

# Package ‘EasyMx’

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**Type** Package

**Title** Easy Model-Builder Functions for 'OpenMx'

**Imports** methods

**Description** Utilities for building certain kinds of common matrices and models in the extended structural equation modeling package, 'OpenMx'.

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**License** GPL

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EasyMx-package	<i>EasyMx: Easy modeling in OpenMx</i>
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## Description

EasyMx is a package for extended structural equation modeling. It is built as a higher-level frontend on top of OpenMx. It is intended as an Easy introduction to OpenMx: Easy Mx. Try the example below.

## Details

All of the functions in the EasyMx package create OpenMx objects. These are most often MxMatrix, MxAlgebra, or MxModel objects. The primary difference between EasyMx and OpenMx is design philosophy. OpenMx has its foundation in WYSIWID: What you say is what it does. This requires the user to be very explicit. The EasyMx package is not as strong or flexible as OpenMx, but it places less burden on the user. Many decisions are made automatically for the user. Some of them are modifiable within EasyMx; for others the user is encouraged to use OpenMx, where nearly everything is modifiable.

The package is broadly divided into two styles of functions: matrix builders and model builders.

The matrix builder functions are utilities for building common structural equation model matrices. These include [emxLoadings](#) for factor loadings, [emxResiduals](#) for residual variances, [emxCovariances](#) for latent or manifest covariances, [emxMeans](#) for means and intercepts matrices, and [emxThresholds](#) for thresholds matrices when ordinal data are involved.

The model builder functions are higher-level utilities for building common kinds of structural equation models. The model builders often call several matrix builders. The model builders include [emxFactorModel](#) for (multiple) factor models, [emxGrowthModel](#) for latent growth curve models, and [emxRegressionModel](#) for full-information likelihood estimation of regression for observed variables.

There are also a few model builder functions for non-standard structural equation models. In particular, the `emxVARModel` function creates vector autoregressive models, and the `emxStateSpaceMixtureModel` function creates state space mixture models.

A third category of functions encompasses special functions for behavior genetics modeling. Some of these functions are matrix builders, and others are model builders. The lowest-level functions for behavior genetics are `emxCholeskyVariance`, `emxGeneticFactorVariance`, `emxRelatednessMatrix`, and `emxKroneckerVariance`.

A higher-level set of behavior genetics matrix builders create all the matrices and algebraic statements needed for e.g. the A component of an ACE model. These functions are `emxCholeskyComponent` and `emxGeneticFactorComponent`.

The highest-level of behavior genetics functions builds some basic twin models. The primary function for this is `emxTwinModel`.

Finally, a mixture model helper is provided: `emxMixtureModel`.

## Examples

```
# Make and run a one factor model
## Not run:
require(EasyMx)

data(demoOneFactor)
fmod <- list(G=names(demoOneFactor))
fit1 <- emxFactorModel(fmod, demoOneFactor, run=TRUE)
summary(fit1)

## End(Not run)
```

---

`emxCholeskyComponent`    *Creates component for a Biometric Cholesky Model*

---

## Description

This function creates all the objects needed for a Cholesky component.

## Usage

```
emxCholeskyComponent(x, xname, xvalues, xfree,
                    h=2, hname=paste0('H', xname), hvalues, hlabels)
```

## Arguments

<code>x</code>	character vector. The base names of the variables used for the matrix with no repetition for twins (x, y, z not x1, y1, z1, x2, y2, z2).
<code>xname</code>	character. Name of the component matrix.
<code>xvalues</code>	numeric vector. Values of the component matrix.

xfree	logical vector. Whether each element of the component matrix is freely estimates.
h	numeric. The number of variables for the relatedness matrix, i.e. the number of critters with relationships
hname	character. Name of the relatedness matrix.
hvalues	numeric vector. Values for the relatedness matrix.
hlabels	character vector. Labels for the relatedness matrix.

### Details

This function is a combination of `emxCholeskyVariance`, `emxRelatednessMatrix`, and `emxKroneckerVariance`.

### Value

A list with elements (1) the lower triangular matrix for the Cholesky, (2) the full positive definite variance matrix, (3) the relatedness matrix, and (4) the Kronecker product of the variance matrix and the relatedness matrix.

### See Also

[emxGeneticFactorComponent](#)

### Examples

```
# Create an ACE model in 22 lines
require(EasyMx)
require(OpenMx)
data(twinData)
twinVar = names(twinData)
selVars <- c('ht1', 'bmi1', 'ht2', 'bmi2')
mzdzData <- subset(twinData, zyg %in% c(1, 3), c(selVars, 'zyg'))
mzdzData$RCcoef <- c(1, NA, .5)[mzdzData$zyg]
nVar = length(selVars)/2
x <- paste0('x', 1:nVar)

acomp <- emxCholeskyComponent(x, 'A', hvalues=c(1, .5, 1), hlabels=c(NA, 'data.RCcoef', NA))
ccomp <- emxCholeskyComponent(x, 'C', hvalues=c(1, 1, 1))
ecomp <- emxCholeskyComponent(x, 'E', hvalues=c(1, 0, 1))
totalVar <- mxAlgebra(AKron + CKron + EKron, 'V', dimnames=list(selVars, selVars))
totalMean <- emxMeans(selVars, type='twin')
expect <- mxExpectationNormal(totalVar$name, totalMean$name)
fitfun <- mxFitFunctionML()

comlist <- c(acomp, ccomp, ecomp, list(totalVar, totalMean, expect, fitfun))

model <- mxModel('model', comlist, mxData(mzdzData, 'raw'))
## Not run:
run2 <- mxRun(model)
```

```
## End(Not run)
```

---

emxCholeskyVariance *Create a variance matrix in Cholesky form*

---

### Description

This function creates a Cholesky variance matrix and associated MxMatrix and MxAlgebra objects.

### Usage

```
emxCholeskyVariance(x, name, values=.8, free=TRUE)
```

### Arguments

x	character vector. The names of the variables used for the matrix.
name	character. The name of the variance matrix created.
values	numeric vector. The starting values for the lower triangular matrix.
free	logical vector. Whether the lower triangular elements are free.

### Details

This is a helper function for creating a matrix that is symmetric and positive definite. Full covariance matrices are the most common case of these. In a behavior genetics modeling context, Cholesky components can be created for Additive genetics, Common environments, and unique Environments. These are unrestrictive models of the covariances of multiple phenotypes.

### Value

A list with two components. The first component is the lower triangular MxMatrix. The second component is an MxAlgebra, the result of which is the positive definite variance matrix.

### See Also

[emxGeneticFactorVariance](#)

### Examples

```
# Create a Cholesky variance matrix called 'A'  
require(EasyMx)  
nVar <- 3  
x <- paste0('x', 1:nVar)  
amat <- emxCholeskyVariance(x, 'A')
```

---

 emxCommonPathwayComponent

*Creates component for a Biometric Common Pathway Model*


---

### Description

UNDER ACTIVE DEVELOPMENT. DO NOT TRUST. This function creates all the objects needed for a Common Pathway component.

### Usage

```
emxCommonPathwayComponent(x, xname, xvalues=.8, xfree=TRUE, xlbound=NA, xubound=NA,
                           h=2, hname=paste0('H', xname), hvalues, hlabels)
```

### Arguments

x	character vector. The base names of the variables used for the matrix with no repetition for twins (x, y, z not x1, y1, z1, x2, y2, z2).
xname	character. Name of the component matrix.
xvalues	Matrix of fixed and/or starting values of parameters
xfree	Matrix of TRUE (for free) and FALSE (for fixed) values
xlbound	Matrix of numeric lower bounds for parameters
xubound	Matrix of numeric upper bounds for parameters
h	numeric. The number of variables for the relatedness matrix, i.e. the number of critters with relationships
hname	character. Name of the relatedness matrix.
hvalues	numeric vector. Values for the relatedness matrix.
hlabels	character vector. Labels for the relatedness matrix.

### Details

This function is a combination of emxCholeskyVariance, emxRelatednessMatrix, and emxKroneckerVariance.

### Value

A list with elements (1) the lower triangular matrix for the Cholesky, (2) the full positive definite variance matrix, (3) the relatedness matrix, and (4) the Kronecker product of the variance matrix and the relatedness matrix.

### See Also

[emxGeneticFactorComponent](#)

**Examples**

```

# Create an ACE model in 22 lines
require(EasyMx)
require(OpenMx)
data(twinData)
twinVar = names(twinData)
selVars <- c('ht1', 'bmi1', 'ht2', 'bmi2')
mzdzData <- subset(twinData, zyg %in% c(1, 3), c(selVars, 'zyg'))
mzdzData$RCoeff <- c(1, NA, .5)[mzdzData$zyg]
nVar = length(selVars)/2
x <- paste0('x', 1:nVar)

acomp <- emxCholeskyComponent(x, 'A', hvalues=c(1, .5, 1), hlabels=c(NA, 'data.RCoef', NA))
ccomp <- emxCholeskyComponent(x, 'C', hvalues=c(1, 1, 1))
ecomp <- emxCholeskyComponent(x, 'E', hvalues=c(1, 0, 1))
totalVar <- mxAlgebra(AKron + CKron + EKron, 'V', dimnames=list(selVars, selVars))
totalMean <- emxMeans(selVars, type='twin')
expect <- mxExpectationNormal(totalVar$name, totalMean$name)
fitfun <- mxFitFunctionML()

comlist <- c(acomp, ccomp, ecomp, list(totalVar, totalMean, expect, fitfun))

model <- mxModel('model', comlist, mxData(mzdzData, 'raw'))
## Not run:
run2 <- mxRun(model)

## End(Not run)

```

---

emxCovariances

*Create a set of covariances*


---

**Description**

This function creates a covariance matrix as an MxMatrix or MxPath object.

**Usage**

```
emxCovariances(x, values, free, path=FALSE, type, name='Variances')
```

**Arguments**

x	character vector. The names of the variables for which covariances are created.
values	numeric vector. See Details.
free	logical vector. See Details.
path	logical. Whether to return the MxPath object instead of the MxMatrix.
type	character. The kind of covariance structure to create. See Details.
name	The name of the matrix created.

## Details

Possible values for the type argument are 'independent', 'full', and 'corr'. When type='independent', the remaining arguments are passed to [emxResiduals](#). The values and free arguments are only used when the type argument is 'independent'. For all other cases, they are ignored.

When type='full', a full covariance matrix is created. That is, a symmetric matrix is created with all unique elements freely estimated. The starting values for the variances are all 1; for the covariances, all 0.5.

When type='corr', a full correlation matrix is created. That is, a symmetric matrix is created with all unique elements not on the diagonal freely estimated. The starting values for the correlations are all 0.5. The variances are fixed at 1.

## Value

Depending on the value of the path argument, either an MxMatrix or an MxPath object that can be inspected, modified, and/or included in MxModel objects.

## See Also

[emxFactorModel](#), [emxGrowthModel](#)

## Examples

```
# Create a covariance matrix
require(EasyMx)
manVars <- paste0('x', 1:6)
latVars <- paste0('F', 1:2)
emxCovariances(manVars, type='full')
emxCovariances(latVars, type='corr', path=TRUE)
```

---

emxFactorModel

*Create a factor model*

---

## Description

This function creates a factor model as an MxModel object.

## Usage

```
emxFactorModel(model, data, name, run=FALSE, identification, use, ordinal,
  ..., parameterization=c("lisrel", "ifa"), weight = as.character(NA))
emxModelFactor(model, data, name, run=FALSE, identification, use, ordinal,
  ..., parameterization=c("lisrel", "ifa"), weight = as.character(NA))
```



**Arguments**

model	named list. Gives the factor loading pattern. See Details.
data	data used for the model
name	character. Optional name of the model created.
run	logical. Whether to run the model before returning.
identification	Not yet implemented. How the model is identified. Currently ignored.
use	character vector. The names of the variables to use.
ordinal	character vector. The names of the ordinal variables.
...	Force later arguments to be named. ... is ignored.
parameterization	character. Whether to specify the model as a LISREL SEM or as an Item Factor Analysis
weight	character. Name of the data column used for sample weights.

**Details**

The `model` argument must be a named list. The names of the list give the names of the latent variables. Each list element gives the names of the variables that load onto that latent variable. This may sound complicated, but the example below makes this more clear. It is intended to be visually intuitive.

**Value**

An `MxModel`.

**See Also**

[emxLoadings](#)

**Examples**

```
# Example
require(EasyMx)
data(myFADDataRaw)
xmap <- list(F1=paste0('x', 1:6), F2=paste0('y', 1:3), F3=paste0('z', 1:3))
## Not run:
mod <- emxFactorModel(xmap, data=myFADDataRaw, run=TRUE)

## End(Not run)
```

---

`emxGeneticFactorComponent`*Creates component for a Genetic Factor Model*

---

**Description**

This function creates all the objects needed for Genetic Factor component

**Usage**

```
emxGeneticFactorComponent(x, xname, xvalues=.8, xfree=TRUE, xlbound=NA, xubound=NA,
                           h=2, hname=paste0('H', xname), hvalues, hlabels)
```

**Arguments**

<code>x</code>	character vector. The base names of the variables used for the matrix with no repetition for twins (x, y, z not x1, y1, z1, x2, y2, z2).
<code>xname</code>	character. Name of the component matrix.
<code>xvalues</code>	numeric vector. Values of the genetic factor loadings.
<code>xfree</code>	logical vector. Whether the genetic factor loadings are free.
<code>xlbound</code>	numeric vector. Lower bounds of the factor loadings.
<code>xubound</code>	numeric vector. Upper bounds of the factor loadings.
<code>h</code>	numeric. The number of variables for the relatedness matrix, i.e. the number of critters with relationships
<code>hname</code>	character. Name of the relatedness matrix.
<code>hvalues</code>	numeric vector. Values for the relatedness matrix.
<code>hlabels</code>	character vector. Labels for the relatedness matrix.

**Details**

This function is a combination of `emxGeneticFactorVariance`, `emxRelatednessMatrix`, and `emxKroneckerVariance`.

**Value**

A list with elements (1) the genetic factor loadings matrix, (2) the full positive definite variance matrix, (3) the relatedness matrix, and (4) the Kronecker product of the variance matrix and the relatedness matrix.

**See Also**

[emxCholeskyComponent](#)

## Examples

```
# Create genetic factor A component for DZ twins
require(EasyMx)
xvars <- paste0('x', 1:4)
acomp <- emxGeneticFactorComponent(xvars, 'A', hvalues=c(1, .5, 1))
```

---

emxGeneticFactorVariance

*Creates a variance matrix accoring to the Genetic Factor Model*

---

## Description

This function creates a variance matrix according to the genetic factor model

## Usage

```
emxGeneticFactorVariance(x, name, values=.8, free=TRUE, lbound=NA, ubound=NA)
```

## Arguments

x	character vector. The names of the variables used for the matrix.
name	character. The name of the variance matrix created.
values	numeric vector. The starting values for the lower triangular matrix.
free	logical vector. Whether the lower triangular elements are free.
lbound	numeric vector. Lower bounds on free parameters.
ubound	numeric vector. Upper bounds on free parameters.

## Value

A list with two components. The first component is the factor loadings matrix. The second component is an MxAlgebra, the result of which is the variance matrix implied by the factor loadings.

## See Also

[emxCholeskyVariance](#)

## Examples

```
# Create a genetic factor variance matrix
require(EasyMx)
xvars <- paste0('x', 1:2)
emxGeneticFactorVariance(xvars, 'D')
```

---

 emxGrowthModel

*Create a latent growth curve model*


---

### Description

This function creates a latent growth curve model as an MxModel object.

### Usage

```
emxGrowthModel(model, data, name, run=FALSE, identification, use, ordinal, times)
emxModelGrowth(model, data, name, run=FALSE, identification, use, ordinal, times)
```

### Arguments

model	character or numeric. See Details.
data	data used for the model
name	character. Optional name of the model created.
run	logical. Whether to run the model before returning.
identification	Not yet implemented. How the model is identified. Currently ignored.
use	character vector. The names of the variables to use.
ordinal	character vector. The names of the ordinal variables.
times	optional character or numeric vector. Either the numeric times of measurement or the names of the variables in data that give the times of measurement.

### Details

The model argument can be either a character or a number that tells the kind of growth curve to make. If it is a character it currently must be one of "Intercept", "Linear", "Quadratic", "Cubic", "Quartic", or "Quintic", and it produces a polynomial growth curve of the corresponding type. If it is a number, the function produces a polynomial growth curve of the corresponding order. Zero is an intercept only, one is linear, two is quadratic; and so on.

When missing, the times are assumed to start at zero and increment by one until the number of variables is completed.

### Value

An MxModel

### See Also

[emxFactorModel](#), [emxGrowthModel](#)

**Examples**

```
# Example
require(EasyMx)
data(myLongitudinalData)
## Not run:
mod <- emxGrowthModel('Linear', data=myLongitudinalData, use=names(myLongitudinalData), run=TRUE)

## End(Not run)
```

---

emxIndependentPathwayComponent

*Creates component for a Biometric Independent Pathway Model*

---

**Description**

UNDER ACTIVE DEVELOPMENT. DO NOT TRUST. This function creates all the objects needed for an Independent Pathway component.

**Usage**

```
emxIndependentPathwayComponent(x, xname, xvalues=.8, xfree=TRUE, xlbound=NA, xubound=NA,
                              h=2, hname=paste0('H', xname), hvalues, hlabels)
```

**Arguments**

x	character vector. The base names of the variables used for the matrix with no repetition for twins (x, y, z not x1, y1, z1, x2, y2, z2).
xname	character. Name of the component matrix.
xvalues	Matrix of fixed and/or starting values of parameters
xfree	Matrix of TRUE (for free) and FALSE (for fixed) values
xlbound	Matrix of numeric lower bounds for parameters
xubound	Matrix of numeric upper bounds for parameters
h	numeric. The number of variables for the relatedness matrix, i.e. the number of critters with relationships
hname	character. Name of the relatedness matrix.
hvalues	numeric vector. Values for the relatedness matrix.
hlabels	character vector. Labels for the relatedness matrix.

**Details**

This function is a combination of emxCholeskyVariance, emxRelatednessMatrix, and emxKroneckerVariance.

**Value**

A list with elements (1) the lower triangular matrix for the Cholesky, (2) the full positive definite variance matrix, (3) the relatedness matrix, and (4) the Kronecker product of the variance matrix and the relatedness matrix.

**See Also**

[emxGeneticFactorComponent](#)

**Examples**

```
# Create an ACE model in 22 lines
require(EasyMx)
require(OpenMx)
data(twinData)
twinVar = names(twinData)
selVars <- c('ht1', 'bmi1', 'ht2', 'bmi2')
mzdzData <- subset(twinData, zyg %in% c(1, 3), c(selVars, 'zyg'))
mzdzData$RCoeff <- c(1, NA, .5)[mzdzData$zyg]
nVar = length(selVars)/2
x <- paste0('x', 1:nVar)

acomp <- emxCholeskyComponent(x, 'A', hvalues=c(1, .5, 1), hlabels=c(NA, 'data.RCcoef', NA))
ccomp <- emxCholeskyComponent(x, 'C', hvalues=c(1, 1, 1))
ecomp <- emxCholeskyComponent(x, 'E', hvalues=c(1, 0, 1))
totalVar <- mxAlgebra(AKron + CKron + EKron, 'V', dimnames=list(selVars, selVars))
totalMean <- emxMeans(selVars, type='twin')
expect <- mxExpectationNormal(totalVar$name, totalMean$name)
fitfun <- mxFitFunctionML()

comlist <- c(acomp, ccomp, ecomp, list(totalVar, totalMean, expect, fitfun))

model <- mxModel('model', comlist, mxData(mzdzData, 'raw'))
## Not run:
run2 <- mxRun(model)

## End(Not run)
```

---

emxKroneckerVariance *Creates a large Variance matrix by Kroneckering two smaller matrices*

---

**Description**

This function creates the wide format variance matrix when combined with a relatedness matrix

**Usage**

```
emxKroneckerVariance(h, v, name)
```

**Arguments**

h	MxMatrix. Left hand side of the Kronecker product. Typically the relatedness matrix.
v	MxMatrix. Right hand side of the Kronecker product. Typically the variance matrix.
name	character. Name of the resulting large matrix.

**Details**

In many behavior genetic models, a relationship matrix is combined with a base variance matrix. The combination is done with a Kronecker product so that the variance exists (possibly weighted by zero or another number) for each member of the relationship.

**Value**

MxAlgebra

**See Also**

[emxRelatednessMatrix](#)

**Examples**

```
# Create a loadings matrix
require(EasyMx)
x <- letters[23:26]
amat <- emxCholeskyVariance(x, 'A')
ahmat <- emxRelatednessMatrix(2, c(1, .5, 1), name='AH')
ab <- emxKroneckerVariance(ahmat, amat[[2]], 'AB')
```

---

emxLoadings

*Create a factor loadings matrix*

---

**Description**

This function creates a factor loadings matrix as an MxMatrix or MxPath object.

**Usage**

```
emxLoadings(x, values=.8, free=TRUE, path=FALSE)
```

**Arguments**

x	named list. Gives the factor loading pattern. See Details.
values	numeric vector. The starting values for the nonzero loadings.
free	logical vector. Whether the nonzero loadings are free.
path	logical. Whether to return the MxPath object instead of the MxMatrix.

**Details**

The `x` argument must be a named list. The names of the list give the names of the latent variables. Each list element gives the names of the variables that load onto that latent variable. This may sound complicated, but the example below makes this more clear. It is intended to be visually intuitive.

**Value**

Depending on the value of the `path` argument, either an `MxMatrix` or an `MxPath` object that can be inspected, modified, and/or included in `MxModel` objects.

**See Also**

[emxFactorModel](#)

**Examples**

```
# Create a loadings matrix
require(EasyMx)
xmap <- list(F1=paste0('x', 1:6), F2=paste0('y', 1:3), F3=paste0('z', 1:3))
emxLoadings(xmap)
emxLoadings(xmap, path=TRUE)
```

---

emxMeans

*Create a set of means*

---

**Description**

This function creates a means matrix as an `MxMatrix` or `MxPath` object.

**Usage**

```
emxMeans(x, values=0, free=TRUE, path=FALSE, type='saturated', name, column=TRUE, labels)
```

**Arguments**

<code>x</code>	character vector. The names of the variables for which means are created.
<code>values</code>	numeric vector. See Details.
<code>free</code>	logical vector. See Details.
<code>path</code>	logical. Whether to return the <code>MxPath</code> object instead of the <code>MxMatrix</code> .
<code>type</code>	character. The kind of covariance structure to create. See Details.
<code>name</code>	The name of the matrix created.
<code>column</code>	logical. Whether to create the means vector as a column or row.
<code>labels</code>	character vector. Optional labels for the means.



**Details**

Possible values for the type argument are 'saturated', 'equal', 'twin', 'special'.

**Value**

Depending on the value of the path argument, either an MxMatrix or and MxPath object that can be inspected, modified, and/or included in MxModel objects.

**See Also**

[emxFactorModel](#), [emxGrowthModel](#)

**Examples**

```
# Create a covariance matrix
require(EasyMx)
manVars <- paste0('x', 1:6)
emxMeans(manVars, type='saturated')
```

---

emxMixtureModel	<i>Create a mixture model</i>
-----------------	-------------------------------

---

**Description**

This function creates a mixture model as an MxModel object.

**Usage**

```
emxMixtureModel(model, data, run=FALSE, p=NA, ...)
emxModelMixture(model, data, run=FALSE, p=NA, ...)
```

**Arguments**

model	list. The MxModel objects that compose the mixture.
data	data used for the model
run	logical. Whether to run the model before returning.
p	character. Optional name of the mixing proportions matrix.
...	Further Mx Objects passed into the mixture model.

**Details**

The model argument is list of MxModel objects. These are the classes over which the mixture model operates.

The p argument is optional. If not specified, the function will create and properly scale the mixing proportions for you. If specified, the Mx Object that gives the mixing proportions should be a column vector (one-column matrix).

**Value**

An MxModel.

**See Also**

[emxLoadings](#)

**Examples**

```
# Factor Mixture Example
require(EasyMx)
data(myFADataRaw)
xmap1 <- list(F1=paste0('x', 1:6), F2=paste0('y', 1:3), F3=paste0('z', 1:3))
mod1 <- emxFactorModel(xmap1, data=myFADataRaw, name='m1')

xmap2 <- list(F1=c(paste0('x', 1:6), paste0('y', 1:3), paste0('z', 1:3)))
mod2 <- emxFactorModel(xmap2, data=myFADataRaw, name='m2')

mod <- emxMixtureModel(list(mod1, mod2), data=myFADataRaw)
# To estimate parameters either
# 1. mod <- mxRun(mod) or
# 2. include run=TRUE in the arguments above
summary(mod)
coef(mod)

# Latent Profile Example
require(EasyMx)

m1 <- omxSaturatedModel(demoOneFactor)[[1]]
m1 <- mxRename(m1, 'profile1')

m2 <- omxSaturatedModel(demoOneFactor)[[1]]
m2 <- mxRename(m2, 'profile2')

mod <- emxMixtureModel(list(m1, m2), data=demoOneFactor)
# To estimate parameters either
# 1. mod <- mxRun(mod) or
# 2. include run=TRUE in the arguments above
summary(mod)
coef(mod)

mxGetExpected(mod$profile1, 'covariance')
mxGetExpected(mod$profile1, 'means')
mxGetExpected(mod$profile2, 'covariance')
mxGetExpected(mod$profile2, 'means')
```

---

emxRegressionModel      *Create a regression model*

---

## Description

This function creates a regression model as an MxModel object.

## Usage

```
emxRegressionModel(model, data, type='Steven', run, ...)  
emxModelRegression(model, data, type='Steven', run, ...)
```

## Arguments

model	formula. See Details.
data	data used for the model
run	logical. Whether to run the model before returning.
type	character. Either 'Steven' or 'Joshua'. See Details.
...	Further named arguments to be passed to <code>lm</code> for the formula

## Details

The `model` argument is a formula identical to what is used in [lm](#).

The `type` argument switches the kind of regression model that is specified. When there are no missing data, the two versions will estimate the same regression parameters but `type='Steven'` will estimate additional parameters that are not estimated by `type='Joshua'`. The `type='Steven'` model is due to Steven Boker and many others. It estimates more parameters than a typical regression analysis and has a different set of assumptions. More exactly, `type='Steven'` models the outcome and all of the predictors as a multivariate Normal distribution. By contrast, `type='Joshua'` is due to Joshua Pritikin and exactly replicates the typical regression model with its usual assumptions. In particular, `type='Joshua'` models the regression residual as a univariate Normal distribution. Predictors are assumed to have no measurement error (see Westfall & Yarkoni, 2016).

The benefit of `type='Steven'` is that it handles missing data with full-information maximum likelihood (FIML; Enders & Bandalos, 2001), at the cost of using a different model with different assumptions from ordinary least squares regression. The benefit of `type='Joshua'` is that it exactly replicates regression as a maximum likelihood model, at the cost of having the same weakness in terms of missing data as OLS regression.

## Value

An MxModel.

## References

Enders, C. K. & Bandalos, D. L. (2001). The relative performance of full information maximum likelihood estimation for missing data in structural equation models. *Structural Equation Modeling*, 8(3), 430-457.

Westfall, J. & Yarkoni, T. (2016). Statistically controlling for confounding constructs is harder than you think. *PLoS ONE*, 11(3). doi:10.1371/journal.pone.0152719

## See Also

[lm](#)

## Examples

```
# Example
require(EasyMx)
data(myRegDataRow)
myrdr <- myRegDataRow
myrdr[1, 4] <- NA

## Not run:
run <- emxRegressionModel(y~1+x*z, data=myrdr, run=TRUE)
summary(run)

## End(Not run)

summary(lm(y~1+x*z, data=myrdr))
```

---

emxRelatednessMatrix *Create a relatedness matrix*

---

## Description

This function creates a relatedness matrix as an MxMatrix, often used in behavior genetics modeling.

## Usage

```
emxRelatednessMatrix(nvar, values, labels, name='h')
```

## Arguments

nvar	numeric. The number of variables for the matrix, i.e. the number of rows or columns.
values	numeric vector. Values used in the matrix.
labels	character vector. Labels of the elements in the matrix. See Details.
name	character. The name of the matrix created.

**Details**

The labels argument can be used to create a "definition variable" which populates the value from one of the data columns for each row in the data. In this context, if the genetic relatedness coefficient between a pair of individuals is given by a column in the data then that information can be used to create in the relatedness matrix. Alternatively, multiple groups can be created

**Value**

An MxMatrix object.

**See Also**

[emxGeneticFactorVariance](#)

**Examples**

```
# Create a Cholesky variance matrix called 'A'
require(EasyMx)
ahmat <- emxRelatednessMatrix(2, c(1, .5, 1), labels=c(NA, 'data.RCoef', NA), name='AH')
# data.RCoef creates a definition variable and ignores the .5 value.
```

---

emxResiduals

---

*Create a residual variances matrix*


---

**Description**

This function creates a factor loadings matrix as an MxMatrix or MxPath object.

**Usage**

```
emxResiduals(x, values=.2, free=TRUE, lbound=NA, ubound=NA, path=FALSE, type='unique')
```

**Arguments**

x	character vector. The names of the variables for which residual variances are created.
values	numeric vector. The starting values for the variances.
free	logical vector. Whether the variances are free.
lbound	numeric vector. Lower bounds for the variances.
ubound	numeric vector. Upper bounds for the variances.
path	logical. Whether to return the MxPath object instead of the MxMatrix.
type	character. The kind of residual variance structure to create. See Details.

**Details**

Possible values for the type argument are 'unique' and 'identical'. When type='unique', each residual variances is a unique free parameter. When type='identical', all of the residual variances are given by a single free parameter. In this case, all the residual variances are constrained to be equal. However, no linear or non-linear constraint function is used. Rather, a single parameter occurs in multiple locations by using the same label.

**Value**

Depending on the value of the path argument, either an MxMatrix or and MxPath object that can be inspected, modified, and/or included in MxModel objects.

**See Also**

[emxFactorModel](#), [emxGrowthModel](#)

**Examples**

```
# Create a residual variance matrix
require(EasyMx)
manVars <- paste0('x', 1:6)
emxResiduals(manVars, lbound=1e-6)
emxResiduals(manVars, type='identical')
emxResiduals(manVars, path=TRUE)
```

---

emxStateSpaceMixtureClassify

*Classify time series in a state space mixture model*

---

**Description**

This function classifies time series (usually people) in a state space mixture model.

**Usage**

```
emxStateSpaceMixtureClassify(model)
```

**Arguments**

model                    MxModel. The output from [emxStateSpaceMixtureModel](#)

**Details**

This is a helper function for state space mixture modeling. The function will almost exclusively be used in conjunction with [emxStateSpaceMixtureModel](#). The present function takes a state space mixture model as input, and returns detailed information about the most likely class for each unique ID.

**Value**

A named list with elements

estimated_classes	A vector of the most likely class for each person. Dimension is people.
joint_m2l1	A matrix of joint minus two summed log likelihoods of each person <i>and</i> each class. Dimension is people by classes.
m2l1	A matrix of minus two summed log likelihoods of each person <i>given</i> each class. Dimension is people by classes.
likelihood	An array of the likelihoods (i.e., probability densities) of each combination of time point, person, and class. Dimension is time points by people by classes.

**See Also**

[emxStateSpaceMixtureModel](#) , [emxMixtureModel](#)

**Examples**

```
# Example
require(EasyMx)
data(myFADDataRaw)

ds0 <- myFADDataRaw[,1:3]

# Make a VAR Model
vm <- emxVARModel(data=ds0, use=names(ds0), name='varmodel')

# Re-label parameters to have different AR parameters
# for class 1 and class 2
vm1 <- OpenMx::omxSetParameters(vm, labels=vm$Dynamics$labels,
  newlabels=paste0(vm$Dynamics$labels, '_k1'), name='klass1')
vm2 <- OpenMx::omxSetParameters(vm, labels=vm$Dynamics$labels,
  newlabels=paste0(vm$Dynamics$labels, '_k2'), name='klass2')

# Pretend you have a data set of 50 people
# each measured 10 times on 3 variables
ds1 <- myFADDataRaw[, 1:3]
ds1$id <- rep(1:50, each=nrow(myFADDataRaw)/50)

## Not run:
# Make the state space mixture model
ssmm <- emxStateSpaceMixtureModel(model=list(vm1, vm2),
  data=ds1, ID='id')

# Fit model
ssmmr <- mxRun(ssmm)

# Extract estimated classes and diagnostics
eclasses <- emxStateSpaceMixtureClassify(ssmmr)

## End(Not run)
```

---

 emxStateSpaceMixtureModel

*Create a state space mixture model*


---

## Description

This function creates a state space mixture model as an MxModel object.

## Usage

```
emxStateSpaceMixtureModel(model, data, name, run=FALSE, use, ID, time, ...)
emxModelStateSpaceMixture(model, data, name, run=FALSE, use, ID, time, ...)
```

## Arguments

model	list of MxModel objects, each of which should be a state space model
data	data used for the model
name	character. Optional name of the model created.
run	logical. Whether to run the model before returning.
use	character vector. The names of the variables to use. Currently ignored.
ID	character. Name of variable that identifies each unique person.
time	character. Name of the variable that gives the time of each observation. Currently ignored.
...	Force later arguments to be named. ... is ignored.

## Details

The idea of state space mixture modeling is to model multiple, multivariate time series while allowing for qualitative differences between the time series. Suppose you have a multivariate time series for several people. You think some people should have the same time series model, but not everyone. You think there should be a small number of homogeneous sets of people that follow the same time series model, but you do not know which people or the exact parameter values of the candidate time series models. This function presents one solution to this problem.

State space mixture modeling begins with a set of candidate state space models, and uses these state space models as the mixture classes. The goal is to simultaneously estimate the free parameters of the state space models, and estimate which multivariate time series (e.g., person) belongs to which mixture class.

The component state space models may share some free parameters or none. Note that free parameters with the same name are constrained to be equal across all models. Conversely, unnamed free parameters are given unique names and are allowed to differ for each person-mixture combination, which creates a very large number of free parameters. We strongly encourage you to name all of your free parameters in the model list to avoid melting your computer's CPU.



The `model` argument currently must be a list. The elements of the list should be `MxModel` objects. Each list element forms a mixture class in the final model.

This function creates a multigroup mixture model where the mixture classes are the elements of the `model` list argument. Each unique ID forms a group.

The `data` argument can be a list of `data.frame` objects with one element for each ID, or a single `data.frame` with an ID variable that separates groups.

## Value

An `MxModel`.

## See Also

[emxStateSpaceMixtureClassify](#) , [emxMixtureModel](#)

## Examples

```
# Example
require(EasyMx)
data(myFADDataRaw)

ds0 <- myFADDataRaw[,1:3]

# Make a VAR Model
vm <- emxVARModel(data=ds0, use=names(ds0), name='varmodel')

# Re-label parameters to have different AR parameters
# for class 1 and class 2
vm1 <- OpenMx::omxSetParameters(vm, labels=vm$Dynamics$labels,
  newlabels=paste0(vm$Dynamics$labels, '_k1'), name='klass1')
vm2 <- OpenMx::omxSetParameters(vm, labels=vm$Dynamics$labels,
  newlabels=paste0(vm$Dynamics$labels, '_k2'), name='klass2')

# Pretend you have a data set of 50 people
# each measured 10 times on 3 variables
ds1 <- myFADDataRaw[, 1:3]
ds1$id <- rep(1:50, each=nrow(myFADDataRaw)/50)

## Not run:
# Make and fit the state space mixture model
ssmm <- emxStateSpaceMixtureModel(model=list(vm1, vm2),
  data=ds1, ID='id', run=TRUE)

## End(Not run)
```

---

emxThresholds                      *Create a set of thresholds for ordinal data*

---

### Description

This function creates a threshold matrix as an MxMatrix object.

### Usage

```
emxThresholds(data, ordinalCols, deviation=TRUE)
```

### Arguments

data	The data frame or matrix for which thresholds should be created.
ordinalCols	optional character vector. The names of the ordinal variables in the data.
deviation	logical. Return the list of OpenMx objects needed for the deviation form of the thresholds (default) or just the raw thresholds matrix

### Value

An MxMatrix giving the thresholds.

### See Also

[emxFactorModel](#), [emxGrowthModel](#)

### Examples

```
# Example
require(EasyMx)
data(jointdata)
jointdata[, c(2, 4, 5)] <- mxFactor(jointdata[,c(2, 4, 5)],
  levels=sapply(jointdata[,c(2, 4, 5)], function(x){sort(unique(x))}))
emxThresholds(jointdata, c(FALSE, TRUE, FALSE, TRUE, TRUE))
```

---

emxTwinModel                      *Creates behavior genetics Twin Model*

---

### Description

This function creates an MxModel and associated objects for a basic Twin model.

### Usage

```
emxTwinModel(model, relatedness, data, run=FALSE, use, name='model', components='ACE')
emxModelTwin(model, relatedness, data, run=FALSE, use, name='model', components='ACE')
```

**Arguments**

model	Description of the model. Currently ignored.
relatedness	Description of the relatedness patterns. Currently the name of the variable that gives the coefficient of relatedness.
data	data.frame or matrix. The data set used in the model.
run	logical. Whether to run the model before returning.
use	character vector. Names of the variables used in the model.
name	character. Name of the model.
components	character. Name of the variance components to include. Current valid options are 'ACE' and 'ADE'

**Details**

Because the model argument is ignored and the relatedness argument has limited use, this function only constructs a very basic and rigid Twin model. It creates a Cholesky model with A, C, and E components or a Cholesky model with A, D, and E components. The means are constrained equal across twins.

**Value**

MxModel.

**See Also**

[emxFactorModel](#)

**Examples**

```
# Create an ACE model in 10 lines
# 8 of those are data handling.
# 2 are the actual model.
require(EasyMx)
require(OpenMx)
data(twinData)
twinVar = names(twinData)
selVars <- c('ht1', 'bmi1', 'ht2', 'bmi2')
mzdzData <- subset(twinData, zyg %in% c(1, 3), c(selVars, 'zyg'))
mzdzData$RCoeff <- c(1, NA, .5)[mzdzData$zyg]

## Not run:
run3 <- emxTwinModel(model='Cholesky', relatedness='RCoeff',
data=mzdzData, use=selVars, run=TRUE, name='TwCh')

## End(Not run)
```

---

emxVarianceComponents *Creates Variance Components Model*

---

### Description

This function creates a variance components model as an MxModel object.

### Usage

```
emxVarianceComponents(model, data, run)
```

### Arguments

model	MxModel. See Details.
data	matrix or data.frame. The used in the model
run	logical. Whether to run the model before returning.

### Details

This function does not really do anything currently. Do not use it.

### Value

MxModel.

### See Also

[emxFactorModel](#)

### Examples

```
# Create a loadings matrix  
require(EasyMx)
```

---

`emxVARModel`*Create a vector autoregressive (VAR) model*

---

## Description

This function creates a vector autoregressive (VAR) model as an MxModel object.

## Usage

```
emxVARModel(model, data, name, run=FALSE, use, ID)
emxModelVAR(model, data, name, run=FALSE, use, ID)
```

## Arguments

<code>model</code>	Currently ignored, but later will specify particular kinds of VAR models
<code>data</code>	data used for the model
<code>name</code>	character. Optional name of the model created.
<code>run</code>	logical. Whether to run the model before returning.
<code>use</code>	character vector. The names of the variables to use. Currently ignored.
<code>ID</code>	character. Name of variable that identifies each unique person.

## Details

The purpose of this function is to quickly specify a vector autoregressive model. It is currently in the early stages of development and might change considerable with regard to the `model` argument and the `ID` argument.

## Value

An MxModel.

## See Also

[emxStateSpaceMixtureModel](#) , [emxFactorModel](#)

## Examples

```
# Example
require(EasyMx)
data(myFADDataRaw)
ds0 <- myFADDataRaw[,1:3]

# Make a VAR Model
vm <- emxVARModel(data=ds0, use=names(ds0), name='varmodel')
```

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