

# OpenMx Scripting

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# What is OpenMx

- A free, full-featured, open source SEM package
- Runs on Windows, Mac OS-X, and Linux
- Runs inside the R statistical programming environment
- Funded by the NIH Roadmap Initiative

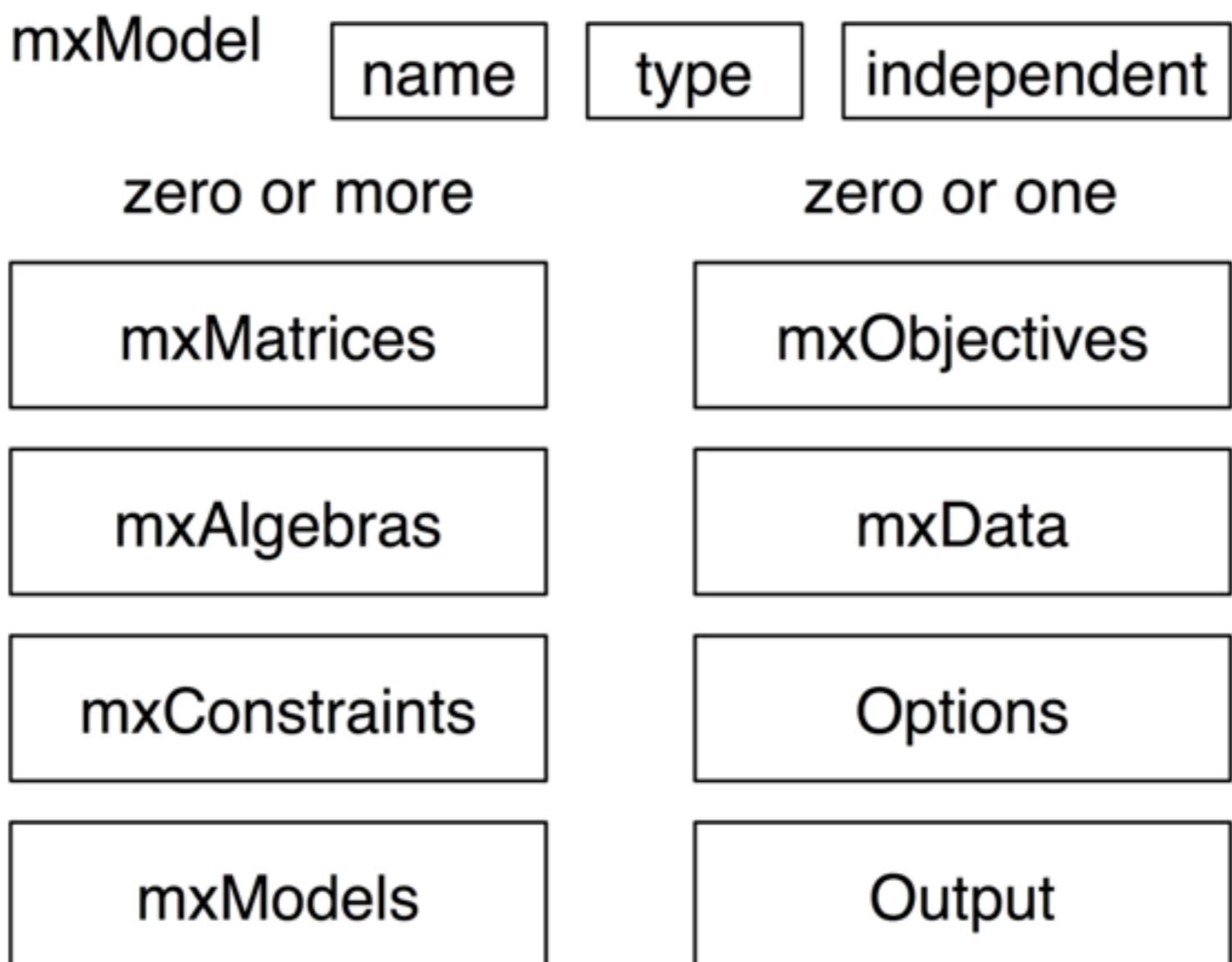
# OpenMx Features

- A new approach to model specification
- Allows both path-style and matrix-style scripting
- Flexible optimization including nonlinear constraints
- Web-based forums, tutorials, and a wiki
- Support for most popular types of modeling
- Advanced features not found in other SEM packages
- An active development team.

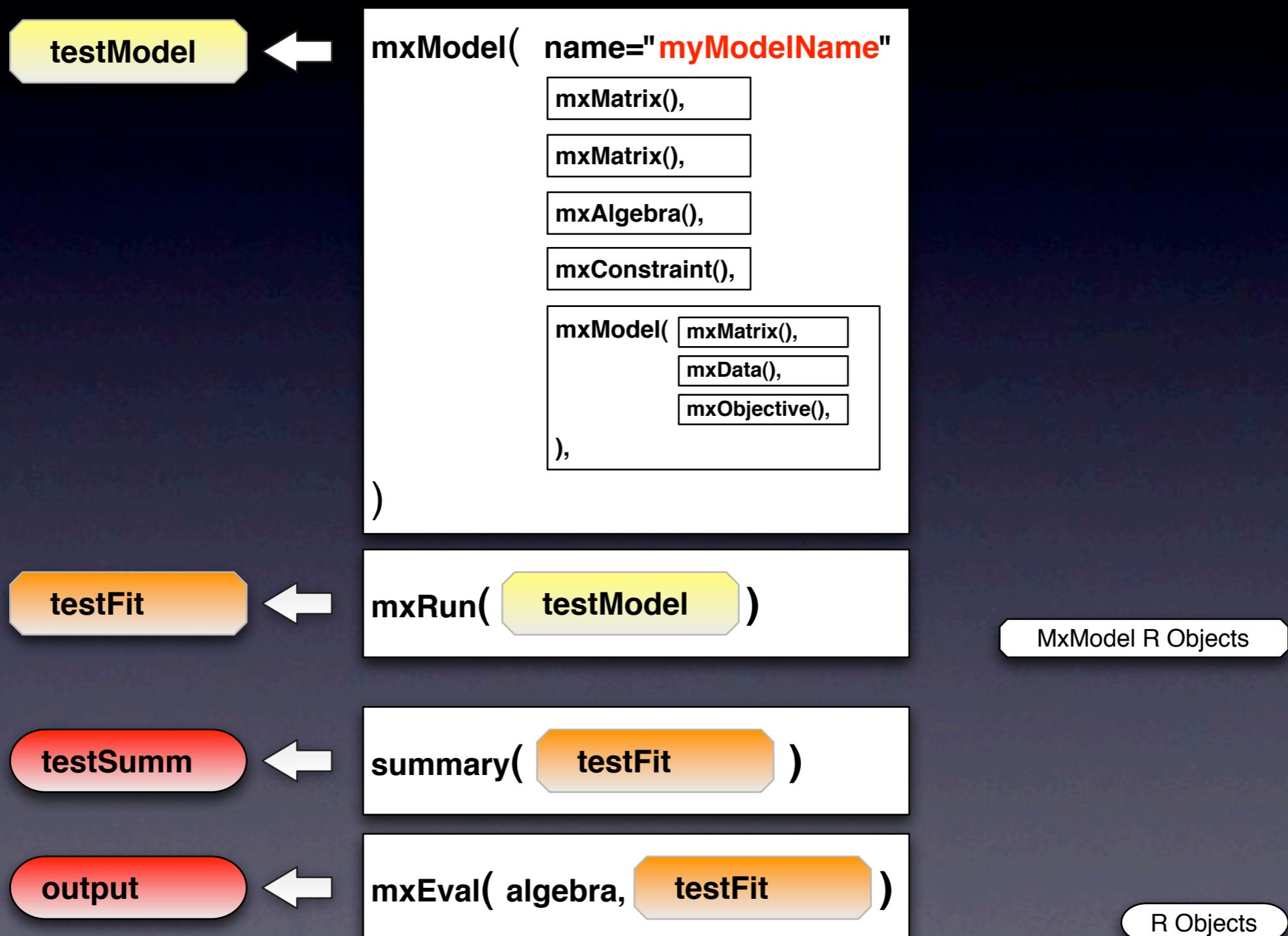
# OpenMx Models

- Multivariate Normal Structural Equation Models
- Multigroup Models, e.g. Behavior Genetic
- Full Information Maximum Likelihood
- Mixed Effects and Multilevel
- Multivariate Categorical Data with Thresholds
- Dynamical Systems Models
- Nonlinear Constraints
- User-supplied Matrix Algebra, Objective Functions

# OpenMx Commands



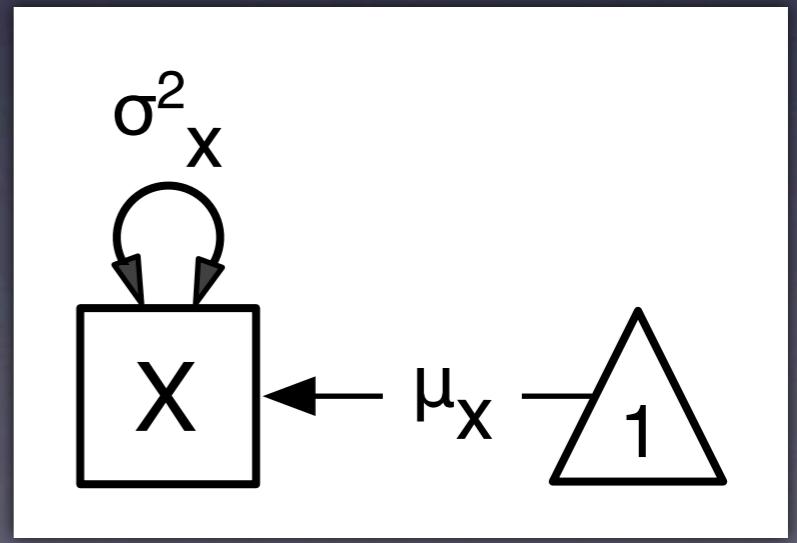
# OpenMx Process



# Univariate Model

## Raw Data -Matrix-Style

```
#example: Model to estimate means/ variances
#-----
require(OpenMx)
univModel <- mxModel("univ",
  mxMatrix( type="Symm", nrow=1, ncol=1, free=T,
    values=1, name="expCov" ),
  mxMatrix( type="Full", nrow=1, ncol=1, free=T,
    values=0, name="expMean" ),
  mxData( observed=testData, type="raw" ),
  mxFIMLObjective(
    covariance="expCov",
    means="expMean",
    dimnames=selVars )
)
univFit <- mxRun(univModel)
```



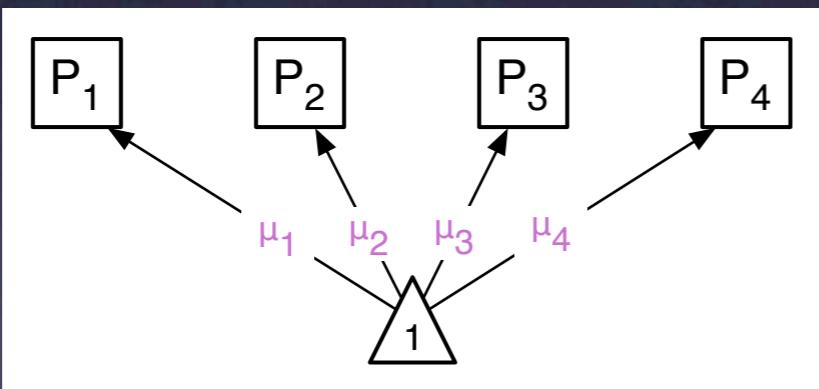
# Multivariate Model

## Multi-Group

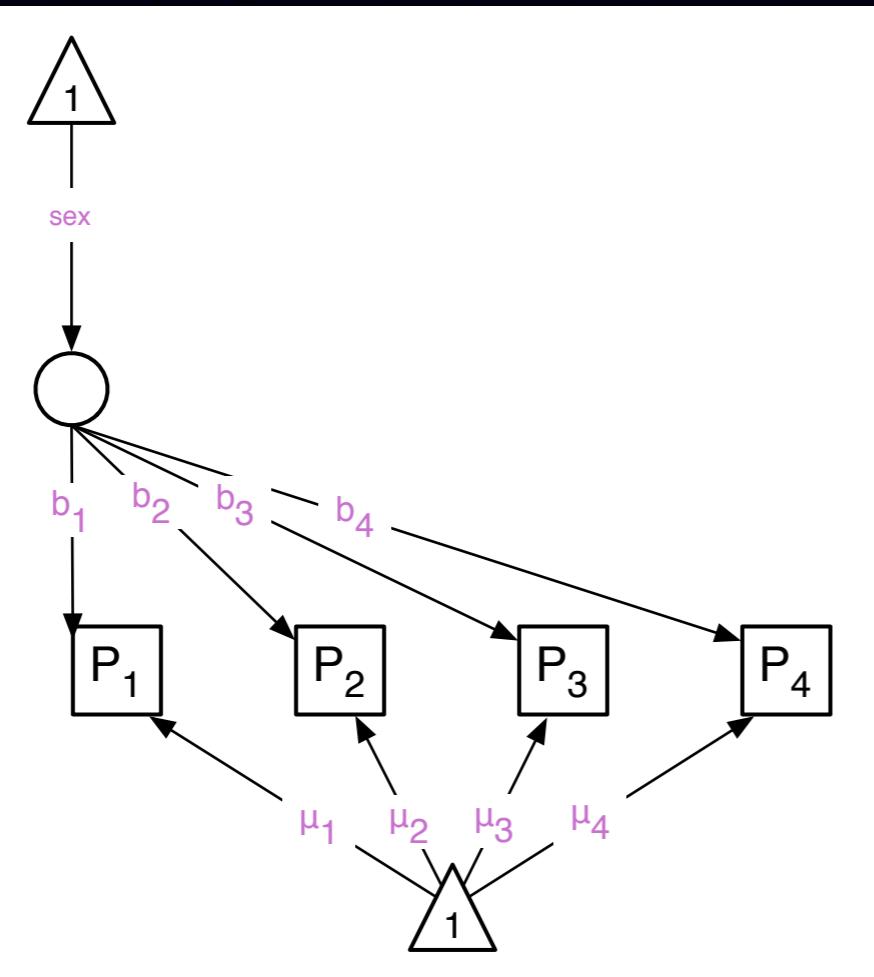
```
manifestVars <-("mo3t1","mo7t1","mo10t1","mo12t1"..)
nv <- 4      # number of variables
factorModel <- mxModel("factor",
mxModel("All", ...),
  # parameters in mxMatrices, mxAlgebras
mxModel("MZM", ...),
  # mxData, definition variables, mxObjective
mxModel("DZM", ...),
mxModel("MZF", ...),
mxModel("DZF", ...),
mxModel("DZO", ...)
)
```

# Means

```
mxMatrix(  
  type="Full",  
  nrow=1,  
  ncol=nv,  
  free=TRUE,  
  values=0,  
  labels=c(  
  "meanm3", "meanm7",  
  "meanm10", "meanm12"),  
  name="Mean"),
```

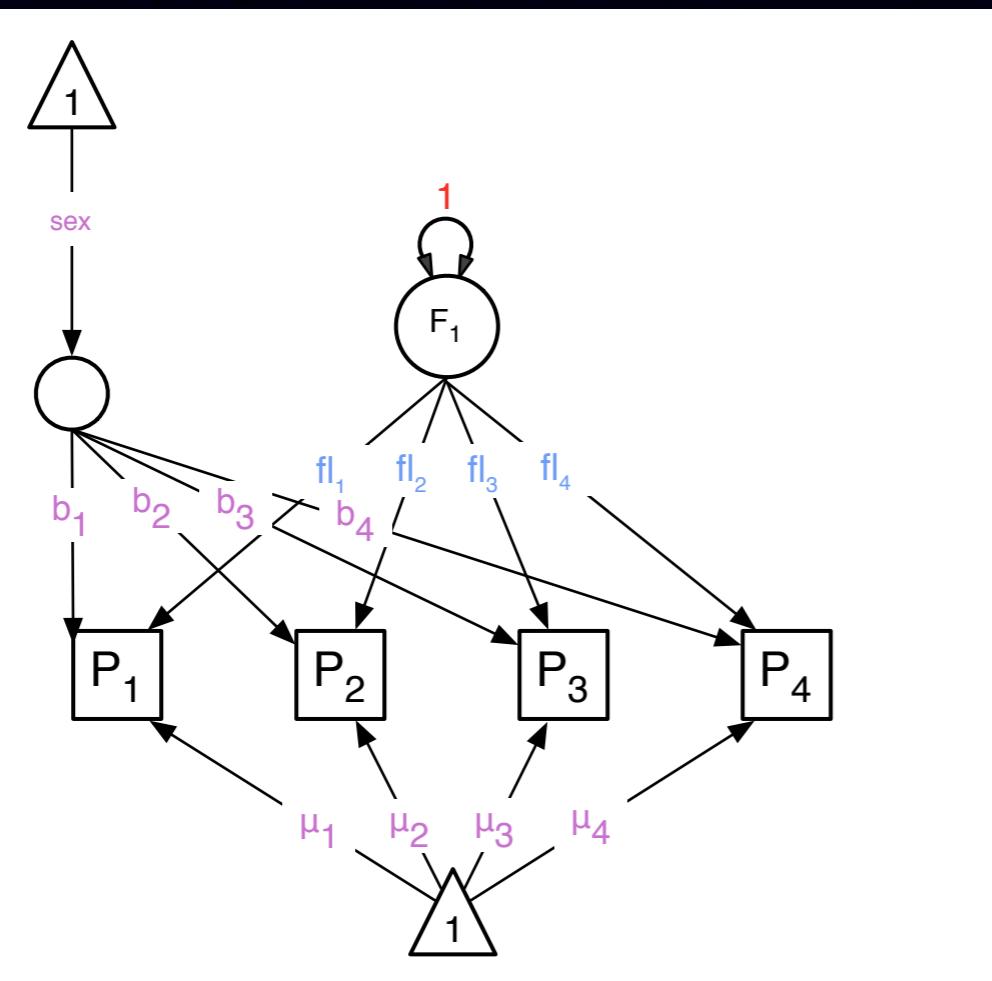


# Regression on Sex



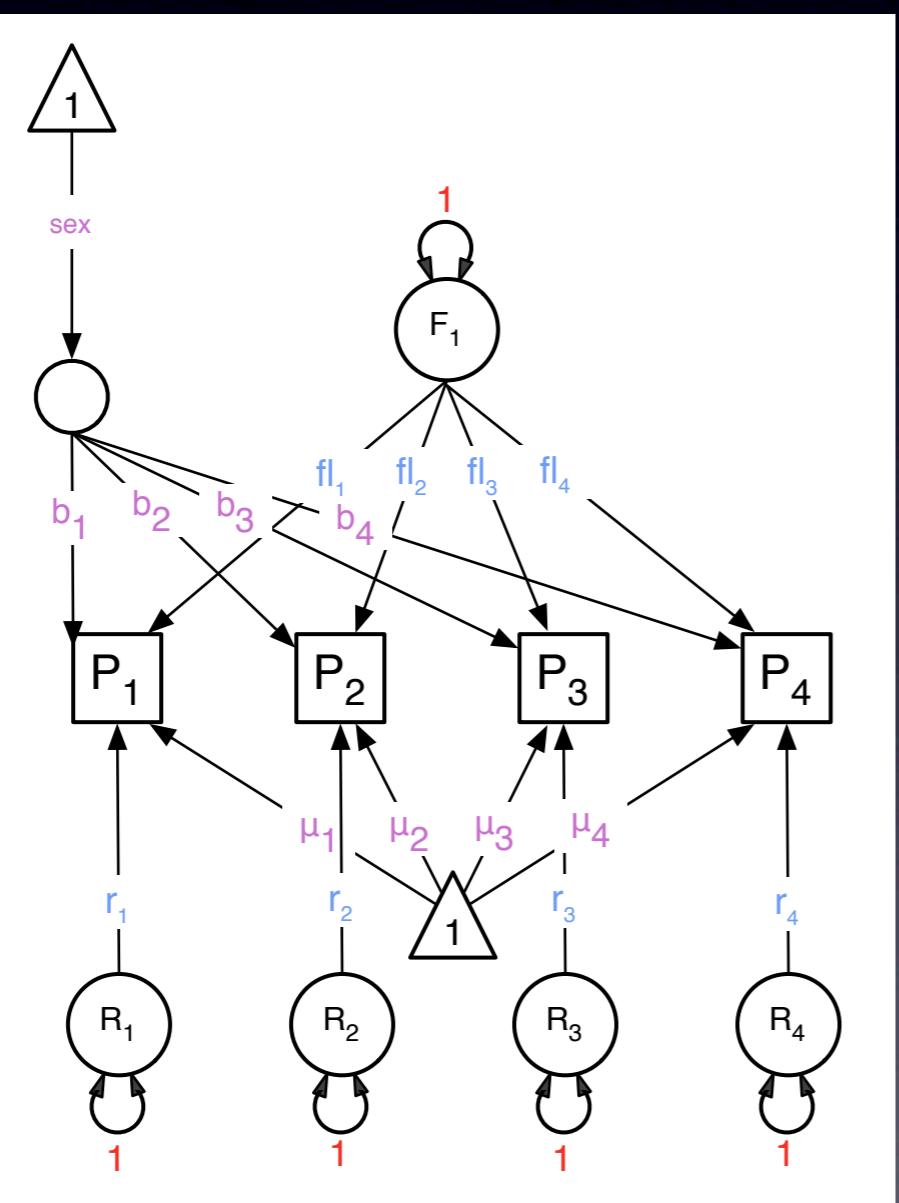
```
mxMatrix(  
  type="Full",  
  nrow=1,  
  ncol=nv,  
  free=TRUE,  
  values=0.1,  
  labels=c(  
  "beta1", "beta2",  
  "beta3", "beta4"),  
  name="Beta"),
```

# Factor Loadings



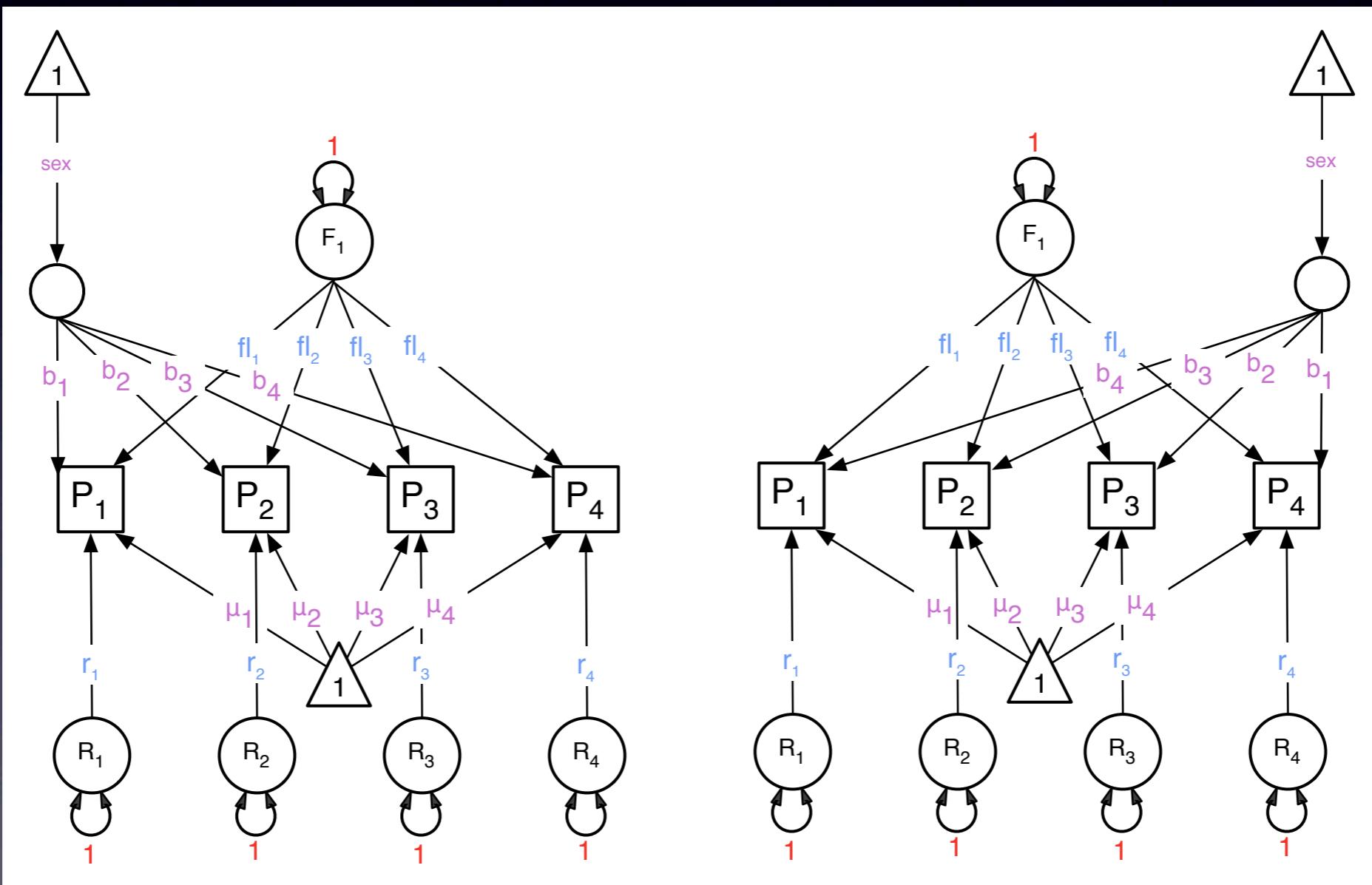
```
mxMatrix(  
  type="Full",  
  nrow=nv,  
  ncol=1,  
  free=TRUE,  
  values=1.5,  
  name="facL"),
```

# Residuals



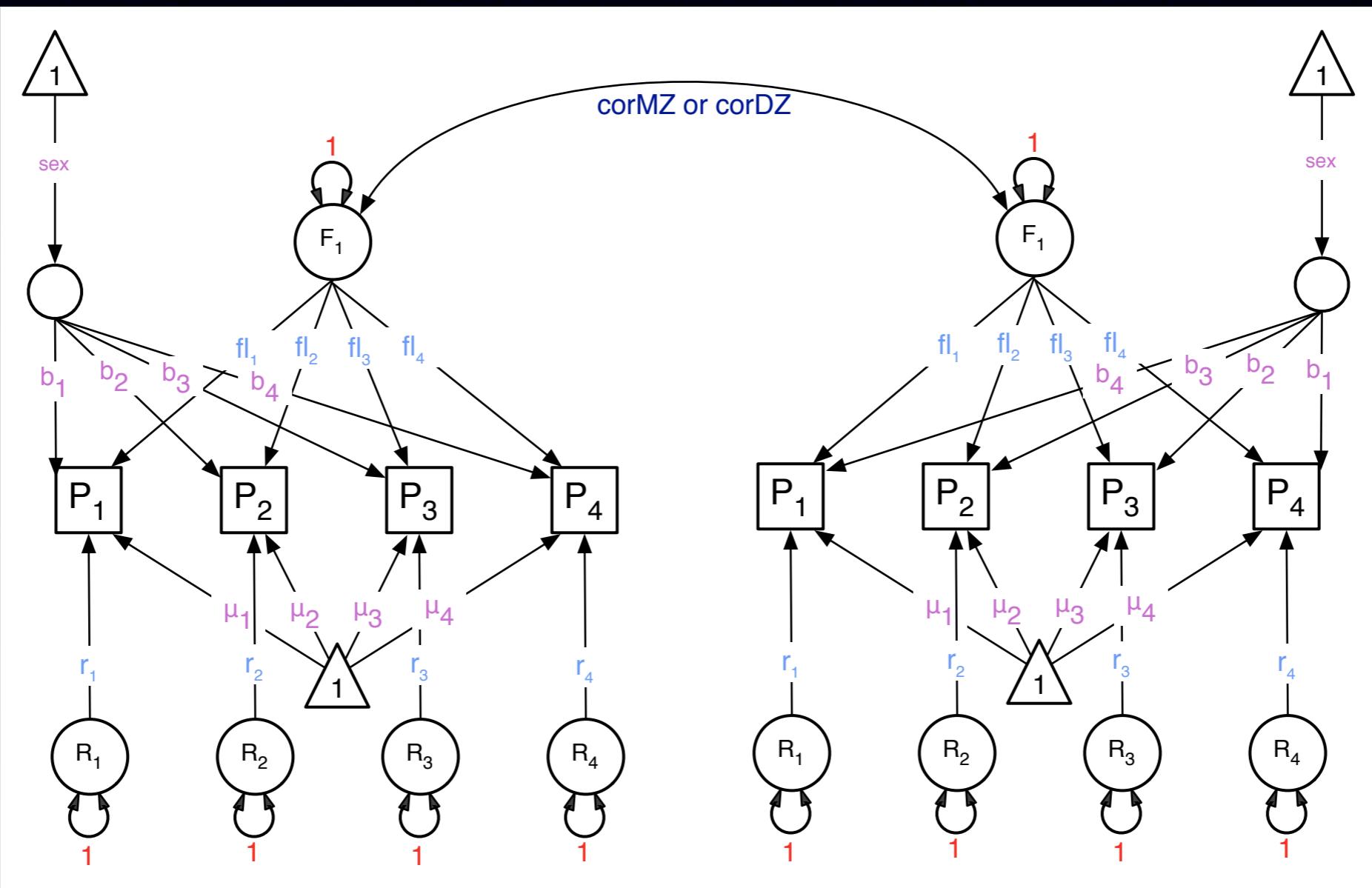
```
mxMatrix(  
  type="Diag",  
  nrow=nv,  
  ncol=nv,  
  free=TRUE,  
  values=2,  
  name="res"),
```

# Data from Twins



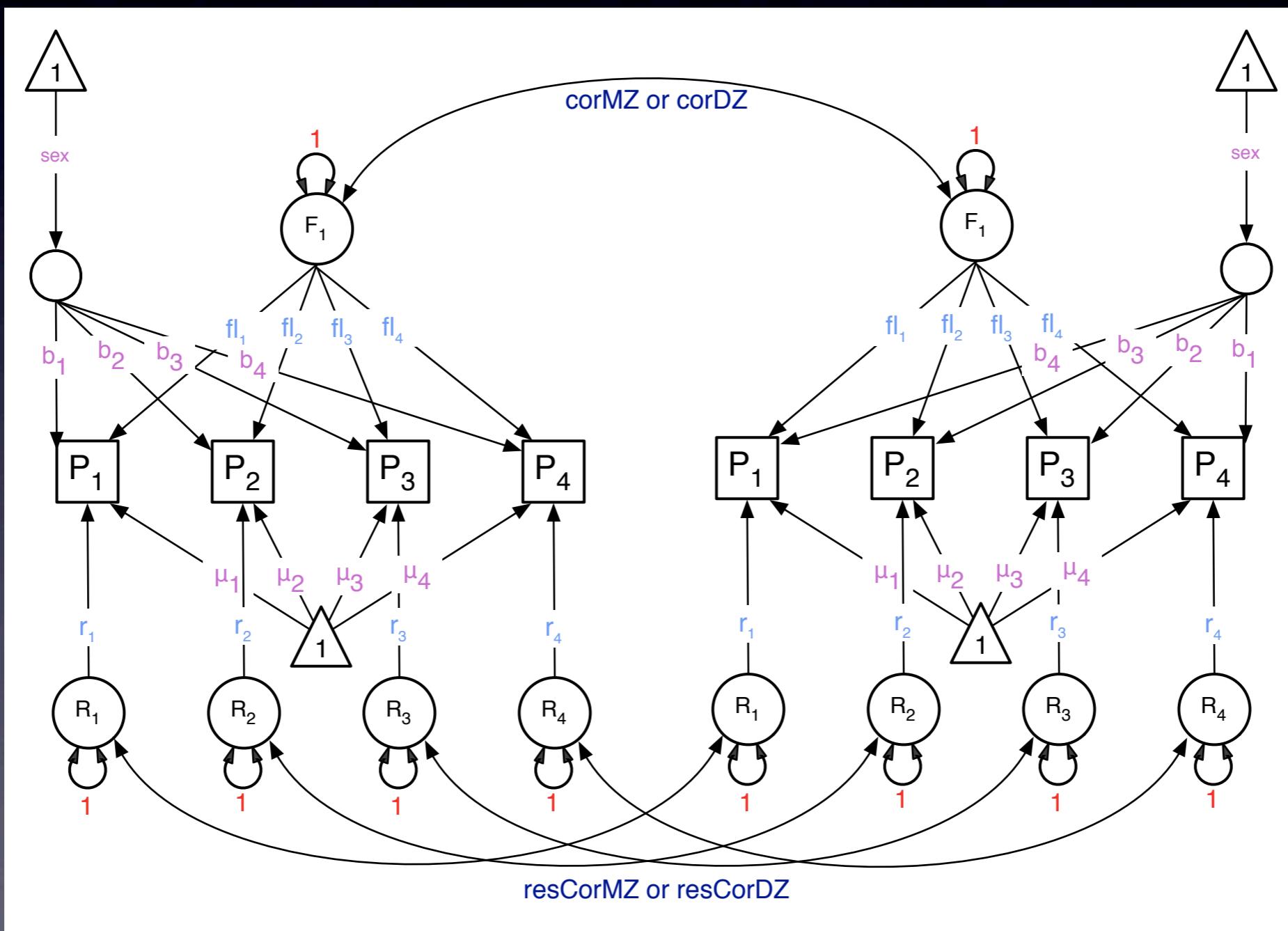
# Factor Correlations

```
mxMatrix( type="Full", nrow=1, ncol=1, free=T,  
values=.6, labels="corMZ", name="facCorMZ"),
```



# Residual Correlations

```
mxMatrix( type="Diag", nrow=nv, ncol=nv, free=T,
values=.1, name="resCorMZ"),
```



# Covariances due to Common Factor -MZ

within twins:

```
mxAlgebra(  
  expression=  
    facL %*% t(facL),  
  name="facVar"),
```

across MZ twins:

```
mxAlgebra(  
  expression=  
    facL %*% facCorMZ %*% t(facL),  
  name="facCovMZ"),
```

		T1				T2			
		m3	m7	m10	m12	m3	m7	m10	m12
T1	m3								
	m7								
	m10								
	m12								
T2	m3								
	m7								
	m10								
	m12								

# Covariances due to Common Factor -DZ

within twins:

```
mxAlgebra(  
  expression=  
    facL %*% t(facL),  
  name="facVar"),
```

across DZ twins:

```
mxAlgebra(  
  expression=  
    facL %*% facCorDZ %*% t(facL),  
  name="facCovDZ"),
```

		T1		T2				
	m3	m7	m10	m12	m3	m7	m10	m12
m3								
m7								
m10								
m12								
T1					facVar			
T2							facCovDZ	
m3								
m7								
m10								
m12								
					facCovDZ			
							facVar	

# Residual Variances

## -MZ

within twins:

```
mxAlgebra(  
  expression=  
    res %*% t(res),  
  name="resVar"),
```

across MZ twins:

```
mxAlgebra(  
  expression=  
    res %*% resCorMZ %*% t(res),  
  name="resCovMZ"),
```

		T1				T2			
		m3	m7	m10	m12	m3	m7	m10	m12
T1	m3								
	m7								
	m10								
	m12								
T2	m3								
	m7								
	m10								
	m12								

The diagram illustrates the structure of residual covariance matrices for MZ twins. It shows a 4x4 grid where rows and columns are indexed by measurement times (m3, m7, m10, m12) and twin ages (T1, T2). Two diagonal bands of cells are highlighted: a purple band running from (m3, T1) to (m12, T2) and a blue band running from (m3, T2) to (m12, T1). The labels 'resVar' and 'resCovMZ' are placed near the center of each band, indicating the elements being estimated by the respective mxAlgebra expressions.

# Residual Variances

## -DZ

within twins:

```
mxAlgebra(  
  expression=  
    res %*% t(res),  
  name="resVar"),
```

across MZ twins:

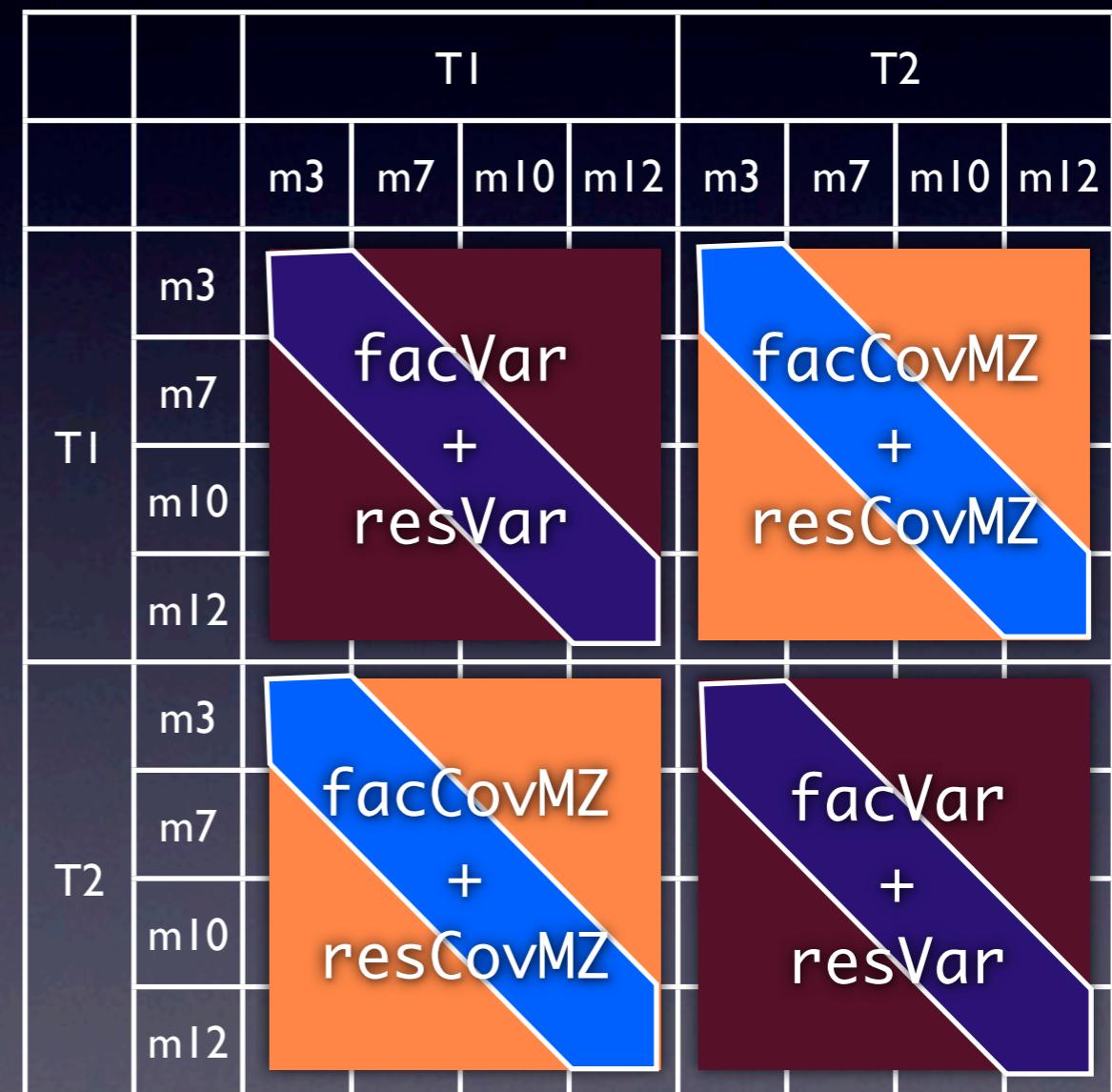
```
mxAlgebra(  
  expression=  
    res %*% resCorMZ %*% t(res),  
  name="resCovDZ")
```

		T1				T2			
		m3	m7	m10	m12	m3	m7	m10	m12
T1	m3								
	m7								
	m10								
	m12								
T2	m3								
	m7								
	m10								
	m12								

The diagram shows a 10x10 grid representing residual variances for two time points (T1 and T2) across four measurement occasions (m3, m7, m10, m12). The main diagonal (from bottom-left to top-right) is shaded blue. Two off-diagonal blocks are highlighted: a purple block below the main diagonal from (T1, m3) to (T2, m12), and a cyan block above the main diagonal from (T2, m3) to (T1, m12). Labels 'resVar' are placed within the purple block, and 'resCovDZ' are placed within the cyan block.

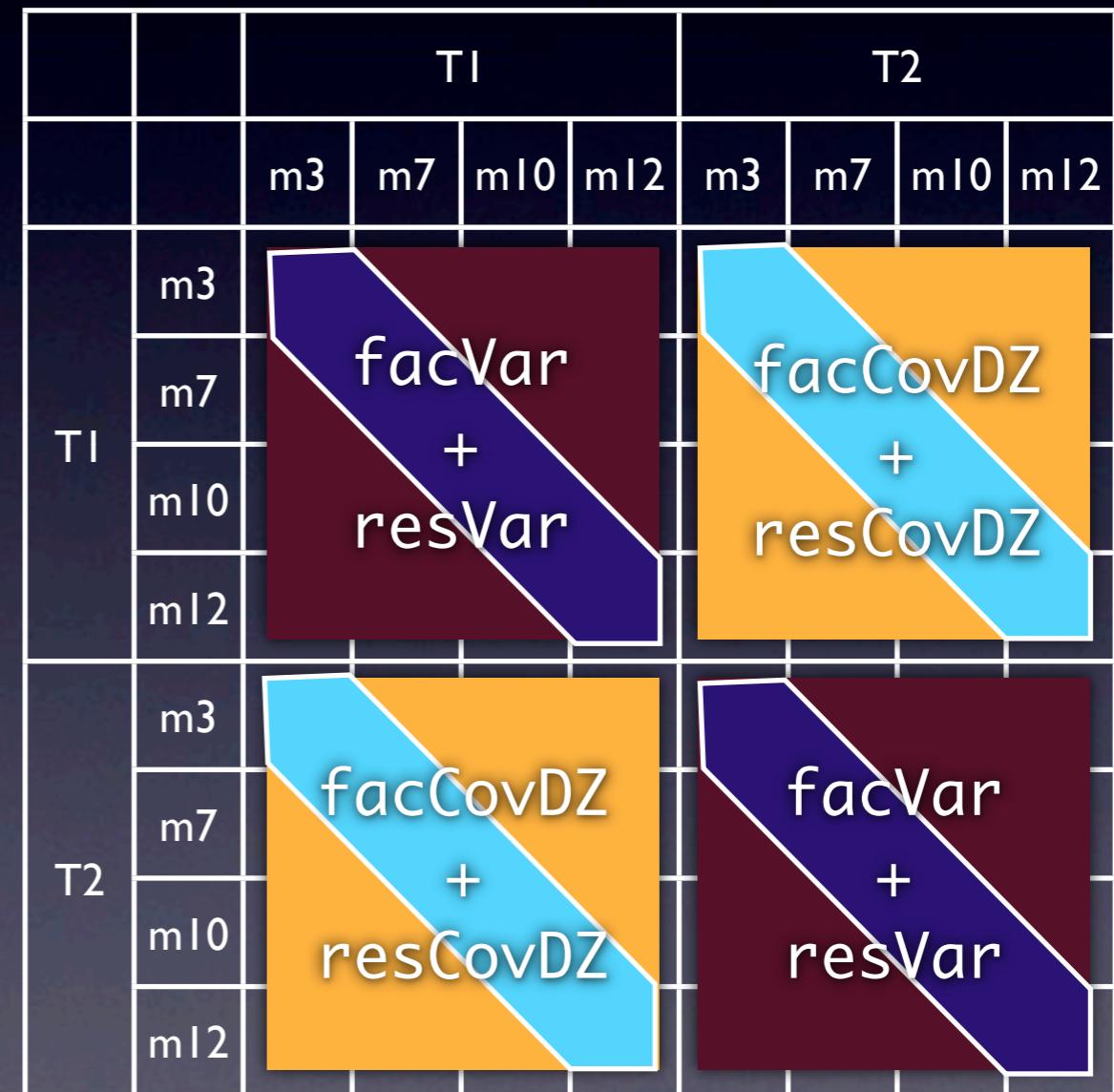
# Total (Co)Variances -MZ

```
mxAlgebra(  
  expression=  
  rbind(  
    cbind(facVar + resVar,  
           facCovMZ + resCovMZ),  
    cbind(facCovMZ + resCovMZ,  
           facVar + resVar)),  
  name="covMZ"),
```



# Total (Co)Variances -DZ

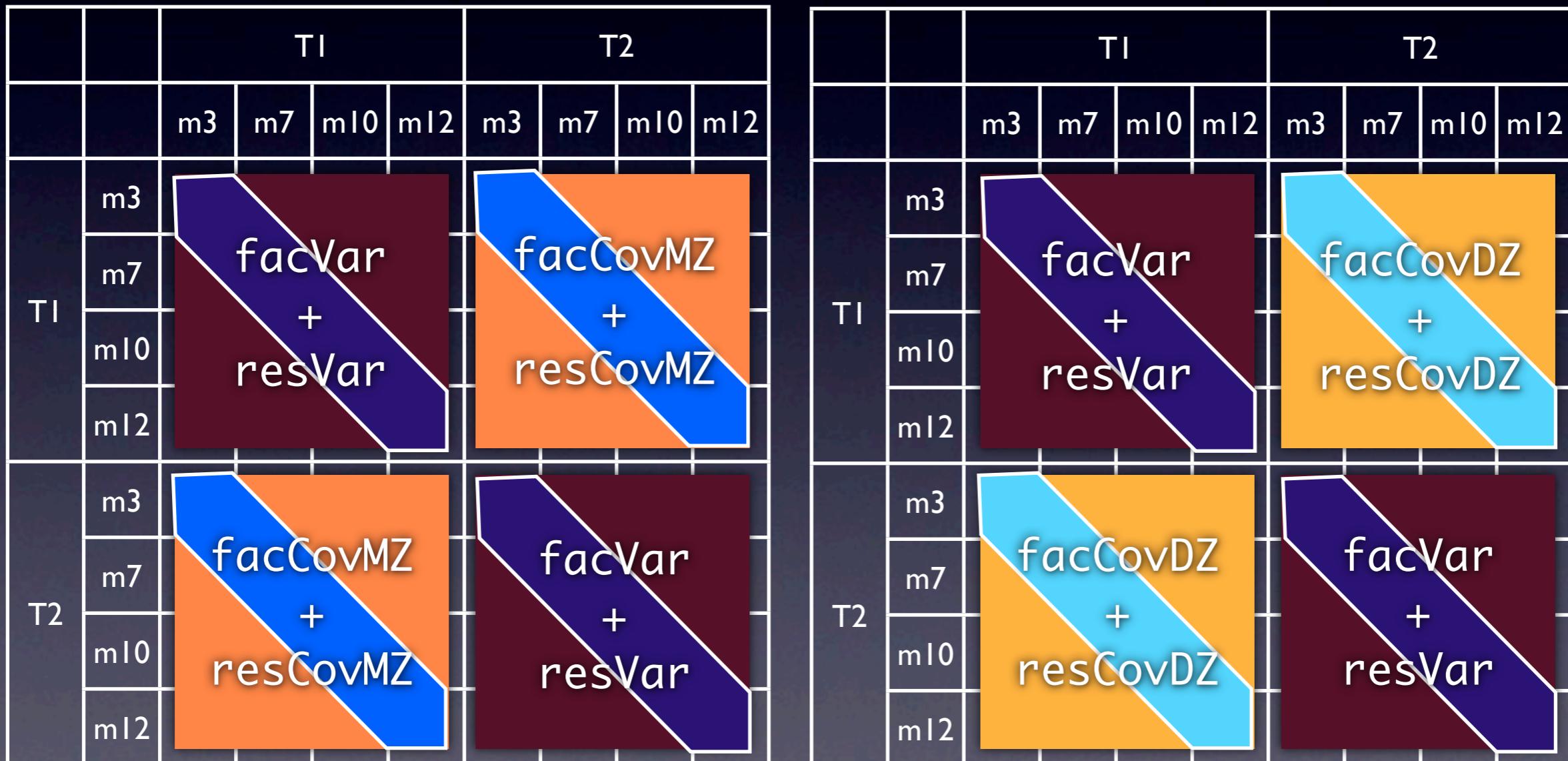
```
mxAlgebra(  
  expression=  
  rbind(  
    cbind(facVar + resVar,  
           facCovDZ + resCovDZ),  
    cbind(facCovDZ + resCovDZ,  
           facVar + resVar)),  
  name="covDZ"),
```



# Total (Co)Variances

## -MZ

## -DZ



# Parameter ‘Group’

```
mxModel("All",  
        mxMatrix(...., name="Mean"),  
        .... Beta, facL, res, facCorMZ, facCorDZ,  
        resCorMZ, resCorDZ  
        mxAlgebra(...., name="facVar"),  
        .... facCovMZ, facCovDZ, resVar, resCovMZ,  
        resCovDZ, covMZ, covDZ  
        .... Var, invSD, stFacL, stRes, StVar  
        )
```

# Data ‘Group’

```
mxModel("MZM",  
        mxData(mzmPData, "raw"),  
        mxMatrix( type="Full", nrow=1, ncol=2, free=F,  
                  labels=c"data.SEXt1","data.SEXt2"), name="sex"),  
        mxAlgebra( expression= cbind(All.Mean,All.Mean) +  
                  sex %x% All.Beta, name="mean"),  
        mxFIMLObjective( covariance="All.covMZ",  
                          means="mean", dimnames=manifestVars)  
,
```

```
mzmPData <-
  “mzmP.dat”
```

```
mo3t1 fa3t1 mo7t1 fa7t1 mo10t1 fa10t1 mo12t1 fa12t1
mo3t2 fa3t2 mo7t2 fa7t2 mo10t2 fa10t2 mo12t2 fa12t2
SEXt1 SEXt2
```

```
284 1 . 2 . 0 . 0 0 3 . 2 . 1 . 0 0 1 1
```

```
285 3 3 2 1 4 3 3 2 4 6 2 2 4 3 3 3 1 1
```

```
287 2 . . 3 1 1 0 2 . . 3 1 1 0 1 1
```

```
289 7 8 . . 8 9 3 4 7 9 . . 6 5 2 2 1 1
```

# Means & Regressions on Sex

```
mean=  
cbind(Mean,Mean)  
+ sex %x% All.Beta
```

```
sex= [data.SEXt1,data.SEXt2]
```

		T1				T2			
		m3	m7	m10	m12	m3	m7	m10	m12
x		Mean				Mean			
		m3	m7	m10	m12	m3	m7	m10	m12
		Beta				Beta			

```
1x8 [meanm3+ beta1*SEXt1, meanm7+ beta2*SEXt1, meanm10+ beta3*SEXt1, meanm12+  
beta4*SEXt1, meanm3+ beta1*SEXt2, meanm7+ beta2*SEXt2, meanm10+ beta3*SEXt2,  
meanm12+ beta4*SEXt2]
```

# Running OpenMx

```
factorModel <- mxModel("factor", ....)
```

```
factorFit <- mxRun(factorModel)
```

```
factorSumm <- summary(factorFit)
```

```
factorSumm
```

```
factorModel$All$facL
```

```
factorFit$All$facL
```

# Exercise

- Run Att4P.R
- Change to include father's ratings

m

