,4)
[1] "Matrix a"
        PathA1  PathA2  PathA3  PathA4  PathA5 PathA6
family  0.6186  0.0000  0.0000  0.0000  0.0000 0.0000
happy   0.4252  0.4489  0.0000  0.0000  0.0000 0.0000
life    0.3618  0.2540  0.1892  0.0000  0.0000 0.0000
anxdep  -0.2639 -0.4421 -0.0299 0.1402  0.0000 0.0000
somatic -0.3021 -0.3193 -0.1527 0.3753  0.1336 0.0000
social  -0.2192 -0.2609 0.5169  -0.0065 0.1356 0.0001

[1] "Matrix c"
        PathC1  PathC2  PathC3  PathC4 PathC5 PathC6
family  0.4277  0.0000  0.0000  0.0000 0.0000 0.0000
happy   0.2889  0.1701  0.0000  0.0000 0.0000 0.0000
life    0.3691  0.1210  0.1583  0.0000 0.0000 0.0000
anxdep  -0.3261 -0.0680 -0.1731 0.3906 0.0000 0.0000
somatic -0.1777 0.0612  -0.5361 0.0699 0.0001 0.0000
social  -0.3123 -0.0377 -0.2629 0.2824 0.0001 0.0001

[1] "Matrix e"
        PathE1  PathE2  PathE3  PathE4 PathE5 PathE6
family  0.6738  0.0000  0.0000  0.0000 0.0000 0.0000
happy   0.1451  0.8594  0.0000  0.0000 0.0000 0.0000
life    0.0925  0.5515  0.6224  0.0000 0.0000 0.0000
anxdep  -0.0449 -0.3008 -0.0691 0.6888 0.0000 0.0000
somatic -0.0081 -0.0538 0.0304  0.3324 0.7914 0.0000
social  -0.0477 -0.0781 -0.1098 0.1850 0.0524 0.8036

[1] "Matrix iSD"
        iSD1   iSD2   iSD3   iSD4   iSD5   iSD6
family  0.9904 0.0000 0.0000 0.0000 0.0000 0.0000
happy   0.0000 0.8929 0.0000 0.0000 0.0000 0.0000
life    0.0000 0.0000 0.9503 0.0000 0.0000 0.0000
anxdep  0.0000 0.0000 0.0000 0.9322 0.0000 0.0000
somatic 0.0000 0.0000 0.0000 0.0000 0.8323 0.0000
social  0.0000 0.0000 0.0000 0.0000 0.0000 0.8598
```

```
[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   0.4008   0.0000   0.0000   0.0000   0.0000
life    0.3438   0.2414   0.1798   0.0000   0.0000   0.0000
anxdep  -0.2460  -0.4121  -0.0279  0.1307   0.0000   0.0000
somatic -0.2514  -0.2658  -0.1271  0.3124   0.1112   0.0000
social  -0.1885  -0.2244  0.4444   -0.0056  0.1166   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  -0.0633  -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
```

ACE Squared Standardized Path Coefficients

```
> formatOutputMatrices(fitACE, matACEpath2, labACEpath2, vars,4)
[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     0.0161     0.0976     0.0124     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     0.4339     0.0000
social  0.0017     0.0045     0.0089     0.0253     0.0020     0.4774
```

ACE Covariance Matrices & Proportions of Variance Matrices

```
> formatOutputMatrices(fitACE, matACEcov, labACEcov, vars,4)
[1] "Matrix A"
        covA1   covA2   covA3   covA4   covA5   covA6
family  0.3826  0.2630  0.2238  -0.1632 -0.1868 -0.1356
happy   0.2630  0.3823  0.2678  -0.3106 -0.2718 -0.2104
life    0.2238  0.2678  0.2312  -0.2134 -0.2193 -0.0478
anxdep  -0.1632 -0.3106 -0.2134 0.2856  0.2780  0.1568
somatic -0.1868 -0.2718 -0.2193 0.2780  0.3752  0.0863
social  -0.1356 -0.2104 -0.0478 0.1568  0.0863  0.4018

[1] "Matrix C"
        covC1   covC2   covC3   covC4   covC5   covC6
family  0.1829  0.1236  0.1579  -0.1395 -0.0760 -0.1336
happy   0.1236  0.1124  0.1272  -0.1058 -0.0409 -0.0967
life    0.1579  0.1272  0.1760  -0.1560 -0.1431 -0.1615
anxdep  -0.1395 -0.1058 -0.1560 0.2935  0.1739  0.2602
somatic -0.0760 -0.0409 -0.1431 0.1739  0.3277  0.2139
social  -0.1336 -0.0967 -0.1615 0.2602  0.2139  0.2478

[1] "Matrix E"
        covE1   covE2   covE3   covE4   covE5   covE6
family  0.4540  0.0978  0.0623  -0.0303 -0.0054 -0.0321
happy   0.0978  0.7596  0.4874  -0.2650 -0.0474 -0.0740
life    0.0623  0.4874  0.7001  -0.2130 -0.0115 -0.1158
anxdep  -0.0303 -0.2650 -0.2130 0.5718  0.2434  0.1606
somatic -0.0054 -0.0474 -0.0115 0.2434  0.7406  0.1042
social  -0.0321 -0.0740 -0.1158 0.1606  0.1042  0.7032

[1] "Matrix V"
        Var1    Var2    Var3    Var4    Var5    Var6
family  1.0195  0.4843  0.4440  -0.3329 -0.2683 -0.3013
happy   0.4843  1.2543  0.8824  -0.6814 -0.3601 -0.3811
life    0.4440  0.8824  1.1073  -0.5824 -0.3738 -0.3251
anxdep  -0.3329 -0.6814 -0.5824 1.1508  0.6953  0.5777
somatic -0.2683 -0.3601 -0.3738 0.6953  1.4435  0.4043
social  -0.3013 -0.3811 -0.3251 0.5777  0.4043  1.3528
```

```
[1] "Matrix A/V"
        stCovA1 stCovA2 stCovA3 stCovA4 stCovA5 stCovA6
family  0.3753  0.5430  0.5041  0.4902  0.6965  0.4501
happy   0.5430  0.3048  0.3035  0.4559  0.7547  0.5520
life    0.5041  0.3035  0.2088  0.3664  0.5865  0.1471
anxdep  0.4902  0.4559  0.3664  0.2482  0.3999  0.2715
somatic 0.6965  0.7547  0.5865  0.3999  0.2599  0.2135
social  0.4501  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  0.2833  0.4433
happy   0.2551  0.0896  0.1442  0.1552  0.1136  0.2536
life    0.3556  0.1442  0.1589  0.2678  0.3827  0.4967
anxdep  0.4188  0.1552  0.2678  0.2550  0.2501  0.4504
somatic 0.2833  0.1136  0.3827  0.2501  0.2270  0.5289
social  0.4433  0.2536  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  0.1316  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  0.1316  0.0308  0.3501  0.5131  0.2576
social  0.1067  0.1943  0.3562  0.2781  0.2576  0.5198
```

ACE Correlation Matrices

```
> formatOutputMatrices(fitACE, matACEcor, labACEcor,
vars, 4)
[1] "Matrix solve(sqrt(I*A)) %&% A"
        corA1   corA2   corA3   corA4   corA5   corA6
family  1.0000  0.6877  0.7524  -0.4937 -0.4931 -0.3459
happy   0.6877  1.0000  0.9010  -0.9401 -0.7176 -0.5367
life    0.7524  0.9010  1.0000  -0.8305 -0.7445 -0.1569
anxdep  -0.4937 -0.9401 -0.8305 1.0000  0.8493  0.4630
somatic -0.4931 -0.7176 -0.7445 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  0.8617  0.8800  -0.6019 -0.3104 -0.6274
happy   0.8617  1.0000  0.9046  -0.5823 -0.2132 -0.5791
life    0.8800  0.9046  1.0000  -0.6864 -0.5958 -0.7733
anxdep  -0.6019 -0.5823 -0.6864 1.0000  0.5607  0.9648
somatic -0.3104 -0.2132 -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
```

Compare Cholesky to Saturated Model

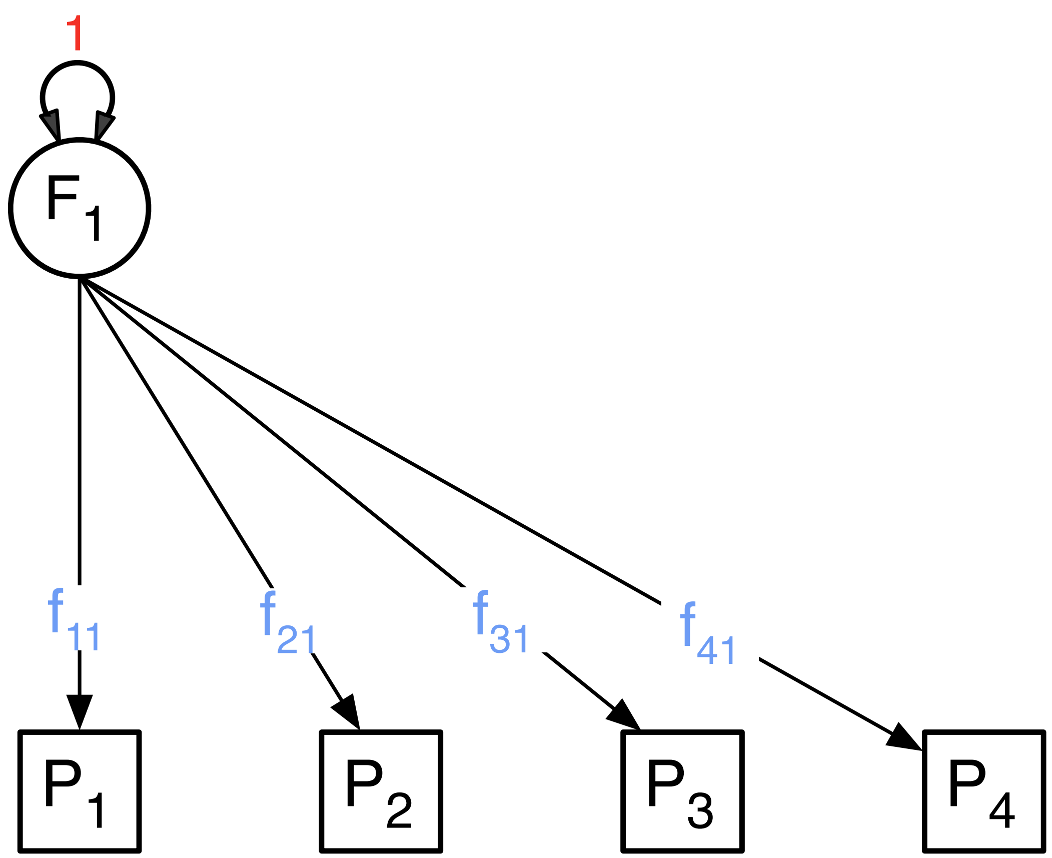
```
> mxCompare( fit, fitACE )
```

base	ep	minus2LL	df	AIC	diffLL	diffdf	p
mulSATc	180	14182.171	5283	3616.1715	NA	NA	NA
mulACEc	69	14362.137	5394	3574.1373	179.96583	111	3.7835027e-05

Theoretical Models

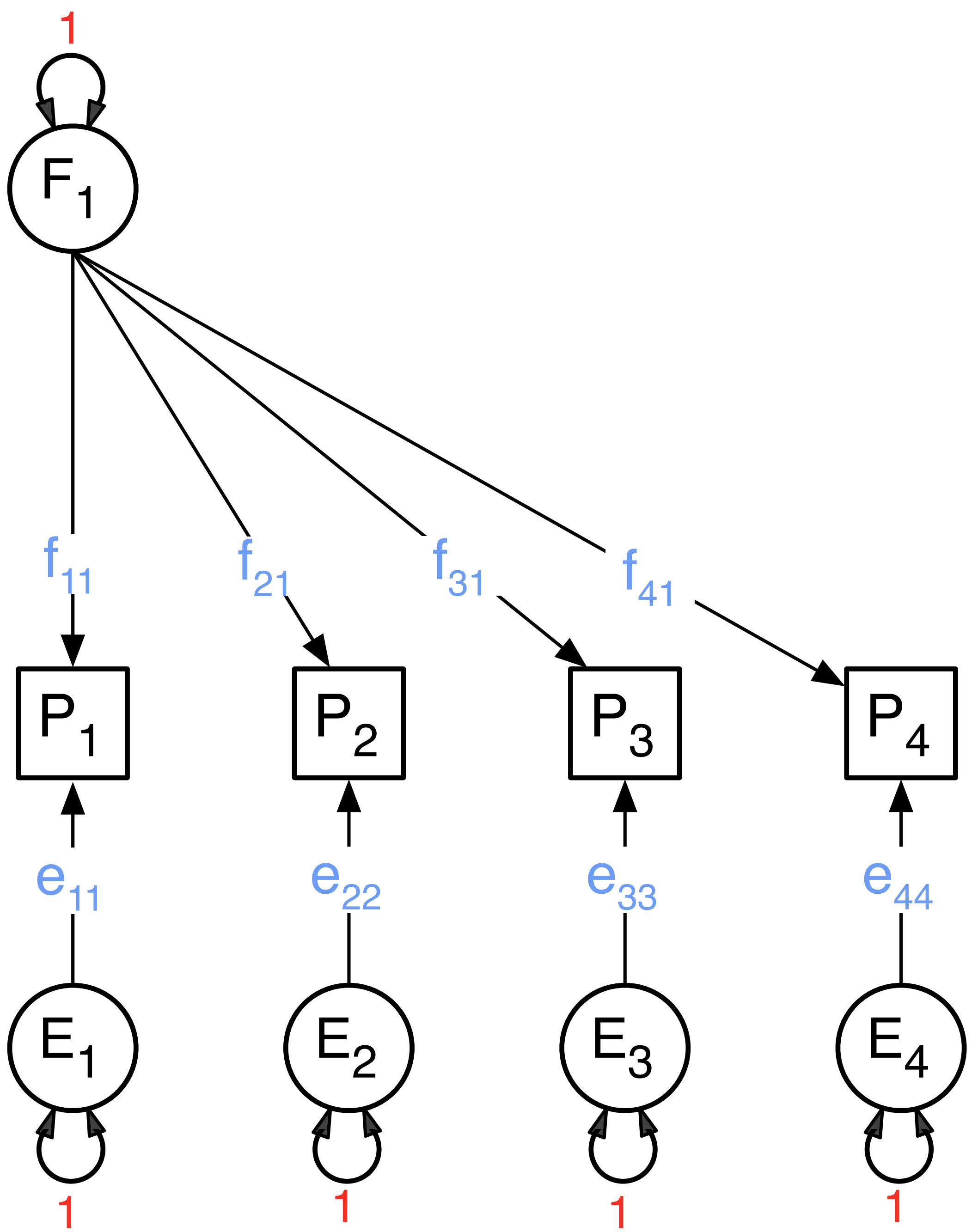
- Independent Pathway
- Common Pathway

Common Factor



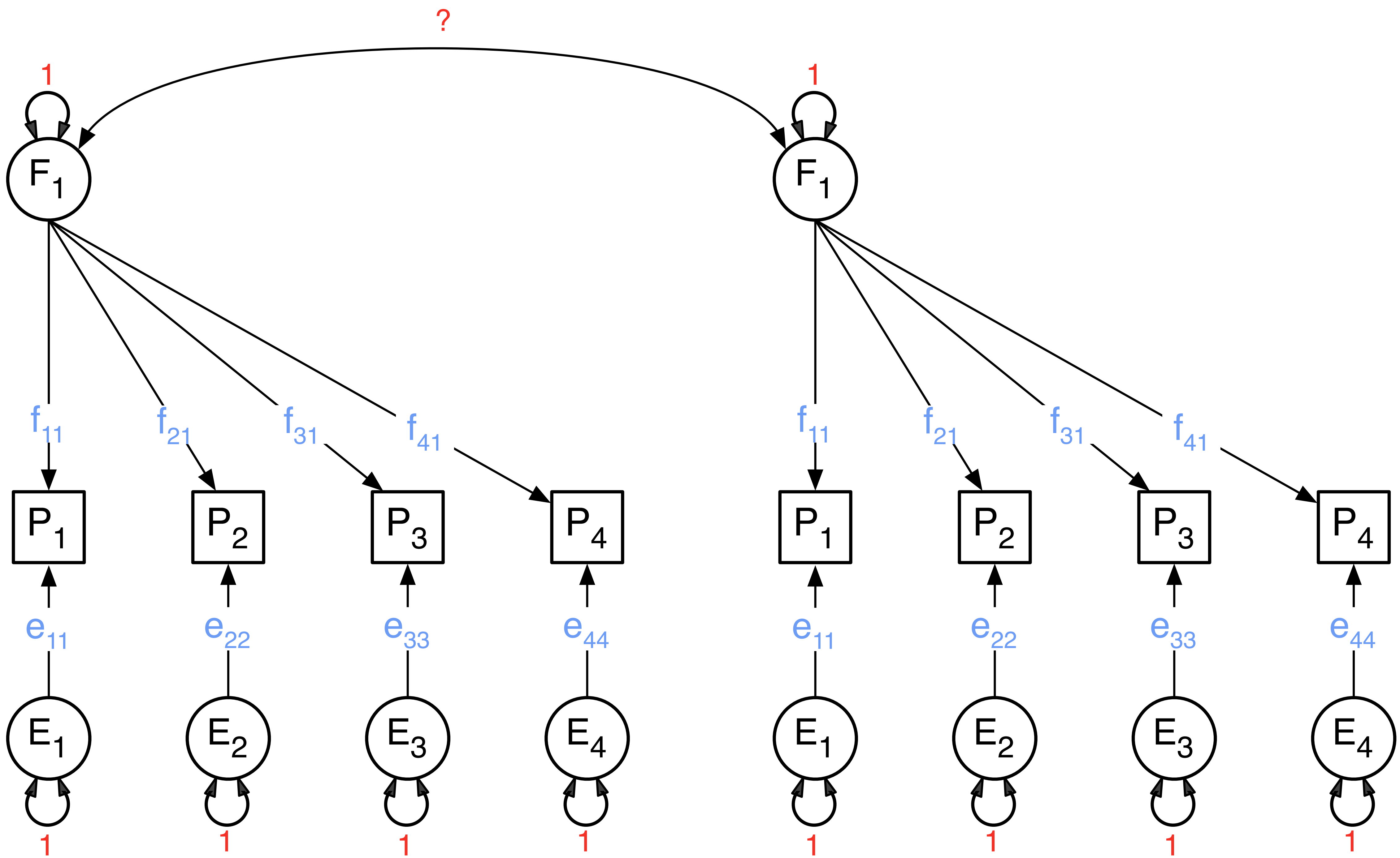
$$\begin{array}{cc} & F_1 \\ \begin{array}{c} P_1 \\ P_2 \\ P_3 \\ P_4 \end{array} & \begin{bmatrix} f_{11} \\ f_{21} \\ f_{31} \\ f_{41} \end{bmatrix} \end{array}$$

Residuals



$$
\begin{array}{c}
P_1 \\ P_2 \\ P_3 \\ P_4
\end{array}
\begin{bmatrix}
e_{11} & 0 & 0 & 0 \\
0 & e_{22} & 0 & 0 \\
0 & 0 & e_{33} & 0 \\
0 & 0 & 0 & e_{44}
\end{bmatrix}
$$

What about Twins

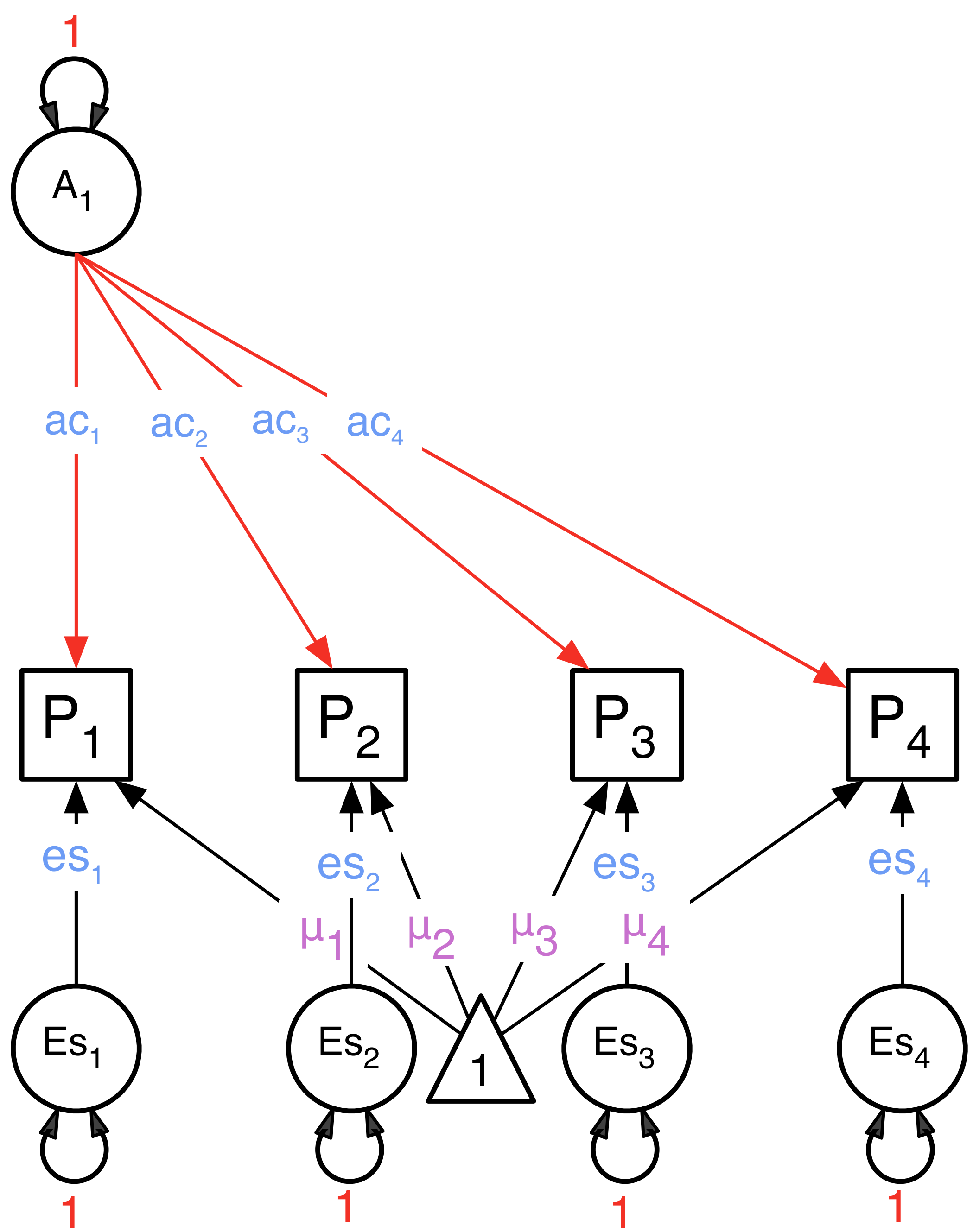


Common Factors
Specifics

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

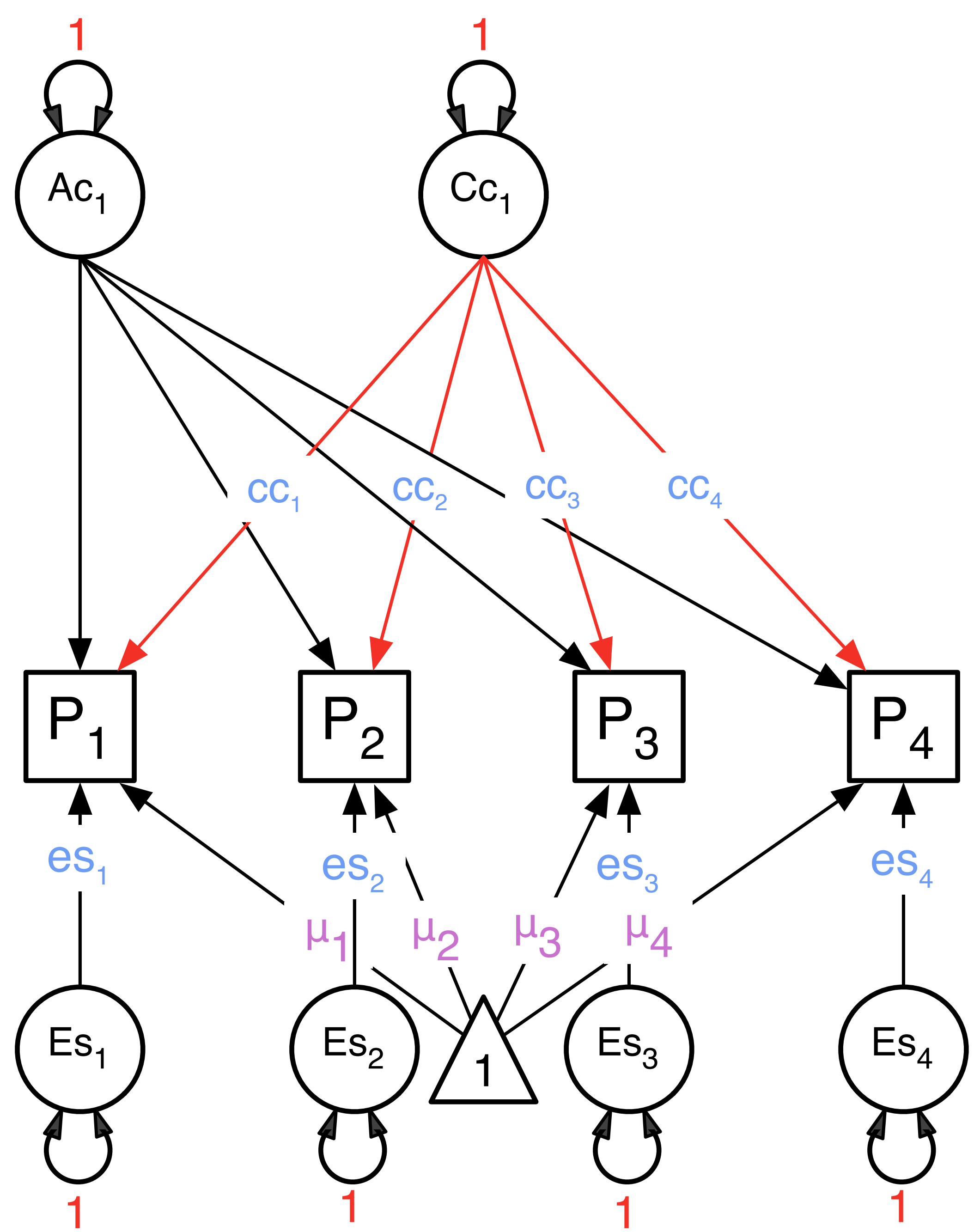
$$\begin{bmatrix} e_{11} & 0 & 0 & 0 \\ 0 & e_{22} & 0 & 0 \\ 0 & 0 & e_{33} & 0 \\ 0 & 0 & 0 & e_{44} \end{bmatrix} \times \begin{bmatrix} e_{11} & 0 & 0 & 0 \\ 0 & e_{22} & 0 & 0 \\ 0 & 0 & e_{33} & 0 \\ 0 & 0 & 0 & e_{44} \end{bmatrix} = \begin{bmatrix} e_{11}^2 & 0 & 0 & 0 \\ 0 & e_{22}^2 & 0 & 0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

Common A Factor



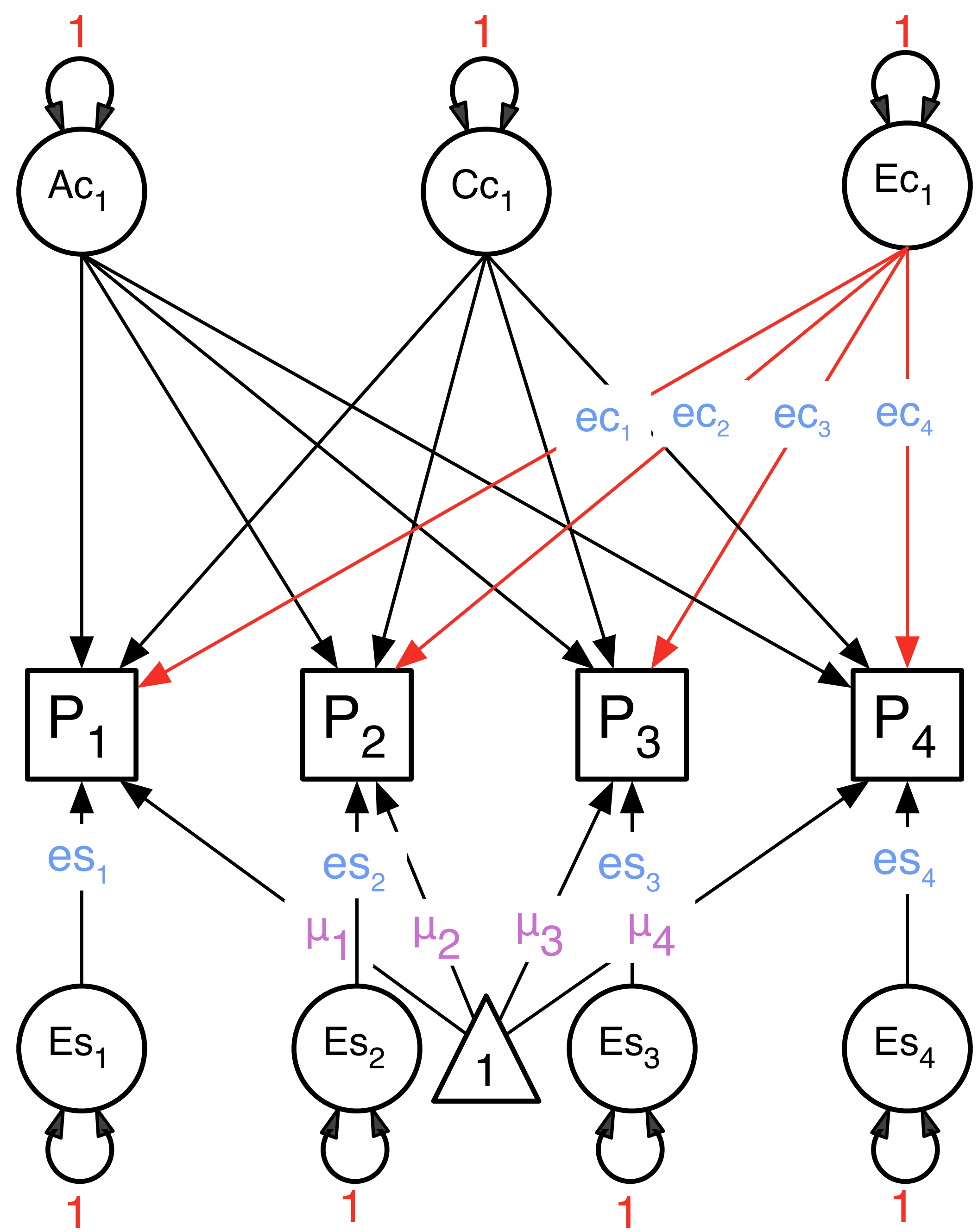
$$
\begin{array}{cc}
 & A_1 \\
\begin{matrix} P_1 \\ P_2 \\ P_3 \\ P_4 \end{matrix} & \begin{bmatrix} ac_{11} \\ ac_{21} \\ ac_{31} \\ ac_{41} \end{bmatrix}
\end{array}
$$

Common C Factor



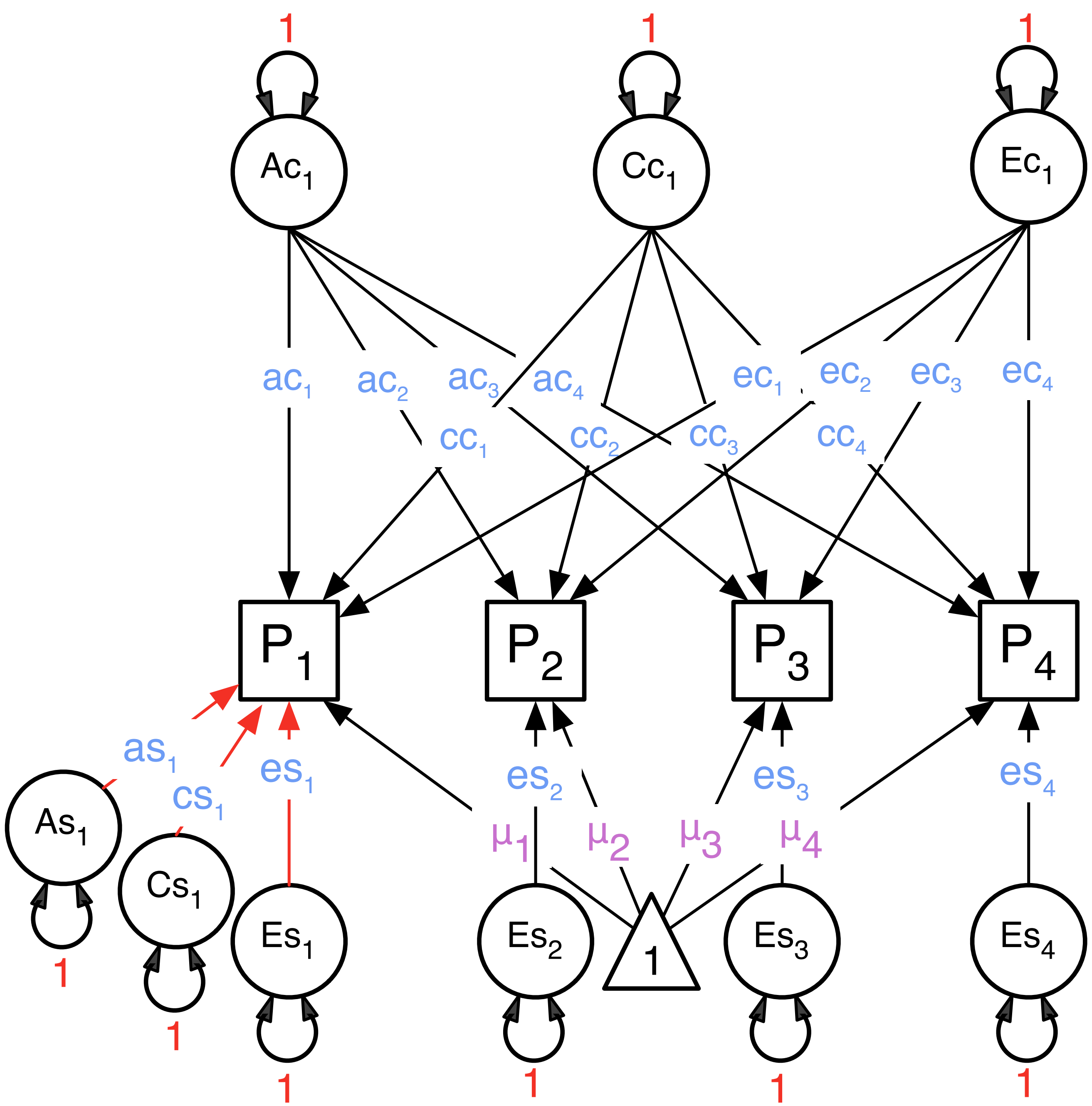
$$\begin{array}{c c} & C_1 \\ \begin{array}{c} P_1 \\ P_2 \\ P_3 \\ P_4 \end{array} & \begin{bmatrix} cc_{11} \\ cc_{21} \\ cc_{31} \\ cc_{41} \end{bmatrix} \end{array}$$

Common E Factor



$$
\begin{array}{c c}
 & E_1 \\
\begin{array}{c} P_1 \\ P_2 \\ P_3 \\ P_4 \end{array} & \begin{bmatrix} ec_{11} \\ ec_{21} \\ ec_{31} \\ ec_{41} \end{bmatrix}
\end{array}
$$

ACE Specifics



$$
\begin{array}{c}
P_1 \\ P_2 \\ P_3 \\ P_4
\end{array}
\begin{bmatrix}
es_{11} & 0 & 0 & 0 \\
0 & es_{22} & 0 & 0 \\
0 & 0 & es_{33} & 0 \\
0 & 0 & 0 & es_{44}
\end{bmatrix}
$$

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

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

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" )
```

Total A Covariance

```
ac %*% t(ac)
```

$$\begin{bmatrix} ac_{11}^2 & ac_{11}ac_{21} & ac_{11}ac_{31} & ac_{11}ac_{41} \\ ac_{21}ac_{11} & ac_{21}^2 & ac_{21}ac_{31} & ac_{21}ac_{41} \\ ac_{31}ac_{11} & ac_{31}ac_{21} & ac_{31}^2 & ac_{31}ac_{41} \\ ac_{41}ac_{11} & ac_{41}ac_{21} & ac_{41}ac_{31} & ac_{41}^2 \end{bmatrix} + \begin{bmatrix} as_{11}^2 & 0 & 0 & 0 \\ 0 & as_{22}^2 & 0 & 0 \\ 0 & 0 & as_{33}^2 & 0 \\ 0 & 0 & 0 & as_{44}^2 \end{bmatrix} = \begin{bmatrix} ac_{11}^2 + as_{11}^2 & ac_{11}ac_{21} & ac_{11}ac_{31} & ac_{11}ac_{41} \\ ac_{21}ac_{11} & ac_{21}^2 + as_{22}^2 & ac_{21}ac_{31} & ac_{21}ac_{41} \\ ac_{31}ac_{11} & ac_{31}ac_{21} & ac_{31}^2 + as_{33}^2 & ac_{31}ac_{41} \\ ac_{41}ac_{11} & ac_{41}ac_{21} & ac_{41}ac_{31} & ac_{41}^2 + as_{44}^2 \end{bmatrix}$$

```
as %*% t(as)
```

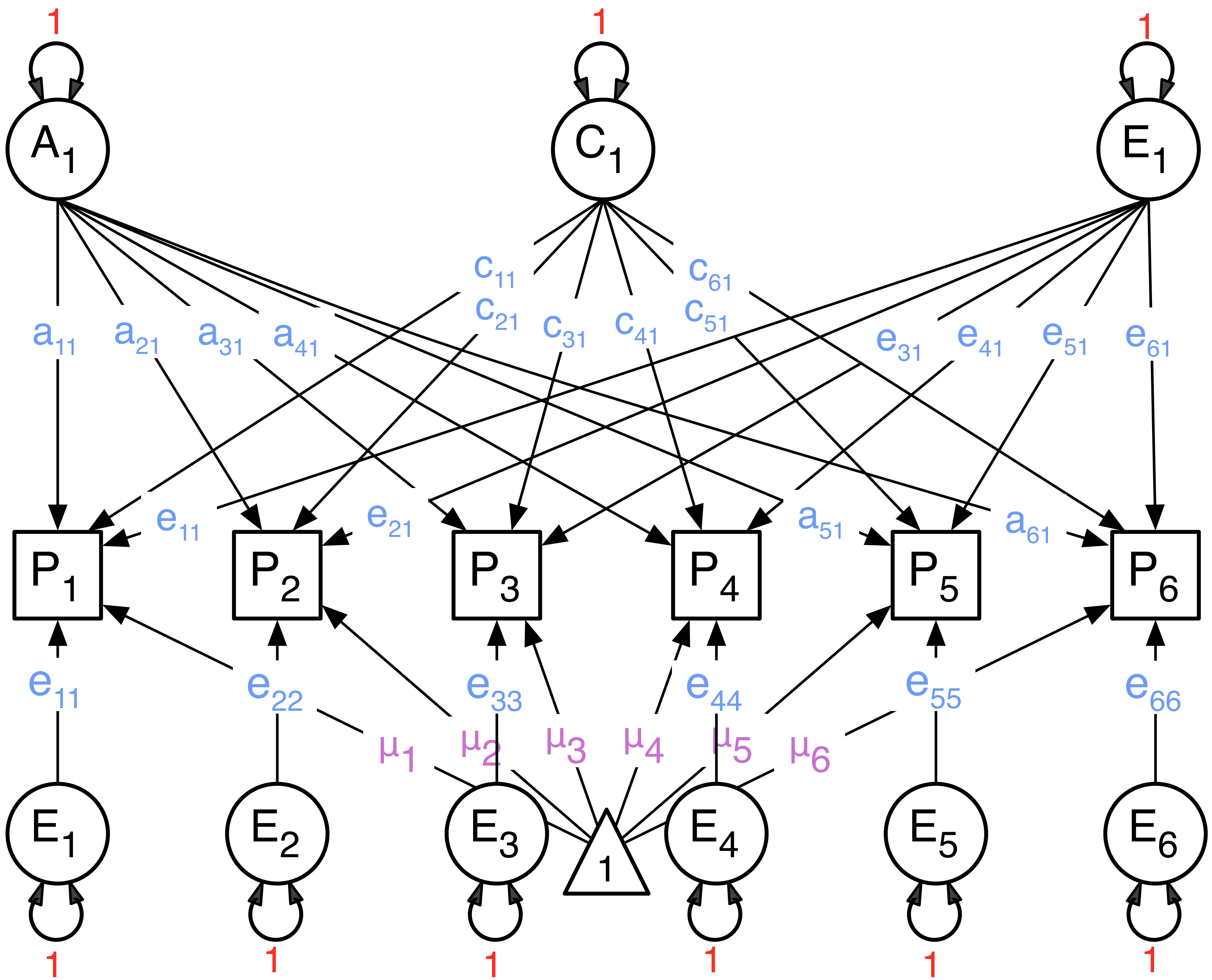
```
object: CovA
matrix name:A
```

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

Independent Pathway Model

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

IP Model



1
1
1
A_1
C_1
E_1
c_{11}
c_{61}
c_{21}
c_{51}
a_{11}
a_{21}
a_{31}
a_{41}
c_{31}
c_{41}
e_{31}
e_{41}
e_{51}
e_{61}
e_{11}
e_{21}
a_{51}
a_{61}
P_1
P_2
P_3
P_4
P_5
P_6
e_{11}
e_{22}
e_{33}
e_{44}
e_{55}
e_{66}
μ_1
μ_2
μ_3
μ_4
μ_5
μ_6
E_1
E_2
E_3
1
E_4
E_5
E_6
1
1
1
1
1
1

Independent Pathway

Variance Component	a2	c2	e2
Common Factors	ac nv x 1	cc nv x 1	ec nv x 1
Residual Factors	as nv x nv	cs nv x nv	es nv x nv

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.

Independent Pathways

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

# 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=TRUE, values=4, labels=labDiag("as",nv), lbound=.00001, name="as" )
pathCs    <- mxMatrix( type="Diag", nrow=nv, ncol=nv, free=TRUE, values=4, labels=labDiag("cs",nv), lbound=.00001, name="cs" )
pathEs    <- mxMatrix( type="Diag", nrow=nv, ncol=nv, free=TRUE, 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 number of independent pathways by source of variance

common factors of size nv x nf

specific factors of size nv x nv (diagonal only)

common factors + specifics

Fitting IP Model

```
# Create Model Objects for Multiple Groups
pars      <- list(meanG, matI, invSD,
                  pathAc, pathCc, pathEc, pathAs, pathCs, pathEs, covA, covC, covE, covP, corA, corC, corE)
modelMZ   <- mxModel( name="MZ", pars, covMZ, expCovMZ, dataMZ, expMZ, funML )
modelDZ   <- mxModel( name="DZ", pars, covDZ, expCovDZ, dataDZ, expDZ, funML )
multi     <- mxFitFunctionMultigroup( c("MZ","DZ") )

# Build & Run Model
modelIP   <- mxModel( "mulIPc", pars, modelMZ, modelDZ, multi )
fitIP     <- mxRun( modelIP, intervals=F )
sumIP     <- summary( fitIP )
mxCompare( fitACE, fitIP )
fitGofs(fitIP)

# Generate List
matIPpaths <- c("iSD %*% ac","iSD %*% cc","iSD %*% ec","iSD %*% as","iSD %*% cs","iSD %*% es")
labIPpaths <- c("stPathAc","stPathCc","stPathEc","stPathAs","stPathCs","stPathEs")
formatOutputMatrices(fitIP, matIPpaths, labIPpaths, vars, 4)
```

include all relevant matrices

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

Independent Pathway Specification

```
> parameterSpecifications(fitIP)
model:mulIPc, 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:mulIPc, 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:mulIPc, 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:mulIPc, 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:mulIPc, 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:mulIPc, 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]
```

Compare IP with Cholesky

```
> mxCompare( fitACE, fitIP )
```

base	ep	minus2LL	df	AIC	diffLL	diffdf	p
mulACEc	69	14362.137	5394	3574.1373	NA	NA	NA
mulIPc	42	14449.871	5421	3607.8713	87.734027	27	2.4154318e-08

Standardized Estimates for fitIP

```
[1] "Matrix iSD %*% ac"
        stPathAc1
family   0.1455
happy    0.2472
life     0.2307
anxdep  -0.7073
somatic -0.5972
social  -0.4640
```

```
[1] "Matrix iSD %*% cc"
        stPathCc1
family  -0.5533
happy   -0.4472
life    -0.4828
anxdep   0.2778
somatic  0.2023
social   0.2418
```

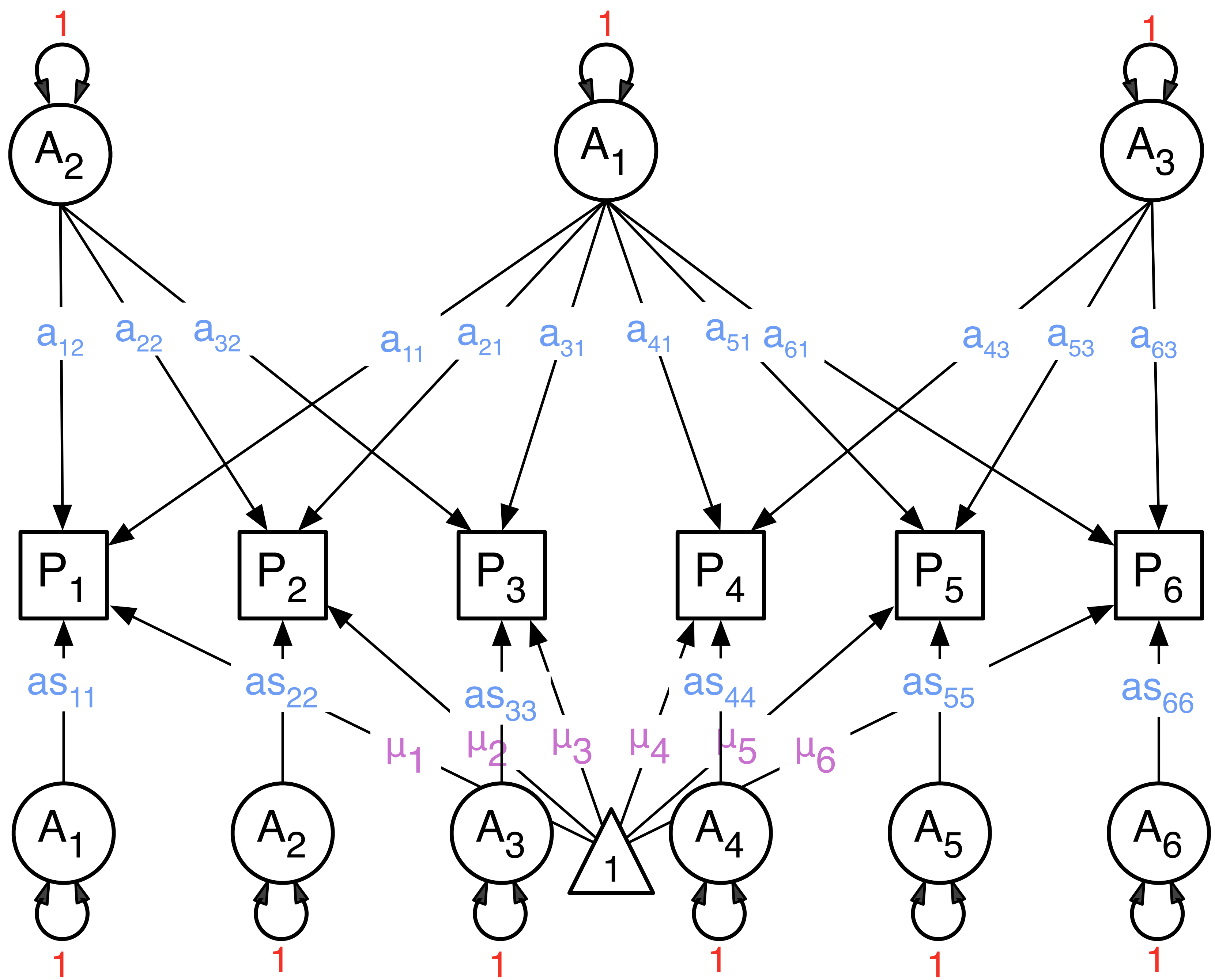
```
[1] "Matrix iSD %*% ec"
        stPathEc1
family  -0.1862
happy   -0.7594
life    -0.6250
anxdep   0.3511
somatic  0.0696
social   0.1002
```

```
[1] "Matrix iSD %*% as"
        stPathAs1 stPathAs2 stPathAs3 stPathAs4 stPathAs5 stPathAs6
family   0.4327    0.0000    0.0000    0.0000    0.0000    0.0000
happy    0.0000    0.1340    0.0000    0.0000    0.0000    0.0000
life     0.0000    0.0000    0.2051    0.0000    0.0000    0.0000
anxdep   0.0000    0.0000    0.0000    0.0000    0.0000    0.0000
somatic  0.0000    0.0000    0.0000    0.0000    0.1742    0.0000
social   0.0000    0.0000    0.0000    0.0000    0.0000    0.4839
```

```
[1] "Matrix iSD %*% cs"
        stPathCs1 stPathCs2 stPathCs3 stPathCs4 stPathCs5 stPathCs6
family   0.0000    0.0000    0.0000    0.0000    0.0000    0.0000
happy    0.0000    0.1275    0.0000    0.0000    0.0000    0.0000
life     0.0000    0.0000    0.0000    0.0000    0.0000    0.0000
anxdep   0.0000    0.0000    0.0000    0.0000    0.0000    0.0000
somatic  0.0000    0.0000    0.0000    0.0000    0.3518    0.0000
social   0.0000    0.0000    0.0000    0.0000    0.0000    0.0000
```

```
[1] "Matrix iSD %*% es"
        stPathEs1 stPathEs2 stPathEs3 stPathEs4 stPathEs5 stPathEs6
family   0.6714    0.0000    0.0000    0.0000    0.0000    0.0000
happy    0.0000    0.3578    0.0000    0.0000    0.0000    0.0000
life     0.0000    0.0000    0.5300    0.0000    0.0000    0.0000
anxdep   0.0000    0.0000    0.0000    0.5470    0.0000    0.0000
somatic  0.0000    0.0000    0.0000    0.0000    0.6659    0.0000
social   0.0000    0.0000    0.0000    0.0000    0.0000    0.6943
```

IP3A Model : bi-factor model



Three Independent A Factors

```
# Fit 3A (1C 1E) Factor - Independent Pathway Model
# ------------------------------------------------------------------------------

# Change Dimension of Additive Genetic Factor Matrix Ac
# Create Free and Values for 3 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    P5  .5   0  .5
# P6   T   F   T    P6  .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" )

# Create Model Objects, Build & Run Model
pars      <- list(meanG, matI, invSD,
                  pathAc, pathCc, pathEc, pathAs, pathCs, pathEs, covA, covC, covE, covP, corA, corC, corE)
modelMZ   <- mxModel( name="MZ", pars, covMZ, expCovMZ, dataMZ, expMZ, funML )
modelDZ   <- mxModel( name="DZ", pars, covDZ, expCovDZ, dataDZ, expDZ, funML )
modelIP3A <- mxModel( "mulIP3Ac", pars, modelMZ, modelDZ, multi )
fitIP3A   <- mxRun( modelIP3A )
mxCompare( fitACE, nested <- list(fitIP, fitIP3A) )
formatOutputMatrices(fitIP, matIPpaths, labIPpaths, vars, 4)
```

changing one matrix

Test Significance of C

```
# Fit 3A (0C 1E) Factor - Independent Pathway Model
# -----------------------------------------------------------------------------
modelIP0C <- mxModel( fitIP3A, name="mulIP0Cc" )
modelIP0C <- omxSetParameters( modelIP0C, labels=c(labFull("cc",nv,nf),labDiag("cs",nv)), free=FALSE, values=0 )
fitIP0C   <- mxRun( modelIP0C )
mxCompare( fitIP3A, fitIP0C )
```

Three Independent E Factors

```
# Fit 3A (0C 3E) Factor - Independent Pathway Model
# -----------------------------------------------------------------------------
nfE <- 3
frEc3     <- c(T,T,T,T,T,T,  T,T,T,F,F,F,  F,F,F,T,T,T)
svEc3     <- c(rep(.5,nv),rep(.5,3),rep(0,3),rep(0,3),rep(.5,3))
pathEc    <- mxMatrix( type="Full", nrow=nv, ncol=nfE, free=frEc3, values=svEc3, labels=labFull("ec",nv,nfE), name="ec" )
```

changing one matrix

```
# Create Model Objects, Build & Run Model
pars      <- list(meanG, matI, invSD,
                  pathAc, pathCc, pathEc, pathAs, pathCs, pathEs, covA, covC, covE, covP, corA, corC, corE)
modelMZ   <- mxModel( name="MZ", pars, covMZ, expCovMZ, dataMZ, expMZ, funML )
modelDZ   <- mxModel( name="DZ", pars, covDZ, expCovDZ, dataDZ, expDZ, funML )
modelIP3E <- mxModel( "mulIP3Ec", pars, modelMZ, modelDZ, multi )
fitIP3E   <- mxRun( modelIP3E )
mxCompare( fitACE, nested <- list(fitIP, fitIP3A, fitIP0C, fitIP3E) )
formatOutputMatrices(fitIP, matIPpaths, labIPpaths, vars, 4)
```

Compare IPs with Cholesky

```
> mxCompare( fitACE, fitIP )
```

base	ep	minus2LL	df	AIC	diffLL	diffdf	p
mulACEc	69	14362.137	5394	3574.1373	NA	NA	NA
mulIPc	42	14449.871	5421	3607.8713	87.734027	27	2.4154318e-08
mulIP3Ac	48	14423.010	5415	3593.0100	60.872650	21	9.4141500e-06
mulIP0Cc	36	14439.733	5427	3585.7332	77.595881	33	1.8718979e-05
mulIP3Ec	54	14381.308	5409	3563.3076	19.170256	15	2.0612213e-01

Standardized Estimates for fitIP3A

```
[1] "Matrix iSD %*% ac"
        stPathAc1 stPathAc2 stPathAc3
family   0.2850   -0.4649    0.0000
happy    0.4007   -0.4145    0.0000
life     0.2280   -0.3638    0.0000
anxdep  -0.6085    0.0000    0.2566
somatic -0.3225    0.0000    0.5586
social  -0.5470    0.0000    0.0240

[1] "Matrix iSD %*% cc"
        stPathCc1
family  -0.3137
happy   -0.1715
life    -0.3986
anxdep   0.3317
somatic  0.3843
social   0.2491

[1] "Matrix iSD %*% ec"
        stPathEc1
family   0.0931
happy    0.6864
life     0.6340
anxdep  -0.3803
somatic -0.1110
social  -0.0695
```

```
[1] "Matrix iSD %*% as"
        stPathAs1 stPathAs2 stPathAs3 stPathAs4 stPathAs5 stPathAs6
family  0.3563    0.0000    0.0000    0.0000    0.0000    0.0000
happy   0.0000    0.0000    0.0000    0.0000    0.0000    0.0000
life    0.0000    0.0000    0.0000    0.0000    0.0000    0.0000
anxdep  0.0000    0.0000    0.0000    0.0000    0.0000    0.0000
somatic 0.0000    0.0000    0.0000    0.0000    0.0000    0.0000
social  0.0000    0.0000    0.0000    0.0000    0.0000    0.3840

[1] "Matrix iSD %*% cs"
        stPathCs1 stPathCs2 stPathCs3 stPathCs4 stPathCs5 stPathCs6
family  0.2133    0.0000    0.0000    0.0000    0.0000    0.0000
happy   0.0000    0.0000    0.0000    0.0000    0.0000    0.0000
life    0.0000    0.0000    0.0000    0.0000    0.0000    0.0000
anxdep  0.0000    0.0000    0.0000    0.0000    0.0000    0.0000
somatic 0.0000    0.0000    0.0000    0.0000    0.0007    0.0000
social  0.0000    0.0000    0.0000    0.0000    0.0000    0.0000

[1] "Matrix iSD %*% es"
        stPathEs1 stPathEs2 stPathEs3 stPathEs4 stPathEs5 stPathEs6
family  0.6505    0.0000    0.0000    0.0000    0.0000    0.0000
happy   0.0000    0.4087    0.0000    0.0000    0.0000    0.0000
life    0.0000    0.0000    0.5049    0.0000    0.0000    0.0000
anxdep  0.0000    0.0000    0.0000    0.5561    0.0000    0.0000
somatic 0.0000    0.0000    0.0000    0.0000    0.6511    0.0000
social  0.0000    0.0000    0.0000    0.0000    0.0000    0.6970
```

Standardized Estimates for fitIP3E

```
[1] "Matrix iSD %*% ac"
        stPathAc1 stPathAc2 stPathAc3
family  -0.3851   0.5341    0.0000
happy   -0.4453   0.1963    0.0000
life    -0.5281   0.2318    0.0000
anxdep  0.4507    0.0000    0.2265
somatic 0.4911    0.0000    0.4729
social  0.2528    0.0000    0.1584

[1] "Matrix iSD %*% cc"
        stPathCc1
family  -0.2738
happy   -0.2695
life    -0.1708
anxdep  0.4163
somatic 0.0790
social  0.4567

[1] "Matrix iSD %*% ec"
        stPathEc1 stPathEc2 stPathEc3
family  -0.0587   -0.1277   0.0000
happy   -0.7056   -0.2824   0.0000
life    -0.5740   -0.0573   0.0000
anxdep  0.3572    0.0000    -0.5685
somatic 0.0376    0.0000    -0.2865
social  0.0810    0.0000    -0.1656
```

```
[1] "Matrix iSD %*% as"
        stPathAs1 stPathAs2 stPathAs3 stPathAs4 stPathAs5 stPathAs6
family  0.0000    0.0000    0.0000    0.0000    0.0000    0.0000
happy   0.0000    0.2357    0.0000    0.0000    0.0000    0.0000
life    0.0000    0.0000    0.0615    0.0000    0.0000    0.0000
anxdep  0.0000    0.0000    0.0000    0.0000    0.0000    0.0000
somatic 0.0000    0.0000    0.0000    0.0000    0.0000    0.0000
social  0.0000    0.0000    0.0000    0.0000    0.0000    0.4194

[1] "Matrix iSD %*% cs"
        stPathCs1 stPathCs2 stPathCs3 stPathCs4 stPathCs5 stPathCs6
family  0.2239    0.0000    0.0000    0.0000    0.0000    0.0000
happy   0.0000    0.0000    0.0000    0.0000    0.0000    0.0000
life    0.0000    0.0000    0.0000    0.0000    0.0000    0.0000
anxdep  0.0000    0.0000    0.0000    0.2302    0.0000    0.0000
somatic 0.0000    0.0000    0.0000    0.0000    0.2032    0.0000
social  0.0000    0.0000    0.0000    0.0000    0.0000    0.0000

[1] "Matrix iSD %*% es"
        stPathEs1 stPathEs2 stPathEs3 stPathEs4 stPathEs5 stPathEs6
family  0.6494    0.0000    0.0000    0.0000    0.0000    0.0000
happy   0.0000    0.2397    0.0000    0.0000    0.0000    0.0000
life    0.0000    0.0000    0.5492    0.0000    0.0000    0.0000
anxdep  0.0000    0.0000    0.0000    0.2617    0.0000    0.0000
somatic 0.0000    0.0000    0.0000    0.0000    0.6357    0.0000
social  0.0000    0.0000    0.0000    0.0000    0.0000    0.7018
```

Behavior Genetics, Vol. 20, No. 5, 1990

Alternative Common Factor Models for Multivariate Biometric Analyses

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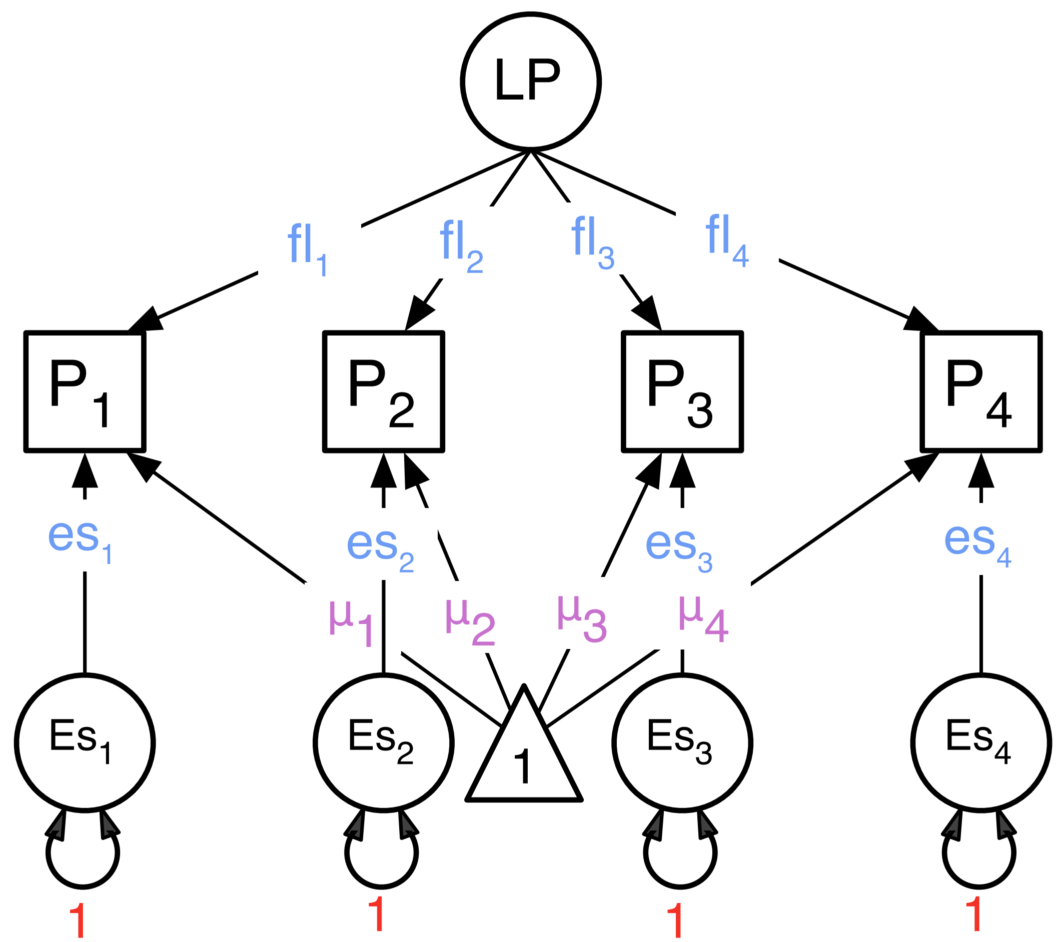
Received 4 Apr. 1988—Final 15 May 1990

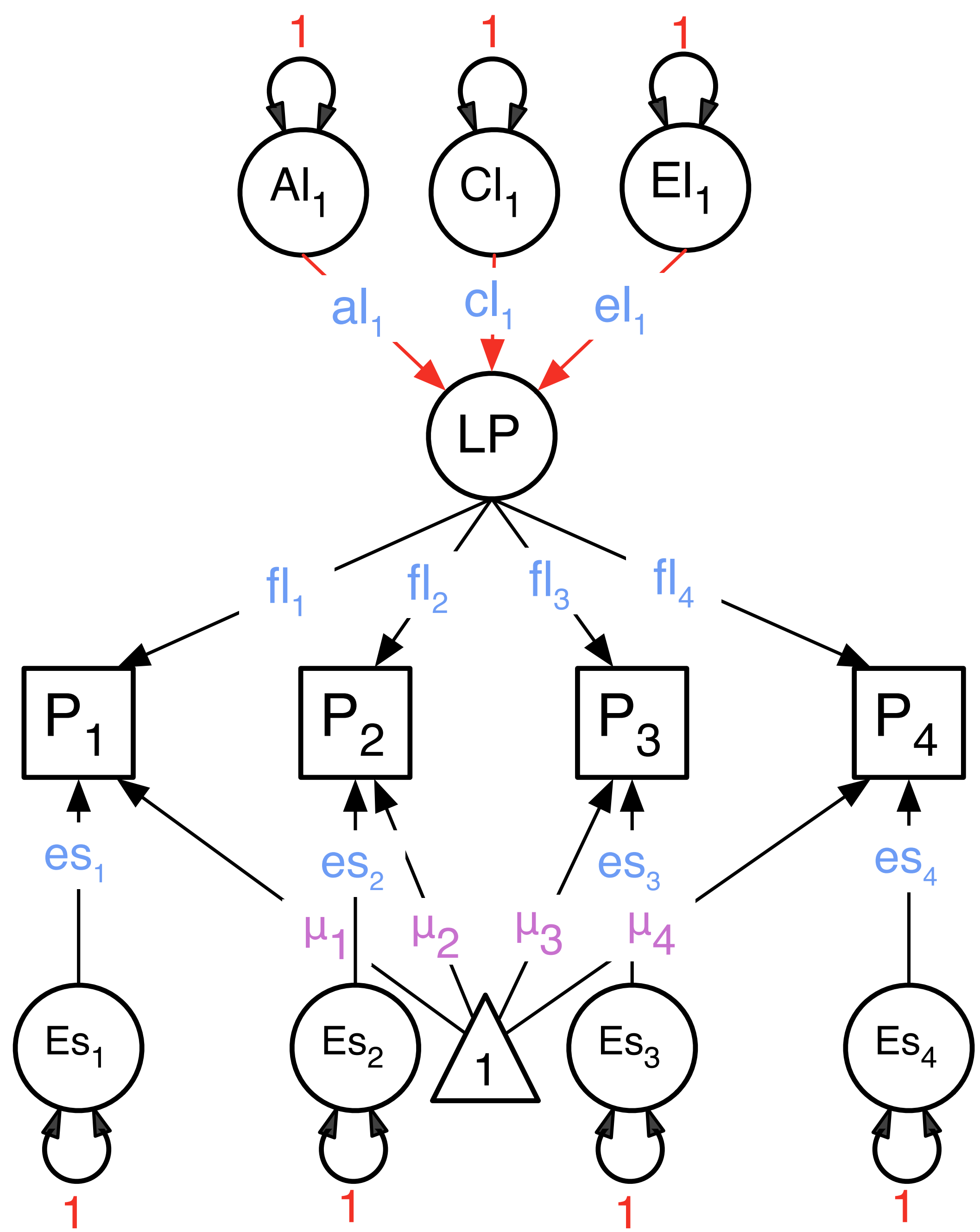
In prior research we have shown how linear structural equation models and computer programs (e.g., LISREL) may be simply and directly used to provide alternatives for the traditional biometric twin design. We use structural equations and path models to define biometric group differences, we write traditional 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



$$\begin{array}{c} P_1 \\ P_2 \\ P_3 \\ P_4 \end{array} \begin{bmatrix} fl_{11} \\ fl_{21} \\ fl_{31} \\ fl_{41} \end{bmatrix}$$

Latent Phenotype ACE

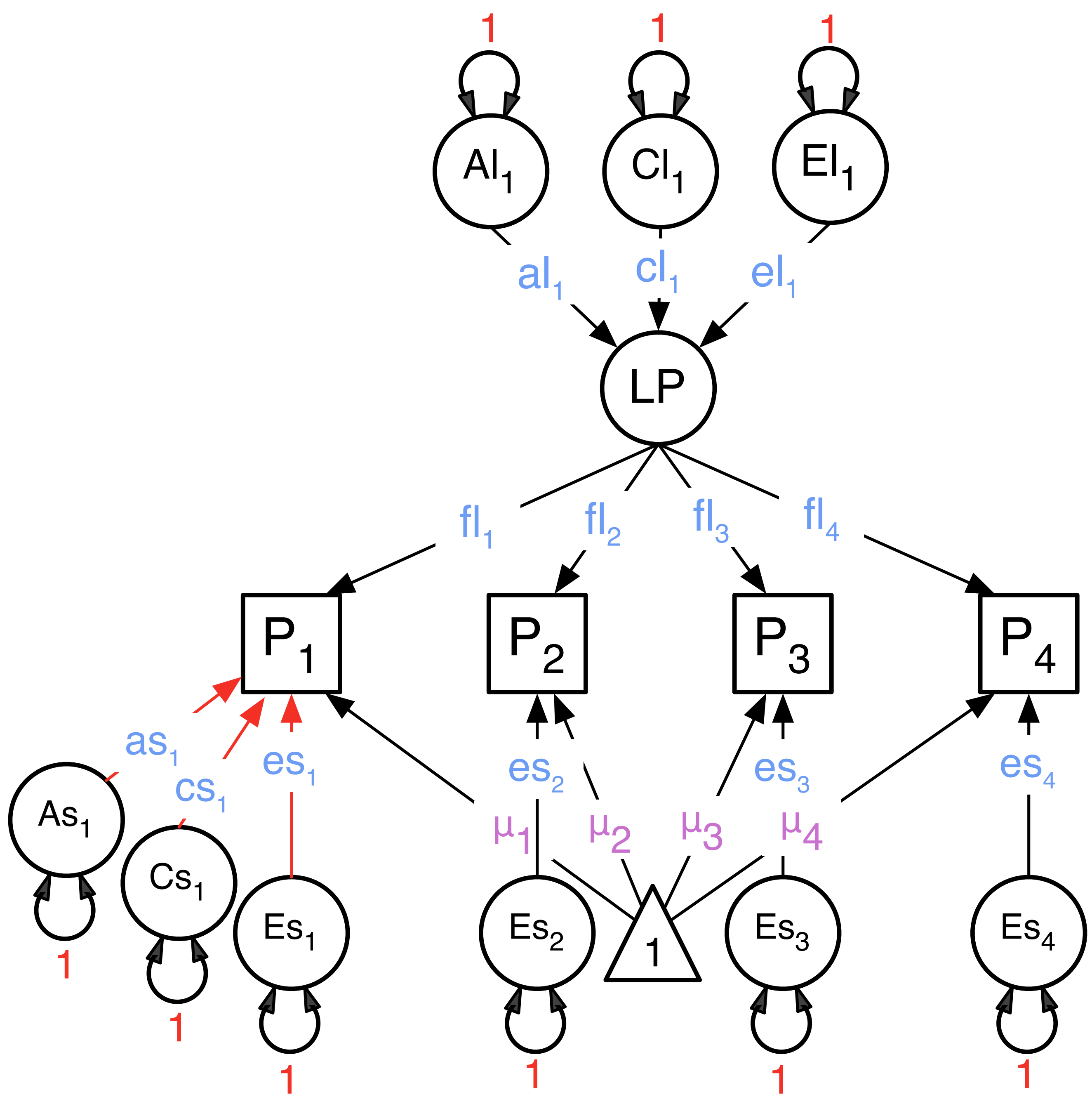


$$\begin{bmatrix} al_{11} \end{bmatrix} \qquad \begin{bmatrix} cl_{11} \end{bmatrix}$$

$$\begin{bmatrix} el_{11} \end{bmatrix}$$

$$\begin{array}{c} P_1 \\ P_2 \\ P_3 \\ P_4 \end{array} \begin{bmatrix} fl_{11} \\ fl_{21} \\ fl_{31} \\ fl_{41} \end{bmatrix}$$

ACE Specifics



$$
\begin{array}{c}
P_1 \\ P_2 \\ P_3 \\ P_4
\end{array}
\begin{bmatrix}
es_{11} & 0 & 0 & 0 \\
0 & es_{22} & 0 & 0 \\
0 & 0 & es_{33} & 0 \\
0 & 0 & 0 & es_{44}
\end{bmatrix}
$$

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

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

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" )
```

Total A Covariance

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

$$\begin{bmatrix} fl_{11}^2 al_{11}^2 & fl_{11} fl_{21} al_{11}^2 & fl_{11} fl_{31} al_{11}^2 & fl_{11} fl_{41} al_{11}^2 \\ fl_{21} fl_{11} al_{11}^2 & fl_{21}^2 al_{11}^2 & fl_{21} fl_{31} al_{11}^2 & fl_{21} fl_{41} al_{11}^2 \\ fl_{31} fl_{11} al_{11}^2 & fl_{31} fl_{21} al_{11}^2 & fl_{31}^2 al_{11}^2 & fl_{31} fl_{41} al_{11}^2 \\ fl_{41} fl_{11} al_{11}^2 & fl_{41} fl_{21} al_{11}^2 & fl_{41} fl_{31} al_{11}^2 & fl_{41}^2 al_{11}^2 \end{bmatrix} + \begin{bmatrix} as_{11}^2 & 0 & 0 & 0 \\ 0 & as_{22}^2 & 0 & 0 \\ 0 & 0 & as_{33}^2 & 0 \\ 0 & 0 & 0 & as_{44}^2 \end{bmatrix} = \begin{bmatrix} fl_{11}^2 al_{11}^2 + as_{11}^2 & fl_{11} fl_{21} al_{11}^2 & fl_{11} fl_{31} al_{11}^2 & fl_{11} fl_{41} al_{11}^2 \\ fl_{21} fl_{11} al_{11}^2 & fl_{21}^2 al_{11}^2 + as_{22}^2 & fl_{21} fl_{31} al_{11}^2 & fl_{21} fl_{41} al_{11}^2 \\ fl_{31} fl_{11} al_{11}^2 & fl_{31} fl_{21} al_{11}^2 & fl_{31}^2 al_{11}^2 + as_{33}^2 & fl_{31} fl_{41} al_{11}^2 \\ fl_{41} fl_{11} al_{11}^2 & fl_{41} fl_{21} al_{11}^2 & fl_{41} fl_{31} al_{11}^2 & fl_{41}^2 al_{11}^2 + as_{44}^2 \end{bmatrix}$$

`as %*% t(as)`

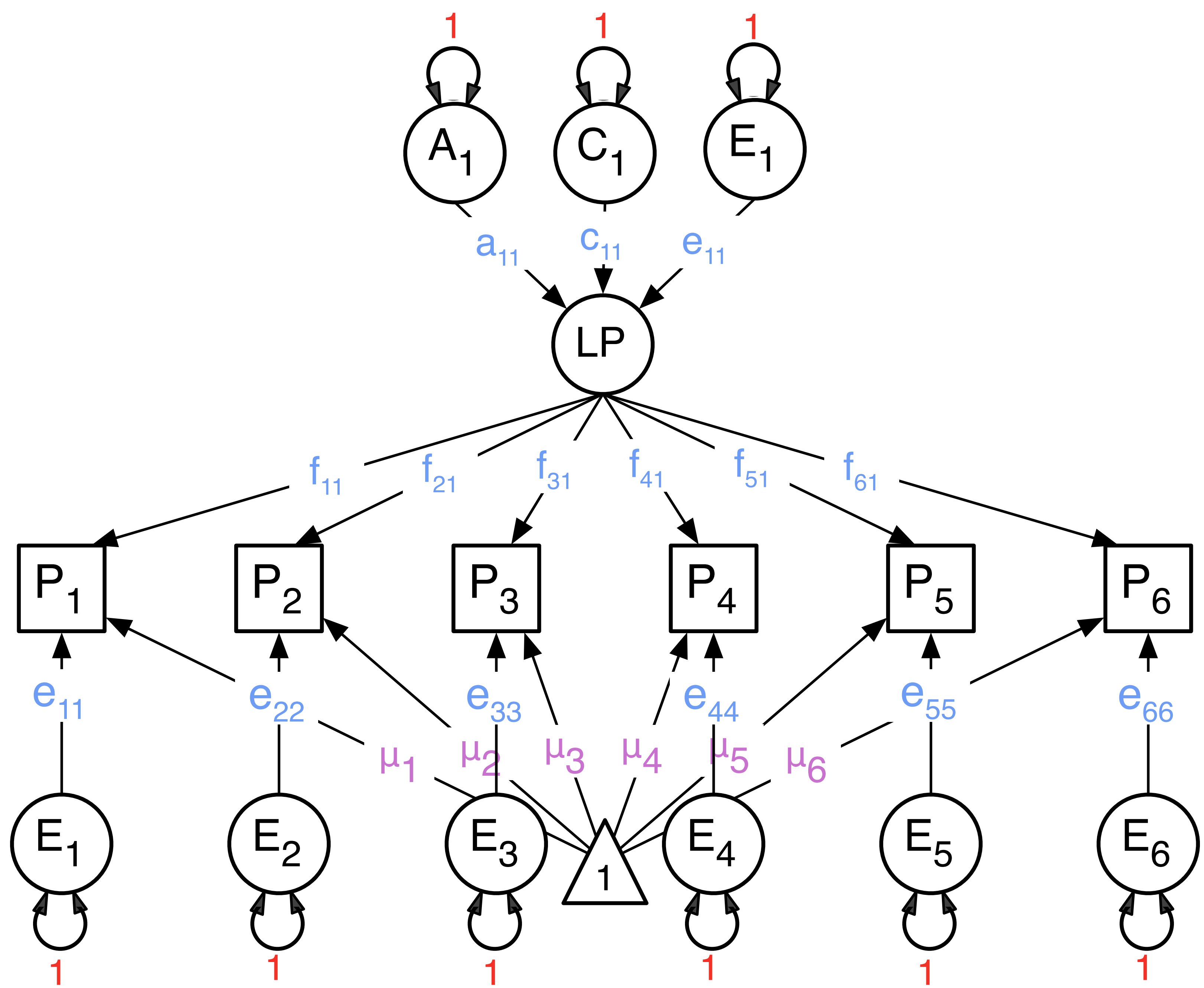
```
object: CovA
matrix name:A
```

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

Common Pathway Model

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

CP Model



1
1
1
A_1
C_1
E_1
a_{11}
c_{11}
e_{11}
LP
f_{11}
f_{21}
f_{31}
f_{41}
f_{51}
f_{61}
P_1
P_2
P_3
P_4
P_5
P_6
e_{11}
e_{22}
e_{33}
e_{44}
e_{55}
e_{66}
μ_1
μ_2
μ_3
μ_4
μ_5
μ_6
E_1
E_2
E_3
1
E_4
E_5
E_6
1
1
1
1
1
1

Common Pathway

Variance Component	a2	c2	e2	
Common Factors	al 1 x 1	cl 1 x 1	el 1 x 1	fl nv x 1
Residual Factors	as nv x nv	cs nv x nv	es nv x nv	

Constraint on Variance of Latent Phenotype

```
# Fit Common Pathway ACE Model
# ------------------------------------------------------------------------------
nl        <- 1

# Matrices ac, cc, and ec to store a, c, and e path coefficients for latent phenotype(s)
pathAl    <- mxMatrix( type="Lower", nrow=nl, ncol=nl, free=TRUE, values=.6, labels=labLower("al",nl), lbound=.00001, name="al" )
pathCl    <- mxMatrix( type="Lower", nrow=nl, ncol=nl, free=TRUE, values=.6, labels=labLower("cl",nl), lbound=.00001, name="cl" )
pathEl    <- mxMatrix( type="Lower", nrow=nl, ncol=nl, free=TRUE, values=.6, labels=labLower("el",nl), lbound=.00001, name="el" )

# Matrix and Algebra for constraint on variance of latent phenotype
covarLP   <- mxAlgebra( expression=al %*% t(al) + cl %*% t(cl) + el %*% t(el), name="CovarLP" )
varLP     <- mxAlgebra( expression= diag2vec(CovarLP), name="VarLP" )
unit      <- mxMatrix( type="Unit", nrow=nl, ncol=1, name="Unit")
varLP1    <- mxConstraint( expression=VarLP == Unit, name="varLP1")

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

# 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" )
```

latent phenotype nf x nf

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

factor loadings

factor loadings x ace on LP
+ specifics

Fitting CP Model

```
# Create Model Objects for Multiple Groups
pars      <- list(meanG, matI, invSD,
                  pathAl, pathCl, pathEl, covarLP, varLP, unit, pathFl, pathAs, pathCs, pathEs, covA, covC, covE, covP)
modelMZ   <- mxModel( name="MZ", pars, covMZ, expCovMZ, dataMZ, expMZ, funML )
modelDZ   <- mxModel( name="DZ", pars, covDZ, expCovDZ, dataDZ, expDZ, funML )
multi     <- mxFitFunctionMultigroup( c("MZ","DZ") )

# Build & Run Model
modelCP   <- mxModel( "mulCPc", pars, varLP1, modelMZ, modelDZ, multi )
fitCP     <- mxRun(modelCP, intervals=F )
sumCP     <- summary( fitCP )
mxCompare( fitACE, fitCP )
parameterSpecifications(fitCP)

# Generate List of Parameter Estimates and Derived Quantities using formatOutputMatrices
matCPpaths <- c("al","cl","el","iSD %*% fl","iSD %*% as","iSD %*% cs","iSD %*% es")
labCPpaths <- c("stPathAl","stPathCl","stPathEl","stPathFl","stPathAs","stPathCs","stPathEs")
formatOutputMatrices(fitCP, matCPpaths, labCPpaths, vars, 4)
```

new objects

constraint object in combined model only

already standardized

Common Pathway Specification

```
parameterSpecifications(fitCP)
model:mulCPc, matrix:al
     [,1]
[1,] [al_1_1]

model:mulCPc, matrix:cl
     [,1]
[1,] [cl_1_1]

model:mulCPc, matrix:el
     [,1]
[1,] [el_1_1]

model:mulCPc, 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]
```

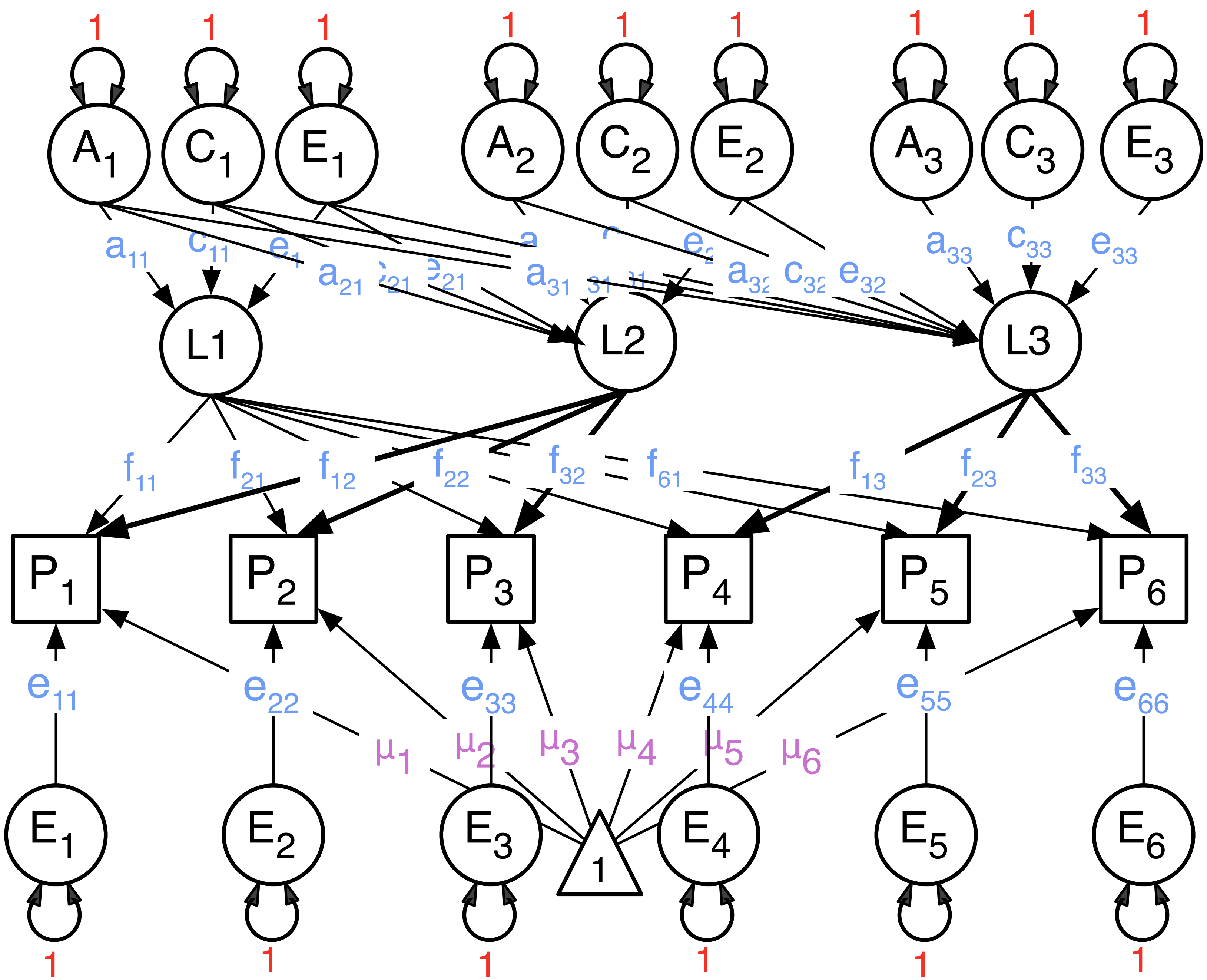
```
model:mulCPc, matrix:as
     [,1]     [,2]     [,3]     [,4]     [,5]     [,6]
[1,] [as_1_1] 0        0        0        0        0
[2,] 0        [as_2_2] 0        0        0        0
[3,] 0        0        [as_3_3] 0        0        0
[4,] 0        0        0        [as_4_4] 0        0
[5,] 0   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

model:mulCPc, 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:mulCPc, 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]
```

Standardized Estimates for fitCP

```
[1] "Matrix al"
    stPathAl1
LP1 0.7208

[1] "Matrix cl"
    stPathCl1
LP1 0.3267

[1] "Matrix el"
    stPathEl1
LP1 0.6113

[1] "Matrix iSD %*% fl"
        stPathFl1
family   0.4768
happy    0.8582
life     0.8228
anxdep  -0.6811
somatic -0.4018
social  -0.3843
```

```
[1] "Matrix iSD %*% as"
        stPathAs1 stPathAs2 stPathAs3 stPathAs4 stPathAs5 stPathAs6
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
life     0.0000    0.0000    0.1387    0.0000    0.0000    0.0000
anxdep   0.0000    0.0000    0.0000    0.1707    0.0000    0.0000
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 iSD %*% cs"
        stPathCs1 stPathCs2 stPathCs3 stPathCs4 stPathCs5 stPathCs6
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
life     0.0000    0.0000    0.0000    0.0000    0.0000    0.0000
anxdep   0.0000    0.0000    0.0000    0.3818    0.0000    0.0000
somatic  0.0000    0.0000    0.0000    0.0000    0.3063    0.0000
social   0.0000    0.0000    0.0000    0.0000    0.0000    0.1828

[1] "Matrix iSD %*% es"
        stPathEs1 stPathEs2 stPathEs3 stPathEs4 stPathEs5 stPathEs6
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
```

CP 3L Model


A1
C1
E1
A2
C2
E2
A3
C3
E3
a11
c11
a21
e21
a31
a32
c32
e32
a33
c33
e33
L1
L2
L3
f11
f21
f12
f22
f32
f61
f13
f23
f33
P1
P2
P3
P4
P5
P6
e11
e22
e33
e44
e55
e66
μ1
μ2
μ3
μ4
μ5
μ6
E1
E2
E3
E4
E5
E6
1

Standardized Estimates for fitCP3L

[1] "Matrix al"

	stPathAl1	stPathAl2	stPathAl3
LP1	0.4446	0.0000	0.0000
LP2	0.2956	0.3004	0.0000
LP3	0.4062	0.3409	0.0187

[1] "Matrix cl"

	stPathCl1	stPathCl2	stPathCl3
LP1	0.4294	0.0000	0.0000
LP2	0.1407	-0.0021	0.0000
LP3	0.1023	0.2202	0.1211

[1] "Matrix el"

	stPathEl1	stPathEl2	stPathEl3
LP1	0.7860	0.0000	0.0000
LP2	0.8910	0.0935	0.0000
LP3	0.7331	-0.0190	0.3272

[1] "Matrix iSD %*% fl"

	stPathFl1	stPathFl2	stPathFl3
family	-1.4243	1.3720	0.0000
happy	-1.1893	1.8167	0.0000
life	-1.2577	1.7095	0.0000
anxdep	0.9893	0.0000	-1.5090
somatic	0.8554	0.0000	-1.0095
social	0.6964	0.0000	-0.8516

[1] "Matrix iSD %*% as"

	stPathAs1	stPathAs2	stPathAs3	stPathAs4	stPathAs5	stPathAs6
family	0.3909	0.0000	0.0000	0.0000	0.0000	0.0000
happy	0.0000	0.1881	0.0000	0.0000	0.0000	0.0000
life	0.0000	0.0000	0.1949	0.0000	0.0000	0.0000
anxdep	0.0000	0.0000	0.0000	0.0092	0.0000	0.0000
somatic	0.0000	0.0000	0.0000	0.0000	0.4129	0.0000
social	0.0000	0.0000	0.0000	0.0000	0.0000	0.5237

[1] "Matrix iSD %*% cs"

	stPathCs1	stPathCs2	stPathCs3	stPathCs4	stPathCs5	stPathCs6
family	0.0196	0.0000	0.0000	0.0000	0.0000	0.0000
happy	0.0000	0.0371	0.0000	0.0000	0.0000	0.0000
life	0.0000	0.0000	0.0174	0.0000	0.0000	0.0000
anxdep	0.0000	0.0000	0.0000	0.0177	0.0000	0.0000
somatic	0.0000	0.0000	0.0000	0.0000	0.2750	0.0000
social	0.0000	0.0000	0.0000	0.0000	0.0000	0.0125

[1] "Matrix iSD %*% es"

	stPathEs1	stPathEs2	stPathEs3	stPathEs4	stPathEs5	stPathEs6
family	0.6502	0.0000	0.0000	0.0000	0.0000	0.0000
happy	0.0000	0.3222	0.0000	0.0000	0.0000	0.0000
life	0.0000	0.0000	0.5422	0.0000	0.0000	0.0000
anxdep	0.0000	0.0000	0.0000	0.3670	0.0000	0.0000
somatic	0.0000	0.0000	0.0000	0.0000	0.6213	0.0000
social	0.0000	0.0000	0.0000	0.0000	0.0000	0.6820

Compare IPs & CPs with Cholesky

```
> mxCompare( fitACE, fitIP )
```

base	ep	minus2LL	df	AIC	diffLL	diffdf	p
mulACEc	69	14362.137	5394	3574.1373	NA	NA	NA
mulIPc	42	14449.871	5421	3607.8713	87.734027	27	2.4154318e-08
mulIP3Ac	48	14423.010	5415	3593.0100	60.872650	21	9.4141500e-06
mulIP0Cc	36	14439.733	5427	3585.7332	77.595881	33	1.8718979e-05
mulIP3Ec	54	14381.308	5409	3563.3076	19.170256	15	2.0612213e-01
mulCPc	33	14713.003	5431	3851.0029	350.865628	37	8.9554069e-53
mulCP3Lc	54	14394.178	5412	3570.1782	32.040945	18	2.1743094e-02

Thanks!