

OpenMx Reference Manual

March 22, 2017

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Title Extended Structural Equation Modelling

URL <http://openmx.ssri.psu.edu>, <https://github.com/OpenMx/OpenMx>

BugReports <http://openmx.ssri.psu.edu/forums>

Description Facilitates treatment of statistical model specifications as things that can be generated and manipulated programmatically. Structural equation models may be specified with reticular action model matrices or paths, linear structural relations matrices or paths, or directly in matrix algebra. Fit functions include full information maximum likelihood, maximum likelihood, and weighted least squares. Example models include confirmatory factor, multiple group, mixture distribution, categorical threshold, modern test theory, differential equations, state space, and many others.

SystemRequirements GNU make

License Apache License (== 2.0)

LinkingTo Rcpp, RcppEigen, StanHeaders (>= 2.10.0.2), BH (>= 1.60), rpf (>= 0.45)

Imports Rcpp, digest,
MASS,
methods,
Matrix,
parallel

Depends R (>= 3.0.2)

Suggests mvtnorm,
numDeriv,
roxygen2 (>= 3.1),
devtools,
Rmpi,
rpf (>= 0.45),
snowfall,
lme4

LazyLoad yes

LazyData yes

Collate '0ClassUnion.R'
'cache.R'
'MxBaseNamed.R'
'MxData.R'
'MxDataWLS.R'
'DefinitionVars.R'
'MxReservedNames.R'
'MxNamespace.R'
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Version 2.7.9

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BaseCompute-class *BaseCompute*

Description

This is an internal class and should not be used directly.

See Also

[mxComputeEM](#), [mxComputeGradientDescent](#), [mxComputeHessianQuality](#), [mxComputeIterate](#), [mx-ComputeNewtonRaphson](#), [mxComputeNumericDeriv](#)

Bollen *Bollen Data on Industrialization and Political Democracy*

Description

Data set used in some of OpenMx's examples, for instance WLS. The data were reported in Bollen (1989, p. 428, Table 9.4) This set includes data from 75 developing countries each assessed on four measures of democracy measured twice (1960 and 1965), and three measures of industrialization measured once (1960).

Usage

```
data("Bollen")
```

Format

A data frame with 75 observations on the following 11 numeric variables.

- y1 Freedom of the press, 1960
- y2 Freedom of political opposition, 1960
- y3 Fairness of elections, 1960
- y4 Effectiveness of elected legislature, 1960
- y5 Freedom of the press, 1965
- y6 Freedom of political opposition, 1965
- y7 Fairness of elections, 1965
- y8 Effectiveness of elected legislature, 1965
- x1 GNP per capita, 1960
- x2 Energy consumption per capita, 1960
- x3 Percentage of labor force in industry, 1960

Details

Variables y1-y4 and y5-y8 are typically used as indicators of the latent trait of “political democracy” in 1960 and 1965 respectively. x1-x3 are used as indicators of industrialization (1960).

Source

The sem package (in turn, via pers. comm Bollen to Fox)

References

Bollen, K. A. (1979). Political democracy and the timing of development. *American Sociological Review*, **44**, 572-587.

Bollen, K. A. (1980). Issues in the comparative measurement of political democracy. *American Sociological Review*, **45**, 370-390.

Bollen, K. A. (1989). *Structural equation models*. New York: Wiley-Interscience.

Examples

```
data(Bollen)
str(Bollen)
plot(y1 ~ y2, data = Bollen)
```

cvectorize

Vectorize By Column

Description

This function returns the vectorization of an input matrix in a column by column traversal of the matrix. The output is returned as a column vector.

Usage

```
cvectorize(x)
```

Arguments

x an input matrix.

See Also

[rvectorize](#), [vech](#), [vechs](#)

Examples

```
cvectorize(matrix(1:9, 3, 3))
cvectorize(matrix(1:12, 3, 4))
```

demoOneFactor

Demonstration data for a one factor model

Description

Data set used in some of OpenMx's examples.

Usage

```
data("demoOneFactor")
```

Format

A data frame with 500 observations on the following 5 numeric variables.

x1

x2

x3

x4

x5

Details

Variables x1-x5 are typically used as indicators of the latent trait.

Source

Simulated.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```
data(demoOneFactor)  
cov(demoOneFactor)  
cor(demoOneFactor)
```

`demoTwoFactor`*Demonstration data for a two factor model*

Description

Data set used in some of OpenMx's examples.

Usage

```
data("demoTwoFactor")
```

Format

A data frame with 500 observations on the following 10 numeric variables.

x1

x2

x3

x4

x5

y1

y2

y3

y4

y5

Details

Variables x1-x5 are typically used as indicators of one latent trait. Variables y1-y5 are typically used as indicators of another latent trait.

Source

Simulated.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```
data(demoTwoFactor)
cov(demoTwoFactor)
cor(demoTwoFactor)
```

`diag2vec`*Extract Diagonal of a Matrix*

Description

Given an input matrix, `diag2vec` returns a column vector of the elements along the diagonal.

Usage

```
diag2vec(x)
```

Arguments

`x` an input matrix.

Details

Similar to the function `diag`, except that the input argument is always treated as a matrix (i.e., it doesn't have `diag()`'s functions of returning an Identity matrix from an `nrow` specification, nor to return a matrix wrapped around a diagonal if provided with a vector). To get vector2matrix functionality, call `vec2diag`.

See Also

[vec2diag](#)

Examples

```
diag2vec(matrix(1:9, nrow=3))
#      [,1]
# [1,]    1
# [2,]    5
# [3,]    9

diag2vec(matrix(1:12, nrow=3, ncol=4))
#      [,1]
# [1,]    1
# [2,]    5
# [3,]    9
```

dzfData	<i>DZ female data</i>
---------	-----------------------

Description

Data for extended twin example ETC88.R

Usage

```
data("dzfData")
```

Format

A data frame with 2007 observations on the following 37 variables.

famid a numeric vector

e1 a numeric vector

e2 a numeric vector

e3 a numeric vector

e4 a numeric vector

e5 a numeric vector

e6 a numeric vector

e7 a numeric vector

e8 a numeric vector

e9 a numeric vector

e10 a numeric vector

e11 a numeric vector

e12 a numeric vector

e13 a numeric vector

e14 a numeric vector

e15 a numeric vector

e16 a numeric vector

e17 a numeric vector

e18 a numeric vector

a1 a numeric vector

a2 a numeric vector

a3 a numeric vector

a4 a numeric vector

a5 a numeric vector

a6 a numeric vector

a7 a numeric vector
a8 a numeric vector
a9 a numeric vector
a10 a numeric vector
a11 a numeric vector
a12 a numeric vector
a13 a numeric vector
a14 a numeric vector
a15 a numeric vector
a16 a numeric vector
a17 a numeric vector
a18 a numeric vector

Examples

```
data(dzfData)  
str(dzfData)
```

dzmData

DZ Male data

Description

Data for extended twin example ETC88.R

Usage

```
data("dzmData")
```

Format

A data frame with 1990 observations on the following 37 variables.

famid a numeric vector
e1 a numeric vector
e2 a numeric vector
e3 a numeric vector
e4 a numeric vector
e5 a numeric vector
e6 a numeric vector
e7 a numeric vector
e8 a numeric vector

e9 a numeric vector
e10 a numeric vector
e11 a numeric vector
e12 a numeric vector
e13 a numeric vector
e14 a numeric vector
e15 a numeric vector
e16 a numeric vector
e17 a numeric vector
e18 a numeric vector
a1 a numeric vector
a2 a numeric vector
a3 a numeric vector
a4 a numeric vector
a5 a numeric vector
a6 a numeric vector
a7 a numeric vector
a8 a numeric vector
a9 a numeric vector
a10 a numeric vector
a11 a numeric vector
a12 a numeric vector
a13 a numeric vector
a14 a numeric vector
a15 a numeric vector
a16 a numeric vector
a17 a numeric vector
a18 a numeric vector

Examples

```
data(dzmData)  
str(dzmData)
```

dzoData	<i>DZ opposite sex data</i>
---------	-----------------------------

Description

Data for extended twin example ETC88.R

Usage

```
data("dzoData")
```

Format

A data frame with 3981 observations on the following 37 variables.

famid a numeric vector

e1 a numeric vector

e2 a numeric vector

e3 a numeric vector

e4 a numeric vector

e5 a numeric vector

e6 a numeric vector

e7 a numeric vector

e8 a numeric vector

e9 a numeric vector

e10 a numeric vector

e11 a numeric vector

e12 a numeric vector

e13 a numeric vector

e14 a numeric vector

e15 a numeric vector

e16 a numeric vector

e17 a numeric vector

e18 a numeric vector

a1 a numeric vector

a2 a numeric vector

a3 a numeric vector

a4 a numeric vector

a5 a numeric vector

a6 a numeric vector

a7 a numeric vector
a8 a numeric vector
a9 a numeric vector
a10 a numeric vector
a11 a numeric vector
a12 a numeric vector
a13 a numeric vector
a14 a numeric vector
a15 a numeric vector
a16 a numeric vector
a17 a numeric vector
a18 a numeric vector

Examples

```
data(dzoData)  
str(dzoData)
```

eigenvec

Eigenvector/Eigenvalue Decomposition

Description

`eigenval` computes the real parts of the eigenvalues of a square matrix. `eigenvec` computes the real parts of the eigenvectors of a square matrix. `ieigenval` computes the imaginary parts of the eigenvalues of a square matrix. `ieigenvec` computes the imaginary parts of the eigenvectors of a square matrix. `eigenval` and `ieigenval` return $n \times 1$ matrices containing the real or imaginary parts of the eigenvalues, sorted in decreasing order of the modulus of the complex eigenvalue. For eigenvalues without an imaginary part, this is equivalent to sorting in decreasing order of the absolute value of the eigenvalue. (See [Mod](#) for more info.) `eigenvec` and `ieigenvec` return $n \times n$ matrices, where each column corresponds to an eigenvector. These are sorted in decreasing order of the modulus of their associated complex eigenvalue.

Usage

```
eigenval(x)  
eigenvec(x)  
ieigenval(x)  
ieigenvec(x)
```

Arguments

x the square matrix whose eigenvalues/vectors are to be calculated.

Details

Eigenvectors returned by `eigenvec` and `ieigenvec` are normalized to unit length.

See Also

[eigen](#)

Examples

```
A <- mxMatrix(values = runif(25), nrow = 5, ncol = 5, name = 'A')
G <- mxMatrix(values = c(0, -1, 1, -1), nrow=2, ncol=2, name='G')

model <- mxModel(A, G, name = 'model')

mxEval(eigenvec(A), model)
mxEval(eigenvec(G), model)
mxEval(eigenval(A), model)
mxEval(eigenval(G), model)
mxEval(ieigenvec(A), model)
mxEval(ieigenvec(G), model)
mxEval(ieigenval(A), model)
mxEval(ieigenval(G), model)
```

example1

Bivariate twin data example from Classic Mx Manual

Description

Data set used in some of OpenMx's examples.

Usage

```
data("example1")
```

Format

A data frame with 400 observations on the following variables.

IDNum Twin pair ID
Zygoty Zygoty of the twin pair
X1 X variable for twin 1
Y1 Y variable for twin 1
X2 X variable for twin 2
Y2 Y variable for twin 2

Details

Same as [example2](#) but in wide format instead of tall.

Source

Classic Mx Manual.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```
data(example1)
plot(X2 ~ X1, data=example1)
```

example2

Bivariate twin data example from Classic Mx Manual

Description

Data set used in some of OpenMx's examples.

Usage

```
data("example2")
```

Format

A data frame with 800 observations on the following variables.

IDNum ID number

TwinNum Twin ID number

Zygoty Zygoty of the twin

X X variable for twins 1 and 2

Y Y variable for twins 1 and 2

Details

Same as [example1](#) but in tall format instead of wide.

Source

Classic Mx Manual.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```
data(example2)
plot(Y ~ X, data=example2)
```

expm	<i>Matrix exponential</i>
------	---------------------------

Description

Matrix exponential

Usage

```
expm(x)
```

Arguments

x	matrix
---	--------

factorExample1	<i>Example Factor Analysis Data</i>
----------------	-------------------------------------

Description

Data set used in some of OpenMx's examples.

Usage

```
data("factorExample1")
```

Format

A data frame with 500 observations on the following variables.

x1
x2
x3
x4
x5
x6
x7
x8
x9

Details

This appears to be a three factor model, but perhaps with an odd loading structure.

Source

Simulated

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```
data(factorExample1)
round(cor(factorExample1), 2)

factanal(covmat=cov(factorExample1), factors=3, rotation="promax")
```

factorScaleExample1 *Example Factor Analysis Data for Scaling the Model*

Description

Data set used in some of OpenMx's examples.

Usage

```
data("factorScaleExample1")
```

Format

A data frame with 200 observations on the following variables.

X1
X2
X3
X4
X5
X6
X7
X8
X9
X10
X11
X12

Details

This appears to be a three factor model with factor 1 loading on X1-X4, factor 2 on X5-X8, and factor 3 on X9-X12.

Source

Simulated

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```
data(factorScaleExample1)
round(cor(factorScaleExample1), 2)
```

factorScaleExample2 *Example Factor Analysis Data for Scaling the Model*

Description

Data set used in some of OpenMx's examples.

Usage

```
data("factorScaleExample2")
```

Format

A data frame with 200 observations on the following variables.

X1
X2
X3
X4
X5
X6
X7
X8
X9
X10
X11
X12

Details

This appears to be a three factor model with factor 1 loading on X1-X4, factor 2 on X5-X8, and factor 3 on X9-X12. It differs from [factorScaleExample1](#) in the scaling of the variables.

Source

Simulated

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```
data(factorScaleExample2)
round(cor(factorScaleExample2), 2)

data(factorScaleExample2)
plot(sapply(factorScaleExample1, var), type='l', ylim=c(0, 6), lwd=3)
lines(1:12, sapply(factorScaleExample2, var), col='blue', lwd=3)
```

genericFitDependencies,MxBaseFitFunction-method
Add dependencies

Description

If there is an expectation, then the fitfunction should always depend on it. Hence, subclasses that implement this method must ignore the passed-in dependencies and use "dependencies <- callNextMethod()" instead.

Usage

```
## S4 method for signature 'MxBaseFitFunction'
genericFitDependencies(.Object, flatModel,
  dependencies)
```

Arguments

.Object	fit function object
flatModel	flat model that lives with .Object
dependencies	accumulated dependency relationships

HS.ability.data	<i>Holzinger and Swineford (1939) Ability data in 301 children from two schools</i>
-----------------	-------------------------------------------------------------------------------------

Description

This classic data set contains of intelligence-test scores from 301 children on 26 distinct tests. The data are also available in the MBESS package.

The tests cover mental speed, memory, mathematical-ability, spatial, and verbal ability as listed below.

Usage

```
data("HS.ability.data")
```

Format

A data frame with 301 observations on the following 2 variables.

id student ID number (int)
 Gender Sex (Factor w/ 2 levels "Female", "Male")
 grade Grade in school (integer 7 or 8)
 agey Age in years (integer)
 agem Age in months (integer)
 school School attended (Factor w/2 levels "Grant-White" and "Pasteur")
 addition A speed test (numeric)
 code A speed test (numeric)
 counting A speed test (numeric)
 straight A speed test (numeric)
 wordr A memory subtest
 numberr A memory subtest
 figurer A memory subtest
 object A memory subtest
 numberf A memory subtest
 figurew A memory subtest
 deduct A mathematical subtest
 numeric A mathematical subtest
 problemr A mathematical subtest
 series A mathematical subtest
 arithmet A mathematical subtest
 visual A spatial subtest

cubes A spatial subtest
paper A spatial subtest
flags A spatial subtest
paperrev A spatial subtest
flagssub A spatial subtest
general A verbal subtest
paragrap A verbal subtest
sentence A verbal subtest
wordc A verbal subtest
wordm A verbal subtest

Details

The data are from children who differ in grade (seventh- and eighth-grade) and are nested in one of two schools (Pasteur and Grant-White). You will see it in use elsewhere, both in R (lavaan, MBESS), and in Joreskog (1969) reporting a cfa on the Grant-White school subject subset).

The last two tests are substitute versions for other tests. paperrev (a paper form board test) can substitute for paper and flagssub for the lozenges test flags.

Source

Holzinger, K., and Swineford, F. (1939).

References

Holzinger, K., and Swineford, F. (1939). A study in factor analysis: The stability of a bifactor solution. *Supplementary Educational Monograph*, no. **48**. Chicago: University of Chicago Press.
Joreskog, K. G. (1969). A general approach to confirmatory maximum likelihood factor analysis. *Psychometrika*, **34**, 183-202.

Examples

```
data(HS.ability.data)
str(HS.ability.data)
levels(HS.ability.data$school)
plot(flags ~ flagssub, data = HS.ability.data)
```

imxAddDependency	<i>Add a dependency</i>
------------------	-------------------------

Description

The dependency tracking system ensures that algebra and fitfunctions are not recomputed if their inputs have not changed. Dependency information is computed prior to handing the model off to the optimizer to reduce overhead during optimization.

Usage

```
imxAddDependency(source, sink, dependencies)
```

Arguments

source	a character vector of the names of the computation sources (inputs)
sink	the name of the computation sink (output)
dependencies	the dependency graph

Details

Each free parameter keeps track of all the objects that store that free parameter and the transitive closure of all algebras and fit functions that depend on that free parameter. Similarly, each definition variable keeps track of all the objects that store that free parameter and the transitive closure of all the algebras and fit functions that depend on that free parameter. At each iteration of the optimization, when the free parameter values are updated, all of the dependencies of that free parameter are marked as dirty (see `omxFitFunction.repopulateFun`). After an algebra or fit function is computed, `omxMarkClean()` is called to indicate that the algebra or fit function is updated. Similarly, when definition variables are populated in FIML, all of the dependencies of the definition variables are marked as dirty. Particularly for FIML, the fact that non-definition-variable dependencies remain clean is a big performance gain.

imxCheckMatrices	<i>imxCheckMatrices</i>
------------------	-------------------------

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxCheckMatrices(model)
```

Arguments

model	model
-------	-------

imxCheckVariables	<i>imxCheckVariables</i>
-------------------	--------------------------

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxCheckVariables(flatModel, namespace)
```

Arguments

flatModel	flatModel
namespace	namespace

imxConDecMatrixSlots	<i>Condense/decondense slots of an MxMatrix</i>
----------------------	-------------------------------------------------

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxConDecMatrixSlots(object)
```

Arguments

object	of class MxMatrix
--------	-------------------

imxConstraintRelations	<i>imxConstraintRelations</i>
------------------------	-------------------------------

Description

A string vector of valid constraint binary relations.

Usage

```
imxConstraintRelations
```

Format

An object of class character of length 3.

`imxConvertIdentifier` *imxConvertIdentifier*

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxConvertIdentifier(identifiers, modelname, namespace, strict = FALSE)
```

Arguments

<code>identifiers</code>	<code>identifiers</code>
<code>modelname</code>	<code>modelname</code>
<code>namespace</code>	<code>namespace</code>
<code>strict</code>	<code>strict</code>

`imxConvertLabel` *imxConvertLabel*

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxConvertLabel(label, modelname, dataname, namespace)
```

Arguments

<code>label</code>	<code>label</code>
<code>modelname</code>	<code>modelname</code>
<code>dataname</code>	<code>dataname</code>
<code>namespace</code>	<code>namespace</code>

```
imxConvertSubstitution
      imxConvertSubstitution
```

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxConvertSubstitution(substitution, modelname, namespace)
```

Arguments

substitution	substitution
modelname	modelname
namespace	namespace

```
imxCreateMatrix      Create a matrix
```

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxCreateMatrix(.Object, labels, values, free, lbound, ubound, nrow, ncol,
  byrow, name, condenseSlots, joinKey, joinModel)
```

Arguments

.Object	the matrix
labels	labels
values	values
free	free
lbound	lbound
ubound	ubound
nrow	nrow
ncol	ncol
byrow	byrow
name	name
condenseSlots	condenseSlots
joinKey	joinKey
joinModel	joinModel

<code>imxDataTypes</code>	<i>Valid types of data that can be contained by MxData</i>
---------------------------	------------------------------------------------------------

Description

Valid types of data that can be contained by MxData

Usage

`imxDataTypes`

Format

An object of class character of length 5.

<code>imxDefaultGetSlotDisplayNames</code>	<i>imxDefaultGetSlotDisplayNames</i>
--------------------------------------------	--------------------------------------

Description

Returns a list of display-friendly object slot names This is an internal function exported for those people who know what they are doing.

Usage

`imxDefaultGetSlotDisplayNames(x, pattern = ".*")`

Arguments

<code>x</code>	The object from which to get slot names
<code>pattern</code>	Initial pattern to match (default of <code>'.*'</code> matches any)

imxDeparse	<i>Deparse for MxObjects</i>
------------	------------------------------

Description

Deparse for MxObjects

Usage

```
imxDeparse(object, indent = "  ")
```

Arguments

object	object
indent	indent

imxDependentModels	<i>Are submodels dependence?</i>
--------------------	----------------------------------

Description

Are submodels dependence?

Usage

```
imxDependentModels(model)
```

Arguments

model	model
-------	-------

imxDetermineDefaultOptimizer	<i>imxDetermineDefaultOptimizer</i>
------------------------------	-------------------------------------

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxDetermineDefaultOptimizer()
```

Details

Returns a character, the default optimizer

imxDiff	<i>Set difference on regular types or S4 objects</i>
---------	------------------------------------------------------

Description

Set difference on regular types or S4 objects

Usage

```
imxDiff(a, b, slots = c("setequal", "intersect"))
```

Arguments

a	a
b	b
slots	slots

imxDmvnorm	<i>A C implementation of dmvnorm</i>
------------	--------------------------------------

Description

This API is visible to permit testing. Please do not use.

Usage

```
imxDmvnorm(loc, mean, sigma)
```

Arguments

loc	loc
mean	mean
sigma	sigma

imxEvalByName	<i>imxEvalByName</i>
---------------	----------------------

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxEvalByName(name, model, compute = FALSE, show = FALSE)
```

Arguments

name	name
model	model
compute	compute
show	show

Details

This function should not be used in MxSummary. All summary information should be extracted from runstate.

imxExtractMethod	<i>imxExtractMethod</i>
------------------	-------------------------

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxExtractMethod(model, index)
```

Arguments

model	model
index	index

<code>imxExtractNames</code>	<i>imxExtractNames</i>
------------------------------	------------------------

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxExtractNames(lst)
```

Arguments

<code>lst</code>	<code>lst</code>
------------------	------------------

<code>imxExtractReferences</code>	<i>imxExtractReferences</i>
-----------------------------------	-----------------------------

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxExtractReferences(lst)
```

Arguments

<code>lst</code>	<code>lst</code>
------------------	------------------

<code>imxExtractSlot</code>	<i>imxExtractSlot</i>
-----------------------------	-----------------------

Description

Checks for and extracts a slot from the object This is an internal function exported for those people who know what they are doing.

Usage

```
imxExtractSlot(x, name)
```

Arguments

<code>x</code>	The object
<code>name</code>	the name of the slot

imxFlattenModel	<i>Remove heirarchical structure from model</i>
-----------------	-------------------------------------------------

Description

Remove heirarchical structure from model

Usage

```
imxFlattenModel(model, namespace)
```

Arguments

model	model
namespace	namespace

imxFreezeModel	<i>Freeze model</i>
----------------	---------------------

Description

Remove free parameters and fit function from model.

Usage

```
imxFreezeModel(model)
```

Arguments

model	model
-------	-------

imxGenerateLabels	<i>imxGenerateLabels</i>
-------------------	--------------------------

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxGenerateLabels(model)
```

Arguments

model	model
-------	-------

```
imxGenerateNamespace  imxGenerateNamespace
```

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxGenerateNamespace(model)
```

Arguments

model	model
-------	-------

```
imxGenericModelBuilder
      imxGenericModelBuilder
```

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxGenericModelBuilder(model, lst, name, manifestVars, latentVars, submodels,
  remove, independent)
```

Arguments

model	model
lst	lst
name	name
manifestVars	manifestVars
latentVars	latentVars
submodels	submodels
remove	remove
independent	independent

 imxGetSlotDisplayNames

imxGetSlotDisplayNames

Description

Returns a list of display-friendly object slot names This is an internal function exported for those people who know what they are doing.

Usage

```
imxGetSlotDisplayNames(object, pattern = ".*", slotList = slotNames(object),
  showDots = FALSE, showEmpty = FALSE)
```

Arguments

object	The object from which to get slot names
pattern	Initial pattern to match (default of '.*' matches any)
slotList	List of slots for which to get display names (default = slotNames(object), i.e., all)
showDots	Include slots whose names start with '.' (default FALSE)
showEmpty	Include slots with length-zero contents (default FALSE)

 imxHasConstraint

imxHasConstraint

Description

This is an internal function exported for those people who know what they are doing. This function checks if a model (or its submodels) has at least one MxConstraint.

Usage

```
imxHasConstraint(model)
```

Arguments

model	model
-------	-------

```
imxHasDefinitionVariable
    imxHasDefinitionVariable
```

Description

This is an internal function exported for those people who know what they are doing. This function checks if a model (or its submodels) has at least one definition variable.

Usage

```
imxHasDefinitionVariable(model)
```

Arguments

```
model          model
```

```
imxHasNPSOL    imxHasNPSOL
```

Description

```
imxHasNPSOL
```

Usage

```
imxHasNPSOL()
```

Value

Returns TRUE if the NPSOL proprietary optimizer is compiled and linked with OpenMx. Otherwise FALSE.

```
imxHasOpenMP   imxHasOpenMP
```

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxHasOpenMP()
```

imxIdentifier	<i>imxIdentifier</i>
---------------	----------------------

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxIdentifier(namespace, name)
```

Arguments

namespace	namespace
name	name

imxIndependentModels	<i>Are submodels independent?</i>
----------------------	-----------------------------------

Description

Are submodels independent?

Usage

```
imxIndependentModels(model)
```

Arguments

model	model
-------	-------

imxInitModel	<i>imxInitModel</i>
--------------	---------------------

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxInitModel(model)
```

Arguments

model	model
-------	-------

```
imxIsDefinitionVariable
      imxIsDefinitionVariable
```

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxIsDefinitionVariable(name)
```

Arguments

name	name
------	------

```
imxIsPath      imxIsPath
```

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxIsPath(value)
```

Arguments

value	value
-------	-------

```
imxJiggle      imxJiggle
```

Description

Jiggle parameter values, subject to box constraints. For internal use by mxTryHard(). This is an internal function exported for those people who know what they are doing.

Usage

```
imxJiggle(params, lbounds, ubounds, dsn, loc, scale)
```

Arguments

params	Numeric vector of current free parameter values.
lbounds	Numeric vector of lower bounds on parameters.
ubounds	Numeric vector of upper bounds on parameters.
dsn	Character string naming the family of distribution to be used.
loc	Numeric vector of location parameters (medians).
scale	Numeric vector of scale parameters (see source code).

<code>imxLocateFunction</code>	<i>imxLocateFunction</i>
--------------------------------	--------------------------

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxLocateFunction(function_name)
```

Arguments

function_name	function_name
---------------	---------------

<code>imxLocateIndex</code>	<i>imxLocateIndex</i>
-----------------------------	-----------------------

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxLocateIndex(model, name, referant)
```

Arguments

model	model
name	name
referant	referant

imxLocateLabel	<i>imxLocateLabel</i>
----------------	-----------------------

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxLocateLabel(label, model, parameter)
```

Arguments

label	label
model	model
parameter	parameter

imxLog	<i>Test thread-safe output code</i>
--------	-------------------------------------

Description

This is the code that the backend uses to write diagnostic information to standard error. This function should not be called from R. We make it available only for testing.

Usage

```
imxLog(str)
```

Arguments

str	the character string to output
-----	--------------------------------

imxLookupSymbolTable	<i>imxLookupSymbolTable</i>
----------------------	-----------------------------

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxLookupSymbolTable(name)
```

Arguments

name	name
------	------

imxModelBuilder	<i>imxModelBuilder</i>
-----------------	------------------------

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxModelBuilder(model, lst, name, manifestVars, latentVars, submodels, remove,
  independent)
```

Arguments

model	model
lst	lst
name	name
manifestVars	manifestVars
latentVars	latentVars
submodels	submodels
remove	remove
independent	independent

Details

TODO: It probably makes sense to split this into separate methods. For example, modelAddVariables and modelRemoveVariables could be their own methods. This would reduce some cut&paste duplication.

imxModelTypes	<i>imxModelTypes</i>
---------------	----------------------

Description

A list of supported model types

Usage

```
imxModelTypes
```

Format

An object of class list of length 3.

imxMpiWrap	<i>imxMpiWrap</i>
------------	-------------------

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxMpiWrap(fun)
```

Arguments

fun	fun
-----	-----

imxOriginalMx	<i>imxOriginalMx</i>
---------------	----------------------

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxOriginalMx(mx.filename, output.directory)
```

Arguments

mx.filename	mx.filename
output.directory	output.directory

imxPPML	<i>imxPPML</i>
---------	----------------

Description

Potentially enable the PPML optimization for the given model.

Usage

```
imxPPML(model, flag = TRUE)
```

Arguments

model	the MxModel to evaluate
flag	whether to potentially enable PPML

`imxPPML.Test.Battery` *imxPPML.Test.Battery*

Description

PPML can be applied to a number of special cases. This function will test the given model for all of these special cases.

Usage

```
imxPPML.Test.Battery(model, verbose = FALSE, testMissingness = TRUE,
  testPermutations = TRUE, testEstimates = TRUE, testFakeLatents = TRUE,
  tolerances = c(0.001, 0.001, 0.001))
```

Arguments

<code>model</code>	the model to test
<code>verbose</code>	whether to print diagnostics
<code>testMissingness</code>	try with missingness
<code>testPermutations</code>	try with permutations
<code>testEstimates</code>	examine estimates
<code>testFakeLatents</code>	try with fake latents
<code>tolerances</code>	a vector of tolerances

Details

Requirements for model passed to this function: - Path-specified - Means vector must be present - Covariance data (with data means vector) - (Recommended) All error variances should be specified on the diagonal of the S matrix, and not as a latent with a loading only on to that manifest

Function will test across all permutations of: - Covariance vs Raw data - Means vector present vs Means vector absent - Path versus Matrix specification - All orders of permutations of latents with manifests

imxPPML.Test.Test	<i>imxPPML.Test.Test</i>
-------------------	--------------------------

Description

Test that PPML solutions match non-PPML solutions.

Usage

```
imxPPML.Test.Test(model, checkLL = TRUE, checkByName = FALSE,
  tolerance = 0.5, testEstimates = TRUE)
```

Arguments

model	the MxModel to evaluate
checkLL	whether to check log likelihood
checkByName	check values using their names
tolerance	closeness tolerance for check
testEstimates	whether to test for the same parameter estimates

Details

This is an internal function used for comparing PPML and non-PPML solutions. Generally, non-developers will not use this function.

imxPreprocessModel	<i>imxPreprocessModel</i>
--------------------	---------------------------

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxPreprocessModel(model)
```

Arguments

model	model
-------	-------

<code>imxReplaceMethod</code>	<i>imxReplaceMethod</i>
-------------------------------	-------------------------

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxReplaceMethod(x, name, value)
```

Arguments

<code>x</code>	the thing
<code>name</code>	name
<code>value</code>	value

<code>imxReplaceModels</code>	<i>Replace parts of a model</i>
-------------------------------	---------------------------------

Description

Replace parts of a model

Usage

```
imxReplaceModels(model, replacements)
```

Arguments

<code>model</code>	model
<code>replacements</code>	replacements

imxReplaceSlot	<i>imxReplaceSlot</i>
----------------	-----------------------

Description

Checks for and replaces a slot from the object This is an internal function exported for those people who know what they are doing.

Usage

```
imxReplaceSlot(x, name, value, check = TRUE)
```

Arguments

x	object
name	the name of the slot
value	replacement value
check	Check replacement value for validity (default TRUE)

imxReportProgress	<i>Report backend progress</i>
-------------------	--------------------------------

Description

Prints a show status string to the console without emitting a newline.

Usage

```
imxReportProgress(info, eraseLen)
```

Arguments

info	the character string to print
eraseLen	the number of characters to erase

imxReservedNames	<i>imxReservedNames</i>
------------------	-------------------------

Description

Vector of reserved names

Usage

imxReservedNames

Format

An object of class character of length 6.

imxReverseIdentifier	<i>imxReverseIdentifier</i>
----------------------	-----------------------------

Description

This is an internal function exported for those people who know what they are doing.

Usage

imxReverseIdentifier(model, name)

Arguments

model	model
name	name

imxRobustSE	<i>imxRobustSE</i>
-------------	--------------------

Description

This is an internal function exported for those people who know what they are doing.

Usage

imxRobustSE(model)

Arguments

model	An OpenMx model object that has been run
-------	------------------------------------------

Details

This function computes robust standard errors via a sandwich estimator. The "bread" of the sandwich is the numerically computed inverse Hessian of the likelihood function. This is what is typically used for standard errors throughout OpenMx. The "meat" of the sandwich is the covariance matrix of the numerically computed row derivatives of the likelihood function (i.e. row gradients).

imxRowGradients	<i>imxRowGradients</i>
-----------------	------------------------

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxRowGradients(model)
```

Arguments

model	An OpenMx model object that has been run
-------	------------------------------------------

Details

This function computes the gradient for each row of data. The returned object is a matrix with the same number of rows as the data, and the same number of columns as there are free parameters.

imxSameType	<i>imxSameType</i>
-------------	--------------------

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxSameType(a, b)
```

Arguments

a	a
b	b

<code>imxSeparatorChar</code>	<i>imxSeparatorChar</i>
-------------------------------	-------------------------

Description

The character between the model name and the named entity inside the model.

Usage

`imxSeparatorChar`

Format

An object of class character of length 1.

<code>imxSfClient</code>	<i>imxSfClient</i>
--------------------------	--------------------

Description

As of snowfall 1.84, the snowfall supervisor process stores an internal state information in a variable named ".sfOption" that is located in the "snowfall" namespace. The snowfall client processes store internal state information in a variable named ".sfOption" that is located in the global namespace.

Usage

`imxSfClient()`

Details

As long as the previous statement is true, then the current process is a snowfall client if-and-only-if `exists(".sfOption")`.

<code>imxSimpleRAMPredicate</code>	<i>imxSimpleRAMPredicate</i>
------------------------------------	------------------------------

Description

This is an internal function exported for those people who know what they are doing.

Usage

`imxSimpleRAMPredicate(model)`

Arguments

<code>model</code>	<code>model</code>
--------------------	--------------------

imxSparseInvert	<i>Sparse symmetric matrix invert</i>
-----------------	---------------------------------------

Description

This API is visible to permit testing. Please do not use.

Usage

```
imxSparseInvert(mat)
```

Arguments

mat	the matrix to invert
-----	----------------------

imxSquareMatrix	<i>imxSquareMatrix</i>
-----------------	------------------------

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxSquareMatrix(.Object)
```

Arguments

.Object	.Object
---------	---------

imxSymmetricMatrix	<i>imxSymmetricMatrix</i>
--------------------	---------------------------

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxSymmetricMatrix(.Object)
```

Arguments

.Object	.Object
---------	---------

<code>imxTypeName</code>	<i>imxTypeName</i>
--------------------------	--------------------

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxTypeName(model)
```

Arguments

<code>model</code>	<code>model</code>
--------------------	--------------------

<code>imxUntitledName</code>	<i>imxUntitledName</i>
------------------------------	------------------------

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxUntitledName()
```

Details

Returns a character, the name of the next untitled entity

<code>imxUntitledNumber</code>	<i>imxUntitledNumber</i>
--------------------------------	--------------------------

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxUntitledNumber()
```

Details

Increments the untitled number counter and returns its value

imxUntitledNumberReset
imxUntitledNumberReset

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxUntitledNumberReset()
```

Details

Resets the [imxUntitledNumber](#) counter

imxUpdateModelValues *imxUpdateModelValues*

Description

Deprecated. This function does not handle parameters with equality constraints. Do not use.

Usage

```
imxUpdateModelValues(model, flatModel, values)
```

Arguments

model	model
flatModel	flat model
values	values to update

imxVariableTypes	<i>imxVariableTypes</i>
------------------	-------------------------

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxVariableTypes
```

Format

An object of class character of length 2.

Details

The acceptable variable types

imxVerifyMatrix	<i>imxVerifyMatrix</i>
-----------------	------------------------

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxVerifyMatrix(.Object)
```

Arguments

.Object	.Object
---------	---------

imxVerifyModel	<i>imxVerifyModel</i>
----------------	-----------------------

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxVerifyModel(model)
```

Arguments

model	model
-------	-------

imxVerifyName	<i>imxVerifyName</i>
---------------	----------------------

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxVerifyName(name, stackNumber)
```

Arguments

name	name
stackNumber	stackNumber

imxVerifyReference	<i>imxVerifyReference</i>
--------------------	---------------------------

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
imxVerifyReference(reference, stackNumber)
```

Arguments

reference	reference
stackNumber	stackNumber

imxWlsChiSquare

Calculate Chi Square for a WLS Model

Description

This is an internal function used to calculate the Chi Square distributed fit statistic for weighted least squares models.

Usage

```
imxWlsChiSquare(model, J=NA)
```

Arguments

model	An MxModel object with acov (WLS) data
J	Optional pre-computed Jacobian matrix

Details

The Chi Square fit statistic for models fit with maximum likelihood depends on the difference in model fit in minus two log likelihood units between the saturated model and the more restricted model under investigation. For models fit with weighted least squares a different expression is required. If J is the first derivative (Jacobian) of the mapping from the free parameters to the unique elements of the expected covariance, means, and thresholds, J_c is the orthogonal complement of J , W is the inverse of the full weight matrix, and e is the difference between the sample-estimated and model-implied covariance, means, and thresholds, then the Chi Square fit statistic is

$$\chi^2 = e' J_c (J_c' W J_c)^{-1} J_c' e$$

with e' indicating the transpose of e . This Equation 2.20a from Browne (1984) where he showed that this statistic is chi-square distributed with the conventional degrees of freedom.

Value

A named list with components

Chi numeric value of the Chi Square fit statistic.

ChiDoF degrees of freedom for the Chi Square fit statistic.

References

M. W. Browne. (1984). Asymptotically Distribution-Free Methods for the Analysis of Covariance Structures. *British Journal of Mathematical and Statistical Psychology*, 37, 62-83.

 imxWlsStandardErrors *Calculate Standard Errors for a WLS Model*

Description

This is an internal function used to calculate standard errors for weighted least squares models.

Usage

```
imxWlsStandardErrors(model)
```

Arguments

model An MxModel object with acov (WLS) data

Details

The standard errors for models fit with maximum likelihood are related to the second derivative (Hessian) of the likelihood function with respect to the free parameters. For models fit with weighted least squares a different expression is required. If J is the first derivative (Jacobian) of the mapping from the free parameters to the unique elements of the expected covariance, means, and thresholds, V is the weight matrix used, W is the inverse of the full weight matrix, and $U = VJ(J'VJ)^{-1}$, then the asymptotic covariance matrix of the free parameters is

$$Acov(\theta) = U'WU$$

with U' indicating the transpose of U .

Value

A named list with components

SE The standard errors of the free parameters

Cov The full covariance matrix of the free parameters. The square root of the diagonal elements of Cov equals SE.

Jac The Jacobian computed to obtain the standard errors.

References

M. W. Browne. (1984). Asymptotically Distribution-Free Methods for the Analysis of Covariance Structures. *British Journal of Mathematical and Statistical Psychology*, 37, 62-83.

F. Yang-Wallentin, K. G. Jöreskog, & H. Luo. (2010). Confirmatory Factor Analysis of Ordinal Variables with Misspecified Models. *Structural Equation Modeling*, 17, 392-423.

jointdata

Joint Ordinal and continuous variables to be modeled together

Description

Data set used in some of OpenMx's examples.

Usage

```
data("jointdata")
```

Format

A data frame with 250 observations on the following variables.

z1 Continuous variable

z2 Ordinal variable with 2 levels (0, 1)

z3 Continuous variable

z4 Ordinal variable with 4 levels (0, 1, 2, 3)

z5 Ordinal variable with 3 levels (0, 1, 3)

Details

Data generated to test the joint ML algorithm thoroughly.

Source

Simulated.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```
data(jointdata)
par(mfrow=c(2, 3))
h <- lapply(jointdata, hist)
par(mfrow=c(1, 1))

plot(z2 ~ z1, jointdata)
```

`latentMultipleRegExample1`*Example data for multiple regression among latent variables*

Description

Data set used in some of OpenMx's examples.

Usage

```
data("latentMultipleRegExample1")
```

Format

A data frame with 200 observations on the following variables.

X1 Factor 1 indicator

X2 Factor 1 indicator

X3 Factor 1 indicator

X4 Factor 1 indicator

X5 Factor 2 indicator

X6 Factor 2 indicator

X7 Factor 2 indicator

X8 Factor 2 indicator

X9 Factor 3 indicator

X10 Factor 3 indicator

X11 Factor 3 indicator

X12 Factor 3 indicator

Details

Factor 1 strongly predicts factor 3. Factor 2 weakly predicts factor 3.

Source

Simulated.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```
data(latentMultipleRegExample1)
round(cor(latentMultipleRegExample1), 2)
```

latentMultipleRegExample2

Example data for multiple regression among latent variables

Description

Data set used in some of OpenMx's examples.

Usage

```
data("latentMultipleRegExample2")
```

Format

A data frame with 200 observations on the following variables.

X1 Factor 1 indicator
X2 Factor 1 indicator
X3 Factor 1 indicator
X4 Factor 1 indicator
X5 Factor 2 indicator
X6 Factor 2 indicator
X7 Factor 2 indicator
X8 Factor 2 indicator
X9 Factor 3 indicator
X10 Factor 3 indicator
X11 Factor 3 indicator
X12 Factor 3 indicator

Details

Factor 1 strongly predicts factor 3. Factor 2 weakly predicts factor 3. Very similar to [latentMultipleRegExample1](#).

Source

Simulated.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```
data(latentMultipleRegExample2)  
round(cor(latentMultipleRegExample2), 2)
```

logm	<i>Matrix logarithm</i>
------	-------------------------

Description

Matrix logarithm

Usage

```
logm(x, tol = .Machine$double.eps)
```

Arguments

x	matrix
tol	tolerance

LongitudinalOverdispersedCounts

Longitudinal, Overdispersed Count Data

Description

Four-timepoint longitudinal data generated from an arbitrary Monte Carlo simulation, for 1000 simulees. The response variable is a discrete count variable. There are three time-invariant covariates. The data are available in both "wide" and "long" format.

Usage

```
data("LongitudinalOverdispersedCounts")
```

Format

The "long" format dataframe, longData, has 4000 rows and the following variables (columns):

1. id: Factor; simulee ID code.
2. tiem: Numeric; represents the time metric, wave of assessment.
3. x1: Numeric; time-invariant covariate.
4. x2: Numeric; time-invariant covariate.
5. x3: Numeric; time-invariant covariate.
6. y: Numeric; the response ("dependent") variable.

The "wide" format dataset, wideData, is a numeric 1000x12 matrix containing the following variables (columns):

1. id: Simulee ID code.

2. x1: Time-invariant covariate.
3. x3: Time-invariant covariate.
4. x3: Time-invariant covariate.
5. y0: Response at initial wave of assessment.
6. y1: Response at first follow-up.
7. y2: Response at second follow-up.
8. y3: Response at third follow-up.
9. t0: Time variable at initial wave of assessment (in this case, 0).
10. t1: Time variable at first follow-up (in this case, 1).
11. t2: Time variable at second follow-up (in this case, 2).
12. t3: Time variable at third follow-up (in this case, 3).

Examples

```

data(LongitudinalOverdispersedCounts)
head(wideData)
str(longData)
#Let's try ordinary least-squares (OLS) regression:
olsmod <- lm(y~tiem+x1+x2+x3, data=longData)
#We will see in the diagnostic plots that the residuals are poorly approximated by normality,
#and are heteroskedastic. We also know that the residuals are not independent of one another,
#because we have repeated-measures data:
plot(olsmod)
#In the summary, it looks like all of the regression coefficients are significantly different
#from zero, but we know that because the assumptions of OLS regression are violated that
#we should not trust its results:
summary(olsmod)

#Let's try a generalized linear model (GLM). We'll use the quasi-Poisson quasiliikelihood
#function to see how well the y variable is approximated by a Poisson distribution
#(conditional on time and covariates):
glm.mod <- glm(y~tiem+x1+x2+x3, data=longData, family="quasipoisson")
#The estimate of the dispersion parameter should be about 1.0 if the data are
#conditionally Poisson. We can see that it is actually greater than 2,
#indicating overdispersion:
summary(glm.mod)

```

multiData1

Data for multiple regression

Description

Data set used in some of OpenMx's examples.

Usage

```
data("multiData1")
```

Format

A data frame with 500 observations on the following variables.

x1
x2
x3
x4
y

Details

x1-x4 are predictor variables, and y is the outcome.

Source

Simulated.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```
data(multiData1)
summary(lm(y ~ ., data=multiData1))
#results can be replicated in OpenMx.
```

mxAlgebra

Create MxAlgebra Object

Description

This function creates a new [MxAlgebra](#) object.

Usage

```
mxAlgebra(expression, name = NA, dimnames = NA, ..., fixed = FALSE,
           joinKey=as.character(NA), joinModel=as.character(NA), verbose=0L)
```

Arguments

expression	An R expression of OpenMx-supported matrix operators and matrix functions.
name	An optional character string indicating the name of the object.
dimnames	list. The dimnames attribute for the algebra: a list of length 2 giving the row and column names respectively. An empty list is treated as NULL, and a list of length one as row names. The list can be named, and the list names will be used as names for the dimensions.
...	Not used. Forces argument 'fixed' to be specified by name.
fixed	If TRUE, this algebra will not be recomputed automatically when things it depends on change. <code>mxComputeOnce</code> can be used to force it to recompute.
joinKey	The name of the column in current model's raw data that is used as a foreign key to match against the primary key in joinModel's raw data.
joinModel	The name of the model that this matrix joins against.
verbose	For values greater than zero, enable runtime diagnostics.

Details

The `mxAlgebra` function is used to create algebraic expressions that operate on one or more `MxMatrix` objects. To evaluate an `MxAlgebra` object, it must be placed in an `MxModel` object, along with all referenced `MxMatrix` objects and the `mxFitFunctionAlgebra` function. The `mxFitFunctionAlgebra` function must reference by name the `MxAlgebra` object to be evaluated.

Note that, if the result for an `MxAlgebra` depends upon one or more "definition variables" (see `mxMatrix()`), then the value returned after the call to `mxRun()` will be computed using the values of those definition variables in the first (i.e., first before any automated sorting is done) row of the raw dataset.

The following operators and functions are supported in `mxAlgebra`:

Operators

`solve()` Inversion

`t()` Transposition

`^` Elementwise powering

`%^%` Kronecker powering

`+` Addition

`-` Subtraction

`%*%` Matrix Multiplication

`*` Elementwise product

`/` Elementwise division

`%x%` Kronecker product

`%&%` Quadratic product: pre- and post-multiply B by A and its transpose `t(A)`, i.e: `A %&% B == A %*% B %*% t(A)`

Functions

cov2cor Convert covariance matrix to correlation matrix
chol Cholesky Decomposition
cbind Horizontal adhesion
rbind Vertical adhesion
colSums Matrix column sums as a column vector
rowSums Matrix row sums as a column vector
det Determinant
tr Trace
sum Sum
mean Arithmetic mean
prod Product
max Maximum
min Min
abs Absolute value
sin Sine
sinh Hyperbolic sine
asin Arcsine
asinh Inverse hyperbolic sine
cos Cosine
cosh Hyperbolic cosine
acos Arccosine
acosh Inverse hyperbolic cosine
tan Tangent
tanh Hyperbolic tangent
atan Arctangent
atanh Inverse hyperbolic tangent
exp Exponent
log Natural Logarithm
sqrt Square root
p2z *Standard*-normal quantile
logp2z *Standard*-normal quantile from log probabilities
lgamma Log-gamma function
lgamma1p Compute $\log(\Gamma(x+1))$ accurately for small x
eigenval Eigenvalues of a square matrix. Usage: eigenval(x); eigenvec(x); ieigenval(x); ieigenvec(x)
rvectorize Vectorize by row
cvectorize Vectorize by column

[vech](#) Half-vectorization
[vechs](#) Strict half-vectorization
[vech2full](#) Inverse half-vectorization
[vechs2full](#) Inverse strict half-vectorization
[vec2diag](#) Create matrix from a diagonal vector (similar to [diag](#))
[diag2vec](#) Extract diagonal from matrix (similar to [diag](#))
[expm](#) Matrix Exponential
[logm](#) Matrix Logarithm
[omxExponential](#) Matrix Exponential
[omxMnor](#) Multivariate Normal Integration
[omxAllInt](#) All cells Multivariate Normal Integration
[omxNot](#) Perform unary negation on a matrix
[omxAnd](#) Perform binary and on two matrices
[omxOr](#) Perform binary or on two matrices
[omxGreaterThan](#) Perform binary greater on two matrices
[omxLessThan](#) Perform binary less than on two matrices
[omxApproxEquals](#) Perform binary equals to (within a specified epsilon) on two matrices
[omxSelectRows](#) Filter rows from a matrix
[omxSelectCols](#) Filter columns from a matrix
[omxSelectRowsAndCols](#) Filter rows and columns from a matrix
[mxEvaluateOnGrid](#) Evaluate an algebra on an abscissa grid and collect column results

There are also several multiargument functions usable in MxAlgebras, which apply themselves elementwise to the matrix provided as their first argument. These functions have slightly different usage from their R counterparts. Their result is always a matrix with the same dimensions as that provided for their first argument. Values must be provided for ALL arguments of these functions, in order. Provide zeroes as logical values of FALSE, and non-zero numerical values as logical values of TRUE. For most of these functions, OpenMx cycles over values of arguments other than the first, by column (i.e., in column-major order), to the length of the first argument. Notable exceptions are the `log`, `log.p`, and `lower.tail` arguments to probability-distribution-related functions, for which only the [1,1] element is used. It is recommended that all arguments after the first be either (1) scalars, or (2) matrices with the same dimensions as the first argument.

Function	Arguments	Notes
<code>besselI</code> & <code>besselK</code>	<code>x, nu, expon.scaled</code>	Note that OpenMx <i>does</i> cycle over the elements of <code>expon.scaled</code>
<code>besselJ</code> & <code>besselY</code>	<code>x, nu</code>	
<code>dbeta</code>	<code>x, shape1, shape2, ncp, log</code>	The algorithm for the non-central beta distribution is used
<code>pbeta</code>	<code>q, shape1, shape2, ncp, lower.tail, log.p</code>	Values of <code>ncp</code> are handled as with <code>dbeta()</code> .
<code>dbinom</code>	<code>x, size, prob, log</code>	
<code>pbinom</code>	<code>q, size, prob, lower.tail, log.p</code>	
<code>dcauchy</code>	<code>x, location, scale, log</code>	
<code>pcauchy</code>	<code>q, location, scale, lower.tail, log.p</code>	
<code>dchisq</code>	<code>x, df, ncp, log</code>	The algorithm for the non-central chi-square distribution is used

pchisq	q,df,ncp,lower.tail,log.p	Values of ncp are handled as with dchisq().
omxDnbinom	x,size,prob,mu,log	Exactly one of arguments size, prob, and mu should be
omxPnbinom	q,size,prob,mu,lower.tail,log.p	Arguments are handled as with omxDnbinom().
dpois	x,lambda,log	
ppois	q,lambda,lower.tail,log.p	

Value

Returns a new [MxAlgebra](#) object.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

[MxAlgebra](#) for the S4 class created by mxAlgebra. [mxFitFunctionAlgebra](#) for an objective function which takes an MxAlgebra or MxMatrix object as the function to be minimized. [MxMatrix](#) and [mxMatrix](#) for objects which may be entered in the expression argument and the function that creates them. More information about the OpenMx package may be found [here](#).

Examples

```
A <- mxMatrix("Full", nrow = 3, ncol = 3, values=2, name = "A")

# Simple example: algebra B simply evaluates to the matrix A
B <- mxAlgebra(A, name = "B")

# Compute A + B
C <- mxAlgebra(A + B, name = "C")

# Compute sin(C)
D <- mxAlgebra(sin(C), name = "D")

# Make a model and evaluate the mxAlgebra object 'D'
A <- mxMatrix("Full", nrow = 3, ncol = 3, values=2, name = "A")
model <- mxModel(model="AlgebraExample", A, B, C, D )
fit <- mxRun(model)
mxEval(D, fit)

# Numbers in mxAlgebras are upgraded to 1x1 matrices
# Example of Kronecker powering (%%) and multiplication (%*)
A <- mxMatrix(type="Full", nrow=3, ncol=3, value=c(1:9), name="A")
m1 <- mxModel(model="kron", A, mxAlgebra(A %% 2, name="KroneckerPower"))
mxRun(m1)$KroneckerPower

# Running kron
# mxAlgebra 'KroneckerPower'
# $formula: A %% 2
```

```
# $result:
#      [,1] [,2] [,3]
# [1,]   1  16  49
# [2,]   4  25  64
# [3,]   9  36  81
```

MxAlgebra-class	<i>MxAlgebra Class</i>
-----------------	------------------------

Description

MxAlgebra is an S4 class. An MxAlgebra object is a [named entity](#). New instances of this class can be created using the function [mxAlgebra](#).

Details

The MxAlgebra class has the following slots:

name	-	The name of the object
formula	-	The R expression to be evaluated
result	-	a matrix with the computation result

The ‘name’ slot is the name of the MxAlgebra object. Use of MxAlgebra objects in the [mxConstraint](#) function or an objective function requires reference by name.

The ‘formula’ slot is an expression containing the expression to be evaluated. These objects are operated on or related to one another using one or more operations detailed in the [mxAlgebra](#) help file.

The ‘result’ slot is used to hold the results of computing the expression in the ‘formula’ slot. If the containing model has not been executed, then the ‘result’ slot will hold a 0 x 0 matrix. Otherwise the slot will store the computed value of the algebra using the final estimates of the free parameters.

Slots may be referenced with the \$ symbol. See the documentation for [Classes](#) and the examples in the [mxAlgebra](#) document for more information.

References

The OpenMx User’s guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

[mxAlgebra](#), [mxMatrix](#), [MxMatrix](#)

MxAlgebraFormula-class
MxAlgebraFormula

Description

This is an internal class for the formulas used in [mxAlgebra](#) calls.

`mxAlgebraFromString` *Create MxAlgebra object from a string*

Description

Create MxAlgebra object from a string

Usage

```
mxAlgebraFromString(algString, name = NA, dimnames = NA, ...)
```

Arguments

<code>algString</code>	the character string to convert into an R expression
<code>name</code>	An optional character string indicating the name of the object.
<code>dimnames</code>	list. The <code>dimnames</code> attribute for the algebra: a list of length 2 giving the row and column names respectively. An empty list is treated as NULL, and a list of length one as row names. The list can be named, and the list names will be used as names for the dimensions.
<code>...</code>	Not used. Forces any remaining arguments to be specified by name.

See Also

[mxAlgebra](#)

Examples

```
A <- mxMatrix(values = runif(25), nrow = 5, ncol = 5, name = 'A')
B <- mxMatrix(values = runif(25), nrow = 5, ncol = 5, name = 'B')
model <- mxModel(A, B, name = 'model',
  mxAlgebraFromString("A * (B + A)", name = 'test'))
model <- mxRun(model)
model[['test']]$result
A$values * (B$values + A$values)
```

mxAlgebraObjective *DEPRECATED: Create MxAlgebraObjective Object*

Description

WARNING: Objective functions have been deprecated as of OpenMx 2.0.

Please use `MxFitFunctionAlgebra()` instead. As a temporary workaround, `MxAlgebraObjective` returns a list containing a NULL `MxExpectation` object and an `MxFitFunctionAlgebra` object.

All occurrences of

`mxAlgebraObjective(algebra, numObs = NA, numStats = NA)`

Should be changed to

`mxFitFunctionAlgebra(algebra, numObs = NA, numStats = NA)`

Arguments

<code>algebra</code>	A character string indicating the name of an MxAlgebra or MxMatrix object to use for optimization.
<code>numObs</code>	(optional) An adjustment to the total number of observations in the model.
<code>numStats</code>	(optional) An adjustment to the total number of observed statistics in the model.

Details

NOTE: THIS DESCRIPTION IS DEPRECATED. Please change to using [mxFitFunctionAlgebra](#) as shown in the example below.

Fit functions are functions for which free parameter values are chosen such that the value of the objective function is minimized. While the other fit functions in OpenMx require an expectation function for the model, the `mxAlgebraObjective` function uses the referenced [MxAlgebra](#) or [MxMatrix](#) object as the function to be minimized.

If a model's primary objective function is a `mxAlgebraObjective` objective function, then the referenced algebra in the objective function must return a 1 x 1 matrix (when using OpenMx's default optimizer). There is no restriction on the dimensions of an objective function that is not the primary, or 'topmost', objective function.

To evaluate an algebra objective function, place the following objects in a [MxModel](#) object: a `MxAlgebraObjective`, [MxAlgebra](#) and [MxMatrix](#) entities referenced by the `MxAlgebraObjective`, and optional [MxBounds](#) and [MxConstraint](#) entities. This model may then be evaluated using the [mxRun](#) function. The results of the optimization may be obtained using the [mxEval](#) function on the name of the [MxAlgebra](#), after the model has been run.

Value

Returns a list containing a NULL `MxExpectation` object and an `MxFitFunctionAlgebra` object. `MxFitFunctionAlgebra` objects should be included with models with referenced [MxAlgebra](#) and [MxMatrix](#) objects.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

[mxAlgebra](#) to create an algebra suitable as a reference function to be minimized. More information about the OpenMx package may be found [here](#).

Examples

```
# Create and fit a very simple model that adds two numbers using mxFitFunctionAlgebra

library(OpenMx)

# Create a matrix 'A' with no free parameters
A <- mxMatrix('Full', nrow = 1, ncol = 1, values = 1, name = 'A')

# Create an algebra 'B', which defines the expression A + A
B <- mxAlgebra(A + A, name = 'B')

# Define the objective function for algebra 'B'
objective <- mxFitFunctionAlgebra('B')

# Place the algebra, its associated matrix and
# its objective function in a model
tmpModel <- mxModel(model="Addition", A, B, objective)

# Evaluate the algebra
tmpModelOut <- mxRun(tmpModel)

# View the results
tmpModelOut$output$minimum
```

mxAvailableOptimizers *mxAvailableOptimizers*

Description

List the Optimizers available in this version, e.g. "SLSQP" "CSOLNP"

Usage

```
mxAvailableOptimizers()
```

Details

note for advanced users: Special-purpose optimizers like Newton-Raphson or EM are not included in this list.

Value

- list of valid Optimizer names

See Also

- [mxOption](#)(model, "Default optimizer")

Examples

```
mxAvailableOptimizers()
```

MxBaseExpectation-class

MxBaseExpectation

Description

The virtual base class for all expectations. Expectations contain enough information to generate simulated data. This is an internal class and should not be used directly.

See Also

[mxExpectationNormal](#), [mxExpectationRAM](#), [mxExpectationLISREL](#), [mxExpectationStateSpace](#), [mxExpectationBA81](#)

MxBaseFitFunction-class

MxBaseFitFunction

Description

The virtual base class for all fit functions. This is an internal class and should not be used directly.

See Also

[mxFitFunctionAlgebra](#), [mxFitFunctionML](#), [mxFitFunctionMultigroup](#), [mxFitFunctionR](#), [mxFitFunctionWLS](#), [mxFitFunctionRow](#), [mxFitFunctionGREML](#)

MxBaseNamed-class

MxBaseNamed

Description

This is an internal class and should not be used directly. It is the base class for named entities. Fit functions, expectations, and computes contain this class.

MxBaseObjectiveMetaData-class
MxBaseObjectiveMetaData

Description

This is an internal class and should not be used directly. It is the virtual base class for all objective functions meta-data

mxBounds *Create MxBounds Object*

Description

This function creates a new [MxBounds](#) object.

Usage

```
mxBounds(parameters, min = NA, max = NA)
```

Arguments

parameters	A character vector indicating the names of the parameters on which to apply bounds.
min	A numeric value for the lower bound. NA means use default value.
max	A numeric value for the upper bound. NA means use default value.

Details

Creates a set of boundaries or limits for a parameter or set of parameters. Parameters may be any free parameter or parameters from an [MxMatrix](#) object. Parameters may be referenced either by name or by referring to their position in the 'spec' matrix of an [MxMatrix](#) object.

Minima and maxima may be specified as scalar numeric values.

Value

Returns a new [MxBounds](#) object. If used as an argument in an [MxModel](#) object, the parameters referenced in the 'parameters' argument must also be included prior to optimization.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

[MxBounds](#) for the S4 class created by `mxBounds`. [MxMatrix](#) and [mxMatrix](#) for free parameter specification. More information about the OpenMx package may be found [here](#).

Examples

```
#Create lower and upper bounds for parameters 'A' and 'B'
bounds <- mxBounds(c('A', 'B'), 3, 5)

#Create a lower bound of zero for a set of variance parameters
varianceBounds <- mxBounds(c('Var1', 'Var2', 'Var3'), 0)
```

MxBounds-class

MxBounds Class

Description

`MxBounds` is an S4 class. New instances of this class can be created using the function [mxBounds](#).

Details

The `MxBounds` class has the following slots:

min	-	The lower bound
max	-	The upper bound
parameters	-	The vector of parameter names

The 'min' and 'max' slots hold scalar numeric values for the lower and upper bounds on the list of parameters, respectively.

Parameters may be any free parameter or parameters from an [MxMatrix](#) object. Parameters may be referenced either by name or by referring to their position in the 'spec' matrix of an `MxMatrix` object. To affect an estimation or optimization, an `MxBounds` object must be included in an [MxModel](#) object with all referenced [MxAlgebra](#) and [MxMatrix](#) objects.

Slots may be referenced with the \$ symbol. See the documentation for [Classes](#) and the examples in the [mxBounds](#) document for more information.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

[mxBounds](#) for the function that creates `MxBounds` objects. [MxMatrix](#) and [mxMatrix](#) for free parameter specification. More information about the OpenMx package may be found [here](#).

MxCharOrList-class *A character, list or NULL*

Description

A character, list or NULL

MxCharOrNumber-class *A character or integer*

Description

A character or integer

mxCheckIdentification *Check that a model is locally identified*

Description

Use the dimension of the null space of the Jacobian to determine whether or not a model is identified local to its current parameter values. The output is a list of the the identification status, the Jacobian, and which parameters are not identified.

Usage

```
mxCheckIdentification(model, details=TRUE)
```

Arguments

model	A MxModel object or list of MxModel objects.
details	logical.

Details

The mxCheckIdentification function is used to check that a model is identified. That is, the function will tell you if the model has a unique solution in parameter space. The function is most useful when applied to either (a) a model that has been run and had some NA standard errors, or (b) a model that has not been run but has reasonable starting values. In the former situation, mxCheckIdentification is used as a diagnostic after a problem was indicated. In the latter situation, mxCheckIdentification is used as a sanity check.

The method uses the Jacobian of the model expected means and the unique elements of the expected covariance matrix with respect to the free parameters. It is the first derivative of the mapping between the free parameters and the sufficient statistics for the Normal distribution. The method

does not depend on data, but does depend on the current values of the free parameters. Thus, it only provides local identification, not global identification. Because the method does not depend on data, the model still could be empirically unidentified due to missing data.

The Jacobian is evaluated numerically and generally takes a few seconds, but much less than a minute.

The identification may not be accurate for model where definition variables are used. Currently, only the first row of the definition variable is evaluated.

When TRUE, the 'details' argument provides the names of the non-identified parameters. Otherwise, only the status and Jacobian are returned.

Value

A named list with components

status logical. TRUE if the model is locally identified; otherwise FALSE.

jacobian matrix. The numerically evaluated Jacobian.

non_identified_parameters vector. The free parameter names that are not identified

References

Bekker, P.A., Merckens, A., Wansbeek, T.J. (1994). Identification, Equivalent Models and Computer Algebra. Academic Press: Orlando, FL.

Bollen, K. A. & Bauldry, S. (2010). Model Identification and Computer Algebra. Sociological Methods & Research, 39, p. 127-156.

See Also

[mxModel](#)

Examples

```
require(OpenMx)

data(demoOneFactor)
manifests <- names(demoOneFactor)
latents <- "G1"
model2 <- mxModel(model="One Factor", type="RAM",
  manifestVars = manifests,
  latentVars = latents,
  mxPath(from = latents[1], to=manifests[1:5]),
  mxPath(from = manifests, arrows = 2, lbound=1e-6),
  mxPath(from = latents, arrows = 2, free = FALSE, values = 1.0),
  mxData(cov(demoOneFactor), type = "cov", numObs=500)
)
fit2 <- mxRun(model2)

id2 <- mxCheckIdentification(fit2)
id2$status
```



```

# The model is locally identified

# Build a model from the solution of the previous one
# but now the factor variance is also free
model2n <- mxModel(fit2, name="Non Identified Two Factor",
  mxPath(from=latents[1], arrows=2, free=TRUE, values=1)
)

mid2 <- mxCheckIdentification(model2n)
mid2$non_identified_parameters
# The factor loadings and factor variance
# are not identified.

```

mxCI

Create mxCI Object

Description

This function creates a new [MxCI](#) object, which are used to estimate likelihood-based confidence intervals.

Usage

```
mxCI(reference, interval = 0.95, type=c("both", "lower", "upper"), ..., boundAdj=TRUE)
```

Arguments

reference	A character vector of free parameters, mxMatrices, mxMatrix elements and mx-Algebras on which confidence intervals are to be estimated, listed by name.
interval	A scalar numeric value indicating the confidence interval to be estimated. Must be between 0 and 1. Defaults to 0.95.
type	A character string indicating whether the upper, lower or both confidence limits are returned. Defaults to "both".
...	Not used. Forces remaining arguments to be specified by name.
boundAdj	Whether to correct the likelihood-based confidence intervals for a lower or upper bound.

Details

The `mxCI` function creates [MxCI](#) objects, which can be used as arguments in [MxModel](#) objects. When models containing [MxCI](#) objects are optimized using `mxRun` with the 'intervals' argument set to TRUE, likelihood-based confidence intervals are returned. The likelihood-based confidence intervals calculated by [MxCI](#) objects are symmetric with respect to the change in likelihood in either direction, and are not necessarily symmetric around the parameter estimate. Estimation of confidence intervals requires both that an [MxCI](#) object be included in the model and that the 'intervals' argument of the `mxRun` function is set to TRUE. When estimated, confidence intervals can be

accessed in the model output at `$output$confidenceIntervals` or by using [summary](#) on a fitted [MxModel](#) object.

A typical use case is when a model includes non-linear constraints, and hence, standard errors are not available. In all cases, a two-sided hypothesis test is assumed. Therefore, the upper bound will exclude 2.5% (for `interval=0.95`) even though only one bound is requested. To obtain a one-sided CI for a one-sided hypothesis test, `interval=0.90` will obtain a 95% confidence interval.

When a confidence interval is requested for a free parameter (not an algebra) constrained by a lower bound or an upper bound (but not both) and `boundAdj=TRUE` then the Wu & Neale (2012) correction is used. This improves the accuracy of the confidence interval when the parameter is estimated close to the bound. For example, this correction will be activated when a variance with a lower bound of 10^{-6} and no upper bound that is estimated close to the bound. The sample size, or more precisely effective sample size for that particular parameter, will determine how close the variance needs to be to the bound at 10^{-6} to activate the correction.

The likelihood-based confidence intervals returned using [MxCI](#) are obtained by increasing or decreasing the value of each parameter until the -2 log likelihood of the model increases by an amount corresponding to the requested interval. The confidence limit specified by the ‘interval’ argument is transformed into a corresponding difference in the model -2 log likelihood based on the likelihood ratio test. Thus, a requested confidence interval for a parameter will first determine the corresponding quantile from the chi-squared distribution with one degree of freedom (a value of 3.841459 when a 95 percent confidence interval is requested). That quantile will be populated into either the ‘lowerdelta’ slot, the ‘upperdelta’ slot, or both in the output [MxCI](#) object.

Estimation of likelihood-based confidence intervals begins after optimization has been completed, with each parameter moved in the direction(s) specified in the ‘type’ argument until the specified increase in -2 log likelihood is reached. All other free parameters are left free for this stage of optimization. This process repeats until all confidence intervals have been calculated. The calculation of likelihood-based confidence intervals can be computationally intensive, and may add a significant amount of time to model estimation when many confidence intervals are requested.

Multiple parameters, [MxMatrices](#) and [MxAlgebras](#) may be listed in the ‘reference’ argument. Individual elements of [MxMatrices](#) and [MxAlgebras](#) may be listed as well, using the syntax “matrix[row,col]” (see [Extract](#) for more information). Only scalar numeric values for the ‘interval’ argument are supported. Users requesting different confidence ranges for different parameters must use separate [mxCI](#) statements. [MxModel](#) objects can hold multiple [MxCI](#) objects, but only one confidence interval may be requested per named-entity.

Confidence interval estimation may result in model non-convergence at the confidence limit. Separate optimizer messages may be passed for each confidence limit. This has no impact on the parameter estimates themselves, but may indicate a problem with the referenced confidence limit. Model non-convergence for a particular confidence limit may indicate parameter interdependence or the influence of a parameter boundary.

These error messages and their meanings are listed in the help for [mxSummary](#)

The validity of a confidence limit can be checked by running a model with the appropriate parameter fixed at the confidence limit in question. If the confidence limit is valid, the -2 log likelihoods of these two models should differ by the specified chi-squared criterion (as set using the ‘lowerdelta’ or ‘upperdelta’ slots in the [MxCI](#) object (you can choose which of these to set via the type parameter of [mxCI](#))).

Value

Returns a new **MxCI** object. If used as an argument in an **MxModel** object, the parameters, **MxMatrices** and **MxAlgebras** listed in the 'reference' argument must also be included prior to optimization.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>. Additional support for mxCI() can be found on the OpenMx wiki at <http://openmx.ssri.psu.edu/wiki>.

Neale, M. C. & Miller M. B. (1997). The use of likelihood based confidence intervals in genetic models. *Behavior Genetics*, 27(2), 113-120.

Pek, J. & Wu, H. (2015). Profile likelihood-based confidence intervals and regions for structural equation models. *Psychometrika*, 80(4), 1123-1145.

Wu, H. & Neale, M. C. (2012). Adjusted confidence intervals for a bounded parameter. *Behavior genetics*, 42(6), 886-898.

See Also

MxCI for the S4 class created by mxCI. **mxComputeConfidenceInterval** is the internal compute plan that implements the algorithm. **MxMatrix** and **mxMatrix** for free parameter specification. More information about the OpenMx package may be found [here](#).

Examples

```
library(OpenMx)

# generate data
covariance <- matrix(c(1.0, 0.5, 0.5, 1.0),
  nrow=2,
  dimnames=list(c("a", "b"), c("a", "b")))

data <- mxData(covariance, "cov", numObs=100)

# create an expected covariance matrix
expect <- mxMatrix("Symm", 2, 2,
  free=TRUE,
  values=c(1, .5, 1),
  labels=c("var1", "cov12", "var2"),
  name="expectedCov")

# request 95 percent confidence intervals
ci <- mxCI(c("var1", "cov12", "var2"))

# specify the model
model <- mxModel(model="Confidence Interval Example",
  data, expect, ci,
  mxExpectationNormal("expectedCov", dimnames=c("a", "b")),
  mxFitFunctionML())

# run the model
```

```

results <- mxRun(model, intervals=TRUE)

# view confidence intervals
print(summary(results)$CI)

# view all results
summary(results)

# remove a specific mxCI from a model
model <- mxModel(model, remove=TRUE, model$intervals[['cov12']])
model$intervals

# remove all mxCI from a model
model <- mxModel(model, remove=TRUE, model$intervals)
model$intervals

```

MxCI-class

MxCI Class

Description

MxCI is an S4 class. An MxCI object is a [named entity](#). New instances of this class can be created using the function [mxCI](#). MxCI objects may be used as arguments in the [mxModel](#) function.

Details

The MxCI class has the following slots:

- reference - The name of the object
- lowerdelta - Either a matrix or a data frame
- upperdelta - A vector for means, or NA if missing

The reference slot contains a character vector of named free parameters, [MxMatrices](#) and [MxAlgebras](#) on which confidence intervals are desired. Individual elements of [MxMatrices](#) and [MxAlgebras](#) may be listed as well, using the syntax “matrix[row,col]” (see [Extract](#) for more information).

The lowerdelta and upperdelta slots give the changes in likelihoods used to define the confidence interval. The upper bound of the likelihood-based confidence interval is estimated by increasing the parameter estimate, leaving all other parameters free, until the model -2 log likelihood increased by ‘upperdelta’. The lower bound of the confidence interval is estimated by decreasing the parameter estimate, leaving all other parameters free, until the model -2 log likelihood increased by ‘lowerdata’.

Likelihood-based confidence intervals may be specified by including one or more MxCI objects in an [MxModel](#) object. Estimation of confidence intervals requires model optimization using the [mxRun](#) function with the ‘intervals’ argument set to TRUE. The calculation of likelihood-based

confidence intervals can be computationally intensive, and may add a significant amount of time to model estimation when many confidence intervals are requested.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

[mxCI](#) for creating MxCI objects. More information about the OpenMx package may be found [here](#).

 mxCompare

Assign Model Parameters

Description

Compare the fit of a model or set of models to a reference model or set of reference models. The output is a table with one row per model comparison.

Usage

```
mxCompare(base, comparison, ..., all = FALSE)
```

Arguments

base	A MxModel object or list of MxModel objects.
comparison	A MxModel object or list of MxModel objects.
...	Not used. Forces remaining arguments to be specified by name.
all	A boolean value on whether to compare all bases with all comparisons. Defaults to FALSE.

Details

The mxCompare function is used to compare the fit of one or more [MxMatrix](#) objects with output to one or more comparison models. Fit statistics for the comparison model or models are subtracted from the fit statistics for the base model or models. All models included in the 'base' argument are also listed without comparison (compared to a <NA> model) to present their raw fit statistics.

Model comparisons are made by subtracting the fit of the comparison model from the fit of a base model. To make sure that the differences between models are positive and yield p-values for likelihood ratio tests, the model or models listed in the 'base' argument should be more saturated (i.e., more estimated parameters and fewer degrees of freedom) than models listed in the 'comparison' argument. If a comparison is made where the comparison model has a higher minus 2 log likelihood (-2LL) than the base model, then the difference in their -2LLs will be negative. P-values for likelihood ratio tests will not be reported when either the -2LL or degrees of freedom for the comparison are negative.

When multiple models are included in both the 'base' and 'comparison' arguments, then comparisons are made between the two lists of models based on the value of the 'all' argument. If 'all'

is set to FALSE (default), then the first model in the 'base' list is compared to the first model in the 'comparison' list, second with second, and so on. If there are an unequal number of 'base' and 'comparison' models, then the shorter list of models is repeated to match the length of the longer list. For example, comparing base models 'B1' and 'B2' with comparison models 'C1', 'C2' and 'C3' will yield three comparisons: 'B1' with 'C1', 'B2' with 'C2', and 'B1' with 'C3'. Each of those comparisons are prefaced by a comparison between the base model and a missing comparison model to present the fit of the base model.

If 'all' is set to TRUE, all possible comparisons between base and comparison models are made, and one entry is made for each base model. All comparisons involving the first model in 'base' are made first, followed by all comparisons with the second 'base' model, and so on. When there are multiple models in either the 'base' or 'comparison' arguments but not both, then the 'all' argument does not affect the set of comparisons made.

The following columns appear in the output:

base Name of the base model.

comparison Name of the comparison model. Is <NA> for the first

ep Estimated parameters of the comparison model.

minus2LL Minus 2*log-likelihood of the comparison model. If the comparison model is <NA>, then the minus 2*log-likelihood of the base model is given.

df Degrees in freedom of the comparison model. If the comparison model is <NA>, then the degrees of freedom of the base model is given.

AIC Akaike's Information Criterion for the comparison model. If the comparison model is <NA>, then the AIC of the base model is given.

diffLL Difference in minus 2*log-likelihoods of the base and comparison models. Will be positive when base model -2LL is higher than comparison model -2LL.

diffdf Difference in degrees of freedoms of the base and comparison models. Will be positive when base model DF is lower than comparison model DF (base model estimated parameters is higher than comparison model estimated parameters)

p P-value for likelihood ratio test based on diffLL and diffdf values.

The mxCompare function will give a p-value for any comparison in which both 'diffLL' and 'diffdf' are non-negative. However, this p-value is based on the assumptions of the likelihood ratio test, specifically that the two models being compared are nested. The likelihood ratio test and associated p-values are not valid when the comparison model is not nested in the referenced base model.

Use options('digits' = N) to set the minimum number of significant digits to be printed in values. The mxCompare function does not directly accept a digits argument, and depends on the value of the 'digits' option.

See Also

[mxModel](#); [options](#) (use options('mxOptions') to see all the OpenMx-specific options)

Examples

```
data(demoOneFactor)
```

```

manifests <- names(demoOneFactor)
latents <- c("G1")
model1 <- mxModel(model="One Factor", type="RAM",
  manifestVars = manifests,
  latentVars = latents,
  mxPath(from = latents, to=manifests),
  mxPath(from = manifests, arrows = 2),
  mxPath(from = latents, arrows = 2, free = FALSE, values = 1.0),
  mxData(cov(demoOneFactor), type = "cov", numObs = 500)
)

fit1 <- mxRun(model1)

latents <- c("G1", "G2")
model2 <- mxModel(model="Two Factor", type="RAM",
  manifestVars = manifests,
  latentVars = latents,
  mxPath(from = latents[1], to=manifests[1:3]),
  mxPath(from = latents[2], to=manifests[4:5]),
  mxPath(from = manifests, arrows = 2),
  mxPath(from = latents, arrows = 2, free = FALSE, values = 1.0),
  mxData(cov(demoOneFactor), type = "cov", numObs=500)
)

fit2 <- mxRun(model2)

mxCompare(fit1, fit2)

# vary precision of the output
oldPrecision = as.numeric(options('digits'))
options('digits' = 1)
mxCompare(fit1, fit2)
options('digits' = oldPrecision)

```

MxCompute-class

MxCompute

Description

This is an internal class and should not be used directly.

mxComputeConfidenceInterval

Find likelihood-based confidence intervals

Description

There are various equivalent ways to pose the optimization problems required to estimate confidence intervals. Most accurate solutions are achieved when the problem is posed using non-linear constraints. However, the available optimizers (NPSOL, SLSQP, and CSOLNP) often have difficulty with non-linear constraints.

Usage

```
mxComputeConfidenceInterval(plan, ..., freeSet = NA_character_,
  verbose = 0L, engine = NULL, fitfunction = "fitfunction",
  tolerance = NA_real_, constraintType = "none")
```

Arguments

plan	compute plan to optimize the model
...	Not used. Forces remaining arguments to be specified by name.
freeSet	names of matrices containing free variables
verbose	level of debugging output
engine	deprecated
fitfunction	the name of the deviance function
tolerance	deprecated
constraintType	one of c('ineq', 'none')

References

Neale, M. C. & Miller M. B. (1997). The use of likelihood based confidence intervals in genetic models. *Behavior Genetics*, 27(2), 113-120.

Pek, J. & Wu, H. (2015). Profile likelihood-based confidence intervals and regions for structural equation models. *Psychometrika*, 80(4), 1123-1145.

Wu, H. & Neale, M. C. (2012). Adjusted confidence intervals for a bounded parameter. *Behavior genetics*, 42(6), 886-898.

mxComputeDefault	<i>Default compute plan</i>
------------------	-----------------------------

Description

The default compute plan is approximately as follows: `mxComputeSequence(list(mxComputeGradientDescent(), mxComp`

Usage

```
mxComputeDefault(freeSet = NA_character_)
```

Arguments

freeSet	names of matrices containing free variables
---------	---------------------------------------------

mxComputeEM	<i>Fit a model using DLR's (1977) Expectation-Maximization (EM) algorithm</i>
-------------	-------------------------------------------------------------------------------

Description

The EM algorithm constitutes the following steps: Start with an initial parameter vector. Predict the missing data to form a completed data model. Optimize the completed data model to obtain a new parameter vector. Repeat these steps until convergence criteria are met.

Usage

```
mxComputeEM(expectation, predict, mstep, observedFit = "fitfunction", ...,
             maxIter = 500L, tolerance = 1e-09, verbose = 0L,
             freeSet = NA_character_, accel = "varadhan2008",
             information = NA_character_, infoArgs = list())
```

Arguments

expectation	a vector of expectation names
predict	what to predict from the observed data (available options depend on the expectation)
mstep	a compute plan to optimize the completed data model
observedFit	the name of the observed data fit function (defaults to "fitfunction")
...	Not used. Forces remaining arguments to be specified by name.
maxIter	maximum number of iterations
tolerance	optimization is considered converged when the maximum relative change in fit is less than tolerance
verbose	level of diagnostic output
freeSet	names of matrices containing free variables
accel	name of acceleration method ("varadhan2008" or "ramsay1975")
information	name of information matrix approximation method
infoArgs	arguments to control the information matrix method

Details

This compute plan does not work with any and all expectations. It requires a special kind of expectation that can predict its missing data to create a completed data model.

The EM algorithm does not produce a parameter covariance matrix for standard errors. The Oakes (1999) direct method and S-EM, an implementation of Meng & Rubin (1991), are included.

Ramsay (1975) was recommended in Bock, Gibbons, & Muraki (1988).

References

- Bock, R. D., Gibbons, R., & Muraki, E. (1988). Full-information item factor analysis. *Applied Psychological Measurement*, 6(4), 431-444.
- Dempster, A. P., Laird, N. M., & Rubin, D. B. (1977). Maximum likelihood from incomplete data via the EM algorithm. *Journal of the Royal Statistical Society. Series B (Methodological)*, 1-38.
- Meng, X.-L. & Rubin, D. B. (1991). Using EM to obtain asymptotic variance-covariance matrices: The SEM algorithm. *Journal of the American Statistical Association*, 86 (416), 899-909.
- Oakes, D. (1999). Direct calculation of the information matrix via the EM algorithm. *Journal of the Royal Statistical Society: Series B (Statistical Methodology)*, 61(2), 479-482.
- Ramsay, J. O. (1975). Solving implicit equations in psychometric data analysis. *Psychometrika*, 40 (3), 337-360.
- Varadhan, R. & Roland, C. (2008). Simple and globally convergent methods for accelerating the convergence of any EM algorithm. *Scandinavian Journal of Statistics*, 35, 335-353.

mxComputeGradientDescent

Optimize parameters using a gradient descent optimizer

Description

This optimizer does not require analytic derivatives of the fit function. The fully open-source CRAN version of OpenMx offers 2 choices, SLSQP (from the NLOPT collection) and CSOLNP. The OpenMx Team's version of OpenMx offers the choice of three optimizers: SLSQP, CSOLNP, and NPSOL.

Usage

```
mxComputeGradientDescent(freeSet = NA_character_, ..., engine = NULL,
  fitfunction = "fitfunction", verbose = 0L, tolerance = NA_real_,
  useGradient = NULL, warmStart = NULL, nudgeZeroStarts = TRUE,
  maxMajorIter = NULL, gradientAlgo = mxOption(NULL, "Gradient algorithm"),
  gradientIterations = mxOption(NULL, "Gradient iterations"),
  gradientStepSize = mxOption(NULL, "Gradient step size"))
```

Arguments

freeSet	names of matrices containing free parameters.
...	Not used. Forces remaining arguments to be specified by name.
engine	specific 'NPSOL', 'SLSQP', or 'CSOLNP'
fitfunction	name of the fitfunction (defaults to 'fitfunction')
verbose	level of debugging output
tolerance	how close to the optimum is close enough (also known as the optimality tolerance)

useGradient	whether to use the analytic gradient (if available)
warmStart	a Cholesky factored Hessian to use as the NPSOL Hessian starting value (pre-conditioner)
nudgeZeroStarts	whether to nudge any zero starting values prior to optimization (default TRUE)
maxMajorIter	maximum number of major iterations
gradientAlgo	one of c('forward','central')
gradientIterations	number of Richardson iterations to use for the gradient
gradientStepSize	the step size for the gradient

Details

One of the most important options for SLSQP is `gradientAlgo`. By default, the central method is used. This method requires 2 times `gradientIterations` function evaluations per parameter per gradient. The central method can be much more accurate than the forward method, which requires `gradientIterations` function evaluations per parameter per gradient. The forward method is faster, and often works well enough, but can result in imprecise gradient estimations that may not allow SLSQP to fully optimize a given model, possibly resulting in code RED (status code 5 or 6).

Currently, only SLSQP uses arguments `gradientIterations` and `gradientAlgo`. CSOLNP always uses the forward method; NPSOL usually uses the forward method, but adaptively switches to central under certain circumstances.

CSOLNP uses the value of argument `gradientStepSize` as-is, whereas SLSQP internally scales it by a factor of 100. The purpose of this transformation is to obtain roughly the same accuracy given other differences in numerical procedure. NPSOL ignores `gradientStepSize`, and instead uses a function of `mxOption` "Function precision" to determine its gradient step size.

Currently, only SLSQP and NPSOL can use analytic gradients, and only NPSOL uses `warmStart`.

References

Luenberger, D. G. & Ye, Y. (2008). *Linear and nonlinear programming*. Springer.

Examples

```
data(demoOneFactor)
factorModel <- mxModel(name = "One Factor",
  mxMatrix(type="Full", nrow=5, ncol=1, free=FALSE, values=0.2, name="A"),
  mxMatrix(type="Symm", nrow=1, ncol=1, free=FALSE, values=1, name="L"),
  mxMatrix(type="Diag", nrow=5, ncol=5, free=TRUE, values=1, name="U"),
  mxAlgebra(expression=A %*% L %*% t(A) + U, name="R"),
  mxExpectationNormal(covariance="R", dimnames=names(demoOneFactor)),
  mxFitFunctionML(),
  mxData(observed=cov(demoOneFactor), type="cov", numObs=500),
  mxComputeSequence(steps=list(
    mxComputeGradientDescent(),
    mxComputeNumericDeriv(),
    mxComputeStandardError(),
```

```

    mxComputeHessianQuality()
  )))
factorModelFit <- mxRun(factorModel)
factorModelFit$output$conditionNumber # 29.5

```

mxComputeHessianQuality

Compute the quality of the Hessian

Description

Tests whether the Hessian is positive definite (model\$output\$infoDefinite) and, if so, computes the approximate condition number (model\$output\$conditionNumber). See Luenberger & Ye (2008) Second Order Test (p. 190) and Condition Number (p. 239).

Usage

```
mxComputeHessianQuality(freeSet = NA_character_, ..., verbose = 0L)
```

Arguments

freeSet	names of matrices containing free variables
...	Not used. Forces remaining arguments to be specified by name.
verbose	Level of debugging output.

Details

The condition number is approximated by $\text{norm}(H) * \text{norm}(H^{-1})$ where H is the Hessian. The norm is either the 1- or infinity-norm (both obtain the same result due to symmetry).

References

Luenberger, D. G. & Ye, Y. (2008). Linear and nonlinear programming. Springer.

mxComputeIterate

Repeatedly invoke a series of compute objects until change is less than tolerance

Description

One step (typically the last) must compute the fit or maxAbsChange.

Usage

```

mxComputeIterate(steps, ..., maxIter = 500L, tolerance = 1e-09,
  verbose = 0L, freeSet = NA_character_, maxDuration = as.numeric(NA))

```

Arguments

steps	a list of compute objects
...	Not used. Forces remaining arguments to be specified by name.
maxIter	the maximum number of iterations
tolerance	iterates until maximum relative change is less than tolerance
verbose	level of debugging output
freeSet	Names of matrices containing free variables.
maxDuration	the maximum amount of time (in seconds) to iterate

mxComputeNelderMead *Optimize parameters using a variation of the Nelder-Mead algorithm.*

Description

OpenMx includes a flexible, options-rich implementation of the Nelder-Mead algorithm.

Usage

```
mxComputeNelderMead(
  freeSet=NA_character_, fitfunction="fitfunction", verbose=0L,
  nudgeZeroStarts=mxOption(NULL,"Nudge zero starts"),
  maxIter=NULL,...,
  alpha=1, betao=0.5, betai=0.5, gamma=2, sigma=0.5, bignum=1e35,
  iniSimplexType=c("regular","right","smartRight","random"),
  iniSimplexEdge=1, iniSimplexMat=NULL, greedyMinimize=FALSE,
  altContraction=FALSE, degenLimit=0, stagnCtrl=c(-1L,-1L),
  validationRestart=TRUE,
  xTolProx=1e-8, fTolProx=1e-8,
  doPseudoHessian=FALSE,
  ineqConstraintMthd=c("soft","eqMthd"),
  eqConstraintMthd=c("soft","backtrack","l1p"),
  backtrackCtrl=c(0.5,5))
```

Arguments

freeSet	Character-string names of MxMatrices containing free parameters.
fitfunction	Character-string name of the fitfunction; defaults to 'fitfunction'.
verbose	Integer level of reporting printed to terminal at runtime ; defaults to 0.
nudgeZeroStarts	Should free parameters with start values of zero be "nudged" to 0.1 at runtime ? Defaults to the current global value of mxOption "Nudge zero starts". May be a logical value, or one of character strings "Yes" or "No".

maxIter	Integer maximum number of iterations. Value of NULL is accepted, in which case the value used at runtime will be 10 times the number of iterations specified by the effective value of mxOption "Major iterations".
...	Not used. Forces remaining arguments to be specified by name.
alpha	Numeric reflection coefficient. Must be positive. Defaults to 1.0.
betao, betai	Numeric outside- and inside-contraction coefficients, respectively. Both must be within unit interval (0,1). Both default to 0.5.
gamma	Numeric expansion coefficient. If positive, must be greater than alpha. If non-positive, expansion transformations will not be carried out. Defaults to 2.0.
sigma	Numeric shrink coefficient. Cannot exceed 1.0. If non-positive, shrink coefficients will not be carried out, and failed contractions will instead be followed by a simplex restart. Defaults to 0.5.
bignum	Numeric value with which the fitfunction value is to be replaced if the fit is non-finite or is evaluated at infeasible parameter values. Defaults to 1e35.
iniSimplexType	Character string naming the method by which to construct the initial simplex from the free-parameter start values. Defaults to "regular".
iniSimplexEdge	Numeric edge-length of the initial simplex. Defaults to 1.0.
iniSimplexMat	Optional numeric matrix providing the vertices of the initial simplex. The matrix must have as many columns as there are free parameters in the MxModel . The matrix's number of rows must be no less than the number of free parameters minus the number of degrees-of-freedom gained from equality MxConstraints , if any. If a non-NULL value is provided, argument iniSimplexEdge is ignored, and argument iniSimplexType is only used in the case of a restart.
greedyMinimize	Logical; should the optimizer use "greedy minimization?" Defaults to FALSE. See below for details.
altContraction	Logical; should the optimizer use an "alternate contraction" transformation? Defaults to FALSE. See below for details.
degenLimit	Numeric "degeneracy limit;" defaults to 0. If positive, the simplex will be restarted if the measure of the angle between any two of its edges is within 0 or pi by less than degenLimit.
stagnCtrl	"Stagnation control;" integer vector of length 2; defaults to c(-1L,-1L). See below for details.
validationRestart	Logical; defaults to TRUE.
xTolProx	Numeric "domain-convergence" criterion; defaults to 1e-8. See below for details.
fTolProx	Numeric "range-convergence" criterion; defaults to 1e-8. See below for details.
doPseudoHessian	Logical; defaults to FALSE.
ineqConstraintMthd	"Inequality constraint method;" character string. Defaults to "soft".
eqConstraintMthd	"Equality constraint method;" character string. Defaults to "soft".
backtrackCtrl	Numeric vector of length two. See below for details.

Details

The state of a Nelder-Mead optimization problem is represented by a simplex (polytope) of $n + 1$ vertices in the space of the free parameters, where n is the number of free parameters minus the number of degrees-of-freedom gained from equality [MxConstraints](#). An iteration of the algorithm first sorts the $n + 1$ vertices by their corresponding fitfunction values (i.e., the values of the fitfunction when evaluated at each vertex), in ascending order (i.e., from "best" fit to "worst" fit). Then, the "subcentroid," which is the centroid of the "best" n vertices, is calculated. Then, the algorithm attempts to improve upon the worst fit by transforming the simplex; see [Singer & Nelder \(2009\)](#) for details.

Argument `iniSimplexType` dictates how the initial simplex will be constructed from the start values if argument `iniSimplexMat` is NULL, and how the simplex will be re-initialized in the case of a restart. In all four cases, the vector of start values constitutes the "starting vertex" of the initial simplex. If `iniSimplexType="regular"`, the initial simplex is merely a regular simplex with edge length equal to `iniSimplexEdge`. A "right" simplex is constructed by incrementing each free parameter by `iniSimplexEdge` from its starting value; thus, all the edges that intersect at the starting vertex do so at right angles. A "smartRight" simplex is constructed similarly, except that each free parameter is both incremented *and* decremented by `iniSimplexEdge`, and of those two points the one with the smaller fitfunction value is retained as a vertex. A "random" simplex is constructed by randomly perturbing the start values, in a manner similar to the default for `mxTryHard()`, to generate the coordinates of the other vertices. The user is advised that bounds on the free parameters may keep the initial simplex from having the requested regularity or edge-length, and that `iniSimplexType` is at best a *suggestion* in the presence of equality [MxConstraints](#).

Note that if argument `iniSimplexMat` has nonzero length, the actual start values of the `MxModel`'s free parameters are not used as a vertex of the initial simplex (unless one of the rows of `iniSimplexMat` happens to contain those start values).

If the simplex is restarted, a new simplex is constructed per argument `iniSimplexType`, with edge length equal to the distance between the current best and second-best vertices, and with the current best vertex used as a starting vertex.

If `greedyMinimize=FALSE`, "greedy expansion" (Singer & Singer, 2004) is used: if the expansion point and reflection point both have smaller fitfunction values than the best vertex, the expansion point is accepted. If `greedyMinimize=TRUE`, "greedy minimization" (Singer & Singer, 2004) is used: if the expansion point and the reflection point both have smaller fitfunction values than the best vertex, the better of the two new points is accepted.

If argument `altContraction=TRUE`, the "modified contraction step" of Gill et al. (1982, Chapter 4) is used, and the candidate point is contracted toward the best vertex instead of toward the subcentroid.

If positive, the first element of argument `stagnCtrl` sets a threshold for the number of successive iterations in which the best vertex of the simplex does not change, after which the algorithm is said to be "stagnant" (in a sense similar to that of Kelley, 1999). To attempt to remedy the stagnation, the simplex is restarted. If positive, the second element of argument `stagnCtrl` sets threshold for the number of restarts conducted, beyond which stagnation no longer triggers a restart. The rationale for the second element is that when the optimizer is close to convergence, the best vertex may not change, but restarting may be counterproductive, and in any event requires many function evaluations.

If argument `validationRestart=TRUE`, then when the optimizer has successfully converged, it will restart the simplex and attempt to improve upon the tentative solution it already found. This

validation restart (Gill et al., 1982, Chapter 4) always re-initializes the simplex as a regular simplex, with edge-length equal to the distance between the best and worst vertices of the tentative solution. Optimization proceeds until convergence to a solution with a better fit value, or $2n$ iterations have elapsed.

The Nelder-Mead optimizer is considered to have successfully converged if (1) the largest l -infinity norm of the vector-differences between the best vertex and the other vertices is less than argument `xTolProx`, or (2) if the largest absolute difference in fit value between the best vertex and the other vertices is less than `fTolProx`.

If argument `doPseudoHessian=TRUE` and there are no equality `MxConstraints`, OpenMx will attempt to calculate the "pseudo-Hessian" or "curvature" matrix as described in the appendix to Nelder & Mead (1965). If successful, this matrix will be stored in the 'output' slot of the post-run `MxComputeNelderMead` object. Although crude, its inverse can be used as an estimate of the repeated-sampling covariance matrix of the free parameters when the usual finite-differences Hessian is unreliable.

OpenMx's implementation of Nelder-Mead can handle nonlinear inequality `MxConstraints` reasonably well. Its default method for doing so, with argument `ineqConstraintMthd="soft"`, imposes a "soft" feasibility constraint by assigning a fitfunction value of `bignum` to points that violate the constraints by more than `mxOption 'Feasibility tolerance'`. Alternately, with argument `ineqConstraintMthd="eqMthd"`, inequality `MxConstraints` can be handled by the same method provided to argument `eqConstraintMthd`, whether or not equality `MxConstraints` are present.

OpenMx's implementation of Nelder-Mead respects equality `MxConstraints`, but as of this writing handles them rather poorly, unless *all* vertices of the initial simplex are feasible. Its default method for equalities is the same as that for inequalities, i.e. a "soft" feasibility constraint. If argument `eqConstraintMthd="backtrack"`, then the optimizer attempts to backtrack from an infeasible point to a feasible point in a manner similar to that of Ghiasi et al. (2008), except that it used with *all* new points, and not just those encountered via reflection, expansion and contraction. In this case, the displacement from the prior point to the candidate point is reduced by the proportion provided as the first element of argument `backtrackCtrl`, and thus a new candidate point is considered. This process is repeated until feasibility of the candidate point is restored, or the number of attempts exceeds the second element of argument `backtrackCtrl`. If argument `eqConstraintMthd="l1p"`, Nelder-Mead is used as part of an l_1 -penalty algorithm, which as of this writing is experimental and subject to change in future releases of OpenMx.

Value

Returns an object of class '`MxComputeNelderMead`'.

References

- Ghiasi, H., Pasini, D., & Lessard, L. (2008). Constrained globalized Nelder-Mead method for simultaneous structural and manufacturing optimization of a composite bracket. *Journal of Composite Materials*, 42(7), p. 717-736. doi: 10.1177/0021998307088592
- Gill, P. E., Murray, W., & Wright, M. H. (1982). *Practical Optimization*. Bingley, UK: Emerald Group Publishing Ltd.
- Kelley, C. T. (1999). Detection and remediation of stagnation in the Nelder-Mead algorithm using a sufficient decrease condition. *SIAM Journal of Optimization* 10(1), p. 43-55.

Nelder, J. A., & Mead, R. (1965) . A simplex method for function minimization. *The Computer Journal*, 7, p. 308-313.

Singer, S., & Nelder, J. (2009). Nelder-Mead algorithm. *Scholarpedia*, 4(7):2928., revision #91557. http://www.scholarpedia.org/article/Nelder-Mead_algorithm .

Singer, S., & Singer, S. (2004). Efficient implementation of the Nelder-Mead search algorithm. *Applied Numerical Analysis & Computational Mathematics Journal*, 1(2), p. 524-534. doi: 10.1002/anac.200410015

Examples

```
foo <- mxComputeNelderMead()
str(foo)
```

mxComputeNewtonRaphson

Optimize parameters using the Newton-Raphson algorithm

Description

This optimizer requires analytic 1st and 2nd derivatives of the fit function. Box constraints are supported. Parameters can approach box constraints but will not leave the feasible region (even by some small $\epsilon > 0$). Non-finite fit values are interpreted as soft feasibility constraints. That is, when a non-finite fit is encountered, line search is continued after the step size is multiplied by 10 available by increasing the verbose level.

Usage

```
mxComputeNewtonRaphson(freeSet = NA_character_, ...,
  fitfunction = "fitfunction", maxIter = 100L, tolerance = 1e-12,
  verbose = 0L)
```

Arguments

freeSet	names of matrices containing free variables
...	Not used. Forces remaining arguments to be specified by name.
fitfunction	name of the fitfunction (defaults to 'fitfunction')
maxIter	maximum number of iterations
tolerance	optimization is considered converged when the maximum relative change in fit is less than tolerance
verbose	level of debugging output

References

Luenberger, D. G. & Ye, Y. (2008). *Linear and nonlinear programming*. Springer.

mxComputeNothing	<i>Compute nothing</i>
------------------	------------------------

Description

Note that this compute plan actually does nothing whereas `mxComputeOnce("expectation", "nothing")` may remove the prediction of an expectation.

Usage

```
mxComputeNothing()
```

mxComputeNumericDeriv	<i>Numerically estimate Hessian using Richardson extrapolation</i>
-----------------------	--------------------------------------------------------------------

Description

For N free parameters, Richardson extrapolation requires $(\text{iterations} * (N^2 + N))$ function evaluations. The implementation is closely based on the `numDeriv` R package.

Usage

```
mxComputeNumericDeriv(freeSet = NA_character_, ...,
  fitfunction = "fitfunction", parallel = TRUE, stepSize = mxOption(NULL,
    "Gradient step size"), iterations = 4L, verbose = 0L,
  knownHessian = NULL, checkGradient = TRUE, hessian = TRUE)
```

Arguments

<code>freeSet</code>	names of matrices containing free variables
<code>...</code>	Not used. Forces remaining arguments to be specified by name.
<code>fitfunction</code>	name of the fitfunction (defaults to 'fitfunction')
<code>parallel</code>	whether to evaluate the fitfunction in parallel (defaults to TRUE)
<code>stepSize</code>	starting set size (defaults to 0.0001)
<code>iterations</code>	number of Richardson extrapolation iterations (defaults to 4L)
<code>verbose</code>	Level of debugging output.
<code>knownHessian</code>	an optional matrix of known Hessian entries
<code>checkGradient</code>	whether to check the first order convergence criterion (gradient is near zero)
<code>hessian</code>	whether to estimate the Hessian. If FALSE then only the gradient is estimated.

Details

In addition to an estimate of the Hessian, forward, central, and backward estimates of the gradient are made available in this compute plan's output slot.

When checkGradient=TRUE, the central difference estimate of the gradient is used to determine whether the first order convergence criterion is met. In addition, the forward and backward difference estimates of the gradient are compared for symmetry. When sufficient asymmetry is detected, the standard error is flagged. In the case, profile likelihood confidence intervals should be used for inference instead of standard errors (see mxComputeConfidenceInterval).

Examples

```
library(OpenMx)
data(demoOneFactor)
factorModel <- mxModel(name = "One Factor",
  mxMatrix(type = "Full", nrow = 5, ncol = 1, free = FALSE, values = .2, name = "A"),
  mxMatrix(type = "Symm", nrow = 1, ncol = 1, free = FALSE, values = 1, name = "L"),
  mxMatrix(type = "Diag", nrow = 5, ncol = 5, free = TRUE, values = 1, name = "U"),
  mxAlgebra(A %*% L %*% t(A) + U, name = "R"),
  mxExpectationNormal(covariance = "R", dimnames = names(demoOneFactor)),
  mxFitFunctionML(),
  mxData(cov(demoOneFactor), type = "cov", numObs = 500),
  mxComputeSequence(
    list(mxComputeNumericDeriv(), mxComputeReportDeriv())
  )
)
factorModelFit <- mxRun(factorModel)
factorModelFit$output$hessian
```

mxComputeOnce

Compute something once

Description

Some models are optimized for a sparse Hessian. Therefore, it can be much more efficient to compute the inverse Hessian in comparison to computing the Hessian and then inverting it.

Usage

```
mxComputeOnce(from, what = "nothing", how = NULL, ...,
  freeSet = NA_character_, verbose = 0L, .is.bestfit = FALSE)
```

Arguments

from	the object to perform the computation (a vector of expectation or fit function names)
what	what to compute (default is "nothing")
how	to compute it (optional)

...	Not used. Forces remaining arguments to be specified by name.
freeSet	names of matrices containing free variables
verbose	the level of debugging output
.is.bestfit	do not use; for backward compatibility

Details

The information matrix is only valid when parameters are at the maximum likelihood estimate. The information matrix is returned in `model$output$hessian`. You cannot request both the information matrix and the Hessian. The information matrix is invariant to the sign of the log likelihood scale whereas the Hessian is not. Use the `how` parameter to specify which approximation to use (one of "default", "hessian", "sandwich", "bread", and "meat").

Examples

```
data(demoOneFactor)
factorModel <- mxModel(name = "One Factor",
  mxMatrix(type="Full", nrow=5, ncol=1, free=TRUE, values=0.2, name="A"),
  mxMatrix(type="Symm", nrow=1, ncol=1, free=FALSE, values=1, name="L"),
  mxMatrix(type="Diag", nrow=5, ncol=5, free=TRUE, values=1, name="U"),
  mxAlgebra(expression=A %*% L %*% t(A) + U, name="R"),
  mxFitFunctionML(), mxExpectationNormal(covariance="R", dimnames=names(demoOneFactor)),
  mxData(observed=cov(demoOneFactor), type="cov", numObs=500),
  mxComputeOnce('fitfunction', 'fit'))
factorModelFit <- mxRun(factorModel)
factorModelFit$output$fit # 972.15
```

mxComputeReportDeriv *Report derivatives*

Description

Copy the internal gradient and Hessian back to R.

Usage

```
mxComputeReportDeriv(freeSet = NA_character_)
```

Arguments

freeSet	names of matrices containing free variables
---------	---------------------------------------------

mxComputeReportExpectation
Report expectation

Description

Copy the internal model expectations back to R.

Usage

```
mxComputeReportExpectation(freeSet = NA_character_)
```

Arguments

freeSet names of matrices containing free variables

mxComputeSequence *Invoke a series of compute objects in sequence*

Description

Invoke a series of compute objects in sequence

Usage

```
mxComputeSequence(steps = list(), ..., freeSet = NA_character_,
  independent = FALSE)
```

Arguments

steps a list of compute objects
 ... Not used; forces argument 'freeSet' to be specified by name.
 freeSet Names of matrices containing free parameters.
 independent Whether the steps could be executed out-of-order.

 mxComputeStandardError

Compute standard errors given the Hessian or inverse Hessian

Description

The fit is assumed to be in deviance units (-2 log likelihood).

Usage

```
mxComputeStandardError(freeSet = NA_character_)
```

Arguments

freeSet names of matrices containing free variables

mxComputeTryHard

Repeatedly attempt a compute plan until successful

Description

The provided compute plan is run until the status code indicates success (0 or 1). It gives up after a small number of retries.

Usage

```
mxComputeTryHard(plan, ..., freeSet = NA_character_, verbose = 0L,
  location = 1, scale = 0.25, maxRetries = 3L)
```

Arguments

plan	compute plan to optimize the model
...	Not used. Forces remaining arguments to be specified by name.
freeSet	names of matrices containing free variables
verbose	level of debugging output
location	location of the perturbation distribution
scale	scale of the perturbation distribution
maxRetries	maximum number of plan evaluations per invocation (including the first evaluation)

Details

Upon failure, start values are randomly perturbed. Currently only the uniform distribution is implemented. The distribution is parametrized by arguments `location` and `scale`. The location parameter is the distribution's median. For the uniform distribution, `scale` is the absolute difference between its median and extrema (i.e., half the width of the rectangle). Each start value is multiplied by a random draw and then added to a random draw from a distribution with the same `scale` but with a median of zero.

References

Shanno, D. F. (1985). On Broyden-Fletcher-Goldfarb-Shanno method. *Journal of Optimization Theory and Applications*, 46(1), 87-94.

See Also

[mxTryHard](#)

mxConstraint

Create MxConstraint Object

Description

This function creates a new [MxConstraint](#) object.

Usage

```
mxConstraint(expression, name=NA, ..., jac=character(0))
```

Arguments

<code>expression</code>	The MxAlgebra -like expression representing the constraint function.
<code>name</code>	An optional character string indicating the name of the object.
<code>...</code>	Not used. Helps <code>OpenMx</code> catch bad input to argument <code>expression</code> , and requires argument <code>jac</code> —meant for advanced users—to be specified by name.
<code>jac</code>	An optional character string naming the MxAlgebra or MxMatrix representing the Jacobian for the constraint function.

Details

The `mxConstraint()` function defines relationships between two [MxAlgebra](#) or [MxMatrix](#) objects. They are used to affect the estimation of free parameters in the referenced objects. The constraint relation is written identically to how a [MxAlgebra](#) expression would be written. The outermost operator in this relation must be either '<', '==' or '>'. To affect an estimation or optimization, an [MxConstraint](#) object must be included in an [MxModel](#) object with all referenced [MxAlgebra](#) and [MxMatrix](#) objects.

Usage Note: Use of `mxConstraint()` should be avoided where it is possible to achieve the constraint by equating free parameters by label or position in an `MxMatrix` or `MxAlgebra` object. Including `mxConstraints` in an `mxEModel` will disable standard errors and the calculation of the final Hessian, and thus should be avoided when standard errors are of importance. Constraints also add computational overhead. If one labels two parameters the same, the optimizer has one fewer parameter to optimize. However, if one uses `mxConstraint` to do the same thing, both parameters remain estimated and a Lagrangian multiplier is added to maintain the constraint. This constraint also has to have its gradients computed and the order of the Hessian grows as well. So while both approaches should work, the `mxConstraint()` will take longer to do so.

Alternatives to `mxConstraints` include using labels, `lbound` or `ubound` arguments or algebras. Free parameters in the same `MxEModel` may be constrained to equality by giving them the same name in their respective 'labels' matrices. Similarly, parameters may be fixed to an individual element in a `MxEModel` object or the result of an `MxAlgebra` object through labeling. For example, assigning a label of "name[1,1]" fixes the value of a parameter at the value in first row and first column of the matrix or algebra "name". The `mxConstraint` function should be used to enforce inequalities that cannot be conveyed using other methods.

Argument `jac` is used to provide the name of an `MxMatrix` or `MxAlgebra` that equals the matrix of first derivatives—the Jacobian—of the constraint function with respect to the free parameters. Here, the "constraint function" refers to the constraint expression in canonical form, with an arbitrary matrix expression on the left-hand side of the comparator, and a matrix with the same dimensions, and constant with respect to free parameters (typically, a matrix of zeroes), on the right-hand side. The rows of the Jacobian correspond to elements of the matrix result of the right-hand side, in column-major order. Each row of the Jacobian is the vector of first partial derivatives, with respect to the free parameters of the `MxEModel`, of its corresponding element. Each column of the Jacobian corresponds to a free parameter of the `MxEModel`; each column must be named with the label of the corresponding free parameter. Only the `gradient-descent` optimizers `NPSOL` and `SLSQP` are able to take advantage of user-supplied Jacobians.

Value

Returns an `MxConstraint` object.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

`MxConstraint` for the S4 class created by `mxConstraint`.

Examples

```
library(OpenMx)

#Create a constraint between MxMatrices 'A' and 'B'
constraint <- mxConstraint(A > B, name = 'AdominatesB')

# Constrain matrix 'K' to be equal to matrix 'limit'
```



```

model <- mxModel(model="con_test",
  mxMatrix(type="Full", nrow=2, ncol=2, free=TRUE, name="K"),
  mxMatrix(type="Full", nrow=2, ncol=2, free=FALSE, name="limit", values=1:4),
  mxConstraint(K == limit, name = "Klimit_equality"),
  mxAlgebra(min(K), name="minK"),
  mxFitFunctionAlgebra("minK")
)

fit <- mxRun(model)
fit$matrices$K$values

#      [,1] [,2]
# [1,]   1   3
# [2,]   2   4

# Constrain both free parameters of a matrix to equality using labels (both are set to "eq")
equal <- mxMatrix("Full", 2, 1, free=TRUE, values=1, labels="eq", name="D")

# Constrain a matrix element in to be equal to the result of an algebra
start <- mxMatrix("Full", 1, 1, free=TRUE, values=1, labels="param", name="F")
alg <- mxAlgebra(log(start), name="logP")

# Force the fixed parameter in matrix G to be the result of the algebra
end <- mxMatrix("Full", 1, 1, free=FALSE, values=1, labels="logP[1,1]", name="G")

```

MxConstraint-class *Class "MxConstraint"*

Description

MxConstraint is an S4 class. An MxConstraint object is a [named entity](#). New instances of this class can be created using the function `mxConstraint()`.

Details

Slots may be referenced with the \$ symbol. See the documentation for [Classes](#) and the examples in the [mxConstraint](#) document for more information.

Slots

name: Character string; the name of the object.

formula: Object of class "MxAlgebraFormula". The [MxAlgebra](#)-like expression representing the constraint function.

alg1: Object of class "MxCharOrNumber". For internal use.

alg2: Object of class "MxCharOrNumber". For internal use.

relation: Object of class "MxCharOrNumber". For internal use.

jac: Object of class "MxCharOrNumber". Identifies the [MxAlgebra](#) representing the Jacobian for the constraint function.

linear: Logical. For internal use.

Methods

```
$<- signature(x = "MxConstraint")
$ signature(x = "MxConstraint")
imxDeparse signature(object = "MxConstraint")
names signature(x = "MxConstraint")
print signature(x = "MxConstraint")
show signature(object = "MxConstraint")
```

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

[mxConstraint\(\)](#) for the function that creates MxConstraint objects.

Examples

```
showClass("MxConstraint")
```

mxData

Create MxData Object

Description

This function creates a new [MxData](#) object.

Usage

```
mxData(observed, type, means = NA, numObs = NA, acov=NA, fullWeight=NA,
        thresholds=NA, ..., sort=NA, primaryKey = as.character(NA))
```

Arguments

observed	A matrix or data.frame which provides data to the MxData object.
type	A character string defining the type of data in the 'observed' argument. Must be one of "raw", "cov", or "cor".
means	An optional vector of means for use when 'type' is "cov", or "cor".
numObs	The number of observations in the data supplied in the 'observed' argument. Required unless 'type' equals "raw".

acov	Asymptotic covariance matrix of observed, means, and thresholds. Used for weighted least squares at weight matrix.
fullWeight	Full asymptotic covariance matrix of observed, means, and thresholds. Used for weighted least squares in standard error and quasi-chi-squared calculation.
thresholds	Observed thresholds. Used for weighted least squares with ordinal data.
...	Not used. Forces remaining arguments to be specified by name.
sort	Whether to sort raw data prior to use (default NA)
primaryKey	The column name of the primary key used to uniquely identify rows (default NA)

Details

The `mxData` function creates `MxData` objects, which can be used as arguments in `MxModel` objects. The ‘observed’ argument may take either a data frame or a matrix, which is then described with the ‘type’ argument. Data types describe compatibility and usage with expectation functions in `MxModel` objects. Four different data types are supported (a fifth, `sscp`, is not yet implemented):

- raw** The contents of the ‘observed’ argument are treated as raw data. Missing values are permitted and must be designated as the system missing value. The ‘means’ and ‘numObs’ arguments cannot be specified, as the ‘means’ argument is not relevant and the ‘numObs’ argument is automatically populated with the number of rows in the data. Data of this type may use fit functions such as `mxFitFunctionML` function in `MxModel` objects, which will automatically use covariance estimation under full-information maximum likelihood for this data type.
- cov** The contents of the ‘observed’ argument are treated as a covariance matrix. The ‘means’ argument is not required, but may be included for estimations involving means. The ‘numObs’ argument is required, which should reflect the number of observations or rows in the data described by the covariance matrix. Data of this type may use the fit functions such as `mxFitFunctionML`, depending on the specified model.
- cor** The contents of the ‘observed’ argument are treated as a correlation matrix. The ‘means’ argument is not required, but may be included for estimations involving means. The ‘numObs’ argument is required, which should reflect the number of observations or rows in the data described by the covariance matrix. Data of this type may use the fit functions such as `mxFitFunctionML` functions, depending on the specified model.
- acov** The best way to have data of the type is to use the `mxDataWLS` function. The contents of the ‘observed’ argument are treated as the polychoric correlation matrix of the ordinal variables. The ‘means’ argument is not required, but may be included for estimations involving means. The ‘thresholds’ argument is not required, but may be included for estimation involving thresholds and ordinal variables. The ‘numObs’ argument is required, which should reflect the number of observations or rows in the data described by the polychoric correlation matrix. Data of this type almost certainly use the `mxFitFunctionWLS` function, but may depend on the specified model.

`MxData` objects may not be included in `MxAlgebra` objects or use the `mxFitFunctionAlgebra` function. If these capabilities are desired, data should be appropriately input or transformed using the `mxMatrix` and `mxAlgebra` functions.

While column names are stored in the ‘observed’ slot of MxData objects, these names are not recognized as variable names in `MxPath` objects. Variable names must be specified using the ‘manifestVars’ argument of the `mxModel` function prior to use in `MxPath` objects.

The `mxData` function does not currently place restrictions on the size, shape, or symmetry of matrices input into the ‘observed’ argument. While it is possible to specify MxData objects as covariance or correlation matrices that do not have the properties commonly associated with these matrices, failure to correctly specify these matrices will likely lead to problems in model estimation.

OpenMx uses the names of variables to map them onto the expectation functions and other elements associated with your model. For data.frames, ensure you have set the `names()`. For matrices set names using, for instance, `row.names=c(“your”, “columns”)`. Covariance and correlation matrices need to have both the row and column names set and these must be identical, for instance by using `dimnames=list(varNames, varNames)`.

When a primary key is provided, sorting is disabled. Otherwise, sort defaults to TRUE.

Value

Returns a new `MxData` object.

References

The OpenMx User’s guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

`MxData` for the S4 class created by `mxData`. `matrix` and `data.frame` for objects which may be entered as arguments in the ‘observed’ slot. More information about the OpenMx package may be found [here](#).

Examples

```
library(OpenMx)

#Create a covariance matrix
covMatrix <- matrix( c(0.77642931, 0.39590663,
  0.39590663, 0.49115615),
  nrow = 2, ncol = 2, byrow = TRUE)
covNames <- c("x", "y")
dimList <- list(covNames, covNames)
dimnames(covMatrix) <- dimList

#Create an MxData object including that covariance matrix
testData <- mxData(observed=covMatrix, type="cov", numObs = 100)

testModel <- mxModel(model="testModel",
  mxMatrix(type="Symm", nrow=2, ncol=2, values=c(.2,.1,.2),
    free=TRUE, name="expCov", dimnames=dimList),
  mxExpectationNormal(covariance="expCov", dimnames=covNames),
  mxFitFunctionML(),
```

```

        testData)

outModel <- mxRun(testModel)

summary(outModel)

```

MxData-class

MxData Class

Description

MxData is an S4 class. An MxData object is a [named entity](#). New instances of this class can be created using the function [mxData](#). MxData is an S4 class union. An MxData object is either [NULL](#) or a MxNonNullData object.

Details

The MxNonNullData class has the following slots:

name	-	The name of the object
observed	-	Either a matrix or a data frame
vector	-	A vector for means, or NA if missing
type	-	Either 'raw', 'cov', or 'cor'
numObs	-	The number of observations

The 'name' slot is the name of the MxData object.

The 'observed' slot is used to contain data, either as a matrix or as a data frame. Use of the data in this slot by other functions depends on the value of the 'type' slot. When 'type' is equal to 'cov' or 'cor', the data input into the 'matrix' slot should be a symmetric matrix or data frame.

The 'vector' slot is used to contain a vector of numeric values, which is used as a vector of means for MxData objects with 'type' equal to 'cov' or 'cor'. This slot may be used in estimation using the [mxFitFunctionML](#) function.

The 'type' slot may take one of four supported values:

raw The contents of the 'observed' slot are treated as raw data. Missing values are permitted and must be designated as the system missing value. The 'vector' and 'numObs' slots cannot be specified, as the 'vector' argument is not relevant and the 'numObs' argument is automatically populated with the number of rows in the data. Data of this type may use the [mxFitFunctionML](#) function as its fit function in MxModel objects, which can deal with covariance estimation under full-information maximum likelihood.

cov The contents of the 'observed' slot are treated as a covariance matrix. The 'vector' argument is not required, but may be included for estimations involving means. The 'numObs' slot is required. Data of this type may use fit functions such as the [mxFitFunctionML](#), depending on the specified model.

cor The contents of the ‘observed’ slot are treated as a correlation matrix. The ‘vector’ argument is not required, but may be included for estimations involving means. The ‘numObs’ slot is required. Data of this type may use fit functions such as the [mxFitFunctionML](#), depending on the specified model.

The ‘numObs’ slot describes the number of observations in the data. If ‘type’ equals ‘raw’, then ‘numObs’ is automatically populated as the number of rows in the matrix or data frame in the ‘observed’ slot. If ‘type’ equals ‘cov’ or ‘cor’, then this slot must be input using the ‘numObs’ argument in the [mxData](#) function when the MxData argument is created.

MxData objects may not be included in [MxAlgebra](#) objects or use the [mxFitFunctionAlgebra](#) function. If these capabilities are desired, data should be appropriately input or transformed using the [mxMatrix](#) and [mxAlgebra](#) functions.

While column names are stored in the ‘observed’ slot of MxData objects, these names are not recognized as variable names in [MxPath](#) objects. Variable names must be specified using the ‘manifestVars’ argument of the [mxModel](#) function prior to use in [MxPath](#) objects.

The mxData function does not currently place restrictions on the size, shape, or symmetry of matrices input into the ‘observed’ argument. While it is possible to specify MxData objects as covariance or correlation matrices that do not have the properties commonly associated with these matrices, failure to correctly specify these matrices will likely lead to problems in model estimation.

References

The OpenMx User’s guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

[mxData](#) for creating MxData objects, [matrix](#) and [data.frame](#) for objects which may be entered as arguments in the ‘matrix’ slot. More information about the OpenMx package may be found [here](#).

mxDataDynamic

Create dynamic data

Description

Create dynamic data

Usage

```
mxDataDynamic(type, ..., expectation, verbose = 0L)
```

Arguments

type	type of data
...	Not used. Forces remaining arguments to be specified by name.
expectation	the name of the expectation to provide the data
verbose	Increase runtime debugging output

MxDataFrameOrMatrix-class
MxDataFrameOrMatrix

Description

Internal class that is the union of data.frame and matrix.

Details

Not to be used.

MxDataStatic-class *Create static data*

Description

Internal static data class.

Details

Not to be used.

mxDataWLS *Create MxData Object for Least Squares (WLS, DLS, ULS) Analyses*

Description

This function creates a new [MxData](#) object of type “ULS” (unweighted least squares), “WLS” (weighted least squares) or “DLS” (diagonally-weighted least squares). The appropriate fit function to include with these models is [mxFitFunctionWLS](#)

Usage

```
mxDataWLS(data, type = "WLS", useMinusTwo = TRUE, returnInverted = TRUE,  
          debug = FALSE, fullWeight = TRUE)
```

Arguments

data	A matrix or data.frame which provides raw data to be used for WLS.
type	A character string 'WLS' (default), 'DLS', or 'ULS' for weighted, diagonal, or unweighted least squares
useMinusTwo	Logical indicating whether to use -2LL (default) or -LL.
returnInverted	Logical indicating whether to return the information matrix (default) or the covariance matrix.
debug	Logical to set debugging on or off (default)
fullWeight	Logical determining if the full weight matrix is returned (default). Needed for standard error and quasi-chi-squared calculation.

Details

The mxDataWLS function creates an [MxData](#) object, which can be used in [MxModel](#) objects. This function takes raw data and returns an MxData object to be used in a model to fit with weighted least squares.

Both Ordinal and continuous data are supported. A combination of these data types also succeeds. Early tests suggested that full 'WLS' might be biased in this joint ordinal and continuous case, whereas 'ULS' and 'DLS' were unbiased. However further investigation revealed that all of these were unbiased when the model is correct, but full 'WLS' is highly sensitive to model misspecification. Full 'WLS' can heavily weight the fourth-order moments of the distribution, so small deviations between the observed fourth-order moments and those implied by the model can lead to poor estimates.

Value

Returns a new [MxData](#) object.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

[mxFitFunctionWLS](#). [MxData](#) for the S4 class created by mxData. [matrix](#) and [data.frame](#) for objects which may be entered as arguments in the 'observed' slot. More information about the OpenMx package may be found [here](#).

Examples

```
# Create and fit a model using mxMatrix, mxAlgebra, mxExpectationNormal, and mxFitFunctionWLS
library(OpenMx)

# Simulate some data

x=rnorm(1000, mean=0, sd=1)
```



```

y= 0.5*x + rnorm(1000, mean=0, sd=1)
tmpFrame <- data.frame(x, y)
tmpNames <- names(tmpFrame)
wdata <- mxDataWLS(tmpFrame)

# Define the matrices

S <- mxMatrix(type = "Full", nrow = 2, ncol = 2, values=c(1,0,0,1),
              free=c(TRUE,FALSE,FALSE,TRUE), labels=c("Vx", NA, NA, "Vy"), name = "S")
A <- mxMatrix(type = "Full", nrow = 2, ncol = 2, values=c(0,1,0,0),
              free=c(FALSE,TRUE,FALSE,FALSE), labels=c(NA, "b", NA, NA), name = "A")
I <- mxMatrix(type="Iden", nrow=2, ncol=2, name="I")

# Define the expectation

expCov <- mxAlgebra(solve(I-A) %*% S %*% t(solve(I-A)), name="expCov")
expFunction <- mxExpectationNormal(covariance="expCov", dimnames=tmpNames)

# Choose a fit function

fitFunction <- mxFitFunctionWLS()

# Define the model

tmpModel <- mxModel(model="exampleModel", S, A, I, expCov, expFunction, fitFunction,
                   wdata)

# Fit the model and print a summary

tmpModelOut <- mxRun(tmpModel)
summary(tmpModelOut)

```

MxDirectedGraph-class *MxDirectedGraph*

Description

This is an internal class and should not be used directly. It is a class for directed graphs.

mxEval	<i>Evaluate Values in MxModel</i>
--------	-----------------------------------

Description

This function can be used to evaluate an arbitrary R expression that includes named entities from a [MxModel](#) object, or labels from a [MxMatrix](#) object.

Usage

```
mxEval(expression, model, compute = FALSE, show = FALSE, defvar.row = 1,
        cache = new.env(parent = emptyenv()), cacheBack = FALSE)
```

```
mxEvalByName(name, model, compute = FALSE, show = FALSE, defvar.row = 1,
             cache = new.env(parent = emptyenv()), cacheBack = FALSE)
```

Arguments

expression	An arbitrary R expression.
model	The model in which to evaluate the expression.
compute	If TRUE then compute the value of algebra expressions and populate square bracket substitutions.
show	If TRUE then print the translated expression.
defvar.row	The row number for definition variables when compute=TRUE; defaults to 1. When compute=FALSE, values for definition variables are always taken from the first (i.e., first before any automated sorting is done) row of the raw data.
cache	An R environment of matrix values used to speedup computation.
cacheBack	If TRUE then return the list pair (value, cache).
name	The character name of an object to evaluate.

Details

The argument ‘expression’ is an arbitrary R expression. Any named entities that are used within the R expression are translated into their current value from the model. Any labels from the matrices within the model are translated into their current value from the model. Finally the expression is evaluated and the result is returned. To enable debugging, the ‘show’ argument has been provided. The most common mistake when using this function is to include named entities in the model that are identical to R function names. For example, if a model contains a named entity named ‘c’, then the following mxEval call will return an error: `mxEval(c(A, B, C), model)`.

The `mxEvalByName` function is a wrapper around `mxEval` that takes a character instead of an R expression.

If ‘compute’ is FALSE, then MxAlgebra expressions return their current values as they have been computed by the optimization call (using `mxRun`). If the ‘compute’ argument is TRUE, then MxAlgebra expressions will be calculated in R and square bracket substitutions will be performed. Any references to an objective function that has not yet been calculated will return a 1 x 1 matrix with a value of NA.

The ‘cache’ is used to speedup calculation by storing previously computing values. The cache is a list of matrices, such that `names(cache)` must all be of the form “modelname.entityname”. Setting ‘cacheBack’ to TRUE will return the pair list(value, cache) where value is the result of the `mxEval()` computation and cache is the updated cache.

References

The OpenMx User’s guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

[mxAlgebra](#) to create algebraic expressions inside your model and [mxModel](#) for the model object `mxEval` looks inside when evaluating.

Examples

```
library(OpenMx)

# Set up a 1x1 matrix
matrixA <- mxMatrix("Full", nrow = 1, ncol = 1, values = 1, name = "A")

# Set up an algebra
algebraB <- mxAlgebra(A + A, name = "B")

# Put them both in a model
testModel <- mxModel(model="testModel", matrixA, algebraB)

# Even though the model has not been run, we can evaluate the algebra
# given the starting values in matrixA.
mxEval(B, testModel, compute=TRUE)

# If we just print the algebra, we can see it has not been evaluated
testModel$B
```

`mxEvaluateOnGrid`*Evaluate an algebra on an abscissa grid and collect column results*

Description

This function evaluates an algebra on a grid of points provided in an auxiliary abscissa matrix.

Usage

```
mxEvaluateOnGrid(algebra, abscissa)
```

Arguments

<code>algebra</code>	the name of the single column matrix to be evaluated.
<code>abscissa</code>	the name of the abscissa matrix. See details.

Details

The abscissa matrix must be in a specific format. The variables are in the rows. Abscissa row names must match names of free variables. The grid points are in columns. For each point (column), the free variables are set to the given values and the algebra is re-evaluated. The resulting columns are collected as the result.

Value

Returns the collected columns.

Examples

```
library(OpenMx)

test2 <- mxModel("test2",
  mxMatrix(values=1.1, nrow=1, ncol=1, free=TRUE, name="thang"),
  mxMatrix(nrow=1, ncol=1, labels="abscissa1", free=TRUE, name="currentAbscissa"),
  mxMatrix(values=-2:2, nrow=1, ncol=5, name="abscissa",
    dimnames=list(c('abscissa1'), NULL)),
  mxAlgebra(rbind(currentAbscissa + thang, currentAbscissa * thang), name="stuff"),
  mxAlgebra(mxEvaluateOnGrid(stuff, abscissa), name="grid"))

test2 <- mxRun(test2)
omxCheckCloseEnough(test2$grid$result, matrix(c(-1:3 + .1, -2:2 * 1.1), ncol=5, nrow=2, byrow=TRUE))
```

MxExpectation-class *MxExpectation*

Description

This is an internal class and should not be used directly.

mxExpectationBA81 *Create a Bock & Aitkin (1981) expectation*

Description

Used in conjunction with [mxFitFunctionML](#), this expectation models ordinal data with a modest number of latent dimensions. Currently, only a multivariate Normal latent distribution is supported. An equal-interval quadrature is used to integrate over the latent distribution. When all items use the graded response model and items are assumed conditionally independent then item factor analysis is equivalent to a factor model.

Usage

```
mxExpectationBA81(ItemSpec, item = "item", ..., qpoints = 49L, qwidth = 6,
  mean = "mean", cov = "cov", verbose = 0L, weightColumn = NA_integer_,
  EstepItem = NULL, debugInternal = FALSE)
```

Arguments

ItemSpec	a single item model (to replicate) or a list of item models in the same order as the column of ItemParam
item	the name of the mxMatrix holding item parameters with one column for each item model with parameters starting at row 1 and extra rows filled with NA
...	Not used. Forces remaining arguments to be specified by name.
qpoints	number of points to use for equal interval quadrature integration (default 49L)
qwidth	the width of the quadrature as a positive Z score (default 6.0)
mean	the name of the mxMatrix holding the mean vector
cov	the name of the mxMatrix holding the covariance matrix
verbose	the level of runtime diagnostics (default 0L)
weightColumn	the name of the column in the data containing the row weights (default NA)
EstepItem	a simple matrix of item parameters for the E-step. This option is mainly of use for debugging derivatives.
debugInternal	when enabled, some of the internal tables are returned in \$debug. This is mainly of use to developers.

Details

The conditional likelihood of response x_{ij} to item j from person i with item parameters ξ_j and latent ability θ_i is

$$L(x_i|\xi, \theta_i) = \prod_j \Pr(\text{pick} = x_{ij}|\xi_j, \theta_i).$$

Items are assumed conditionally independent. That is, the outcome of one item is assumed to not influence another item after controlling for ξ and θ_i . The unconditional likelihood is obtained by integrating over the latent distribution θ_i ,

$$L(x_i|\xi) = \int L(x_i|\xi, \theta_i)L(\theta_i)d\theta_i.$$

With an assumption that examinees are independently and identically distributed, we can sum the individual log likelihoods,

$$\mathcal{L} = \sum_i \log L(x_i|\xi).$$

Response models $\Pr(\text{pick} = x_{ij}|\xi_j, \theta_i)$ are not implemented in OpenMx, but are imported from the **RPF** package. You must pass a list of models obtained from the RPF package in the 'ItemSpec' argument. All item models must use the same number of latent factors although some of these factor loadings can be constrained to zero in the item parameter matrix. The 'item' matrix contains item parameters with one item per column in the same order as ItemSpec.

The ‘qpoints’ and ‘qwidth’ argument control the fineness and width, respectively, of the equal-interval quadrature grid. The integer ‘qpoints’ is the number of points per dimension. The quadrature extends from negative qwidth to positive qwidth for each dimension. Since the latent distribution defaults to standard Normal, qwidth can be regarded as a value in Z-score units.

The optional ‘mean’ and ‘cov’ arguments permit modeling of the latent distribution in multigroup models (in a single group, the latent distribution must be fixed). A separate latent covariance model is used in combination with mxExpectationBA81. The point mass distribution contained in the quadrature is converted into a multivariate Normal distribution by `mxDataDynamic`. Typically `mxExpectationNormal` is used to fit a multivariate Normal model to these data. Some intricate programming is required. Examples are given in the manual. mxExpectationBA81 uses a sample size of N for the covariance matrix. This differs from `mxExpectationNormal` which uses a sample size of $N - 1$.

The ‘verbose’ argument enables diagnostics that are mainly of interest to developers.

When a two-tier covariance matrix is recognized, this expectation automatically enables analytic dimension reduction (Cai, 2010).

The optional ‘weightColumn’ argument names a column in `mxData` that contains the per-row weights. For data with many repeated response patterns, model evaluation time can be reduced. An easy way to transform your data into this form is to use `compressDataFrame`. By default, each row is given unit weight. Non-integer weights are supported except for `EAPscores`.

mxExpectationBA81 requires `mxComputeEM`. During a typical optimization run, latent abilities are assumed for examinees during the E-step. These examinee scores are implied by the previous iteration’s parameter vector. This can be overridden using the ‘Estepltem’ argument. This is mainly of use to developers for checking item parameter derivatives.

Common univariate priors are available from `univariatePrior`. The standard Normal distribution of the quadrature acts like a prior distribution for difficulty. It is not necessary to impose any additional Bayesian prior on difficulty estimates (Baker & Kim, 2004, p. 196).

Many estimators are available for standard errors. Oakes is recommended (see `mxComputeEM`). Also available are Supplement EM (`mxComputeEM`), Richardson extrapolation (`mxComputeNumericDeriv`), likelihood-based confidence intervals (`mxCI`), and the covariance of the rowwise gradients.

References

- Bock, R. D., & Aitkin, M. (1981). Marginal maximum likelihood estimation of item parameters: Application of an EM algorithm. *Psychometrika*, *46*, 443-459.
- Cai, L. (2010). A two-tier full-information item factor analysis model with applications. *Psychometrika*, *75*, 581-612.
- Pritikin, J. N., Hunter, M. D., & Boker, S. M. (2015). Modular open-source software for Item Factor Analysis. *Educational and Psychological Measurement*, *75*(3), 458-474
- Pritikin, J. N. & Schmidt, K. M. (in press). Model builder for Item Factor Analysis with OpenMx. *R Journal*.
- Seong, T. J. (1990). Sensitivity of marginal maximum likelihood estimation of item and ability parameters to the characteristics of the prior ability distributions. *Applied Psychological Measurement*, *14*(3), 299-311.

See Also**RPF****Examples**

```

library(OpenMx)
library(rpf)

numItems <- 14

# Create item specifications
spec <- list()
for (ix in 1:numItems) { spec[[ix]] <- rpf.grm(outcomes=sample(2:7, 1)) }
names(spec) <- paste("i", 1:numItems, sep="")

# Generate some random "true" parameter values
correct.mat <- mxSimplify2Array(lapply(spec, rpf.rparam))

# Generate some example data
data <- rpf.sample(500, spec, correct.mat)

# Create a matrix of item parameters with starting values
imat <- mxMatrix(name="item",
                 values=mxSimplify2Array(lapply(spec, rpf.rparam)))
rownames(imat)[1] <- 'f1'
imat$free[!is.na(correct.mat)] <- TRUE
imat$values[!imat$free] <- NA

# Create a compute plan
plan <- mxComputeSequence(list(
  mxComputeEM('expectation', 'scores',
             mxComputeNewtonRaphson(), information="oakes1999",
             infoArgs=list(fitfunction='fitfunction')),
  mxComputeHessianQuality(),
  mxComputeStandardError(),
  mxComputeReportDeriv()))

# Build the OpenMx model
grmModel <- mxModel(model="grm1", imat,
                  mxData(observed=data, type="raw"),
                  mxExpectationBA81(ItemSpec=spec),
                  mxFitFunctionML(),
                  plan)

grmModel <- mxRun(grmModel)
summary(grmModel)

```

Description

This function creates a new `MxExpectationGREML` object.

Usage

```
mxExpectationGREML(V, yvars=character(0), Xvars=list(), addOnes=TRUE, blockByPheno=TRUE,
  staggerZeroes=TRUE, dataset.is.yX=FALSE, casesToDropFromV=integer(0))
```

Arguments

- `V` Character string; the name of the `MxAlgebra` or `MxMatrix` to serve as the 'V' matrix (the model-expected covariance matrix). Internally, the 'V' matrix is assumed to be symmetric, and its elements above the main diagonal are ignored.
- `yvars`, `Xvars`, `addOnes`, `blockByPheno`, `staggerZeroes`
Passed to `mxGREMLDataHandler()`.
- `dataset.is.yX` Logical; defaults to FALSE. If TRUE, then the first column of the raw dataset is taken as-is to be the 'y' phenotype vector, and the remaining columns are taken as-is to be the 'X' matrix of covariates. In this case, `mxGREMLDataHandler()` is never internally called at runtime, and all other arguments besides `V` and `casesToDropFromV` are ignored.
- `casesToDropFromV` Integer vector. Its elements are the numbers of the rows and columns of covariance matrix 'V' to be dropped at runtime, usually because they correspond to rows of 'y' or 'X' that contained missing observations. By default, no cases are dropped from 'V.' Ignored unless `dataset.is.yX=TRUE`.

Details

"GREML" stands for "genomic-relatedness-matrix restricted maximum-likelihood." In the strictest sense of the term, it refers to genetic variance-component estimation from matrices of subjects' pairwise degree of genetic relatedness, as calculated from genome-wide marker data. It is from this original motivation that some of the terminology originates, such as calling 'y' the "phenotype" vector. However, OpenMx's implementation of GREML is applicable for analyses from any subject-matter domain, and in which the following assumptions are reasonable:

1. Conditional on 'X' (the covariates), the phenotype vector (response variable) 'y' is a single realization from a multivariate-normal distribution having (in general) a dense covariance matrix, 'V.'
2. The parameters of the covariance matrix, such as variance components, are of primary interest.
3. The random effects are normally distributed.
4. Weighted least-squares regression, using the inverse of 'V' as a weight matrix, is an adequate model for the phenotypic means. Note that the regression coefficients are not actually free parameters to be numerically optimized.

Computationally, the chief distinguishing feature of an OpenMx GREML analysis is that the phenotype vector, 'y,' is a single realization of a random vector that, in general, cannot be partitioned into independent subvectors. For this reason, definition variables are not compatible (and should be

unnecessary with) GREML expectation. GREML expectation can still be used if the covariance matrix is sparse, but as of this writing, OpenMx does not take advantage of the sparseness to improved performance. Because of the limitations of restricted maximum likelihood, GREML expectation is presently incompatible with ordinal variables.

Value

Returns a new object of class `MxExpectationGREML`.

References

One of the first uses of the acronym "GREML":

Benjamin DJ, Cesarini D, van der Loos MJHM, Dawes CT, Koellinger PD, et al. (2012) The genetic architecture of economic and political preferences. *Proceedings of the National Academy of Sciences* 109: 8026-8031. doi: 10.1073/pnas.1120666109

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

See `MxExpectationGREML` for the S4 class created by `mxExpectationGREML()`. More information about the OpenMx package may be found [here](#).

Examples

```
dat <- cbind(rnorm(100),rep(1,100))
colnames(dat) <- c("y","x")

ge <- mxExpectationGREML(V="V",yvars="y",Xvars=list("X"),addOnes=FALSE)
gff <- mxFitFunctionGREML(dV=c("ve","I"))
plan <- mxComputeSequence(freeSet=c("Ve"),steps=list(
  mxComputeNewtonRaphson(fitfunction="fitfunction"),
  mxComputeOnce('fitfunction',
    c('fit','gradient','hessian','ihessian')),
  mxComputeStandardError(),
  mxComputeReportDeriv(),
  mxComputeReportExpectation()
))

testmod <- mxModel(
  "GREML test",
  mxData(observed = dat, type="raw"),
  mxMatrix(type = "Full", nrow = 1, ncol=1, free=TRUE,
    values = 1, labels = "ve", lbound = 0.0001, name = "Ve"),
  mxMatrix("Iden",nrow=100,name="I",condenseSlots=TRUE),
  mxAlgebra(I %x% Ve,name="V"),
  ge,
  gff,
  plan
)
str(testmod)
```

MxExpectationGREML-class

Class "MxExpectationGREML"

Description

MxExpectationGREML is a type of expectation class. It contains the necessary elements for specifying a GREML model. For more information, see [mxExpectationGREML\(\)](#).

Objects from the Class

Objects can be created by calls of the form `mxExpectationGREML(V, yvars, Xvars, addOnes, blockByPheno,`

Slots

V: Object of class "MxCharOrNumber". Identifies the [MxAlgebra](#) or [MxMatrix](#) to serve as the 'V' matrix.

yvars: Character vector. Each string names a column of the raw dataset, to be used as a phenotypes.

Xvars: A list of data column names, specifying the covariates to be used with each phenotype.

addOnes: Logical; pertains to data-handling at runtime.

blockByPheno: Logical; pertains to data-handling at runtime.

staggerZeroes: Logical; pertains to data-handling at runtime.

dataset.is.yX: Logical; pertains to data-handling at runtime.

y: Object of class "MxData". Its observed slot will contain the phenotype vector, 'y.'

X: A matrix, to contain the 'X' matrix of covariates.

yXcolnames: Character vector; used to store the column names of 'y' and 'X.'

casesToDrop: Integer vector, specifying the rows and columns of the 'V' matrix to be removed at runtime.

b: A matrix, to contain the vector of regression coefficients calculated at runtime.

bcov: A matrix, to contain the sampling covariance matrix of the regression coefficients calculated at runtime.

numFixEff: Integer number of covariates in 'X.'

dims: Object of class "character".

numStats: Numeric; number of observed statistics.

dataColumns: Object of class "numeric".

name: Object of class "character".

data: Object of class "MxCharOrNumber".

.runDims: Object of class "character".

Extends

Class "MxBaseExpectation", directly. Class "MxBaseNamed", by class "MxBaseExpectation", distance 2. Class "MxExpectation", by class "MxBaseExpectation", distance 2.

Methods

No methods defined with class "MxExpectationGREML" in the signature.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

See `mxExpectationGREML()` for creating MxExpectationGREML objects, and for more information generally concerning GREML analyses, including a complete example. More information about the OpenMx package may be found [here](#).

Examples

```
showClass("MxExpectationGREML")
```

```
mxExpectationHiddenMarkov
```

Hidden Markov expectation

Description

Used in conjunction with `mxFitFunctionML`, this expectation can express a mixture model (with the transition matrix omitted) or a Hidden Markov model.

Usage

```
mxExpectationHiddenMarkov(components, initial="initial", transition=NULL,
  ..., verbose=0L, scale=c('softmax','sum'))
```

Arguments

<code>components</code>	A character vector of model names.
<code>initial</code>	The name of the matrix or algebra column that specifies the initial probabilities.
<code>transition</code>	The name of the matrix or algebra that specifies the left stochastic transition probabilities.
<code>...</code>	Not used. Forces remaining arguments to be specified by name.
<code>verbose</code>	the level of runtime diagnostics
<code>scale</code>	How the probabilities are rescaled. For 'softmax', the coefficient-wise exponential is taken and then each column is divided by its column sum. For 'sum', each column is divided by its column sum.

Details

Parameters are estimated in the given scale. To obtain the initial column vector and left stochastic transition matrix in probability units then examine the expectation's output slot.

[mxGenerateData](#) is not implemented for this type of expectation.

Examples

```
library(OpenMx)

start_prob <- c(.2,.4,.4)
transition_prob <- matrix(c(.8, .1, .1,
.3, .6, .1,
.1, .3, .6), 3, 3)
noise <- .5

# simulate a trajectory
state <- sample.int(3, 1, prob=transition_prob %*% start_prob)
trail <- c(state)

for (rep in 1:500) {
  state <- sample.int(3, 1, prob=transition_prob[,state])
  trail <- c(trail, state)
}

# add noise
trailN <- sapply(trail, function(v) rnorm(1, mean=v, sd=sqrt(noise)))

classes <- list()

for (cl in 1:3) {
  classes[[cl]] <- mxModel(paste0("cl", cl), type="RAM",
    manifestVars=c("ob"),
    mxPath("one", "ob", value=cl, free=FALSE),
    mxPath("ob", arrows=2, value=noise, free=FALSE),
    mxFitFunctionML(vector=TRUE))
}

m1 <-
  mxModel("hmm", classes,
    mxData(data.frame(ob=trailN), "raw"),
    mxMatrix(nrow=3, ncol=1,
      labels=paste0('i',1:3), name="initial"),
    mxMatrix(nrow=length(classes), ncol=length(classes),
      labels=paste0('t', 1:(length(classes) * length(classes))),
      name="transition"),
    mxExpectationHiddenMarkov(
      components=sapply(classes, function(m) m$name),
      initial="initial",
      transition="transition", scale="softmax"),
    mxFitFunctionML())

m1$transition$free[1:(length(classes)-1), 1:length(classes)] <- TRUE
```

```

m1 <- mxRun(m1)

summary(m1)

print(m1$expectation$output)

```

mxExpectationLISREL *Create MxExpectationLISREL Object*

Description

This function creates a new MxExpectationLISREL object.

Usage

```

mxExpectationLISREL(LX=NA, LY=NA, BE=NA, GA=NA, PH=NA, PS=NA, TD=NA, TE=NA, TH=NA,
  TX = NA, TY = NA, KA = NA, AL = NA,
  dimnames = NA, thresholds = NA, threshnames = dimnames)

```

Arguments

LX	An optional character string indicating the name of the 'LX' matrix.
LY	An optional character string indicating the name of the 'LY' matrix.
BE	An optional character string indicating the name of the 'BE' matrix.
GA	An optional character string indicating the name of the 'GA' matrix.
PH	An optional character string indicating the name of the 'PH' matrix.
PS	An optional character string indicating the name of the 'PS' matrix.
TD	An optional character string indicating the name of the 'TD' matrix.
TE	An optional character string indicating the name of the 'TE' matrix.
TH	An optional character string indicating the name of the 'TH' matrix.
TX	An optional character string indicating the name of the 'TX' matrix.
TY	An optional character string indicating the name of the 'TY' matrix.
KA	An optional character string indicating the name of the 'KA' matrix.
AL	An optional character string indicating the name of the 'AL' matrix.
dimnames	An optional character vector that is currently ignored
thresholds	An optional character string indicating the name of the thresholds matrix.
threshnames	An optional character vector to be assigned to the column names of the thresholds matrix.

Details

Expectation functions define the way that model expectations are calculated. The mxExpectation-LISREL calculates the expected covariance and means of a given [MxData](#) object given a LISREL model. This model is defined by Linear Structural Relations (LISREL; Jöreskog & Sörbom, 1982, 1996). Arguments 'LX' through 'AL' must refer to [MxMatrix](#) objects with the associated properties of their respective matrices in the LISREL modeling approach.

The full LISREL specification has 13 matrices and is sometimes called the extended LISREL model. It is defined by the following equations.

$$\eta = \alpha + B\eta + \Gamma\xi + \zeta$$

$$y = \tau_y + \Lambda_y\eta + \epsilon$$

$$x = \tau_x + \Lambda_x\xi + \delta$$

The table below is provided as a quick reference to the numerous matrices in LISREL models. Note that NX is the number of manifest exogenous (independent) variables, the number of Xs. NY is the number of manifest endogenous (dependent) variables, the number of Ys. NK is the number of latent exogenous variables, the number of Ksis or Xis. NE is the number of latent endogenous variables, the number of etas.

Matrix	Word	Abbreviation	Dimensions	Expression	Description
Λ_x	Lambda x	LX	NX x NK		Exogenous Factor Loading Matrix
Λ_y	Lambda y	LY	NY x NE		Endogenous Factor Loading Matrix
B	Beta	BE	NE x NE		Regressions of Latent Endogenous Variables Predicted by Latent Exogenous Variables
Γ	Gamma	GA	NE x NK		Regressions of Latent Exogenous Variables Predicted by Latent Endogenous Variables
Φ	Phi	PH	NK x NK	cov(ξ)	Covariance Matrix of Latent Exogenous Variables
Ψ	Psi	PS	NE x NE	cov(ζ)	Residual Covariance Matrix of Latent Endogenous Variables
Θ_δ	Theta delta	TD	NX x NX	cov(δ)	Residual Covariance Matrix of Manifest Exogenous Variables
Θ_ϵ	Theta epsilon	TE	NY x NY	cov(ϵ)	Residual Covariance Matrix of Manifest Endogenous Variables
$\Theta_{\delta\epsilon}$	Theta delta epsilon	TH	NX x NY	cov(δ, ϵ)	Residual Covariance Matrix of Manifest Exogenous and Manifest Endogenous Variables
τ_x	tau x	TX	NX x 1		Residual Means of Manifest Exogenous Variables
τ_y	tau y	TY	NY x 1		Residual Means of Manifest Endogenous Variables
κ	kappa	KA	NK x 1	mean(ξ)	Means of Latent Exogenous Variables
α	alpha	AL	NE x 1		Residual Means of Latent Endogenous Variables

From the extended LISREL model, several submodels can be defined. Subtypes of the LISREL model are defined by setting some of the arguments of the LISREL expectation function to NA. Note that because the default values of each LISREL matrix is NA, setting a matrix to NA can be accomplished by simply not giving it any other value.

The first submodel is the LISREL model without means.

$$\eta = B\eta + \Gamma\xi + \zeta$$

$$y = \Lambda_y\eta + \epsilon$$

$$x = \Lambda_x\xi + \delta$$

The LISREL model without means requires 9 matrices: LX, LY, BE, GA, PH, PS, TD, TE, and TH. Hence this LISREL model has TX, TY, KA, and AL as NA. This can be accomplished by leaving these matrices at their default values.

The TX, TY, KA, and AL matrices must be specified if either the mxData type is “cov” or “cor” and a means vector is provided, or if the mxData type is “raw”. Otherwise the TX, TY, KA, and AL matrices are ignored and the model without means is estimated.

A second submodel involves only endogenous variables.

$$\eta = B\eta + \zeta$$

$$y = \Lambda_y\eta + \epsilon$$

The endogenous-only LISREL model requires 4 matrices: LY, BE, PS, and TE. The LX, GA, PH, TD, and TH must be NA in this case. However, means can also be specified, allowing TY and AL if the data are raw or if observed means are provided.

Another submodel involves only exogenous variables.

$$x = \Lambda_x\xi + \delta$$

The exogenous-model model requires 3 matrices: LX, PH, and TD. The LY, BE, GA, PS, TE, and TH matrices must be NA. However, means can also be specified, allowing TX and KA if the data are raw or if observed means are provided.

The model that is run depends on the matrices that are not NA. If all 9 matrices are not NA, then the full model is run. If only the 4 endogenous matrices are not NA, then the endogenous-only model is run. If only the 3 exogenous matrices are not NA, then the exogenous-only model is run. If some endogenous and exogenous matrices are not NA, but not all of them, then appropriate errors are thrown. Means are included in the model whenever their matrices are provided.

The **MxMatrix** objects included as arguments may be of any type, but should have the properties described above. The mxExpectationLISREL will not return an error for incorrect specification, but incorrect specification will likely lead to estimation problems or errors in the **mxRun** function.

Like the **mxExpectationRAM**, the mxExpectationLISREL evaluates with respect to an **MxData** object. The **MxData** object need not be referenced in the mxExpectationLISREL function, but must be included in the **MxModel** object. mxExpectationLISREL requires that the ‘type’ argument in the associated **MxData** object be equal to ‘cov’, ‘cor’, or ‘raw’.

To evaluate, place mxExpectationLISREL objects, the **mxData** object for which the expected covariance approximates, referenced **MxAlgebra** and **MxMatrix** objects, and optional **MxBounds** and **MxConstraint** objects in an **MxModel** object. This model may then be evaluated using the **mxRun** function. The results of the optimization can be found in the ‘output’ slot of the resulting model, and may be obtained using the **mxEval** function.

Value

Returns a new MxExpectationLISREL object. One and only one MxExpectationLISREL object can be included with models using one and only one fit function object (e.g., MxFitFunctionML) and with referenced **MxAlgebra**, **MxData** and **MxMatrix** objects.

References

Jöreskog, K. G. & Sörbom, D. (1996). LISREL 8: User's Reference Guide. Lincolnwood, IL: Scientific Software International.

Jöreskog, K. G. & Sörbom, D. (1982). Recent developments in structural equation modeling. *Journal of Marketing Research*, 19, 404-416.

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

```
demo("LISRELJointFactorModel")
```

Examples

```
# Create and fit a model using mxExpectationLISREL, and mxFitFunctionML

library(OpenMx)

vNames <- paste("v",as.character(1:6),sep="")
dimList <- list(vNames, vNames)
covData <- matrix(
  c(0.9223099, 0.1862938, 0.4374359, 0.8959973, 0.9928430, 0.5320662,
    0.1862938, 0.2889364, 0.3927790, 0.3321639, 0.3371594, 0.4476898,
    0.4374359, 0.3927790, 1.0069552, 0.6918755, 0.7482155, 0.9013952,
    0.8959973, 0.3321639, 0.6918755, 1.8059956, 1.6142005, 0.8040448,
    0.9928430, 0.3371594, 0.7482155, 1.6142005, 1.9223567, 0.8777786,
    0.5320662, 0.4476898, 0.9013952, 0.8040448, 0.8777786, 1.3997558
  ), nrow=6, ncol=6, byrow=TRUE, dimnames=dimList)

# Create LISREL matrices

mLX <- mxMatrix("Full", values=c(.5, .6, .8, rep(0, 6), .4, .7, .5),
  name="LX", nrow=6, ncol=2,
  free=c(TRUE,TRUE,TRUE,rep(FALSE, 6),TRUE,TRUE,TRUE),
  dimnames=list(vNames, c("x1","x2")))
mTD <- mxMatrix("Diag", values=c(rep(.2, 6)),
  name="TD", nrow=6, ncol=6, free=TRUE,
  dimnames=dimList)
mPH <- mxMatrix("Symm", values=c(1, .3, 1),
  name="PH", nrow=2, ncol=2, free=c(FALSE, TRUE, FALSE),
  dimnames=list(c("x1","x2"),c("x1","x2")))

# Create a LISREL expectation with LX, TD, and PH matrix names

expFunction <- mxExpectationLISREL(LX="LX", TD="TD", PH="PH")

# Create fit function and data

tmpData <- mxData(observed=covData, type="cov", numObs=100)
fitFunction <- mxFitFunctionML()
```



```

# Create the model, fit it, and print a summary.

tmpModel <- mxModel(model="exampleModel",
                    mLX, mTD, mPH, expFunction, fitFunction, tmpData)
tmpModelOut <- mxRun(tmpModel)
summary(tmpModelOut)

#-----
# Fit factor model with means

require(OpenMx)

data(demoOneFactor)
nvar <- ncol(demoOneFactor)
varnames <- colnames(demoOneFactor)

factorMeans <- mxMatrix("Zero", 1, 1, name="Kappa",
                        dimnames=list("F1", NA))
xIntercepts <- mxMatrix("Full", nvar, 1, free=TRUE, name="TauX",
                        dimnames=list(varnames, NA))
factorLoadings <- mxMatrix("Full", nvar, 1, TRUE, .6, name="LambdaX",
                          labels=paste("lambda", 1:nvar, sep=""),
                          dimnames=list(varnames, "F1"))
factorCovariance <- mxMatrix("Diag", 1, 1, FALSE, 1, name="Phi")
xResidualVariance <- mxMatrix("Diag", nvar, nvar, TRUE, .2, name="ThetaDelta",
                              labels=paste("theta", 1:nvar, sep=""))

liModel <- mxModel(model="LISREL Factor Model",
                  factorMeans, xIntercepts, factorLoadings,
                  factorCovariance, xResidualVariance,
                  mxExpectationLISREL(LX="LambdaX", PH="Phi",
                                      TD="ThetaDelta", TX="TauX", KA="Kappa"),
                  mxFitFunctionML(),
                  mxData(cov(demoOneFactor), "cov",
                        means=colMeans(demoOneFactor), numObs=nrow(demoOneFactor))
                  )

liRun <- mxRun(liModel)

summary(liRun)

```

mxExpectationNormal *Create MxExpectationNormal Object*

Description

This function creates an MxExpectationNormal object.

Usage

```
mxExpectationNormal(covariance, means, dimnames = NA, thresholds = NA,
                    threshnames = dimnames)
```

Arguments

covariance	A character string indicating the name of the expected covariance algebra.
means	A character string indicating the name of the expected means algebra.
dimnames	An optional character vector to be assigned to the dimnames of the covariance and means algebras.
thresholds	An optional character string indicating the name of the thresholds matrix.
threshnames	An optional character vector to be assigned to the column names of the thresholds matrix.

Details

Expectation functions define the way that model expectations are calculated. The `mxExpectationNormal` function uses the algebra defined by the 'covariance' and 'means' arguments to define the expected covariance and means under the assumption of multivariate normality. The 'covariance' argument takes an `MxAlgebra` object, which defines the expected covariance of an associated `MxData` object. The 'means' argument takes an `MxAlgebra` object, which defines the expected means of an associated `MxData` object. The 'dimnames' arguments takes an optional character vector. If this argument is not a single NA, then this vector is used to assign the dimnames of the means vector as well as the row and columns dimnames of the covariance matrix.

thresholds: The name of the thresholds matrix. When needed (for modelling ordinal data), this matrix should be created using `mxMatrix()`. The thresholds matrix must have as many columns as there are ordinal variables in the model, and number of rows equal to one fewer than the maximum number of levels found in the ordinal variables. The starting values of this matrix must also be set to reasonable values. Fill each column with a set of ordered start thresholds, one for each level of this column's factor levels minus 1. These thresholds may be free if you wish them to be estimated, or fixed. The unused rows in each column, if any, can be set to any value including NA.

threshnames: A character vector consisting of the variables in the thresholds matrix, i.e., the names of ordinal variables in a model. This is necessary for OpenMx to map the thresholds matrix columns onto the variables in your data. If you set the `dimnames` of the columns in the thresholds matrix then `threshnames` is not needed.

Usage Notes: `dimnames` must be supplied where the matrices referenced by the covariance and means algebras are not themselves labeled. Failure to do so leads to an error noting that the covariance or means matrix associated with the FIML objective does not contain dimnames.

`mxExpectationNormal` evaluates with respect to an `MxData` object. The `MxData` object need not be referenced in the `mxExpectationNormal` function, but must be included in the `MxModel` object. When the 'type' argument in the associated `MxData` object is equal to 'raw', missing values are permitted in the associated `MxData` object.

To evaluate, place an `mxExpectationNormal` object, the `mxData` object for which the expected covariance approximates, referenced `MxAlgebra` and `MxMatrix` objects, optional `MxBounds` or `MxConstraint` objects, and an `mxFitFunction` such as `mxFitFunctionML` in an `MxModel` object. This model may then be evaluated using the `mxRun` function.

The results of the optimization can be reported using the [summary](#) function, or accessed directly in the 'output' slot of the resulting model (i.e., modelName\$output). Components of the output may be referenced using the [Extract](#) functionality.

Value

Returns an MxExpectationNormal object.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```
# Create and fit a model using mxMatrix, mxAlgebra,
# mxExpectationNormal, and mxFitFunctionML

library(OpenMx)

# Simulate some data

x=rnorm(1000, mean=0, sd=1)
y= 0.5*x + rnorm(1000, mean=0, sd=1)
tmpFrame <- data.frame(x, y)
tmpNames <- names(tmpFrame)

# Define the matrices

M <- mxMatrix(type = "Full", nrow = 1, ncol = 2, values=c(0,0),
              free=c(TRUE,TRUE), labels=c("Mx", "My"), name = "M")
S <- mxMatrix(type = "Full", nrow = 2, ncol = 2, values=c(1,0,0,1),
              free=c(TRUE,FALSE,FALSE,TRUE), labels=c("Vx", NA, NA, "Vy"),
              name = "S")
A <- mxMatrix(type = "Full", nrow = 2, ncol = 2, values=c(0,1,0,0),
              free=c(FALSE,TRUE,FALSE,FALSE), labels=c(NA, "b", NA, NA),
              name = "A")
I <- mxMatrix(type="Iden", nrow=2, ncol=2, name="I")

# Define the expectation

expCov <- mxAlgebra(solve(I-A) %*% S %*% t(solve(I-A)), name="expCov")
expFunction <- mxExpectationNormal(covariance="expCov", means="M",
dimnames=tmpNames)

# Choose a fit function

fitFunction <- mxFitFunctionML()

# Define the model

tmpModel <- mxModel(model="exampleModel", M, S, A, I,
```

```

expCov, expFunction, fitFunction,
mxData(observed=tmpFrame, type="raw"))

# Fit the model and print a summary

tmpModelOut <- mxRun(tmpModel)
summary(tmpModelOut)

```

mxExpectationRAM

Create an MxExpectationRAM Object

Description

This function creates an MxExpectationRAM object.

Usage

```

mxExpectationRAM(A="A", S="S", F="F", M = NA, dimnames = NA, thresholds = NA,
  threshnames = dimnames, ..., between=NULL, verbose=0L)

```

Arguments

A	A character string indicating the name of the 'A' matrix.
S	A character string indicating the name of the 'S' matrix.
F	A character string indicating the name of the 'F' matrix.
M	An optional character string indicating the name of the 'M' matrix.
dimnames	An optional character vector to be assigned to the column names of the 'F' and 'M' matrices.
thresholds	An optional character string indicating the name of the thresholds matrix.
threshnames	An optional character vector to be assigned to the column names of the thresholds matrix.
...	Not used. Forces remaining arguments to be specified by name.
between	A character vector of matrices that specify cross model relationships.
verbose	integer. Level of runtime diagnostic output.

Details

Expectation functions define the way that model expectations are calculated. The mxExpectationRAM calculates the expected covariance and means of a given [MxData](#) object given a RAM model. This model is defined by reticular action modeling (McArdle and McDonald, 1984). The 'A', 'S', and 'F' arguments must refer to [MxMatrix](#) objects with the associated properties of the A, S, and F matrices in the RAM modeling approach.

The 'dimnames' argument takes an optional character vector. If this argument is not a single NA, then this vector be assigned to be the column names of the 'F' matrix and optionally to the 'M' matrix, if the 'M' matrix exists.

The 'A' argument refers to the A or asymmetric matrix in the RAM approach. This matrix consists of all of the asymmetric paths (one-headed arrows) in the model. A free parameter in any row and column describes a regression of the variable represented by that row regressed on the variable represented in that column.

The 'S' argument refers to the S or symmetric matrix in the RAM approach, and as such must be square. This matrix consists of all of the symmetric paths (two-headed arrows) in the model. A free parameter in any row and column describes a covariance between the variable represented by that row and the variable represented by that column. Variances are covariances between any variable at itself, which occur on the diagonal of the specified matrix.

The 'F' argument refers to the F or filter matrix in the RAM approach. If no latent variables are included in the model (i.e., the A and S matrices are of both of the same dimension as the data matrix), then the 'F' should refer to an identity matrix. If latent variables are included (i.e., the A and S matrices are not of the same dimension as the data matrix), then the 'F' argument should consist of a horizontal adhesion of an identity matrix and a matrix of zeros.

The 'M' argument refers to the M or means matrix in the RAM approach. It is a 1 x n matrix, where n is the number of manifest variables + the number of latent variables. The M matrix must be specified if either the mxData type is "cov" or "cor" and a means vector is provided, or if the mxData type is "raw". Otherwise the M matrix is ignored.

The [MxMatrix](#) objects included as arguments may be of any type, but should have the properties described above. The mxExpectationRAM will not return an error for incorrect specification, but incorrect specification will likely lead to estimation problems or errors in the [mxRun](#) function.

mxExpectationRAM evaluates with respect to an [MxData](#) object. The [MxData](#) object need not be referenced in the mxExpectationRAM function, but must be included in the [MxModel](#) object.

To evaluate, place mxExpectationRAM objects, the [mxData](#) object for which the expected covariance approximates, referenced [MxAlgebra](#) and [MxMatrix](#) objects, and optional [MxBounds](#) and [MxConstraint](#) objects in an [MxModel](#) object. This model may then be evaluated using the [mxRun](#) function. The results of the optimization can be found in the 'output' slot of the resulting model, and may be obtained using the [mxEval](#) function..

Value

Returns a new MxExpectationRAM object. mxExpectationRAM objects should be included with models with referenced [MxAlgebra](#), [MxData](#) and [MxMatrix](#) objects.

References

McArdle, J. J. and MacDonald, R. P. (1984). Some algebraic properties of the Reticular Action Model for moment structures. *British Journal of Mathematical and Statistical Psychology*, 37, 234-251.

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```

# Create and fit a model using mxMatrix, mxAlgebra,
# mxExpectationNormal, and mxFitFunctionML

library(OpenMx)

# Simulate some data

x=rnorm(1000, mean=0, sd=1)
y= 0.5*x + rnorm(1000, mean=0, sd=1)
tmpFrame <- data.frame(x, y)
tmpNames <- names(tmpFrame)

# Define the matrices

matrixS <- mxMatrix(type = "Full", nrow = 2, ncol = 2, values=c(1,0,0,1),
                    free=c(TRUE,FALSE,FALSE,TRUE), labels=c("Vx", NA, NA, "Vy"),
                    name = "S")
matrixA <- mxMatrix(type = "Full", nrow = 2, ncol = 2, values=c(0,1,0,0),
                    free=c(FALSE,TRUE,FALSE,FALSE), labels=c(NA, "b", NA, NA),
                    name = "A")
matrixF <- mxMatrix(type="Iden", nrow=2, ncol=2, name="F")
matrixM <- mxMatrix(type = "Full", nrow = 1, ncol = 2, values=c(0,0),
                    free=c(TRUE,TRUE), labels=c("Mx", "My"), name = "M")

# Define the expectation

expFunction <- mxExpectationRAM(M="M", dimnames = tmpNames)

# Choose a fit function

fitFunction <- mxFitFunctionML()

# Define the model

tmpModel <- mxModel(model="exampleRAMModel",
                    matrixA, matrixS, matrixF, matrixM,
                    expFunction, fitFunction,
                    mxData(observed=tmpFrame, type="raw"))

# Fit the model and print a summary

tmpModelOut <- mxRun(tmpModel)
summary(tmpModelOut)

```

mxExpectationStateSpace

Create an MxExpectationStateSpace Object

Description

This function creates a new MxExpectationStateSpace object.

Usage

```
mxExpectationStateSpace(A, B, C, D, Q, R, x0, P0, u,
                        dimnames = NA, thresholds = NA, threshnames = dimnames,
                        ..., t = NA, scores=FALSE)
```

Arguments

A	A character string indicating the name of the 'A' matrix.
B	A character string indicating the name of the 'B' matrix.
C	A character string indicating the name of the 'C' matrix.
D	A character string indicating the name of the 'D' matrix.
Q	A character string indicating the name of the 'Q' matrix.
R	A character string indicating the name of the 'R' matrix.
x0	A character string indicating the name of the 'x0' matrix.
P0	A character string indicating the name of the 'P0' matrix.
u	A character string indicating the name of the 'u' matrix.
dimnames	An optional character vector to be assigned to the row names of the 'C' matrix.
thresholds	Not Yet Implemented. An optional character string indicating the name of the thresholds matrix.
threshnames	Not Yet Implemented. An optional character vector to be assigned to the column names of the thresholds matrix.
...	Unused. Requires further arguments to be named.
t	Not to be used
scores	Not to be used

Details

Expectation functions define the way that model expectations are calculated. When used in conjunction with the [mxFitFunctionML](#), the mxExpectationStateSpace uses maximum likelihood prediction error decomposition (PED) to obtain estimates of free parameters in a model of the raw [MxData](#) object. State space expectations treat the raw data as a multivariate time series of equally spaced times with each row corresponding to a single occasion. This is not a model of the block Toeplitz lagged autocovariance matrix. State space expectations implement a classical Kalman filter to produce expectations.

The hybrid Kalman filter (combination of classical Kalman and Kalman-Bucy filters) for continuous latent time with discrete observations is implemented and is available as [mxExpectationStateSpace-ContinuousTime](#). The following alternative filters are not yet implemented: square root Kalman filter (in Cholesky or singular value decomposition form), extended Kalman filter for linear approximations to nonlinear state space models, unscented Kalman filter for highly nonlinear state space

models, and Rauch-Tung-Striebel smoother for updating forecast state estimates after a complete forward pass through the data has been made.

Missing data handling is implemented in the same fashion as full information maximum likelihood for partially missing rows of data. Additionally, completely missing rows of data are handled by only using the prediction step from the Kalman filter and omitting the update step.

This model uses notation for the model matrices commonly found in engineering and control theory.

The 'A', 'B', 'C', 'D', 'Q', 'R', 'x0', and 'P0' arguments must be the names of [MxMatrix](#) or [MxAlgebra](#) objects with the associated properties of the A, B, C, D, Q, R, x0, and P0 matrices in the state space modeling approach.

The state space expectation is defined by the following model equations.

$$x_t = Ax_{t-1} + Bu_t + q_t$$

$$y_t = Cx_t + Du_t + r_t$$

with q_t and r_t both independently and identically distributed random Gaussian (normal) variables with mean zero and covariance matrices Q and R , respectively.

The first equation is called the state equation. It describes how the latent states change over time. Also, the state equation in state space modeling is directly analogous to the structural model in LISREL structural equation modeling.

The second equation is called the output equation. It describes how the latent states relate to the observed states at a single point in time. The output equation shows how the observed output is produced by the latent states. Also, the output equation in state space modeling is directly analogous to the measurement model in LISREL structural equation modeling.

Note that the covariates, u , have "instantaneous" effects on both the state and output equations. If lagged effects are desired, then the user must create a lagged covariate by shifting their observed variable to the desired lag.

The state and output equations, together with some minimal assumptions and the Kalman filter, imply a new expected covariance matrix and means vector for every row of data. The expected covariance matrix of row t is

$$S_t = C(AP_{t-1}A^T + Q)C^T + R$$

The expected means vector of row t is

$$\hat{y}_t = Cx_t + Du_t$$

The 'dimnames' arguments takes an optional character vector.

The 'A' argument refers to the A matrix in the State Space approach. This matrix consists of time regressive coefficients from the latent variable in column j at time $t - 1$ to the latent variable in row i at time t . Entries in the diagonal are autoregressive coefficients. Entries in the off-diagonal are cross-lagged regressive coefficients. If the A and B matrices are zero matrices, then the state space model reduces to a factor analysis. The A matrix is sometimes called the state-transition model.

The 'B' argument refers to the B matrix in the State Space approach. This matrix consists of regressive coefficients from the input (manifest covariate) variable j at time t to the latent variable

in row i at time t . Note that the covariate effect is contemporaneous: the covariate at time t has influence on the latent state also at time t . A lagged effect can be created by lagged the observed variable. The B matrix is sometimes called the control-input model.

The 'C' argument refers to the C matrix in the State Space approach. This matrix consists of contemporaneous regression coefficients from the latent variable in column j to the observed variable in row i . This matrix is directly analogous to the factor loadings matrix in LISREL and Mplus models. The C matrix is sometimes called the observation model.

The 'D' argument refers to the D matrix in the State Space approach. This matrix consists of contemporaneous regressive coefficients from the input (manifest covariate) variable j to the observed variable in row i . The D matrix is sometimes called the feedthrough or feedforward matrix.

The 'Q' argument refers to the Q matrix in the State Space approach. This matrix consists of residual covariances among the latent variables. This matrix must be symmetric. As a special case, it is often diagonal. The Q matrix is the covariance of the process noise. Just as in factor analysis and general structural equation modeling, the scale of the latent variables is usually set by fixing some factor loadings in the C matrix, or fixing some factor variances in the Q matrix.

The 'R' argument refers to the R matrix in the State Space approach. This matrix consists of residual covariances among the observed (manifest) variables. This matrix must be symmetric. As a special case, it is often diagonal. The R matrix is the covariance of the observation noise.

The 'x0' argument refers to the x_0 matrix in the State Space approach. This matrix consists of the column vector of the initial values for the latent variables. The state space expectation uses the x_0 matrix as the starting point to recursively estimate the latent variables' values at each time. These starting values can be difficult to pick, however, for sufficiently long time series they often do not greatly impact the estimation.

The 'P0' argument refers to the P_0 matrix in the State Space approach. This matrix consists of the initial values of the covariances of the error in the initial latent variable estimates given in x_0 . That is, the P_0 matrix gives the covariance of $x_0 - x_{true_0}$ where x_{true_0} is the vector of true initial values. P_0 is a measure of the accuracy of the initial latent state estimates. The Kalman filter uses this initial covariance to recursively generated a new covariance for each time point based on the previous time point. The Kalman filter updates this covariance so that it is as small as possible (minimum trace). Similar to the x_0 matrix, these starting values are often difficult to choose.

The 'u' argument refers to the u matrix in the State Space approach. This matrix consists of the inputs or manifest covariates of the state space expectation. The u matrix must be a column vector with the same number of rows as the B and D matrices have columns. If no inputs are desired, u can be a zero matrix. If time-varying inputs are desired, then they should be included as columns in the [MxData](#) object and referred to in the labels of the u matrix as definition variables. There is an example of this below.

The [MxMatrix](#) objects included as arguments may be of any type, but should have the properties described above. The `mxExpectationStateSpace` will not return an error for incorrect specification, but incorrect specification will likely lead to estimation problems or errors in the [mxRun](#) function.

`mxExpectationStateSpace` evaluates with respect to an [MxData](#) object. The [MxData](#) object need not be referenced in the `mxExpectationStateSpace` function, but must be included in the [MxModel](#) object. `mxExpectationStateSpace` requires that the 'type' argument in the associated [MxData](#) object be equal to 'raw'. Neighboring rows of the [MxData](#) object are treated as adjacent, equidistant time points increasing from the first to the last row.

To evaluate, place `mxExpectationStateSpace` objects, the [mxData](#) object for which the expected covariance approximates, referenced [MxAlgebra](#) and [MxMatrix](#) objects, and optional [MxBounds](#)

and `MxConstraint` objects in an `MxModel` object. This model may then be evaluated using the `mxRun` function. The results of the optimization can be found in the 'output' slot of the resulting model, and may be obtained using the `mxEval` function.

Value

Returns a new `MxExpectationStateSpace` object. `MxExpectationStateSpace` objects should be included with models with referenced `MxAlgebra`, `MxData` and `MxMatrix` objects.

References

- K.J. Åström and R.M. Murray (2010). *Feedback Systems: An Introduction for Scientists and Engineers*. Princeton University Press.
- J. Durbin and S.J. Koopman. (2001). *Time Series Analysis by State Space Methods*. Oxford University Press.
- R.E. Kalman (1960). A New Approach to Linear Filtering and Prediction Problems. *Basic Engineering*, 82, 35-45.
- G. Petris (2010). An R Package for Dynamic Linear Models. *Journal of Statistical Software*, 36, 1-16.
- The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

[mxExpectationStateSpaceContinuousTime](#)

Examples

```
# Create and fit a model using mxMatrix, mxExpectationStateSpace, and mxFitFunctionML
require(OpenMx)
data(demoOneFactor)
nvar <- ncol(demoOneFactor)
varnames <- colnames(demoOneFactor)
ssModel <- mxModel(model="State Space Manual Example",
  mxMatrix("Full", 1, 1, TRUE, .3, name="A"),
  mxMatrix("Zero", 1, 1, name="B"),
  mxMatrix("Full", nvar, 1, TRUE, .6, name="C", dimnames=list(varnames, "F1")),
  mxMatrix("Zero", nvar, 1, name="D"),
  mxMatrix("Diag", 1, 1, FALSE, 1, name="Q"),
  mxMatrix("Diag", nvar, nvar, TRUE, .2, name="R"),
  mxMatrix("Zero", 1, 1, name="x0"),
  mxMatrix("Diag", 1, 1, FALSE, 1, name="P0"),
  mxMatrix("Zero", 1, 1, name="u"),
  mxData(observed=demoOneFactor[1:100,], type="raw"),#fewer rows = fast
  mxExpectationStateSpace("A", "B", "C", "D", "Q", "R", "x0", "P0", "u"),
  mxFitFunctionML()
)
ssRun <- mxRun(ssModel)
summary(ssRun)
# Note the freely estimated Autoregressive parameter (A matrix)
```

```

# is near zero as it should be for the independent rows of data
# from the factor model.

# Create and fit a model with INPUTS using mxMatrix, mxExpectationStateSpace, and mxFitFunctionML
require(OpenMx)
data(demoOneFactor)
nvar <- ncol(demoOneFactor)
varnames <- colnames(demoOneFactor)
#demoOneFactorInputs <- cbind(demoOneFactor, V1=rep(1, nrow(demoOneFactor)))
demoOneFactorInputs <- cbind(demoOneFactor, V1=rnorm(nrow(demoOneFactor)))
ssModel <- mxModel(model="State Space Inputs Manual Example",
  mxMatrix("Full", 1, 1, TRUE, .3, name="A"),
  mxMatrix("Full", 1, 1, TRUE, values=1, name="B"),
  mxMatrix("Full", nvar, 1, TRUE, .6, name="C", dimnames=list(varnames, "F1")),
  mxMatrix("Zero", nvar, 1, name="D"),
  mxMatrix("Diag", 1, 1, FALSE, 1, name="Q"),
  mxMatrix("Diag", nvar, nvar, TRUE, .2, name="R"),
  mxMatrix("Zero", 1, 1, name="x0"),
  mxMatrix("Diag", 1, 1, FALSE, 1, name="P0"),
  mxMatrix("Full", 1, 1, FALSE, labels="data.V1", name="u"),
  mxData(observed=demoOneFactorInputs[1:100,], type="raw"),#fewer rows = fast
  mxExpectationStateSpace("A", "B", "C", "D", "Q", "R", "x0", "P0", u="u"),
  mxFitFunctionML()
)
ssRun <- mxRun(ssModel)
summary(ssRun)
# Note the freely estimated Autoregressive parameter (A matrix)
# and the freely estimated Control-Input parameter (B matrix)
# are both near zero as they should be for the independent rows of data
# from the factor model that does not have inputs, covariates,
# or exogenous variables.

```

```
mxExpectationStateSpaceContinuousTime
```

Create an MxExpectationStateSpace Object

Description

This function creates a new MxExpectationStateSpace object.

Usage

```

mxExpectationStateSpaceContinuousTime(A, B, C, D, Q, R, x0, P0, u, t = NA,
  dimnames = NA, thresholds = NA, threshnames = dimnames,
  ..., scores=FALSE)
mxExpectationSSCT(A, B, C, D, Q, R, x0, P0, u, t = NA,
  dimnames = NA, thresholds = NA, threshnames = dimnames,
  ..., scores=FALSE)

```

Arguments

A	A character string indicating the name of the 'A' matrix.
B	A character string indicating the name of the 'B' matrix.
C	A character string indicating the name of the 'C' matrix.
D	A character string indicating the name of the 'D' matrix.
Q	A character string indicating the name of the 'Q' matrix.
R	A character string indicating the name of the 'R' matrix.
x0	A character string indicating the name of the 'x0' matrix.
P0	A character string indicating the name of the 'P0' matrix.
u	A character string indicating the name of the 'u' matrix.
t	A character string indicating the name of the 't' matrix.
dimnames	An optional character vector to be assigned to the row names of the 'C' matrix.
thresholds	Not Yet Implemented. An optional character string indicating the name of the thresholds matrix.
threshnames	Not Yet Implemented. An optional character vector to be assigned to the column names of the thresholds matrix.
...	Unused. Requires further arguments to be named.
scores	Not to be used

Details

The `mxExpectationStateSpaceContinuousTime` and `mxExpectationSSCT` functions are identical. The latter is simply an abbreviated name. When using the former, tab completion is strongly encouraged to save tedious typing. Both of these functions are wrappers for the [mxExpectationStateSpace](#) function, which could be used for both discrete and continuous time modeling. However, there is a strong possibility of misunderstanding the model parameters when switching between discrete time and continuous time. The expectation matrices have the same names, but mean importantly different things so caution is warranted. The best practice is to use `mxExpectationStateSpace` for discrete time models, and `mxExpectationStateSpaceContinuousTime` for continuous time models.

Expectation functions define the way that model expectations are calculated. That is to say, expectation functions define how a set of model matrices get turned into expectations for the data. When used in conjunction with the [mxFitFunctionML](#), the `mxExpectationStateSpace` uses maximum likelihood prediction error decomposition (PED) to obtain estimates of free parameters in a model of the raw [MxData](#) object. Continuous time state space expectations treat the raw data as a multivariate time series of possibly unevenly spaced times with each row corresponding to a single occasion. Continuous time state space expectations implement a hybrid Kalman filter to produce expectations. The hybrid Kalman filter uses a Kalman-Bucy filter for the prediction step and the classical Kalman filter for the update step. It is a hybrid between the classical Kalman filter used for the discrete (but possibly unequally spaced) measurement occasions and the continuous time Kalman-Bucy filter for latent variable predictions.

Missing data handling is implemented in the same fashion as full information maximum likelihood for partially missing rows of data. Additionally, completely missing rows of data are handled by only using the prediction step from the Kalman-Bucy filter and omitting the update step.

This model uses notation for the model matrices commonly found in engineering and control theory. The 'A', 'B', 'C', 'D', 'Q', 'R', 'x0', and 'P0' arguments must be the names of [MxMatrix](#) or [MxAlgebra](#) objects with the associated properties of the A, B, C, D, Q, R, x0, and P0 matrices in the state space modeling approach. The 't' matrix must be a 1x1 matrix using definition variables that gives the times at which measurements occurred.

The state space expectation is defined by the following model equations.

$$\frac{d}{dt}x(t) = Ax(t) + Bu_t + q(t)$$

$$y_t = Cx_t + Du_t + r_t$$

with $q(t)$ and r_t both independently and identically distributed random Gaussian (normal) variables with mean zero and covariance matrices Q and R , respectively. Subscripts or square brackets indicate discrete indices; parentheses indicate continuous indices. The derivative of $x(t)$ with respect to t is $\frac{d}{dt}x(t)$.

The first equation is called the state equation. It describes how the latent states change over time with a first-order linear differential equation. Unlike some other programs, we do not require that the continuous time A matrix has an inverse. This allows zero dynamics (i.e. no growth models) and many other important kinds of processes.

The second equation is called the output equation. It describes how the latent states relate to the observed states at a single point in time. The output equation shows how the observed output is produced by the latent states. Also, the output equation in state space modeling is directly analogous to the measurement model in LISREL structural equation modeling.

Note that the covariates, u , have "instantaneous" effects on both the state and output equations. If lagged effects are desired, then the user must create a lagged covariate by shifting their observed variable to the desired lag.

The state and output equations, together with some minimal assumptions and the Kalman filter, imply a new expected covariance matrix and means vector for every row of data. The expected covariance matrix of row t is

$$S_t = C(AP_{t-1}A^T + Q)C^T + R$$

The expected means vector of row t is

$$\hat{y}_t = Cx_t + Du_t$$

The 'dimnames' arguments takes an optional character vector.

The 'A' argument refers to the A matrix in the State Space approach. This matrix gives the dynamics. Entries in the diagonal give the strength of the influence of a variable's position on its slope. Entries in the off-diagonal give the coupling strength from one variable to another. The A matrix is sometimes called the state-transition model.

The 'B' argument refers to the B matrix in the State Space approach. This matrix consists of exogenous forces that influence the dynamics. Note that the covariate effect is contemporaneous: the covariate at time t has influence on the slope of the latent state also at time t . A lagged effect can be created by lagged the observed variable. The B matrix is sometimes called the control-input model.

The 'C' argument refers to the C matrix in the State Space approach. This matrix consists of contemporaneous regression coefficients from the latent variable in column j to the observed variable in row i . This matrix is directly analogous to the factor loadings matrix in LISREL and Mplus models. The C matrix is sometimes called the observation model.

The 'D' argument refers to the D matrix in the State Space approach. This matrix consists of contemporaneous regressive coefficients from the input (manifest covariate) variable j to the observed variable in row i . The D matrix is sometimes called the feedthrough or feedforward matrix.

The 'Q' argument refers to the Q matrix in the State Space approach. This matrix gives the covariance of the dynamic noise. The dynamic noise can be thought of as unmeasured covariate inputs active at all times. This matrix must be symmetric, diagonal, or zero. As a special case, it is often diagonal. The Q matrix is the covariance of the process noise. Just as in factor analysis and general structural equation modeling, the scale of the latent variables is usually set by fixing some factor loadings in the C matrix, or fixing some factor variances in the Q matrix.

The 'R' argument refers to the R matrix in the State Space approach. This matrix consists of residual covariances among the observed (manifest) variables. This matrix must be symmetric. As a special case, it is often diagonal. The R matrix is the covariance of the observation noise.

The 'x0' argument refers to the x_0 matrix in the State Space approach. This matrix consists of the column vector of the initial values for the latent variables. The state space expectation uses the x_0 matrix as the starting point to recursively estimate the latent variables' values at each time. These starting values can be difficult to pick, however, for sufficiently long time series they often do not greatly impact the estimation.

The 'P0' argument refers to the P_0 matrix in the State Space approach. This matrix consists of the initial values of the covariances of the error in the initial latent variable estimates given in x_0 . That is, the P_0 matrix gives the covariance of $x_0 - x_{true_0}$ where x_{true_0} is the vector of true initial values. P_0 is a measure of the accuracy of the initial latent state estimates. The Kalman filter uses this initial covariance to recursively generate a new covariance for each time point based on the previous time point. The Kalman filter updates this covariance so that it is as small as possible (minimum trace). Similar to the x_0 matrix, these starting values are often difficult to choose.

The 'u' argument refers to the u matrix in the State Space approach. This matrix consists of the inputs or manifest covariates of the state space expectation. The u matrix must be a column vector with the same number of rows as the B and D matrices have columns. If no inputs are desired, u can be a zero matrix. If time-varying inputs are desired, then they should be included as columns in the [MxData](#) object and referred to in the labels of the u matrix as definition variables. There is an example of this below.

The 't' argument refers to the t matrix in the State Space approach. This matrix should be 1x1 (1 row and 1 column) and not free. The label for the element of this matrix should be 'data.YourTimeVariable'. The 'data' part does not change, but 'YourTimeVariable' should be a name in your data set that gives the times at which measurement happened. The units of time are up to you. Your choice of time units will influence the values of the parameters you estimate. Also, recall that the model is given x_0 and P_0 . These always happen at $t = 0$. So the first row of data happens some amount of time after zero.

The [MxMatrix](#) objects included as arguments may be of any type, but should have the properties described above. The `mxExpectationStateSpace` will not return an error for incorrect specification, but incorrect specification will likely lead to estimation problems or errors in the `mxRun` function.

`mxExpectationStateSpaceContinuousTime` evaluates with respect to an [MxData](#) object. The [MxData](#) object need not be referenced in the `mxExpectationStateSpace` function, but must be included

in the `MxModel` object. `mxExpectationStateSpace` requires that the `'type'` argument in the associated `MxData` object be equal to `'raw'`. Neighboring rows of the `MxData` object are treated as adjacent, equidistant time points increasing from the first to the last row.

To evaluate, place an `mxExpectationStateSpaceContinuousTime` object, the `mxData` object for which the expected covariance approximates, referenced `MxAlgebra` and `MxMatrix` objects, and optional `MxBounds` and `MxConstraint` objects in an `MxModel` object. This model may then be evaluated using the `mxRun` function. The results of the optimization can be found in the `'output'` slot of the resulting model, and may be obtained using the `mxEval` function.

Value

Returns a new `MxExpectationStateSpace` object. `mxExpectationStateSpace` objects should be included with models with referenced `MxAlgebra`, `MxData` and `MxMatrix` objects.

References

K.J. Åström and R.M. Murray (2010). *Feedback Systems: An Introduction for Scientists and Engineers*. Princeton University Press.

J. Durbin and S.J. Koopman. (2001). *Time Series Analysis by State Space Methods*. Oxford University Press.

R.E. Kalman (1960). A New Approach to Linear Filtering and Prediction Problems. *Basic Engineering*, 82, 35-45.

R.E. Kalman and R.S. Bucy (1961). New Results in Linear Filtering and Prediction Theory. *Transactions of the ASME, Series D, Journal of Basic Engineering*, 83, 95-108.

G. Petris (2010). An R Package for Dynamic Linear Models. *Journal of Statistical Software*, 36, 1-16.

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

[mxExpectationStateSpace](#)

Examples

```
#-----
# Example 1
# Undamped linear oscillator, i.e. a noisy sine wave.
# Measurement error, but no dynamic error, single indicator.
# This example works great.

#-----
# Data Generation

require(OpenMx)

set.seed(405)
tlen <- 200
t <- seq(1.2, 50, length.out=tlen)
```

```

freqParam <- .5
initialCond <- matrix(c(2.5, 0))
x <- initialCond[1,1]*cos(freqParam*t)
plot(t, x, type='l')

measVar <- 1.5
y <- cbind(obs=x+rnorm(tlen, sd=sqrt(measVar)), tim=t)

plot(t, y[,1], type='l')

#-----
# Model Specification

#Note: the bounds are here only to keep SLSQP from
# stepping too far off a cliff. With the bounds in
# place, SLSQP finds the right solution. Without
# the bounds, SLSQP goes crazy.

cdim <- list('obs', c('ksi', 'ksiDot'))

amat <- mxMatrix('Full', 2, 2, c(FALSE, TRUE, FALSE, TRUE), c(0, -.1, 1, -.2),
name='A', lbound=-10)
bmat <- mxMatrix('Zero', 2, 1, name='B')
cmat <- mxMatrix('Full', 1, 2, FALSE, c(1, 0), name='C', dimnames=cdim)
dmat <- mxMatrix('Zero', 1, 1, name='D')
qmat <- mxMatrix('Zero', 2, 2, name='Q')
rmat <- mxMatrix('Diag', 1, 1, TRUE, .4, name='R', lbound=1e-6)
xmat <- mxMatrix('Full', 2, 1, TRUE, c(0, 0), name='x0', lbound=-10, ubound=10)
pmat <- mxMatrix('Diag', 2, 2, FALSE, 1, name='P0')
umat <- mxMatrix('Zero', 1, 1, name='u')
tmat <- mxMatrix('Full', 1, 1, name='time', labels='data.tim')

osc <- mxModel("LinearOscillator",
amat, bmat, cmat, dmat, qmat, rmat, xmat, pmat, umat, tmat,
mxExpectationSSCT('A', 'B', 'C', 'D', 'Q', 'R', 'x0', 'P0', 'u', 'time'),
mxFitFunctionML(),
mxData(y, 'raw'))

oscr <- mxRun(osc)

#-----
# Results Examination

summary(oscr)

(ssFreqParam <- mxEval(sqrt(-A[2,1]), oscr))
freqParam

```



```
(ssMeasVar <- mxEval(R, oscr))
measVar

dampingParam <- 0
(ssDampingParam <- mxEval(-A[2,2], oscr))
dampingParam
```

mxFactor

Fail-safe Factors

Description

This is a wrapper for the R function [factor](#).

OpenMx requires ordinal data to be ordered. R's `factor` function doesn't enforce this, hence this wrapper exists to throw an error should you accidentally try and run with `ordered = FALSE`.

Also, the 'levels' parameter is optional in R's `factor` function. However, relying on the data to specify the data is foolhardy for the following reasons: The `factor` function will skip levels missing from the data: Specifying these in levels leaves the list of levels complete. Data will often not explore the min and max level that the user knows are possible. For these reasons this function forces you to write out all possible levels explicitly.

Usage

```
mxFactor(x = character(), levels, labels = levels,
         exclude = NA, ordered = TRUE, collapse = FALSE)
```

Arguments

<code>x</code>	either a vector of data or a <code>data.frame</code> object.
<code>levels</code>	a mandatory vector of the values that 'x' might have taken.
<code>labels</code>	<i>_either_</i> an optional vector of labels for the levels, <i>_or_</i> a character string of length 1.
<code>exclude</code>	a vector of values to be excluded from the set of levels.
<code>ordered</code>	logical flag to determine if the levels should be regarded as ordered (in the order given). Required to be TRUE.
<code>collapse</code>	logical flag to determine if duplicate labels should collapsed into a single level

Details

If 'x' is a `data.frame`, then all of the columns of 'x' are converted into ordered factors. If 'x' is a `data.frame`, then 'levels' and 'labels' may be either a list or a vector. When 'levels' is a list, then different levels are assigned to different columns of the constructed `data.frame` object. When 'levels' is a vector, then the same levels are assigned to all the columns of the `data.frame` object. The function will throw an error if 'ordered' is not TRUE or if 'levels' is missing. See [factor](#) for more information on creating ordered factors.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```
myVar <- c("s", "t", "a", "t", "i", "s", "t", "i", "c", "s")
ff <- mxFactor(myVar, levels=letters)
# Note: letters is a built in list of all lowercase letters of the alphabet
ff
# [1] s t a t i s t i c s
# Levels: a < b < c < d < e < f < g < h < i < j < k < l < m < n < o < p < q <
# r < s < t < u < v < w < x < y < z

as.integer(ff) # the internal codes

factor(ff)      # NOTE: drops the levels that do not occur.
                # mxFactor prevents you doing this unintentionally.

# This example works on a dataframe
foo <- data.frame(x=c(1:3),y=c(4:6),z=c(7:9))

# Applies one set of levels to all three columns
mxFactor(foo, c(1:9))

# Apply unique sets of levels to each variable
mxFactor(foo, list(c(1:3), c(4:6), c(7:9)))

mxFactor(foo, c(1:9), labels=c(1,1,1,2,2,2,3,3,3), collapse=TRUE)
```

mxFactorScores

Estimate factor scores and standard errors

Description

This function creates the factor scores and their standard errors under different methods for an MxModel object that has either a RAM or LISREL expectation.

Usage

```
mxFactorScores(model, type=c('ML', 'WeightedML', 'Regression'),
  minManifests=as.integer(NA))
```

Arguments

model	An MxModel object with either an MxExpectationLISREL or MxExpectationRAM
type	The type of factor scores to compute

minManifests Set scores to NA when there are less than minManifests non-NA manifest variables

Details

This is a helper function to compute or estimate factor scores along with their standard errors. The two maximum likelihood methods create a new model for each data row. They then estimate the factor scores as free parameters in a model with a single data row. For 'ML', the conditional likelihood of the data given the factor scores is optimized:

$$L(D|F)$$

. For 'WeightedML', the joint likelihood of the data and the factor scores is optimized:

$$L(D, F) = L(D|F)L(F)$$

. The WeightedML scores are akin to the empirical Bayes random effects estimates from mixed effects modeling. They display the same kind of shrinkage as random effects estimates, and for the same reason: they account for the latent variable distribution in their estimation.

In many cases, especially for ordinal data or missing data, the weighted ML scores are to be preferred over alternatives (Estabrook & Neale, 2013). For example, when using ordinal data, a person whose observations are all in the highest ordinal category theoretically has an 'ML' factor score of positive infinity. A similar situation arises for a person whose observations are all in the lowest ordinal category: their 'ML' factor score is theoretically negative infinity. Weighted ML factor scores in these cases remain reasonable.

For type='Regression', with LISREL expectation, factor scores are computed based on a simple formula. This formula is equivalent to the formula for the Kalman updated scores in a state space model with zero dynamics (Priestly & Subba Rao, 1975). Thus, to compute the regression factor scores, the appropriate state space model is set-up and the [mxKalmanScores](#) function is used to produce the factor scores and their standard errors. With RAM expectation, factor scores are predicted from the non-missing manifest variables for each row of the raw data, using a general linear prediction formula analytically equivalent to that used with LISREL expectation. The standard errors for regression-predicted RAM factor scores are the square roots of the indeterminate variances of the latent variables, given the data row's missing-data pattern and the values of any relevant definition variables. The RAM and LISREL methods for computing regression factor scores with their standard errors are analytically identical. They produce the same score and standard error estimates.

If you have missing data then you must specify minManifests. This option will set scores to NA when there are too few items to make an accurate score estimate. If you are using the scores as point estimates without considering the standard error then you should set minManifests as high as you can tolerate. This will increase the amount of missing data but scores will be more accurate. If you are carefully considering the standard errors of the scores then you can set minManifests to 0. When set to 0, all NA rows are scored to the prior distribution.

Note that for compatibility with [factanal](#), type='regression' is also acceptable.

Value

An array with dimensions (Number of Rows of Data, Number of Latent Variables, 2). The third dimension has the scores in the first slot and the standard errors in the second slot. The rows are in the order of the *unsorted* data. Multigroup models are an exception, in that the returned value is instead a list of such arrays, containing one per group.

References

Estabrook, R. & Neale, M. C. (2013). A Comparison of Factor Score Estimation Methods in the Presence of Missing Data: Reliability and an Application to Nicotine Dependence. *Multivariate Behavioral Research*, 48, 1-27.

Priestley, M. & Subba Rao, T. (1975). The estimation of factor scores and Kalman filtering for discrete parameter stationary processes. *International Journal of Control*, 21, 971-975.

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

[mxKalmanScores](#)

Examples

```
# Create and estimate a factor model
require(OpenMx)
data(demoOneFactor)
manifests <- names(demoOneFactor)
latents <- c("G")
factorModel <- mxModel("OneFactor",
                        type="LISREL",
                        manifestVars=list(exo=manifests),
                        latentVars=list(exo=latents),
                        mxPath(from=latents, to=manifests),
                        mxPath(from=manifests, arrows=2),
                        mxPath(from=latents, arrows=2, free=FALSE, values=1.0),
                        mxPath(from='one', to=manifests),
                        mxData(observed=cov(demoOneFactor), type="cov", numObs=500,
                              means = colMeans(demoOneFactor)))
summary(factorRun <- mxRun(factorModel))

# Swap in raw data in place of summary data
factorRun <- mxModel(factorRun, mxData(observed=demoOneFactor[1:50,], type="raw"))

# Estimate factor scores for the model
r1 <- mxFactorScores(factorRun, 'Regression')
```

mxFIMLObjective

DEPRECATED: Create MxFIMLObjective Object

Description

WARNING: Objective functions have been deprecated as of OpenMx 2.0.

Please use `mxExpectationNormal()` and `mxFitFunctionML()` instead. As a temporary workaround, `mxFIMLObjective` returns a list containing an `MxExpectationNormal` object and an `MxFitFunctionML` object.

All occurrences of

```
mxFIMLObjective(covariance, means, dimnames = NA, thresholds = NA, vector = FALSE, threshnames = dimnames)
```

Should be changed to

```
mxExpectationNormal(covariance, means, dimnames = NA, thresholds = NA, threshnames = dimnames)
mxFitFunctionML(vector = FALSE)
```

Arguments

<code>covariance</code>	A character string indicating the name of the expected covariance algebra.
<code>means</code>	A character string indicating the name of the expected means algebra.
<code>dimnames</code>	An optional character vector to be assigned to the <code>dimnames</code> of the covariance and means algebras.
<code>thresholds</code>	An optional character string indicating the name of the thresholds matrix.
<code>vector</code>	A logical value indicating whether the objective function result is the likelihood vector.
<code>threshnames</code>	An optional character vector to be assigned to the column names of the thresholds matrix.

Details

NOTE: THIS DESCRIPTION IS DEPRECATED. Please change to using [mxExpectationNormal](#) and [mxFitFunctionML](#) as shown in the example below.

Objective functions were functions for which free parameter values are chosen such that the value of the objective function is minimized. The `mxFIMLObjective` function used full-information maximum likelihood to provide maximum likelihood estimates of free parameters in the algebra defined by the 'covariance' and 'means' arguments. The 'covariance' argument takes an [MxAlgebra](#) object, which defines the expected covariance of an associated [MxData](#) object. The 'means' argument takes an [MxAlgebra](#) object, which defines the expected means of an associated [MxData](#) object. The 'dimnames' arguments takes an optional character vector. If this argument is not a single NA, then this vector is used to assign the `dimnames` of the means vector as well as the row and columns `dimnames` of the covariance matrix.

The 'vector' argument is either TRUE or FALSE, and determines whether the objective function returns a column vector of the likelihoods, or a single $-2 * (\log \text{likelihood})$ value.

`thresholds`: The name of the thresholds matrix. When needed (for modelling ordinal data), this matrix should be created using [mxMatrix\(\)](#). The thresholds matrix must have as many columns as there are ordinal variables in the model, and number of rows equal to one fewer than the maximum number of levels found in the ordinal variables. The starting values of this matrix must also be set to reasonable values. Fill each column with a set of ordered start thresholds, one for each level of this column's factor levels minus 1. These thresholds may be free if you wish them to be estimated, or fixed. The unused rows in each column, if any, can be set to any value including NA.

threshnames: A character vector consisting of the variables in the thresholds matrix, i.e., the names of ordinal variables in a model. This is necessary for OpenMx to map the thresholds matrix columns onto the variables in your data. If you set the `dimnames` of the columns in the thresholds matrix then `threshnames` is not needed.

Usage Notes: `dimnames` must be supplied where the matrices referenced by the covariance and means algebras are not themselves labeled. Failure to do so leads to an error noting that the covariance or means matrix associated with the FIML objective does not contain `dimnames`.

`mxFIMLObjective` evaluates with respect to an `MxData` object. The `MxData` object need not be referenced in the `mxFIMLObjective` function, but must be included in the `MxModel` object. `mxFIMLObjective` requires that the 'type' argument in the associated `MxData` object be equal to 'raw'. Missing values are permitted in the associated `MxData` object.

To evaluate, place `MxFIMLObjective` objects, the `mxData` object for which the expected covariance approximates, referenced `MxAlgebra` and `MxMatrix` objects, and optional `MxBounds` and `MxConstraint` objects in an `MxModel` object. This model may then be evaluated using the `mxRun` function.

The results of the optimization can be reported using the `summary` function, or accessed directly in the 'output' slot of the resulting model (i.e., `modelName$output`). Components of the output may be referenced using the `Extract` functionality.

Value

Returns a list containing an `MxExpectationNormal` object and an `MxFitFunctionML` object.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```
# Create and fit a model using mxMatrix, mxAlgebra, mxExpectationNormal, and mxFitFunctionML

library(OpenMx)

# Simulate some data

x=rnorm(1000, mean=0, sd=1)
y= 0.5*x + rnorm(1000, mean=0, sd=1)
tmpFrame <- data.frame(x, y)
tmpNames <- names(tmpFrame)

# Define the matrices

M <- mxMatrix(type = "Full", nrow = 1, ncol = 2, values=c(0,0),
              free=c(TRUE,TRUE), labels=c("Mx", "My"), name = "M")
S <- mxMatrix(type = "Full", nrow = 2, ncol = 2, values=c(1,0,0,1),
              free=c(TRUE,FALSE,FALSE,TRUE), labels=c("Vx", NA, NA, "Vy"), name = "S")
A <- mxMatrix(type = "Full", nrow = 2, ncol = 2, values=c(0,1,0,0),
              free=c(FALSE,TRUE,FALSE,FALSE), labels=c(NA, "b", NA, NA), name = "A")
I <- mxMatrix(type="Iden", nrow=2, ncol=2, name="I")
```

```

# Define the expectation

expCov <- mxAlgebra(solve(I-A) %*% S %*% t(solve(I-A)), name="expCov")
expFunction <- mxExpectationNormal(covariance="expCov", means="M", dimnames=tmpNames)

# Choose a fit function

fitFunction <- mxFitFunctionML()

# Define the model

tmpModel <- mxModel(model="exampleModel", M, S, A, I, expCov, expFunction, fitFunction,
                    mxData(observed=tmpFrame, type="raw"))

# Fit the model and print a summary

tmpModelOut <- mxRun(tmpModel)
summary(tmpModelOut)

```

MxFitFunction-class *MxFitFunction*

Description

This is an internal class and should not be used directly.

mxFitFunctionAlgebra *Create MxFitFunctionAlgebra Object*

Description

mxFitFunctionAlgebra returns an MxFitFunctionAlgebra object.

Usage

```

mxFitFunctionAlgebra(algebra, numObs = NA, numStats = NA, ..., gradient =
                    NA_character_, hessian = NA_character_, verbose = 0L, units="-2lnL")

```

Arguments

algebra	A character string indicating the name of an MxAlgebra or MxMatrix object to use for optimization.
numObs	(optional) An adjustment to the total number of observations in the model.
numStats	(optional) An adjustment to the total number of observed statistics in the model.

...	Not used. Forces remaining arguments to be specified by name.
gradient	(optional) A character string indicating the name of an MxAlgebra object.
hessian	(optional) A character string indicating the name of an MxAlgebra object.
verbose	(optional) An integer to increase the level of runtime log output.
units	(optional) The units of the fit statistic.

Details

If you want to fit a multigroup model, the preferred way is to use [mxFitFunctionMultigroup](#).

Fit functions are functions for which free parameter values are chosen such that the value of the objective function is minimized. While the other fit functions in OpenMx require an expectation function for the model, the [mxAlgebraObjective](#) function uses the referenced [MxAlgebra](#) or [MxMatrix](#) object as the function to be minimized.

If a model's fit function is an [mxFitFunctionAlgebra](#) objective function, then the referenced algebra in the objective function must return a 1 x 1 matrix (when using OpenMx's default optimizer). There is no restriction on the dimensions of an fit function that is not the primary, or 'topmost', objective function.

To evaluate an algebra fit function, place the following objects in a [MxModel](#) object: a [mxFitFunctionAlgebra](#), [MxAlgebra](#) and [MxMatrix](#) entities referenced by the [MxAlgebraObjective](#), and optional [MxBounds](#) and [MxConstraint](#) objects. This model may then be evaluated using the [mxRun](#) function. The results of the optimization may be obtained using the [mxEval](#) function on the name of the [MxAlgebra](#), after the model has been run.

First and second derivatives can be provided with the algebra fit function. The dimnames on the gradient and hessian [MxAlgebras](#) are matched against names of free variables. Names that do not match are ignored. The fit is assumed to be in deviance units (-2 log likelihood units). If you are working in log likelihood units, the -2 scaling factor is not applied automatically. You have to multiply by -2 yourself.

Value

Returns an [MxFitFunctionAlgebra](#) object. [MxFitFunctionAlgebra](#) objects should be included with models with referenced [MxAlgebra](#) and [MxMatrix](#) objects.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

Other fit functions: [mxFitFunctionMultigroup](#), [mxFitFunctionML](#), [mxFitFunctionWLS](#), [mxFitFunctionGREML](#), [mxFitFunctionR](#), [mxFitFunctionRow](#)

To create an algebra suitable as a reference function to be minimized see: [mxAlgebra](#)

More information about the OpenMx package may be found [here](#).

Examples

```
# Create and fit a very simple model that adds two numbers using mxFitFunctionAlgebra

library(OpenMx)

# Create a matrix 'A' with no free parameters
A <- mxMatrix('Full', nrow = 1, ncol = 1, values = 1, name = 'A')

# Create an algebra 'B', which defines the expression A + A
B <- mxAlgebra(A + A, name = 'B')

# Define the objective function for algebra 'B'
objective <- mxFitFunctionAlgebra('B')

# Place the algebra, its associated matrix and
# its objective function in a model
tmpModel <- mxModel(model="Addition", A, B, objective)

# Evaluate the algebra
tmpModelOut <- mxRun(tmpModel)

# View the results
tmpModelOut$output$minimum
```

mxFitFunctionGREML *Create MxFitFunctionGREML Object*

Description

This function creates a new [MxFitFunctionGREML](#) object.

Usage

```
mxFitFunctionGREML(dV=character(0), aug=character(0),
  augGrad=character(0), augHess=character(0))
```

Arguments

dV Vector of character strings; defaults to a character vector of length zero. If a value of non-zero length is provided, it must be a *named* character vector. This vector's names must be the labels of each free parameter in the model. The vector's elements (i.e., the character strings themselves) must be the names of [MxAlgebra](#) or [MxMatrix](#) object(s), each of which equals the first partial derivative of the 'V' matrix with respect to the corresponding free parameter.

aug	Character string; defaults to a character vector of length zero. Any elements after the first are ignored. The string should name a 1x1 <code>MxMatrix</code> or an <code>MxAlgebra</code> that evaluates to a 1x1 matrix. The named object will be used as an "augmentation" to the GREML fitfunction—specifically, the [1,1] value of the object named by <code>aug</code> will be added to the GREML fitfunction value at each function evaluation during optimization. The augmentation can be used to regularize estimation with a prior likelihood, or to use penalty functions to approximate constraints.
augGrad	Character string; defaults to a character vector of length zero. Any elements after the first are ignored. The string should name a <code>MxMatrix</code> or an <code>MxAlgebra</code> that evaluates to the gradient of <code>aug</code> with respect to free parameters. The gradient can be either a column or row vector. The free parameters corresponding to the elements of the gradient vector are taken from the names of argument <code>dV</code> , e.g. if the third name of <code>dV</code> is 'va', then the third element of the gradient vector should be the first partial derivative of the augmentation function with respect to 'va'. Ignored unless both <code>dV</code> and <code>aug</code> have nonzero length.
augHess	Character string; defaults to a character vector of length zero. Any elements after the first are ignored. The string should name a <code>MxMatrix</code> or an <code>MxAlgebra</code> that evaluates to the Hessian of <code>aug</code> with respect to free parameters. The free parameters corresponding to each row and column of this matrix are dictated by the names of argument <code>dV</code> , in the same manner as for the elements of <code>augGrad</code> . Ignored unless both <code>dV</code> and <code>aug</code> have nonzero length. Providing a nonzero-length value for <code>augHess</code> but not <code>augGrad</code> will result in an error at runtime.

Details

Making effective use of arguments `dV`, `augGrad`, and `augHess` will usually require a custom `mxComputeSequence()`. The derivatives of the REML loglikelihood function with respect to parameters can be internally computed from the derivatives of the 'V' matrix supplied via `dV`. These loglikelihood derivatives will be valid as long as (1) the derivatives of 'V' evaluate to symmetric matrices the same size as 'V,' and (2) the model contains no `MxConstraints`. Internally, the derivatives of the 'V' matrix are assumed to be symmetric, and the elements above their main diagonals are ignored.

Currently, if any derivatives are provided via `dV`, then derivatives must be provided for *every* free parameter in the `MxModel`.

Argument `aug` is intended to allow users to provide penalty functions or prior likelihoods in order to approximate constraints or to regularize optimization. The user is warned that careless use of this augmentation feature may undermine the validity of his/her statistical inferences.

Value

Returns a new object of class `MxFitFunctionGREML`.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

See `MxFitFunctionGREML` for the S4 class created by `mxFitFunctionGREML()`. For more information generally concerning GREML analyses, including a complete example, see `mxExpectationGREML()`.

Other fit functions: [mxFitFunctionMultigroup](#), [mxFitFunctionML](#), [mxFitFunctionWLS](#), [mxFitFunctionAlgebra](#), [mxFitFunctionR](#), [mxFitFunctionRow](#)

More information about the OpenMx package may be found [here](#).

Examples

```
gff <- mxFitFunctionGREML()
str(gff)
```

```
MxFitFunctionGREML-class
      Class "MxFitFunctionGREML"
```

Description

MxFitFunctionGREML is the fitfunction class for GREML analyses.

Objects from the Class

Objects can be created by calls of the form `mxFitFunctionGREML(dV)`.

Slots

dV: Object of class "MxCharOrNumber". Identifies the [MxAlgebra](#) or [MxMatrix](#) object(s) to serve as the derivatives of 'V' with respect to free parameters.

dVnames: Vector of character strings; names of the free parameters corresponding to slot dV.

MLfit: Object of class "numeric", equal to the maximum-likelihood fitfunction value (as opposed to the restricted maximum-likelihood value).

numObs: Object of class "integer". Number of observations.

aug: Object of class "MxCharOrNumber". Identifies the [MxAlgebra](#) or [MxMatrix](#) object used to "augment" the fitfunction value at each function evaluation during optimization.

augGrad: Object of class "MxCharOrNumber". Identifies the [MxAlgebra](#) or [MxMatrix](#) object(s) to serve as the first derivatives of aug with respect to free parameters.

augHess: Object of class "MxCharOrNumber". Identifies the [MxAlgebra](#) or [MxMatrix](#) object(s) to serve as the second derivatives of aug with respect to free parameters.

info: Object of class "list".

dependencies: Object of class "integer".

expectation: Object of class "integer".

vector: Object of class "logical".

rowDiagnostics: Object of class "logical".

result: Object of class "matrix".

name: Object of class "character".

Extends

Class "MxBaseFitFunction", directly. Class "MxBaseNamed", by class "MxBaseFitFunction", distance 2. Class "MxFitFunction", by class "MxBaseFitFunction", distance 2.

Methods

No methods defined with class "MxFitFunctionGREML" in the signature.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

See [mxFitFunctionGREML\(\)](#) for creating MxFitFunctionGREML objects. See [mxExpectationGREML\(\)](#) for creating MxExpectationGREML objects, and for more information generally concerning GREML analyses, including a complete example. More information about the OpenMx package may be found [here](#).

Examples

```
showClass("MxFitFunctionGREML")
```

 mxFitFunctionML

Create MxFitFunctionML Object

Description

This function creates a new MxFitFunctionML object.

Usage

```
mxFitFunctionML(vector = FALSE, rowDiagnostics = FALSE, ..., fellner =
  as.logical(NA), verbose=0L, profileOut=c(),
  rowwiseParallel=as.logical(NA), jointConditionOn = c("auto", "ordinal", "continuous"))
```

Arguments

vector	A logical value indicating whether the objective function result is the likelihood vector.
rowDiagnostics	A logical value indicating whether the row-wise results of the objective function should be returned as an attribute of the fit function.
...	Not used. Forces remaining arguments to be specified by name.
fellner	Whether to fully expand the covariance matrix for maximum flexibility.
verbose	Level of diagnostic output

profileOut	Character vector naming constant coefficients to profile out of the likelihood (sometimes known as REML)
rowwiseParallel	For raw data only, whether to use OpenMP to parallelize the evaluation of rows
jointConditionOn	The evaluation strategy when both continuous and ordinal data are present.

Details

Fit functions are functions for which free parameter values are optimized such that the value of a cost function is minimized. The `mxFitFunctionML` function computes $-2 \times (\log \text{likelihood})$ of the data given the current values of the free parameters and the expectation function (e.g., `mxExpectationNormal` or `mxExpectationRAM`) selected for the model.

The 'vector' argument is either TRUE or FALSE, and determines whether the objective function returns a column vector of the likelihoods, or a single $-2 \times (\log \text{likelihood})$ value.

The 'rowDiagnostics' argument is either TRUE or FALSE, and determines whether the row likelihoods are returned as an attribute of the fit function. It is sometimes useful to inspect the likelihoods for outliers, diagnostics, or other anomalies.

When `vector=FALSE` and `rowDiagnostics=TRUE`, `fitfunction` can be referenced in the model and included in algebras as a scalar. The row likelihoods are an attribute of the fit function but are not accessible in the model during optimization. The row likelihoods are accessible to the user after the model has been run.

By default, `jointConditionOn='auto'` and a heuristic will be used to select the fastest algorithm. Conditioning the continuous data on ordinal will be superior when there are relatively few unique ordinal patterns. Otherwise, conditioning the ordinal data on continuous will perform better when there are relatively many ordinal patterns.

Usage Notes:

The results of the optimization can be reported using the `summary` function, or accessed directly in the 'output' slot of the resulting model (i.e., `modelName$output`). Components of the output may be referenced using the `Extract` functionality.

Value

Returns a new `MxFitFunctionML` object. One and only one `MxFitFunctionML` object should be included in each model along with an associated `mxExpectationNormal` or `mxExpectationRAM` object.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

Other fit functions: `mxFitFunctionMultigroup`, `mxFitFunctionWLS`, `mxFitFunctionAlgebra`, `mxFitFunctionGREML`, `mxFitFunctionR`, `mxFitFunctionRow`

More information about the OpenMx package may be found [here](#).

Examples

```

# Create and fit a model using mxMatrix, mxAlgebra, mxExpectationNormal, and mxFitFunctionML

library(OpenMx)

# Simulate some data

x=rnorm(1000, mean=0, sd=1)
y= 0.5*x + rnorm(1000, mean=0, sd=1)
tmpFrame <- data.frame(x, y)
tmpNames <- names(tmpFrame)

# Define the matrices

M <- mxMatrix(type = "Full", nrow = 1, ncol = 2, values=c(0,0),
              free=c(TRUE,TRUE), labels=c("Mx", "My"), name = "M")
S <- mxMatrix(type = "Full", nrow = 2, ncol = 2, values=c(1,0,0,1),
              free=c(TRUE,FALSE,FALSE,TRUE), labels=c("Vx", NA, NA, "Vy"), name = "S")
A <- mxMatrix(type = "Full", nrow = 2, ncol = 2, values=c(0,1,0,0),
              free=c(FALSE,TRUE,FALSE,FALSE), labels=c(NA, "b", NA, NA), name = "A")
I <- mxMatrix(type="Iden", nrow=2, ncol=2, name="I")

# Define the expectation

expCov <- mxAlgebra(solve(I-A) %*% S %*% t(solve(I-A)), name="expCov")
expFunction <- mxExpectationNormal(covariance="expCov", means="M", dimnames=tmpNames)

# Choose a fit function

fitFunction <- mxFitFunctionML(rowDiagnostics=TRUE)
# also return row likelihoods, even though the fit function
# value is still 1x1

# Define the model

tmpModel <- mxModel(model="exampleModel", M, S, A, I, expCov, expFunction, fitFunction,
                    mxData(observed=tmpFrame, type="raw"))

# Fit the model and print a summary

tmpModelOut <- mxRun(tmpModel)
summary(tmpModelOut)

fitResOnly <- mxEval(fitfunction, tmpModelOut)
attributes(fitResOnly) <- NULL
fitResOnly

# Look at the row likelihoods alone
fitLikeOnly <- attr(mxEval(fitfunction, tmpModelOut), 'likelihoods')
head(fitLikeOnly)

```

 mxFitFunctionMultigroup

Create MxFitFunctionMultigroup object

Description

The fit function used to fit a multiple group model

Usage

```
mxFitFunctionMultigroup(groups, ..., verbose = 0L)
```

Arguments

groups	vector of fit function names (strings)
...	Not used. Forces subsequent arguments to be specified by name.
verbose	the level of debugging output

Details

The `mxFitFunctionMultigroup` creates a fit function consisting of the sum of the fit statistics from a list of submodels provided. Thus, it aggregates fit statistics from multiple submodels.

This is conceptually similar to creating an `mxAlgebra` consisting of the sum of the `subModel` objectives and also creating an `mxFitFunctionAlgebra` to optimize the model based on this aggregate value.

This call to `mxFitFunctionMultigroup`:

```
mxFitFunctionMultigroup(c("model1", "model2"))
```

then, is almost equivalent to the following pair of statements:

```
mxAlgebra(model1.objective + model2.objective, name="myAlgebra")
```

```
mxFitFunctionAlgebra("myAlgebra")
```

The preferred method of specifying such a fit function is with this multigroup fit function, not the algebra fit function.

In addition to being more compact and readable, using `mxFitFunctionMultigroup` has additional side effects which are valuable for multi-group modeling.

Firstly, it aggregates analytic derivative calculations. Secondly, it allows `mxRefModels` to compute saturated models for raw data, as this function can learn which are the constituent submodels. Thirdly, it allows `mxCheckIdentification` to evaluate the local identification of the multigroup model.

Note: You can refer to the algebra generated by `mxFitFunctionMultigroup` when used in a group "modelName" as:

```
modelName.fitfunction
```

See Also

Other fit functions: [mxFitFunctionML](#), [mxFitFunctionWLS](#), [mxFitFunctionAlgebra](#), [mxFitFunctionGREML](#), [mxFitFunctionR](#), [mxFitFunctionRow](#)

More information about the OpenMx package may be found [here](#).

Examples

```
#-----
# Brief non-running example
require("OpenMx")
mxFitFunctionMultigroup(c("model1", "model2")) # names of sub-models to be jointly optimised

#-----
# Longer, fully featured, running example
#
#
# Create and fit a model using mxMatrix, mxExpectationRAM, mxFitFunctionML,
# and mxFitFunctionMultigroup.
# The model is multiple group regression.
# Only the residual variances are allowed to differ across groups.

library(OpenMx)

# Simulate some data

# Group 1
N1=100
x=rnorm(N1, mean=0, sd=1)
y= 0.5*x + rnorm(N1, mean=0, sd=1)
ds1 <- data.frame(x, y)
dsNames <- names(ds1)

# Group 2
N2=150
x=rnorm(N2, mean=0, sd=1)
y= 0.5*x + rnorm(N2, mean=0, sd=sqrt(1.5))
ds2 <- data.frame(x, y)

# Define the matrices
M <- mxMatrix(type = "Full", nrow = 1, ncol = 2, values=0,
              free=TRUE, labels=c("Mx", "My"), name = "M")
S1 <- mxMatrix(type = "Diag", nrow = 2, ncol = 2, values=1,
              free=TRUE, labels=c("Vx", "ResidVy1"), name = "S")
S2 <- mxMatrix(type = "Diag", nrow = 2, ncol = 2, values=1,
              free=TRUE, labels=c("Vx", "ResidVy2"), name = "S")
A <- mxMatrix(type = "Full", nrow = 2, ncol = 2, values=c(0,1,0,0),
              free=c(FALSE,TRUE,FALSE,FALSE), labels=c(NA, "b", NA, NA),
              name = "A")
I <- mxMatrix(type="Iden", nrow=2, ncol=2, name="I")
```



```

# Define the expectation
expect <- mxExpectationRAM('A', 'S', 'I', 'M', dimnames=dsNames)

# Choose a fit function
fitFunction <- mxFitFunctionML(rowDiagnostics=TRUE)
# also return row likelihoods, even though the fit function
# value is still 1x1

# Multiple group fit function sums the model likelihoods
# from its component models
mgFitFun <- mxFitFunctionMultigroup(c('g1model', 'g2model'))

# Define the models
m1 <- mxModel(model="g1model", M, S1, A, I, expect, fitFunction,
              mxData(observed=cov(ds1), type="cov", numObs=nrow(ds1),
                    means=colMeans(ds1)))
m2 <- mxModel(model="g2model", M, S2, A, I, expect, fitFunction,
              mxData(observed=cov(ds2), type="cov", numObs=nrow(ds2),
                    means=colMeans(ds2)))
mg <- mxModel(model='multipleGroup', m1, m2, mgFitFun)

# Fit the model and print a summary

mgOut <- mxRun(mg)

# Look at summary of model
summary(mgOut)

# Examine fit function results
fitResOnly <- mxEval(fitfunction, mgOut)
( g1Fit <- mxEval(g1model.fitfunction, mgOut) )
( g2Fit <- mxEval(g2model.fitfunction, mgOut) )

```

mxFitFunctionR

Create MxFitFunctionR Object

Description

mxFitFunctionR returns an MxFitFunctionR object.

Usage

```
mxFitFunctionR(fitfun, ..., units="-2lnL")
```

Arguments

fitfun	A function that accepts two arguments.
...	The initial state information to the objective function.
units	(optional) The units of the fit statistic.

Details

The `mxFitFunctionR` function evaluates a user-defined R function called the 'fitfun'. `mxFitFunctionR` is useful in defining new `mxFitFunctions`, since any calculation that can be performed in R can be treated as an `mxFitFunction`.

The 'fitfun' argument must be a function that accepts two arguments. The first argument is the `mxModel` that should be evaluated, and the second argument is some persistent state information that can be stored between one iteration of optimization to the next iteration. It is valid for the function to simply ignore the second argument.

The function must return either a single numeric value, or a list of exactly two elements. If the function returns a list, the first argument must be a single numeric value and the second element will be the new persistent state information to be passed into this function at the next iteration. The single numeric value will be used by the optimizer to perform optimization.

The initial default value for the persistent state information is NA.

Throwing an exception (via `stop`) from inside `fitfun` may result in unpredictable behavior. You may want to wrap your code in `tryCatch` while experimenting.

`fitfun` should not call R functions that use OpenMx's compiled backend, including (but not limited to) `omxMnor()`, because doing so can crash R.

Value

Returns an `MxFitFunctionR` object.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

Other fit functions: [mxFitFunctionMultigroup](#), [mxFitFunctionML](#), [mxFitFunctionWLS](#), [mxFitFunctionAlgebra](#), [mxFitFunctionGREML](#), [mxFitFunctionRow](#)

More information about the OpenMx package may be found [here](#).

Examples

```
# Create and fit a model using mxFitFunctionR

library(OpenMx)

A <- mxMatrix(nrow = 2, ncol = 2, values = c(1:4), free = TRUE, name = 'A')
squared <- function(x) { x ^ 2 }
```

```

# Define the objective function in R

objFunction <- function(model, state) {
  values <- model$A$values
  return(squared(values[1,1] - 4) + squared(values[1,2] - 3) +
         squared(values[2,1] - 2) + squared(values[2,2] - 1))
}

# Define the expectation function

fitFunction <- mxFitFunctionR(objFunction)

# Define the model

tmpModel <- mxModel(model="exampleModel", A, fitFunction)

# Fit the model and print a summary

tmpModelOut <- mxRun(tmpModel)
summary(tmpModelOut)

```

mxFitFunctionRow

Create an MxFitFunctionRow Object

Description

mxFitFunctionRow returns an MxFitFunctionRow object.

Usage

```

mxFitFunctionRow(rowAlgebra, reduceAlgebra, dimnames,
  rowResults = "rowResults", filteredDataRow = "filteredDataRow",
  existenceVector = "existenceVector", units="-2lnL")

```

Arguments

rowAlgebra	A character string indicating the name of the algebra to be evaluated row-wise.
reduceAlgebra	A character string indicating the name of the algebra that collapses the row results into a single number which is then optimized.
dimnames	A character vector of names corresponding to columns be extracted from the data set.
rowResults	The name of the auto-generated "rowResults" matrix. See details.
filteredDataRow	The name of the auto-generated "filteredDataRow" matrix. See details.
existenceVector	The name of the auto-generated "existenceVector" matrix. See details.
units	(optional) The units of the fit statistic.

Details

Fit functions are functions for which free parameter values are optimized such that the value of a cost function is minimized. The `mxFitFunctionRow` function evaluates a user-defined `MxAlgebra` object called the 'rowAlgebra' in a row-wise fashion. It then stores results of the row-wise evaluation in another `MxAlgebra` object called the 'rowResults'. Finally, the `mxFitFunctionRow` function collapses the row results into a single number which is then used for optimization. The `MxAlgebra` object named by the 'reduceAlgebra' collapses the row results into a single number.

The 'filteredDataRow' is populated in a row-by-row fashion with all the non-missing data from the current row. You cannot assume that the length of the filteredDataRow matrix remains constant (unless you have no missing data). The 'existenceVector' is populated in a row-by-row fashion with a value of 1.0 in column j if a non-missing value is present in the data set in column j, and a value of 0.0 otherwise. Use the functions `omxSelectRows`, `omxSelectCols`, and `omxSelectRowsAndCols` to shrink other matrices so that their dimensions will be conformable to the size of 'filteredDataRow'.

Value

Returns a new `MxFitFunctionRow` object. Only one `MxFitFunction` object should be included in each model. There is no need for an `MxExpectation` object when using `mxFitFunctionRow`.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

Other fit functions: `mxFitFunctionMultigroup`, `mxFitFunctionML`, `mxFitFunctionWLS`, `mxFitFunctionAlgebra`, `mxFitFunctionGREML`, `mxFitFunctionR`

More information about the OpenMx package may be found [here](#).

Examples

```
# Model that adds two data columns row-wise, then sums that column
# Notice no optimization is performed here.
```

```
library(OpenMx)

xdat <- data.frame(a=rnorm(10), b=1:10) # Make data set
amod <- mxModel(model="example1",
  mxData(observed=xdat, type='raw'),
  mxAlgebra(sum(filteredDataRow), name = 'rowAlgebra'),
  mxAlgebra(sum(rowResults), name = 'reduceAlgebra'),
  mxFitFunctionRow(
    rowAlgebra='rowAlgebra',
    reduceAlgebra='reduceAlgebra',
    dimnames=c('a','b'))
)
amodOut <- mxRun(amod)
mxEval(rowResults, model=amodOut)
mxEval(reduceAlgebra, model=amodOut)
```

```

# Model that find the parameter that minimizes the sum of the
# squared difference between the parameter and a data row.

bmod <- mxModel(model="example2",
  mxData(observed=xdat, type='raw'),
  mxMatrix(values=.75, ncol=1, nrow=1, free=TRUE, name='B'),
  mxAlgebra((filteredDataRow - B) ^ 2, name='rowAlgebra'),
  mxAlgebra(sum(rowResults), name='reduceAlgebra'),
  mxFitFunctionRow(
    rowAlgebra='rowAlgebra',
    reduceAlgebra='reduceAlgebra',
    dimnames=c('a'))
)
bmodOut <- mxRun(bmod)
mxEval(B, model=bmodOut)
mxEval(reduceAlgebra, model=bmodOut)
mxEval(rowResults, model=bmodOut)

```

mxFitFunctionWLS	<i>Create MxFitFunctionWLS Object</i>
------------------	---------------------------------------

Description

This function creates a new MxFitFunctionWLS object.

Usage

```
mxFitFunctionWLS(weights = "ULS")
```

Arguments

weights Ignored. Uses weights from [mxData](#)

Details

Fit functions are functions for which free parameter values are optimized such that the value of a cost function is minimized. The `mxFitFunctionWLS` function computes the weighted least squares difference between the data and the model-implied expectations for the data based on the free parameters and the expectation function (e.g., [mxExpectationNormal](#) or [mxExpectationRAM](#)) selected for the model.

The 'weights' argument is ignored. Rather the weights are provided in the [mxData](#) object, often generated by the [mxDataWLS](#) function.

Usage Notes:

The results of the optimization can be reported using the [summary](#) function, or accessed directly in the 'output' slot of the resulting model (i.e., `modelName$output`). Components of the output may be referenced using the [Extract](#) functionality.

Value

Returns a new MxFitFunctionWLS object. One and only one MxFitFunctionWLS object should be included in each model along with an associated [mxExpectationNormal](#) or [mxExpectationRAM](#) object.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

Other fit functions: [mxFitFunctionMultigroup](#), [mxFitFunctionML](#), [mxFitFunctionAlgebra](#), [mxFitFunctionGREML](#), [mxFitFunctionR](#), [mxFitFunctionRow](#)

More information about the OpenMx package may be found [here](#).

Examples

```
# Create and fit a model using mxMatrix, mxAlgebra, mxExpectationNormal, and mxFitFunctionWLS

library(OpenMx)

# Simulate some data

x=rnorm(1000, mean=0, sd=1)
y= 0.5*x + rnorm(1000, mean=0, sd=1)
tmpFrame <- data.frame(x, y)
tmpNames <- names(tmpFrame)
wdata <- mxDataWLS(tmpFrame)

# Define the matrices

S <- mxMatrix(type = "Full", nrow = 2, ncol = 2, values=c(1,0,0,1),
              free=c(TRUE,FALSE,FALSE,TRUE), labels=c("Vx", NA, NA, "Vy"), name = "S")
A <- mxMatrix(type = "Full", nrow = 2, ncol = 2, values=c(0,1,0,0),
              free=c(FALSE,TRUE,FALSE,FALSE), labels=c(NA, "b", NA, NA), name = "A")
I <- mxMatrix(type="Iden", nrow=2, ncol=2, name="I")

# Define the expectation

expCov <- mxAlgebra(solve(I-A) %*% S %*% t(solve(I-A)), name="expCov")
expFunction <- mxExpectationNormal(covariance="expCov", dimnames=tmpNames)

# Choose a fit function

fitFunction <- mxFitFunctionWLS()

# Define the model

tmpModel <- mxModel(model="exampleModel", S, A, I, expCov, expFunction, fitFunction,
```

```

wdata)

# Fit the model and print a summary

tmpModelOut <- mxRun(tmpModel)
summary(tmpModelOut)

```

MxFlatModel-class *MxFlatModel*

Description

This is an internal class and should not be used.

mxGenerateData *Generate data based on an MxModel object*

Description

This function returns a new (simulated) data set based on the model-implied distribution provided.

Usage

```
mxGenerateData(model, nrows, returnModel=FALSE, use.miss = TRUE)
```

Arguments

model	A data.frame or MxModel object upon which the data are generated.
nrows	Numeric. The number of rows of data to generate.
returnModel	Logical. Return data.frames if FALSE or model populated with new data if TRUE.
use.miss	Logical. Whether to approximate the missingness pattern of the original data.

Details

When given a data.frame as a model, the model is assumed to be saturated multivariate Gaussian and the expected distribution is obtained using [mxDataWLS](#). In this case, the default number of rows is assumed to be the number of rows in the original data.frame, but any other number of rows can also be requested.

When given an MxModel, the model-implied means and covariance are extracted. It then generates data with the same mean and covariance. Data can be generated based on Normal ([mxExpectationNormal](#)), RAM ([mxExpectationRAM](#)), LISREL ([mxExpectationLISREL](#)), and state space ([mxExpectationStateSpace](#)) models.

Please note that this function samples data from the model-implied distribution(s); it does not sample from the data object in the model. That is, this function generates new data rather than pulling data that already exist from the model.

Thresholds and ordinal data are implemented by generating continuous data and then using `cut` and `mxFactor` to break the continuous data at the thresholds into an ordered factor.

If the model has definition variables, then a data set must be included in the model object and the number of rows requested must match the number of rows in the model data. In this case the means, covariance, and thresholds are reevaluated for each row of data, potentially creating a different mean, covariance, and threshold structure for every generated row of data.

For state space models (i.e. models with an `mxExpectationStateSpace` or `mxExpectationStateSpaceContinuousTime` expectation), the data are generated based on the autoregressive structure of the model. The rows of data in a state space model are not independent replicates of a stationary process. Rather, they are the result of a latent (possibly non-stationary) autoregressive process. For state space models different rows of data often correspond to different times. As alluded to above, data generation works for discrete time state space models and hybrid continuous-discrete time state space models. The latter have a continuous process that is measured as discrete times.

Value

A data.frame, list of data.frames, or model populated with the new data (depending on the `returnModel` parameter).

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```
#-----
# Create data based on state space model.
require(OpenMx)
nvar <- 5
varnames <- paste("x", 1:nvar, sep="")
ssModel <- mxModel(model="State Space Manual Example",
  mxMatrix("Full", 1, 1, TRUE, .3, name="A"),
  mxMatrix("Zero", 1, 1, name="B"),
  mxMatrix("Full", nvar, 1, TRUE, .6, name="C", dimnames=list(varnames, "F1")),
  mxMatrix("Zero", nvar, 1, name="D"),
  mxMatrix("Diag", 1, 1, FALSE, 1, name="Q"),
  mxMatrix("Diag", nvar, nvar, TRUE, .2, name="R"),
  mxMatrix("Zero", 1, 1, name="x0"),
  mxMatrix("Diag", 1, 1, FALSE, 1, name="P0"),
  mxMatrix("Zero", 1, 1, name="u"),
  mxExpectationStateSpace("A", "B", "C", "D", "Q", "R", "x0", "P0", "u"),
  mxFitFunctionML()
)

ssData <- mxGenerateData(ssModel, 200) # 200 time points
```



```

# Add simulated data to model
ssModel <- mxModel(ssModel, mxData(ssData, 'raw'))

# Fit model to simulated data
ssRun <- mxRun(ssModel)

# Compare parameters estimated from random data to
# their true generating values
cbind(Rand = omxGetParameters(ssRun), Gen = omxGetParameters(ssModel))
# Note the parameters should be "close" (up to sampling error)
# to the generating values

#-----
require(OpenMx)
manifests <- paste("x", 1:5, sep="")
latents <- c("G")
factorModel <- mxModel("One Factor",
  type="RAM",
  manifestVars = manifests,
  latentVars = latents,
  mxPath(from=latents, to=manifests, values=.8),
  mxPath(from=manifests, arrows=2, values=.2),
  mxPath(from=latents, arrows=2,
    free=FALSE, values=1.0),
  mxPath(from = 'one', to = manifests))

factorData <- mxGenerateData(factorModel, 100)

factorModel <- mxModel(factorModel,
  mxData(observed=cov(factorData), type="cov",
    numObs=nrow(factorData),
    means = colMeans(factorData)))
factorRun <- mxRun(factorModel)
cbind(Rand=omxGetParameters(factorRun), Gen=omxGetParameters(factorModel))

```

mxGetExpected

Extract the component from a model's expectation

Description

This function extracts the expected means, covariance, or thresholds from a model.

Usage

```

mxGetExpected(model, component, defvar.row=1, subname=model$name)
imxGetExpectationComponent(model, component, defvar.row=1, subname=model$name)

```

Arguments

model	MxModel object from which to extract the expectation component.
component	A character. The name of the component to extract.
defvar.row	A row index. Which row to load for definition variables.
subname	Name of the submodel to evaluate.

Details

The expected means, covariance, or thresholds can be extracted from Normal ([mxExpectationNormal](#)), RAM ([mxExpectationRAM](#)), and LISREL ([mxExpectationLISREL](#)) models. When more than one component is requested, the components will be returned as a list.

If component 'vector' is requested then the non-redundent coefficients of the expected manifest distribution will be returned as a vector.

If component 'standVector' is requested then the same parameter structure as 'vector' is returned, but it is standardized. For Normal expectations the covariances are returned as correlations, the means are returned as zeros, and the thresholds are returned as z-scores. For the thresholds the z-scores are computed by using the model-implied means and variances.

Note that capitalization is ignored for the 'standVector' option, so 'standvector' is also acceptable.

Value

See details.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```
#-----
require(OpenMx)
manifests <- paste("x", 1:5, sep="")
latents <- c("G")
factorModel <- mxModel("One Factor",
  type="RAM",
  manifestVars = manifests,
  latentVars = latents,
  mxPath(from=latents, to=manifests),
  mxPath(from=manifests, arrows=2),
  mxPath(from=latents, arrows=2,
    free=FALSE, values=1.0),
  mxPath(from = 'one', to = manifests))

mxGetExpected(factorModel, "covariance")
# oops. Starting values indicate a zero covariance matrix.
# Probably should adjust them.
```

 mxGREMLDataHandler *Helper Function for Structuring GREML Data*

Description

This function takes a dataframe or matrix and uses it to setup the 'y' and 'X' matrices for a GREML analysis; this includes trimming out NAs from 'X' and 'y.' The result is a matrix the first column of which is the 'y' vector, and the remaining columns of which constitute 'X.'

Usage

```
mxGREMLDataHandler(data, yvars=character(0), Xvars=list(), addOnes=TRUE,
                    blockByPheno=TRUE, staggerZeroes=TRUE)
```

Arguments

data	Either a dataframe or matrix, with column names, containing the variables to be used as phenotypes and covariates in 'y' and 'X,' respectively.
yvars	Character vector. Each string names a column of the raw dataset, to be used as a phenotype.
Xvars	A list of data column names, specifying the covariates to be used with each phenotype. The list should have the same length as argument yvars.
addOnes	Logical; should lead columns of ones (for the regression intercepts) be adhered to the covariates when assembling the 'X' matrix? Defaults to TRUE.
blockByPheno	Logical; relevant to polyphenotype analyses. If TRUE (default), then the resulting 'y' will contain phenotype #1 for individuals 1 thru <i>n</i> , phenotype #2 for individuals 1 thru <i>n</i> , ... If FALSE, then observations are "blocked by individual", and the resulting 'y' will contain individual #1's scores on phenotypes 1 thru <i>p</i> , individual #2's scores on phenotypes 1 thru <i>p</i> , ... Note that in either case, 'X' will be structured appropriately for 'y.'
staggerZeroes	Logical; relevant to polyphenotype analyses. If TRUE (default), then each phenotype's covariates in 'X' are "staggered," and 'X' is padded out with zeroes. If FALSE, then 'X' is formed simply by stacking the phenotypes' covariates; this requires each phenotype to have the same number of covariates (i.e., each character vector in Xvars must be of the same length). The default (TRUE) is intended for instances where the multiple phenotypes truly are different variables, whereas staggerZeroes=FALSE is intended for instances where the multiple "phenotypes" actually represent multiple observations on the same variable. One example of the latter case is longitudinal data where the multiple "phenotypes" are repeated measures on a single phenotype.

Details

For a monophenotype analysis (only), argument Xdata can be a character vector. In a polyphenotype analysis, if the same covariates are to be used with all phenotypes, then Xdata can be a list of length 1.

Note the synergy between the output of `mxGREMLDataHandler()` and arguments `dataset.is.yX` and `casesToDropFromV` to `mxExpectationGREML()`.

If the dataframe or matrix supplied for argument `data` has n rows, and argument `yvars` is of length p , then the resulting 'y' and 'X' matrices will have np rows. Then, if either matrix contains any NA's, the rows containing the NA's are trimmed from both 'X' and 'y' before being returned in the output (in which case they will obviously have fewer than np rows). Function `mxGREMLDataHandler()` reports which rows of the full-size 'X' and 'y' were trimmed out due to missing observations. These row indices can be provided as argument `casesToDropFromV` to `mxExpectationGREML()`.

Value

A list with these two components:

<code>yX</code>	Numeric matrix. The first column is the phenotype vector, 'y,' while the remaining columns constitute the 'X' matrix of covariates. If this matrix is used as the raw dataset for a model, then the model's GREML expectation can be constructed with <code>dataset.is.yX=TRUE</code> in <code>mxExpectationGREML()</code> .
<code>casesToDrop</code>	Numeric vector. Contains the indices of the rows of the 'y' and 'X' that were dropped due to containing NA's. Can be provided as argument <code>casesToDropFromV</code> to <code>mxExpectationGREML()</code> .

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

For more information generally concerning GREML analyses, including a complete example, see `mxExpectationGREML()`. More information about the OpenMx package may be found [here](#).

Examples

```
dat <- cbind(rnorm(100),rep(1,100))
colnames(dat) <- c("y","x")
dat[42,1] <- NA
dat[57,2] <- NA
dat2 <- mxGREMLDataHandler(data=dat, yvars="y", Xvars=list("x"),
  addOnes = FALSE)
str(dat2)
```

MxInterval-class

MxInterval

Description

This is an internal class and should not be used directly.

See Also

[mxCI](#)

mxKalmanScores	<i>Estimate Kalman scores and error covariance matrices</i>
----------------	-------------------------------------------------------------

Description

This function creates the Kalman predicted, Kalman updated, and Rauch-Tung-Striebel smoothed latent state and error covariance estimates for an MxModel object that has an MxExpectationStateSpace object.

Usage

```
mxKalmanScores(model, data=NA, frontend=TRUE)
```

Arguments

model	An MxModel object with an MxExpectationStateSpace.
data	An optional data.frame or matrix.
frontend	When TRUE, compute score in the frontend, otherwise use the backend.

Details

This is a helper function that computes the results of the classical Kalman filter. In particular, for every row of data there is a predicted latent score, an error covariance matrix for the predicted latent scores that provides an estimate of the predictions precision, an updated latent score, and an updated error covariance matrix for the updated lated scores. Additionally, the Rauch-Tung-Striebel (RTS) smoothed latent scores and error covariance matrices are returned.

Value

A list with components xPredicted, PPredicted, xUpdated, PUpdated, xSmoothed, PSmoothed, m2ll, and L. When using backend scores, this list also has components for yPredicted and SPredicted which have the same number of time points as the other components but relate to the observed variables instead of the latent variables. The rows of xPredicted, xUpdated, and xSmoothed correspond to different time points. The columns are the different latent variables. The third index of PPredicted, PUpdated, and PSmoothed corresponds to different times. This works nicely with the R default print method for arrays. At each time there is a covariance matrix of the latent variable scores. For all items listed below, the first element goes with the zeroth time point (See example).

xPredicted matrix of Kalman predicted scores
PPredicted array of Kalman predicted error covariances
xUpdated matrix of Kalman updated scores
PUpdated array of Kalman updated error covariances
xSmoothed matrix of RTS smoothed scores
PSmoothed array of RTS smoothed error covariances
m2ll minus 2 log likelihood

L likelihood, i.e., the multivariate normal probability density

yPredicted matrix of Kalman predicted scores for the observed variables, i.e., the predicted means.
Only available for backend scores.

SPredicted array of Kalman predicted error covariances for the observed variables, i.e., the predicted covariances. Only available for backend scores.

References

J. Durbin and S.J. Koopman. (2001). *Time Series Analysis by State Space Methods*. Oxford University Press.

R.E. Kalman (1960). A New Approach to Linear Filtering and Prediction Problems. *Basic Engineering*, 82, 35-45.

H.E. Rauch, F. Tung, C.T. Striebel. (1965). Maximum Likelihood Estimates of Linear Dynamic Systems. *American Institute of Aeronautics and Astronautics Journal*, 3, 1445-1450.

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

[mxExpectationStateSpace](#)

Examples

```
# Create and fit a model using mxMatrix, mxExpectationStateSpace, and mxFitFunctionML
require(OpenMx)
data(demoOneFactor)
# Use only first 50 rows, for speed of example
data <- demoOneFactor[1:50,]
nvar <- ncol(demoOneFactor)
varnames <- colnames(demoOneFactor)
ssModel <- mxModel(model="State Space Manual Example",
  mxMatrix("Full", 1, 1, TRUE, .3, name="A"),
  mxMatrix("Zero", 1, 1, name="B"),
  mxMatrix("Full", nvar, 1, TRUE, .6, name="C", dimnames=list(varnames, "F1")),
  mxMatrix("Zero", nvar, 1, name="D"),
  mxMatrix("Diag", 1, 1, FALSE, 1, name="Q"),
  mxMatrix("Diag", nvar, nvar, TRUE, .2, name="R"),
  mxMatrix("Zero", 1, 1, name="x0"),
  mxMatrix("Diag", 1, 1, FALSE, 1, name="P0"),
  mxMatrix("Zero", 1, 1, name="u"),
  mxData(observed=data, type="raw"),
  mxExpectationStateSpace("A", "B", "C", "D", "Q", "R", "x0", "P0", "u"),
  mxFitFunctionML()
)
ssRun <- mxRun(ssModel)
summary(ssRun)
# Note the freely estimated Autoregressive parameter (A matrix)
# is near zero as it should be for the independent rows of data
# from the factor model.
```

```

ssScores <- mxKalmanScores(ssRun)

cor(cbind(ssScores$xPredicted[,1], ssScores$xUpdated[,1], ssScores$xSmoothed[,1]))
# Because the autoregressive dynamics are near zero, the predicted and updated scores
# correlate minimally, and the updated and smoothed latent state estimates
# are extremely close.

# The first few latent predicted scores
head(ssScores$xPredicted)

# The predicted latent score for time 10
ssScores$xPredicted[10+1,]

# The error covariance of the predicted score at time 10
ssScores$PPredicted[,10+1]

```

MxLISRELMModel-class *MxLISRELMModel*

Description

This is an internal class and should not be used directly.

mxLISRELObjective *Create MxLISRELObjective Object*

Description

This function creates a new MxLISRELObjective object.

Usage

```

mxLISRELObjective(LX=NA, LY=NA, BE=NA, GA=NA, PH=NA, PS=NA, TD=NA, TE=NA, TH=NA,
  TX = NA, TY = NA, KA = NA, AL = NA,
  dimnames = NA, thresholds = NA, vector = FALSE, threshnames = dimnames)

```

Arguments

LX	An optional character string indicating the name of the 'LX' matrix.
LY	An optional character string indicating the name of the 'LY' matrix.
BE	An optional character string indicating the name of the 'BE' matrix.
GA	An optional character string indicating the name of the 'GA' matrix.
PH	An optional character string indicating the name of the 'PH' matrix.
PS	An optional character string indicating the name of the 'PS' matrix.

TD	An optional character string indicating the name of the 'TD' matrix.
TE	An optional character string indicating the name of the 'TE' matrix.
TH	An optional character string indicating the name of the 'TH' matrix.
TX	An optional character string indicating the name of the 'TX' matrix.
TY	An optional character string indicating the name of the 'TY' matrix.
KA	An optional character string indicating the name of the 'KA' matrix.
AL	An optional character string indicating the name of the 'AL' matrix.
dimnames	An optional character vector that is currently ignored
thresholds	An optional character string indicating the name of the thresholds matrix.
vector	A logical value indicating whether the objective function result is the likelihood vector.
threshnames	An optional character vector to be assigned to the column names of the thresholds matrix.

Details

Objective functions are functions for which free parameter values are chosen such that the value of the objective function is minimized. The `mxLISRELObjective` provides maximum likelihood estimates of free parameters in a model of the covariance of a given `MxData` object. This model is defined by Linear Structural Relations (LISREL; Jöreskog & Sörbom, 1982, 1996). Arguments 'LX' through 'AL' must refer to `MxMatrix` objects with the associated properties of their respective matrices in the LISREL modeling approach.

The full LISREL specification has 13 matrices and is sometimes called the extended LISREL model. It is defined by the following equations.

$$\eta = \alpha + B\eta + \Gamma\xi + \zeta$$

$$y = \tau_y + \Lambda_y\eta + \epsilon$$

$$x = \tau_x + \Lambda_x\xi + \delta$$

The table below is provided as a quick reference to the numerous matrices in LISREL models. Note that NX is the number of manifest exogenous (independent) variables, the number of Xs. NY is the number of manifest endogenous (dependent) variables, the number of Ys. NK is the number of latent exogenous variables, the number of Ks or Xis. NE is the number of latent endogenous variables, the number of etas.

Matrix	Word	Abbreviation	Dimensions	Expression	Description
Λ_x	Lambda x	LX	NX x NK		Exogenous Factor Loading Matrix
Λ_y	Lambda y	LY	NY x NE		Endogenous Factor Loading Matrix
B	Beta	BE	NE x NE		Regressions of Latent Endogenous Variables Pre
Γ	Gamma	GA	NE x NK		Regressions of Latent Exogenous Variables Pred
Φ	Phi	PH	NK x NK	$\text{cov}(\xi)$	Covariance Matrix of Latent Exogenous Variable
Ψ	Psi	PS	NE x NE	$\text{cov}(\zeta)$	Residual Covariance Matrix of Latent Endogeno
Θ_δ	Theta delta	TD	NX x NX	$\text{cov}(\delta)$	Residual Covariance Matrix of Manifest Exogeno
Θ_ϵ	Theta epsilon	TE	NY x NY	$\text{cov}(\epsilon)$	Residual Covariance Matrix of Manifest Endogeno

$\Theta_{\delta\epsilon}$	Theta delta epsilon	TH	NX x NY	cov(δ, ϵ)	Residual Covariance Matrix of Manifest Exogenous Variables
τ_x	tau x	TX	NX x 1		Residual Means of Manifest Exogenous Variables
τ_y	tau y	TY	NY x 1		Residual Means of Manifest Endogenous Variables
κ	kappa	KA	NK x 1	mean(ξ)	Means of Latent Exogenous Variables
α	alpha	AL	NE x 1		Residual Means of Latent Endogenous Variables

From the extended LISREL model, several submodels can be defined. Subtypes of the LISREL model are defined by setting some of the arguments of the LISREL objective to NA. Note that because the default values of each LISREL matrix is NA, setting a matrix to NA can be accomplished by simply not giving it any other value.

The first submodel is the LISREL model without means.

$$\eta = B\eta + \Gamma\xi + \zeta$$

$$y = \Lambda_y\eta + \epsilon$$

$$x = \Lambda_x\xi + \delta$$

The LISREL model without means requires 9 matrices: LX, LY, BE, GA, PH, PS, TD, TE, and TH. Hence this LISREL model has TX, TY, KA, and AL as NA. This can be accomplished by leaving these matrices at their default values.

The TX, TY, KA, and AL matrices must be specified if either the mxData type is “cov” or “cor” and a means vector is provided, or if the mxData type is “raw”. Otherwise the TX, TY, KA, and AL matrices are ignored and the model without means is estimated.

A second submodel involves only endogenous variables.

$$\eta = B\eta + \zeta$$

$$y = \Lambda_y\eta + \epsilon$$

The endogenous-only LISREL model requires 4 matrices: LY, BE, PS, and TE. The LX, GA, PH, TD, and TH must be NA in this case. However, means can also be specified, allowing TY and AL if the data are raw or if observed means are provided.

Another submodel involves only exogenous variables.

$$x = \Lambda_x\xi + \delta$$

The exogenous-only model requires 3 matrices: LX, PH, and TD. The LY, BE, GA, PS, TE, and TH matrices must be NA. However, means can also be specified, allowing TX and KA if the data are raw or if observed means are provided.

The model that is run depends on the matrices that are not NA. If all 9 matrices are not NA, then the full model is run. If only the 4 endogenous matrices are not NA, then the endogenous-only model is run. If only the 3 exogenous matrices are not NA, then the exogenous-only model is run. If some endogenous and exogenous matrices are not NA, but not all of them, then appropriate errors are thrown. Means are included in the model whenever their matrices are provided.

The `MxMatrix` objects included as arguments may be of any type, but should have the properties described above. The `mxLISRELObjective` will not return an error for incorrect specification, but incorrect specification will likely lead to estimation problems or errors in the `mxRun` function.

Like the `mxRAMObjective`, the `mxLISRELObjective` evaluates with respect to an `MxData` object. The `MxData` object need not be referenced in the `mxLISRELObjective` function, but must be included in the `MxModel` object. `mxLISRELObjective` requires that the 'type' argument in the associated `MxData` object be equal to 'cov', 'cor', or 'raw'.

To evaluate, place `MxLISRELObjective` objects, the `mxData` object for which the expected covariance approximates, referenced `MxAlgebra` and `MxMatrix` objects, and optional `MxBounds` and `MxConstraint` objects in an `MxModel` object. This model may then be evaluated using the `mxRun` function. The results of the optimization can be found in the 'output' slot of the resulting model, and may be obtained using the `mxEval` function.

Value

Returns a new `MxLISRELObjective` object. `MxLISRELObjective` objects should be included with models with referenced `MxAlgebra`, `MxData` and `MxMatrix` objects.

References

Jöreskog, K. G. & Sörbom, D. (1996). LISREL 8: User's Reference Guide. Lincolnwood, IL: Scientific Software International.

Jöreskog, K. G. & Sörbom, D. (1982). Recent developments in structural equation modeling. *Journal of Marketing Research*, 19, 404-416.

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```
#####-----#####
##### Factor Model
mLX <- mxMatrix("Full", values=c(.5, .6, .8, rep(0, 6), .4, .7, .5),
  name="LX", nrow=6, ncol=2,
  free=c(TRUE,TRUE,TRUE,rep(FALSE, 6),TRUE,TRUE,TRUE))
mTD <- mxMatrix("Diag", values=c(rep(.2, 6)), name="TD", nrow=6, ncol=6,
  free=TRUE)
mPH <- mxMatrix("Symm", values=c(1, .3, 1), name="PH", nrow=2, ncol=2,
  free=c(FALSE, TRUE, FALSE))

# Create a LISREL objective with LX, TD, and PH matrix names
objective <- mxLISRELObjective(LX="LX", TD="TD", PH="PH")

testModel <- mxModel(model="testModel", mLX, mTD, mPH, objective)
```

MxListOrNull-class	<i>An optional list</i>
--------------------	-------------------------

Description

An optional list

mxMakeNames	<i>mxMakeNames</i>
-------------	--------------------

Description

Adjust a character vector so that it can be used as MxMatrix column or row names. OpenMx is (much) more restrictive than base R's `make.names`.

Usage

```
mxMakeNames(names, unique = FALSE)
```

Arguments

names	a character vector
unique	whether the pass the result through make.unique

See Also

[make.names](#)

Examples

```
demo <- c("", "103", "data", "foo.bar[3,2]", "+!", "!+")
mxMakeNames(demo, unique=TRUE)
```

mxMatrix

*Create MxMatrix Object***Description**

This function creates a new [MxMatrix](#) object.

Usage

```
mxMatrix(type = "Full", nrow = NA, ncol = NA,
         free = FALSE, values = NA, labels = NA, lbound = NA,
         ubound = NA, byrow = getOption('mxByrow'), dimnames = NA, name = NA,
         condenseSlots=getOption('mxCondenseMatrixSlots'),
         ..., joinKey=as.character(NA), joinModel=as.character(NA))
```

Arguments

type	A character string indicating the matrix type, where type indicates the range of values and equalities in the matrix. Must be one of: 'Diag', 'Full', 'Iden', 'Lower', 'Sdiag', 'Stand', 'Symm', 'Unit', or 'Zero'.
nrow	Integer; the desired number of rows. One or both of 'nrow' and 'ncol' is required when 'values', 'free', 'labels', 'lbound', and 'ubound' arguments are not matrices, depending on the desired MxMatrix type.
ncol	Integer; the desired number of columns. One or both of 'nrow' and 'ncol' is required when 'values', 'free', 'labels', 'lbound', and 'ubound' arguments are not matrices, depending on the desired MxMatrix type.
free	A vector or matrix of logicals for free parameter specification. A single 'TRUE' or 'FALSE' will set all allowable variables to free or fixed, respectively.
values	A vector or matrix of numeric starting values. By default, all values are set to zero.
labels	A vector or matrix of characters for variable label specification.
lbound	A vector or matrix of numeric lower bounds. Default bounds are specified with an NA.
ubound	A vector or matrix of numeric upper bounds. Default bounds are specified with an NA.
byrow	Logical; defaults to value of global option 'mxByRow'. If FALSE (default), the 'values', 'free', 'labels', 'lbound', and 'ubound' matrices are populated by column rather than by row.
dimnames	List. The dimnames attribute for the matrix: a list of length 2 giving the row and column names respectively. An empty list is treated as NULL, and a list of length one as row names. The list can be named, and the list names will be used as names for the dimensions.
name	An optional character string indicating the name of the MxMatrix object.

condenseSlots	Logical; defaults to value of global option 'mxBByRow' If TRUE, then the resulting MxMatrix will "condense" its 'labels', 'free', 'lbound', and 'ubound' down to 1x1 matrices if they contain only FALSE ('free') or NA (the other three). If FALSE, those four matrices and the 'values' matrix will all be of equal dimensions.
...	Not used. Forces remaining arguments to be specified by name.
joinKey	The name of the column in current model's raw data that is used as a foreign key to match against the primary key in joinModel's raw data.
joinModel	The name of the model that this matrix joins against.

Details

The `mxMatrix` function creates [MxMatrix](#) objects, which consist of five matrices and a 'type' argument. The 'values' matrix is made up of numeric elements whose usage and capabilities in other functions are defined by the 'free' matrix. If an element is specified as a fixed parameter in the 'free' matrix, then the element in the 'values' matrix is treated as a constant value and cannot be altered or updated by an objective function when included in an `mxRun` function. If an element is specified as a free parameter in the 'free' matrix, the element in the 'value' matrix is considered a starting value and can be changed by an objective function when included in an `mxRun` function.

Element labels beginning with 'data.' can be used if the [MxMatrix](#) is to be used in an [MxModel](#) object that has a raw dataset (i.e., an [MxData](#) object of type="raw"). Such a label instructs OpenMx to use a particular column of the raw dataset to fill in the value of that element. For historical reasons, the variable contained in that column is called a "definition variable." For example, if an [MxMatrix](#) element has the label 'data.x', then OpenMx will use the first value of the data column named "x" when evaluating the fitfunction for the first row, and will use the second value of column "x" when evaluating the fitfunction for the second row, and so on. After the call to `mxRun()`, the values for elements labeled with 'data.x' are returned as the value from the first (i.e., first before any automated sorting is done) element of column "x" in the data.

Objects created by the `mxMatrix()` function are of a specific 'type', which specifies the number and location of parameters in the 'labels' matrix and the starting values in the 'values' matrix. Input 'values', 'free', and 'labels' matrices must be of appropriate shape and have appropriate values for the matrix type requested. Nine types of matrices are supported:

'Diag'	matrices must be square, and only elements on the principal diagonal may be specified as free parameters or take no
'Full'	matrices may be either rectangular or square, and all elements in the matrix may be freely estimated. This type is th
'Iden'	matrices must be square, and consist of no free parameters. Matrices of this type have a value of 1 for all entries on
'Lower'	matrices must be square, with a value of 0 for all entries in the upper triangle and no free parameters in the upper tr
'Sdiag'	matrices must be square, with a value of 0 for all entries in the upper triangle and along the diagonal. No free paran
'Symm'	matrices must be square, and elements in the principle diagonal and lower triangular portion of the matrix may be f
'Stand'	matrices are symmetric matrices (see 'Symm') with 1's along the main diagonal.
'Unit'	matrices may be either rectangular or square, and contain no free parameters. All elements in matrices of this type
'Zero'	matrices may be either rectangular or square, and contain no free parameters. All elements in matrices of this type

When 'type' is 'Lower' or 'Symm', then the arguments to 'free', 'values', 'labels', 'lbound', or 'ubound' may be vectors of length $N * (N + 1) / 2$, where N is the number of rows and columns of the matrix. When 'type' is 'Sdiag' or 'Stand', then the arguments to 'free', 'values', 'labels',

‘lbound’, or ‘ubound’ may be vectors of length $N * (N - 1)/2$.

Value

Returns a new `MxMatrix` object, which consists of a ‘values’ matrix of numeric starting values, a ‘free’ matrix describing free parameter specification, a ‘labels’ matrix of labels for the variable names, and ‘lbound’ and ‘ubound’ matrices of the lower and upper parameter bounds. This `MxMatrix` object can be used as an argument in the `mxAlgebra()`, `mxBounds()`, `mxConstraint()` and `mxModel()` functions.

References

The OpenMx User’s guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

`MxMatrix` for the S4 class created by `mxMatrix`. More information about the OpenMx package may be found [here](#).

Examples

```
# Create a 3 x 3 identity matrix

idenMatrix <- mxMatrix(type = "Iden", nrow = 3,
  ncol = 3, name = "I")

# Create a full 4 x 2 matrix from existing
# value matrix with all free parameters

vals <- matrix(1:8, nrow = 4)
fullMatrix <- mxMatrix(type = "Full", values = vals,
  free = TRUE, name = "foo")

# Create a 3 x 3 symmetric matrix with free off-
# diagonal parameters and starting values

symmMatrix <- mxMatrix(type = "Symm", nrow = 3, ncol = 3,
  free = c(FALSE, TRUE, TRUE, FALSE, TRUE, FALSE),
  values = c(1, .8, .8, 1, .8, 1),
  labels = c(NA, "free1", "free2", NA, "free3", NA),
  name = "bar")

# Create an mxMatrix from a character matrix. All numbers are
# interpreted as fixed and non-numbers are interpreted as free
# parameters.

matrixFromChar <- function(inputm, name=NA) {
  inputmFixed <- suppressWarnings(matrix(
    as.numeric(inputm), nrow = nrow(inputm), ncol = ncol(inputm)))
  inputmCharacter <- inputm
  inputmCharacter[!is.na(inputmFixed)] <- NA
  mxMatrix(nrow=nrow(inputm), ncol=ncol(inputm),
```

```

        free=!is.na(inputmCharacter),
        values=inputmFixed,
        labels=inputmCharacter,
        dimnames=dimnames(inputm), name=name)
    }

# Demonstrate some of the behavior of the condensed slots
# Create a 3x3 matrix with condensed slots

a <- mxMatrix('Full', 3, 3, values=1, condenseSlots=TRUE)
a@free # at operator returns the stored 1x1 matrix
a$free # dollar operator constructs full matrix for printing

# assignment with the dollar operator
# de-condenses the slots to create the
# full 3x3 matrix
a$free[1,1] <- TRUE
a@free

```

MxMatrix-class

MxMatrix Class

Description

MxMatrix is a virtual S4 class that comprises the nine types of matrix objects used by OpenMx (see [mxMatrix\(\)](#) for details). An MxMatrix object is a [named entity](#). New instances of this class can be created using the function [mxMatrix\(\)](#). MxMatrix objects may be used as arguments in other functions from the OpenMx package, including [mxAlgebra\(\)](#), [mxConstraint\(\)](#), and [mxModel\(\)](#).

Objects from the Class

All nine types of object that the class comprises can be created via [mxMatrix\(\)](#).

Slots

name: Character string; the name of the MxMatrix object. Note that this is the object's "Mx name" (so to speak), which identifies it in OpenMx's internal namespace, rather than the symbol identifying it in R's workspace. Use of MxMatrix objects in an [mxAlgebra](#) or [mxConstraint](#) function requires reference by name.

values: Numeric matrix of values. If an element is specified as a fixed parameter in the 'free' matrix, then the element in the 'values' matrix is treated as a constant value and cannot be altered or updated by an objective function when included in an [mxRun\(\)](#) function. If an element is specified as a free parameter in the 'free' matrix, the element in the 'value' matrix is considered a starting value and can be changed by an objective function when included in an [mxRun\(\)](#) function.

- labels:** Matrix of character strings which provides the labels of free and fixed parameters. Fixed parameters with identical labels must have identical values. Free parameters with identical labels impose an equality constraint. The same label cannot be applied to a free parameter and a fixed parameter. A free parameter with the label 'NA' implies a unique free parameter, that cannot be constrained to equal any other free parameter.
- free:** Logical matrix specifying whether each element is free versus fixed. An element is a free parameter if-and-only-if the corresponding value in the 'free' matrix is 'TRUE'. Free parameters are elements of an MxMatrix object whose values may be changed by a fitfunction when that MxMatrix object is included in an MxModel object and evaluated using the `mxRun()` function.
- lbound:** Numeric matrix of lower bounds on free parameters.
- ubound:** Numeric matrix of upper bounds on free parameters.
- .squareBrackets:** Logical matrix; used internally by OpenMx. Identifies which elements have labels with square brackets in them.
- .persist:** Logical; used internally by OpenMx. Governs how `mxRun()` handles the MxMatrix object when it is inside the MxModel being run.
- .condenseSlots:** Logical; used internally by OpenMx. If FALSE, then the matrices in the 'values', 'labels', 'free', 'lbound', and 'ubound' slots are all of equal dimensions. If TRUE, then the last four of those slots will "condense" a matrix consisting entirely of FALSE or NA down to 1x1.
- display:** Character string; used internally by OpenMx when parsing MxAlgebras.
- dependencies:** Integer; used internally by OpenMx when parsing MxAlgebras.

Methods

```

$ signature(x = "MxMatrix"): ...
$<- signature(x = "MxMatrix"): ...
[ signature(x = "MxMatrix"): ...
[<- signature(x = "MxMatrix"): ...
dim signature(x = "MxMatrix"): ...
dimnames signature(x = "MxMatrix"): ...
dimnames<- signature(x = "MxMatrix"): ...
length signature(x = "MxMatrix"): ...
names signature(x = "MxMatrix"): ...
ncol signature(x = "MxMatrix"): ...
nrow signature(x = "MxMatrix"): ...
print signature(x = "MxMatrix"): ...
show signature(object = "MxMatrix"): ...

```

Note that some methods are documented separately (see below, under "See Also").

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

`mxMatrix()` for creating MxMatrix objects. Note that functions `imxCreateMatrix()`, `imxDeparse()`, `imxSquareMatrix()`, `imxSymmetricMatrix()`, and `imxVerifyMatrix()` are separately documented methods for this class. More information about the OpenMx package may be found [here](#).

Examples

```
showClass("MxMatrix")
```

 mxMI

Estimate Modification Indices for MxModel Objects

Description

This function estimates the change in fit function value resulting from freeing currently fixed parameters.

Usage

```
mxMI(model, matrices=NA, full=TRUE)
```

Arguments

<code>model</code>	An MxModel for which modification indices are desired.
<code>matrices</code>	Character vector. The names of the matrices in which to search for modification
<code>full</code>	Logical. Whether or not to return the full modification index in addition to the restricted.

Details

Modification indices provide an estimate of how much the fit function value would change if a parameter that is currently fixed was instead freely estimated. There are two versions of this estimate: a restricted version and an full version. The restricted version is reported as the MI and is much faster to compute. The full version is reported as MI.Full. The full version accounts for the *total* change in fit function value resulting from the newly freed parameter. The restricted version only accounts for the change in the fit function due to the movement of the new free parameter. In particular, the restricted version does not account for the change in fit function value due to the other free parameters moving in response to the new parameter.

The algorithm respects fixed parameter labels. That is, when a fixed parameter has a label and occurs in more than one spot, then that fixed parameter is freed in all locations in which it occurs to evaluate the modification index for that fixed parameter.

When the fit function is in minus two log likelihood units (e.g. `mxFitFunctionML`), then the MI will be approximately chi squared distributed with 1 degree of freedom. Using a p-value of 0.01 has been suggested. Hence, a MI greater than `qchisq(p=1-0.01, df=1)`, or 6.63, is suggestive of a modification.

Users should be cautious in their use of modification indices. If a model was created with the aid of MIs, then it should *always* be reported. *Do not pretend that you have a theoretical reason for part of a model that was put there because it was suggested by a modification index. This is fraud.* When using modification indices there are two options for best practices. First, you can report the analyses as exploratory. Document all the explorations that you did, and know that your results may or may not generalize. Second, you can use cross-validation. Reserve part of your data for exploration, and use the remaining data to test if the exploratory model generalizes to new data.

Value

A named list with components

MI The restricted modification index.

MI.Full The full modification index.

plusOneParamModels A list of models with one additional free parameter

References

Sörbom, D. (1989). Model Modification. *Psychometrika*, 54, 371-384.

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```
# Create a model
require(OpenMx)
data(demoOneFactor)
manifests <- names(demoOneFactor)
latents <- c("G")
factorModel <- mxModel("One Factor",
  type="RAM",
  manifestVars = manifests,
  latentVars = latents,
  mxPath(from=latents, to=manifests),
  mxPath(from=manifests, arrows=2),
  mxPath(from=latents, arrows=2,
    free=FALSE, values=1.0),
  mxPath(from = 'one', to = manifests),
  mxData(observed=cov(demoOneFactor), type="cov", numObs=500,
    means = colMeans(demoOneFactor)))
#No SEs for speed
factorModel <- mxOption(factorModel, 'Standard Errors', 'No')
factorRun <- mxRun(factorModel)

# See if it should be modified
# Notes
# Using full=FALSE for faster performance
# Using matrices= 'A' and 'S' to not get MIs for
# the F matrix which is always fixed.
fim <- mxMI(factorRun, matrices=c('A', 'S'), full=FALSE)
round(fim$MI, 3)
plot(fim$MI, ylim=c(0, 10))
```

```
abline(h=qchisq(p=1-0.01, df=1)) # line of "significance"
```

 mxMLObjective

DEPRECATED: Create MxMLObjective Object

Description

WARNING: Objective functions have been deprecated as of OpenMx 2.0.

Please use `mxExpectationNormal()` and `mxFitFunctionML()` instead. As a temporary workaround, `mxMLObjective` returns a list containing an `MxExpectationNormal` object and an `MxFitFunctionML` object.

`mxMLObjective(covariance, means = NA, dimnames = NA, thresholds = NA)` All occurrences of `mxMLObjective(covariance, means = NA, dimnames = NA, thresholds = NA)`

Should be changed to

`mxExpectationNormal(covariance, means = NA, dimnames = NA, thresholds = NA, threshnames = dimnames)` `mxFitFunctionML(vector = FALSE)`

Arguments

<code>covariance</code>	A character string indicating the name of the expected covariance algebra.
<code>means</code>	An optional character string indicating the name of the expected means algebra.
<code>dimnames</code>	An optional character vector to be assigned to the dimnames of the covariance and means algebras.
<code>thresholds</code>	An optional character string indicating the name of the thresholds matrix.

Details

NOTE: THIS DESCRIPTION IS DEPRECATED. Please change to using [mxExpectationNormal](#) and [mxFitFunctionML](#) as shown in the example below.

Objective functions are functions for which free parameter values are chosen such that the value of the objective function is minimized. The `mxMLObjective` function uses full-information maximum likelihood to provide maximum likelihood estimates of free parameters in the algebra defined by the 'covariance' argument given the covariance of an [MxData](#) object. The 'covariance' argument takes an [MxAlgebra](#) object, which defines the expected covariance of an associated [MxData](#) object. The 'dimnames' arguments takes an optional character vector. If this argument is not a single NA, then this vector be assigned to be the dimnames of the means vector, and the row and columns dimnames of the covariance matrix.

`mxMLObjective` evaluates with respect to an [MxData](#) object. The [MxData](#) object need not be referenced in the `mxMLObjective` function, but must be included in the [MxModel](#) object. `mxMLObjective` requires that the 'type' argument in the associated [MxData](#) object be equal to 'cov' or 'cov'. The 'covariance' argument of this function evaluates with respect to the 'matrix' argument of the associated [MxData](#) object, while the 'means' argument of this function evaluates with respect to the 'vector' argument of the associated [MxData](#) object. The 'means' and 'vector' arguments are

optional in both functions. If the 'means' argument is not specified (NA), the optional 'vector' argument of the `MxData` object is ignored. If the 'means' argument is specified, the associated `MxData` object should specify a 'means' argument of equivalent dimension as the 'means' algebra.

dimnames must be supplied where the matrices referenced by the covariance and means algebras are not themselves labeled. Failure to do so leads to an error noting that the covariance or means matrix associated with the ML objective does not contain dimnames.

To evaluate, place `MxMLObjective` objects, the `mxData` object for which the expected covariance approximates, referenced `MxAlgebra` and `MxMatrix` objects, and optional `MxBounds` and `MxConstraint` objects in an `MxModel` object. This model may then be evaluated using the `mxRun` function. The results of the optimization can be found in the 'output' slot of the resulting model, or using the `mxEval` function.

Value

Returns a list containing an `MxExpectationNormal` object and an `MxFitFunctionML` object.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```
# Create and fit a model using mxMatrix, mxAlgebra, mxExpectationNormal, and mxFitFunctionML

library(OpenMx)

# Simulate some data

x=rnorm(1000, mean=0, sd=1)
y= 0.5*x + rnorm(1000, mean=0, sd=1)
tmpFrame <- data.frame(x, y)
tmpNames <- names(tmpFrame)

# Define the matrices

S <- mxMatrix(type = "Full", nrow = 2, ncol = 2, values=c(1,0,0,1),
              free=c(TRUE,FALSE,FALSE,TRUE), labels=c("Vx", NA, NA, "Vy"), name = "S")
A <- mxMatrix(type = "Full", nrow = 2, ncol = 2, values=c(0,1,0,0),
              free=c(FALSE,TRUE,FALSE,FALSE), labels=c(NA, "b", NA, NA), name = "A")
I <- mxMatrix(type="Iden", nrow=2, ncol=2, name="I")

# Define the expectation

expCov <- mxAlgebra(solve(I-A) %*% S %*% t(solve(I-A)), name="expCov")
expFunction <- mxExpectationNormal(covariance="expCov", dimnames=tmpNames)

# Choose a fit function

fitFunction <- mxFitFunctionML()
```

```

# Define the model

tmpModel <- mxModel(model="exampleModel", S, A, I, expCov, expFunction, fitFunction,
                    mxData(observed=cov(tmpFrame), type="cov", numObs=dim(tmpFrame)[1]))

# Fit the model and print a summary

tmpModelOut <- mxRun(tmpModel)
summary(tmpModelOut)

```

mxModel *Create MxModel Object*

Description

This function creates a new [MxModel](#) object.

Usage

```

mxModel(model = NA, ..., manifestVars = NA, latentVars = NA,
        remove = FALSE, independent = NA, type = NA, name = NA)

```

Arguments

model	This argument is either an MxModel object or a string. If 'model' is an Mx-Model object, then all elements of that model are placed in the resulting Mx-Model object. If 'model' is a string, then a new model is created with the string as its name. If 'model' is either unspecified or 'model' is a named entity, data source, or MxPath object, then a new model is created.
...	An arbitrary number of mxMatrix , mxPath , mxData , and other functions such as mxConstraints and mxCI . These will all be added or removed from the model as specified in the 'model' argument, based on the 'remove' argument.
manifestVars	For RAM-type models, A list of manifest variables to be included in the model.
latentVars	For RAM-type models, A list of latent variables to be included in the model.
remove	logical. If TRUE, elements listed in this statement are removed from the original model. If FALSE, elements listed in this statement are added to the original model.
independent	logical. If TRUE then the model is evaluated independently of other models.
type	character vector. The model type to assign to this model. Defaults to options("mxDefaultType"). See below for valid types
name	An optional character vector indicating the name of the object.

Details

The `mxModel` function is used to create `MxModel` objects. Objects created by this function may be new, or may be modified versions of existing `MxModel` objects. By default a new `MxModel` object will be created: To create a modified version of an existing `MxModel` object, include this model in the 'model' argument.

Other `named-entities` may be added as arguments to the `mxModel` function, which are then added to or removed from the model specified in the 'model' argument. Other functions you can use to add objects to the model to this way are `mxCI`, `mxAlgebra`, `mxBounds`, `mxConstraint`, `mxData`, and `mxMatrix` objects, as well as objective functions. You can also include `MxModel` objects as sub-models of the output model, and may be estimated separately or jointly depending on shared parameters and the 'independent' flag discussed below. Only one `MxData` object and one objective function may be included per model, but there are no restrictions on the number of other `named-entities` included in an `mxModel` statement.

All other arguments must be named (i.e. 'latentVars = names'), or they will be interpreted as elements of the ellipsis list. The 'manifestVars' and 'latentVars' arguments specify the names of the manifest and latent variables, respectively, for use with the `mxPath` function. The 'remove' argument may be used when `mxModel` is used to create a modified version of an existing `MxMatrix` object. When 'remove' is set to TRUE, the listed objects are removed from the model specified in the 'model' argument. When 'remove' is set to FALSE, the listed objects are added to the model specified in the 'model' argument.

Model independence may be specified with the 'independent' argument. If a model is independent ('independent = TRUE'), then the parameters of this model are not shared with any other model. An independent model may be estimated with no dependency on any other model. If a model is not independent ('independent = FALSE'), then this model shares parameters with one or more other models such that these models must be jointly estimated. These dependent models must be entered as arguments in another model, so that they are simultaneously optimized.

The model type is determined by a character vector supplied to the 'type' argument. The type of a model is a dynamic property, ie. it is allowed to change during the lifetime of the model. To see a list of available types, use the `mxTypes` command. When a new model is created and no type is specified, the type specified by `options("mxDefaultType")` is used.

To be estimated, `MxModel` objects must include objective functions as arguments (`mxAlgebraObjective`, `mxFIMLObjective`, `mxMLObjective` or `mxRAMObjective`) and executed using the `mxRun` function. When `MxData` objects are included in models, the 'type' argument of these objects may require or exclude certain objective functions, or set an objective function as default.

`Named entities` in `MxModel` objects may be viewed and referenced by name using the \$ symbol. For instance, for an `MxModel` named "yourModel" containing an `MxMatrix` named "yourMatrix", the contents of "yourMatrix" can be accessed as `yourModel$yourMatrix`. Slots (i.e., matrices, algebras, etc.) in an `MxMatrix` may also be referenced with the \$ symbol (e.g., `yourModel$matrices` or `yourModel$algebras`). See the documentation for `Classes` and the examples in `Classes` for more information.

Value

Returns a new `MxModel` object. `MxModel` objects must include an objective function to be used as arguments in `mxRun` functions.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

See [mxCI](#) for information about adding Confidence Interval calculations to a model. See [mxPath](#) for information about adding paths to RAM-type models. See [mxMatrix](#) for information about adding matrices to models. See [mxData](#) for specifying the data a model is to be evaluated against. See [MxModel](#) for the S4 class created by mxMatrix. Many advanced options can be set via [mxOption](#) (such as calculating the Hessian). More information about the OpenMx package may be found [here](#).

Examples

```
library(OpenMx)

# At the simplest, you can create an empty model,
# placing it in an object, and add to it later
emptyModel <- mxModel(model="IAmEmpty")

# Create a model named 'firstdraft' with one matrix 'A'
firstModel <- mxModel(model='firstdraft',
  mxMatrix(type='Full', nrow = 3, ncol = 3, name = "A"))

# Update 'firstdraft', and rename the model 'finaldraft'
finalModel <- mxModel(model=firstModel,
  mxMatrix(type='Symm', nrow = 3, ncol = 3, name = "S"),
  mxMatrix(type='Iden', nrow = 3, name = "F"),
  name= "finaldraft")

# Add data to the model from an existing data frame in object 'data'
data(twinData) # load some data
finalModel <- mxModel(model=finalModel, mxData(twinData, type='raw'))

# Two ways to view the matrix named "A" in MxModel object 'model'

finalModel$A

finalModel$matrices$A

# A working example using OpenMx Path Syntax
data(HS.ability.data) # load the data

# The manifest variables loading on each proposed latent variable
Spatial <- c("visual", "cubes", "paper")
Verbal <- c("general", "paragrap", "sentence")
Math <- c("numeric", "series", "arithmet")

latents <- c("vis", "math", "text")
manifests <- c(Spatial, Math, Verbal)

HSModel <- mxModel(model="Holzinger_and_Swineford_1939", type="RAM",
```

```

manifestVars = manifests, # list the measured variables (boxes)
latentVars   = latents,   # list the latent variables (circles)
# factor loadings from latents to manifests
mxPath(from="vis", to=Spatial),# factor loadings
mxPath(from="math", to=Math),  # factor loadings
mxPath(from="text", to=Verbal), # factor loadings

# Allow latent variables to covary
mxPath(from="vis" , to="math", arrows=2, free=TRUE),
mxPath(from="vis" , to="text", arrows=2, free=TRUE),
mxPath(from="math", to="text", arrows=2, free=TRUE),

# Allow latent variables to have variance
mxPath(from=latents, arrows=2, free=FALSE, values=1.0),
# Manifest have residual variance
mxPath(from=manifests, arrows=2),
# the data to be analysed
mxData(cov(HS.ability.data[,manifests]), type = "cov", numObs = 301))

fitModel <- mxRun(HSModel) # run the model
summary(fitModel) # examine the output: Fit statistics and path loadings

```

MxModel-class

MxModel Class

Description

MxModel is an S4 class. An MxModel object is a [named entity](#).

Details

The ‘matrices’ slot contains a list of the [MxMatrix](#) objects included in the model. These objects are listed by name. Two objects may not share the same name. If a new [MxMatrix](#) is added to an MxModel object with the same name as an [MxMatrix](#) object in that model, the added version replaces the previous version. There is no imposed limit on the number of [MxMatrix](#) objects that may be added here.

The ‘algebras’ slot contains a list of the [MxAlgebra](#) objects included in the model. These objects are listed by name. Two objects may not share the same name. If a new [MxAlgebra](#) is added to an MxModel object with the same name as an [MxAlgebra](#) object in that model, the added version replaces the previous version. All [MxMatrix](#) objects referenced in the included [MxAlgebra](#) objects must be included in the ‘matrices’ slot prior to estimation. There is no imposed limit on the number of [MxAlgebra](#) objects that may be added here.

The ‘constraints’ slot contains a list of the [MxConstraint](#) objects included in the model. These objects are listed by name. Two objects may not share the same name. If a new [MxConstraint](#) is added to an MxModel object with the same name as an [MxConstraint](#) object in that model, the added version replaces the previous version. All [MxMatrix](#) objects referenced in the included [MxConstraint](#) objects must be included in the ‘matrices’ slot prior to estimation. There is no imposed limit on the number of [MxConstraint](#) objects that may be added here.

The 'intervals' slot contains a list of the confidence intervals requested by included [MxCI](#) objects. These objects are listed by the free parameters, [MxMatrices](#) and [MxAlgebras](#) referenced in the [MxCI](#) objects, not the list of [MxCI](#) objects themselves. If a new [MxCI](#) object is added to an MxModel object referencing one or more free parameters [MxMatrices](#) or [MxAlgebras](#) previously listed in the 'intervals' slot, the new confidence interval(s) replace the existing ones. All listed confidence intervals must refer to free parameters [MxMatrices](#) or [MxAlgebras](#) in the model.

The 'latentVars' slot contains a list of latent variable names, which may be referenced by [MxPath](#) objects. This slot defaults to 'NA', and is only used when the [mxPath](#) function is used.

The 'manifestVars' slot contains a list of latent variable names, which may be referenced by [MxPath](#) objects. This slot defaults to 'NA', and is only used when the [mxPath](#) function is used.

The 'data' slot contains an [MxData](#) object. This slot must be filled prior to execution when a fitfunction referencing data is used. Only one [MxData](#) object may be included per model, but submodels may have their own data in their own 'data' slots. If an [MxData](#) object is added to an MxModel which already contains an [MxData](#) object, the new object replaces the existing one.

The 'submodels' slot contains references to all of the MxModel objects included as submodels of this MxModel object. Models held as arguments in other models are considered to be submodels. These objects are listed by name. Two objects may not share the same name. If a new submodel is added to an MxModel object with the same name as an existing submodel, the added version replaces the previous version. When a model containing other models is executed using [mxRun](#), all included submodels are executed as well. If the submodels are dependent on one another, they are treated as one larger model for purposes of estimation.

The 'independent' slot contains a logical value indicating whether or not the model is independent. If a model is independent (`independent=TRUE`), then the parameters of this model are not shared with any other model. An independent model may be estimated with no dependency on any other model. If a model is not independent (`independent=FALSE`), then this model shares parameters with one or more other models such that these models must be jointly estimated. These dependent models must be entered as submodels of another MxModel objects, so that they are simultaneously optimized.

The 'options' slot contains a list of options for the model. The name of each entry in the list is the option name to be used at runtime. The values in this list are the values of the optimizer options. The standard interface for updating options is through the [mxOption](#) function.

The 'output' slot contains a list of output added to the model by the [mxRun](#) function. Output includes parameter estimates, optimization information, model fit, and other information. If a model has not been optimized using the [mxRun](#) function, the 'output' slot will be 'NULL'.

[Named entities](#) in [MxModel](#) objects may be viewed and referenced by name using the \$ symbol. For instance, for an MxModel named "yourModel" containing an MxMatrix named "yourMatrix", the contents of "yourMatrix" can be accessed as `yourModel$yourMatrix`. Slots (i.e., matrices, algebras, etc.) in an `mxMatrix` may also be referenced with the \$ symbol (e.g., `yourModel$matrices` or `yourModel$algebras`). See the documentation for [Classes](#) and the examples in [mxModel](#) for more information.

Objects from the Class

Objects can be created by calls of the form `mxModel()`.

Slots

name: Character string. The name of the model object.
matrices: List of the model's [MxMatrix](#) objects.
algebras: List of the model's [MxAlgebra](#) objects.
constraints: List of the model's [MxConstraint](#) objects.
intervals: List of the model's [MxInterval](#) objects, requested via [mxCI\(\)](#).
latentVars: "Latent variables;" object of class "MxCharOrList".
manifestVars: "Manifest variables;" object of class "MxCharOrList".
data: Object of class [MxData](#).
submodels: List of [MxModel](#) objects.
expectation: Object of class [MxExpectation](#); dictates the model's specification.
fitfunction: Object of class [MxFitFunction](#); dictates the cost function to be minimized when fitting the model.
compute: Object of class [MxCompute](#)—the model's compute plan, which contains instructions on what the model is to compute and how to do so.
independent: Logical; is the model to be run independently from other submodels?
options: List of model-specific options, set by [mxOption\(\)](#).
output: List of model output produced during a call to [mxRun\(\)](#).
runstate: List produced by [mxRun\(\)](#), which contains the pre-run state of the model object.
.newobjects: Logical; for internal use.
.resetdata: Logical; for internal use.
.wasRun: Logical; for internal use.
.modifiedSinceRun: Logical; for internal use.
.version: Object of class "package_version"; for internal use.

Methods

\$ signature(x = "MxModel"): Accessor. Accesses slots by slot-name. Also accesses constituent [named entities](#), by name.
\$<- signature(x = "MxModel"): Assignment. Generally, this method will not allow the user to make unsafe changes to the [MxModel](#) object.
[[signature(x = "MxModel"): Accessor for constituent [named entities](#).
[[<- signature(x = "MxModel"): Assignment for a [named entity](#).
names signature(x = "MxModel"): Returns names of slots and [named entities](#).
print signature(x = "MxModel"): "Print" method.
show signature(object = "MxModel"): "Show" method.
 Note that [imxInitModel\(\)](#), [imxModelBuilder\(\)](#), [imxTypeName\(\)](#), and [imxVerifyModel\(\)](#) are separately documented methods for class "MxModel".

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

[mxModel](#) for creating MxModel objects. More information about the OpenMx package may be found [here](#).

Examples

```
showClass("MxModel")
```

mxNormalQuantiles *mxNormalQuantiles*

Description

Get quantiles from a normal distribution

Usage

```
mxNormalQuantiles(nBreaks, mean = 0, sd = 1)
```

Arguments

nBreaks	the number of thresholds, or a vector of the number of thresholds
mean	the mean of the underlying normal distribution
sd	the standard deviation of the underlying normal distribution

Value

a vector of quantiles

Examples

```
mxNormalQuantiles(3)
mxNormalQuantiles(3, mean=7)
mxNormalQuantiles(2, mean=1, sd=3)
```

mxOption	<i>Set or Clear an Optimizer Option</i>
----------	-----------------------------------------

Description

The function sets, shows, or clears an option that is specific to the optimizer in the back-end.

Usage

```
mxOption(model, key, value, reset = FALSE)
```

Arguments

model	An MxModel object or NULL
key	The name of the option.
value	The value of the option.
reset	If TRUE then reset all options to their defaults.

Details

mxOption is used to set, clear, or query an option (given in the ‘key’ argument) in the back-end optimizer. Valid option keys are listed below.

Use value = NULL to remove an existing option. Leaving value blank will return the current value of the option specified by ‘key’.

To reset all options to their default values, use ‘reset = TRUE’. When reset = TRUE, ‘key’ and ‘value’ are ignored.

If the ‘model’ argument is set to NULL, the default optimizer option (i.e those applying to all models by default) will be set.

To see the defaults, use `getOption('mxOptions')`.

Before the model is submitted to the back-end, all keys and values are converted into strings using the [as.character](#) function.

The “Default optimizer” option can only be set globally (i.e., with model=NULL), and not locally (i.e., specifically to a given MxModel). Although the checkpointing options may be set globally, OpenMx’s behavior is only affected by locally set checkpointing options (that is, global checkpointing options are ignored at [runtime](#)).

Options “Gradient step size”, “Gradient iterations”, and “Function precision” have on-load global defaults of “Auto”. If value “Auto” is in effect for any of these three options at [runtime](#), then OpenMx selects a reasonable numerical value in its place. These automated numerical values are intended to (1) adjust for the limited precision of the algorithm for computing multivariate-normal probability integrals, and (2) calculate accurate numeric derivatives at the optimizer’s solution. If the user replaces “Auto” with a valid numerical value, then OpenMx uses that value as-is.

Some options only affect certain optimizers. Currently, options “Gradient algorithm” and “Gradient iterations” are ignored by all optimizers other than SLSQP. Also, currently option “Analytic Gradients” only affects SLSQP and NPSOL. Option “Gradient step size” is used slightly differently

by SLSQP and CSOLNP, and is ignored by NPSOL (see `mxComputeGradientDescent()` for details). If the `MxModel` contains `MxConstraints`, `OpenMx`'s interface to NPSOL scales "Feasibility tolerance" by multiplying it by 0.02 and dividing it by 0.05 before passing it to NPSOL; if there are no `MxConstraints`, `OpenMx` passes NPSOL a hardcoded value of 1e-5. Note that NPSOL's criterion for returning a status code of 0 versus 1 for a given solution depends partly on "Optimality tolerance".

For a block of n ordinal variables, the maximum number of integration points that `OpenMx` may use to calculate multivariate-normal probability integrals is given by $mvnMaxPointsA + mvnMaxPointsB*n + mvnMaxPointsC*n$.

The maximum number of major iterations (the option "Major iterations") for optimization for NPSOL can be specified either by using a numeric value (such as 50, 1000, etc) or by specifying a user-defined function. The user-defined function should accept two arguments as input, the number of parameters and the number of constraints, and return a numeric value as output.

OpenMx options

Calculate Hessian	[Yes No]	calculate the Hessian explicitly after optimization.
Standard Errors	[Yes No]	return standard error estimates from the explicitly calculate hessian.
Default optimizer	[NPSOL SLSQP CSOLNP]	the gradient-descent optimizer to use
Number of Threads	[0 1 2 ... 10 ...]	number of threads used for optimization. Default value is taken from
Feasibility tolerance	r	the maximum acceptable absolute violations in linear and nonlinear c
Optimality tolerance	r	the accuracy with which the final iterate approximates a solution to th
Gradient algorithm	see list	finite difference method, either 'forward' or 'central'.
Gradient iterations	1:4	the number of Richardson extrapolation iterations
Gradient step size	r	amount of change made to free parameters when numerically calculat
Analytic Gradients	[Yes No]	should the optimizer use analytic gradients (if available)?
loglikelihoodScale	i	factor by which the loglikelihood is scaled.
Parallel diagnostics	[Yes No]	whether to issue diagnostic messages about use of multiple threads
Nudge zero starts	[TRUE FALSE]	Should <code>OpenMx</code> "nudge" starting values of zero to 0.1 at runtime?

NPSOL-specific options

Nolist		this option suppresses printing of the options
Print level	i	the value of i controls the amount of printout produced by the major iterations
Minor print level	i	the value of i controls the amount of printout produced by the minor iterations
Print file	i	for $i > 0$ a full log is sent to the file with logical unit number i .
Summary file	i	for $i > 0$ a brief log will be output to file i .
Function precision	r	a measure of accuracy with which the fitfunction and constraint functions can be co
Infinite bound size	r	if $r > 0$ defines the "infinite" bound <code>bigbnd</code> .
Major iterations	i or a function	the maximum number of major iterations before termination.
Verify level	[-1:3 Yes No]	see NPSOL manual.
Line search tolerance	r	controls the accuracy with which a step is taken.
Derivative level	[0-3]	see NPSOL manual.
Hessian	[Yes No]	return the Hessian (Yes) or the transformed Hessian (No).
Step Limit	r	maximum change in free parameters at first step of linesearch.

Checkpointing options

Always Checkpoint	[Yes No]	whether to checkpoint all models during optimization.
-------------------	------------	-------------------------------------------------------

Checkpoint Directory	path	the directory into which checkpoint files are written.
Checkpoint Prefix	string	the string prefix to add to all checkpoint filenames.
Checkpoint Fullpath	path	overrides the directory and prefix (useful to output to /dev/fd/2)
Checkpoint Units	see list	the type of units for checkpointing: 'minutes', 'iterations', or 'evaluations'.
Checkpoint Count	<i>i</i>	the number of units between checkpoint intervals.

Model transformation options

Error Checking	[Yes No]	whether model consistency checks are performed in the OpenMx front-end
No Sort Data		character vector of model names for which FIML data sorting is not performed
RAM Inverse Optimization	[Yes No]	whether to enable solve(I - A) optimization
RAM Max Depth	<i>i</i>	the maximum depth to be used when solve(I - A) optimization is enabled

Multivariate normal integration parameters

maxOrdinalPerBlock	<i>i</i>	maximum number of ordinal variables to evaluate together
mvnMaxPointsA	<i>i</i>	base number of integration points
mvnMaxPointsB	<i>i</i>	number of integration points per row
mvnMaxPointsC	<i>i</i>	number of integration points per rows^2
mvnAbsEps	<i>i</i>	absolute error tolerance
mvnRelEps	<i>i</i>	relative error tolerance

Value

If a model is provided, it is returned with the optimizer option either set or cleared. If value is empty, the current value is returned.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

See [mxModel\(\)](#), as almost all uses of [mxOption\(\)](#) are via an [mxModel](#) whose options are set or cleared. See [mxComputeGradientDescent\(\)](#) for details on how different optimizers are affected by different options.

Examples

```
# set the Number of Threads (cores to use)
mxOption(NULL, "Number of Threads", parallel::detectCores() - 1)

testModel <- mxModel(model = "testModel") # make a model to use for example
testModel$options # show the model options (none yet)
options()$mxOptions # list all mxOptions (global settings)
```

```

testModel <- mxOption(testModel, "Function precision", 1e-5) # set precision
testModel <- mxOption(testModel, "Function precision", NULL) # clear precision
# N.B. This is model-specific precision (defaults to global setting)

# may optimize for speed
# at cost of not getting standard errors
testModel <- mxOption(testModel, "Calculate Hessian", "No")
testModel <- mxOption(testModel, "Standard Errors" , "No")

testModel$options # see the list of options you set

```

MxOptionalChar-class *An optional character*

Description

An optional character

MxOptionalCharOrNumber-class
A character, integer, or NULL

Description

A character, integer, or NULL

MxOptionalLogical-class
An optional logical

Description

This is an internal class, the union of NULL and logical.

MxOptionalMatrix-class
An optional matrix

Description

An optional matrix

MxOptionalNumeric-class

An optional numeric

Description

An optional numeric

mxPath

Create List of Paths

Description

This function creates a list of paths.

Usage

```
mxPath(from, to = NA, connect = c("single", "all.pairs", "unique.pairs",
  "all.bivariate", "unique.bivariate"), arrows = 1,
  free = TRUE, values = NA, labels = NA,
  lbound = NA, ubound = NA, ..., joinKey = as.character(NA))
```

Arguments

from	character vector. These are the sources of the new paths.
to	character vector. These are the sinks of the new paths.
connect	String. Specifies the type of source to sink connection: "single", "all.pairs", "all.bivariate", "unique.pairs", "unique.bivariate". Default value is "single".
arrows	numeric value. Must be either 1 (for single-headed) or 2 (for double-headed arrows).
free	boolean vector. Indicates whether paths are free or fixed.
values	numeric vector. The starting values of the parameters.
labels	character vector. The names of the paths.
lbound	numeric vector. The lower bounds of free parameters.
ubound	numeric vector. The upper bounds of free parameters.
...	Not used. Allows OpenMx to catch the use of the deprecated 'all' argument.
joinKey	character vector. The name of the foreign key to join against some other model to create a cross model path (regression or factor loading).

Details

The `mxPath` function creates `MxPath` objects. These consist of a list of paths describing the relationships between variables in a model using the RAM modeling approach (McArdle and MacDonald, 1984). Variables are referenced by name, and these names must appear in the ‘manifestVar’ and ‘latentVar’ arguments of the `mxModel` function.

Paths are specified as going "from" one variable (or set of variables) "to" another variable or set of variables using the ‘from’ and ‘to’ arguments, respectively. If ‘to’ is left empty, it will be set to the value of ‘from’.

‘connect’ has five possible connection types: "single", "all.pairs", "all.bivariate", "unique.pairs", "unique.bivariate". The default value is "single". Assuming the values c(‘a’, ‘b’, ‘c’) for the ‘to’ and ‘from’ fields the paths produced by each connection type are as follows:

"all.pairs": (a,a), (a,b), (a,c), (b,a), (b,b), (b,c), (c,a), (c,b), (c,c).

"unique.pairs": (a,a), (a,b), (a,c), (b,b), (b,c), (c,c).

"all.bivariate": (a,b), (a,c), (b,a), (b,c), (c,a), (c,b).

"unique.bivariate": (a,b), (a,c), (b,c).

"single": (a,a), (b,b), (c,c).

Multiple variables may be input as a vector of variable names. If the ‘connect’ argument is set to "single", then paths are created going from each entry in the ‘from’ vector to the corresponding entry in the ‘to’ vector. If the ‘to’ and ‘from’ vectors are of different lengths when the ‘connect’ argument is set to "single", the shorter vector is repeated to make the vectors of equal length.

The ‘free’ argument specifies whether the paths created by the `mxPath` function are free or fixed parameters. This argument may take either TRUE for free parameters, FALSE for fixed parameters, or a vector of TRUEs and FALSEs to be applied in order to the created paths.

The ‘arrows’ argument specifies the type of paths created. A value of 1 indicates a one-headed arrow representing regression. This path represents a regression of the ‘to’ variable on the ‘from’ variable, such that the arrow points to the ‘to’ variable in a path diagram. A value of 2 indicates a two-headed arrow, representing a covariance or variance. If multiple paths are created in the same `mxPath` function, then the ‘arrows’ argument may take a vector of 1s and 2s to be applied to the set of created paths.

The ‘values’ is a numeric vectors containing the starting values of the created paths. ‘values’ gives a starting value for estimation. The ‘labels’ argument specifies the names of the resulting `MxPath` object. The ‘lbound’ and ‘ubound’ arguments specify lower and upper bounds for the created paths.

Value

Returns a list of paths.

Note

The previous implementation of ‘all’ had unsafe features. Its use is now deprecated, and has been replaced by the new mechanism ‘connect’ which supports safe and controlled generation of desired combinations of paths.

References

McArdle, J. J. and MacDonald, R. P. (1984). Some algebraic properties of the Reticular Action Model for moment structures. *British Journal of Mathematical and Statistical Psychology*, 37, 234-251.

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

[mxMatrix](#) for a matrix-based approach to path specification; [mxModel](#) for the container in which mxPaths are embedded. More information about the OpenMx package may be found [here](#).

Examples

```
# A simple Example: 1 factor Confirmatory Factor Analysis

library(OpenMx)

data(demoOneFactor)
manifests <- names(demoOneFactor)
latents <- c("G")
factorModel <- mxModel(model="One Factor", type="RAM",
  manifestVars = manifests,
  latentVars = latents,
  mxPath(from=latents, to=manifests),
  mxPath(from=manifests, arrows=2),
  mxPath(from=latents, arrows=2, free=FALSE, values=1.0),
  mxData(cov(demoOneFactor), type="cov", numObs=500)
)
factorFit <- mxRun(factorModel)
summary(factorFit)

# A more complex example using features of R to compress
# what would otherwise be a long and error-prone script

# list of 100 variable names: "01" "02" "03"...
myManifest <- sprintf("%02d", c(1:100))

# the latent variables for the model
myLatent <- c("G1", "G2", "G3", "G4", "G5")

# Start building the model:
# Define its type, and add the manifest and latent variable name lists
testModel <- mxModel(model="testModel", type = "RAM",
  manifestVars = myManifest, latentVars = myLatent)

# Create covariances between the latent variables and add to the model
# Here we use combn to create the covariances
# nb: To create the variances and covariances in one operation you could use
# expand.grid(myLatent,myLatent) to specify from and to
```

```

uniquePairs <- combn(myLatent,2)
covariances <- mxPath(from = uniquePairs[1,],
                      to=uniquePairs[2,], arrows = 2, free = TRUE, values = 1)
testModel <- mxModel(model=testModel, covariances)

# Create variances for the latent variables
variances <- mxPath(from = myLatent,
                    to=myLatent, arrows = 2, free = TRUE, values = 1)
testModel <- mxModel(model=testModel, variances) # add variances to the model

# Make a list of paths from each packet of 20 manifests
# to one of the 5 latent variables
# nb: The first loading to each latent is fixed to 1 to scale its variance.
singles <- list()
for (i in 1:5) {
  j <- i*20
  singles <- append(singles, mxPath(
    from = myLatent[i], to = myManifest[(j - 19):j],
    arrows = 1,
    free = c(FALSE, rep(TRUE, 19)),
    values = c(1, rep(0.75, 19))))
}

# add single-headed paths to the model
testModel <- mxModel(model=testModel, singles)

```

MxRAMGraph-class *MxRAMGraph*

Description

This is an internal class and should not be used directly. It is a class for RAM directed graphs.

MxRAMMetaData-class *Meta Data for RAM*

Description

This is an internal class, the meta data for RAM.

MxRAMModel-class *MxRAMModel*

Description

This is an internal class and should not be used directly.

mxRAMObjective

*DEPRECATED: Create MxRAMObjective Object***Description**

WARNING: Objective functions have been deprecated as of OpenMx 2.0.

Please use `mxExpectationRAM()` and `mxFitFunctionML()` instead. As a temporary workaround, `mxRAMObjective` returns a list containing an `MxExpectationNormal` object and an `MxFitFunctionML` object.

All occurrences of

`mxRAMObjective(A, S, F, M = NA, dimnames = NA, thresholds = NA, vector = FALSE, threshnames = dimnames)`

Should be changed to

`mxExpectationRAM(A, S, F, M = NA, dimnames = NA, thresholds = NA, threshnames = dimnames) mxFitFunctionML(vector = FALSE)`

Arguments

A	A character string indicating the name of the 'A' matrix.
S	A character string indicating the name of the 'S' matrix.
F	A character string indicating the name of the 'F' matrix.
M	An optional character string indicating the name of the 'M' matrix.
dimnames	An optional character vector to be assigned to the column names of the 'F' and 'M' matrices.
thresholds	An optional character string indicating the name of the thresholds matrix.
vector	A logical value indicating whether the objective function result is the likelihood vector.
threshnames	An optional character vector to be assigned to the column names of the thresholds matrix.

Details

NOTE: THIS DESCRIPTION IS DEPRECATED. Please change to using `mxExpectationRAM` and `mxFitFunctionML` as shown in the example below.

Objective functions were functions for which free parameter values are chosen such that the value of the objective function was minimized. The `mxRAMObjective` provided maximum likelihood estimates of free parameters in a model of the covariance of a given `MxData` object. This model is defined by reticular action modeling (McArdle and McDonald, 1984). The 'A', 'S', and 'F' arguments must refer to `MxMatrix` objects with the associated properties of the A, S, and F matrices in the RAM modeling approach.

The 'dimnames' argument takes an optional character vector. If this argument is not a single NA, then this vector be assigned to be the column names of the 'F' matrix and optionally to the 'M' matrix, if the 'M' matrix exists.

The 'A' argument refers to the A or asymmetric matrix in the RAM approach. This matrix consists of all of the asymmetric paths (one-headed arrows) in the model. A free parameter in any row and column describes a regression of the variable represented by that row regressed on the variable represented in that column.

The 'S' argument refers to the S or symmetric matrix in the RAM approach, and as such must be square. This matrix consists of all of the symmetric paths (two-headed arrows) in the model. A free parameter in any row and column describes a covariance between the variable represented by that row and the variable represented by that column. Variances are covariances between any variable at itself, which occur on the diagonal of the specified matrix.

The 'F' argument refers to the F or filter matrix in the RAM approach. If no latent variables are included in the model (i.e., the A and S matrices are of both of the same dimension as the data matrix), then the 'F' should refer to an identity matrix. If latent variables are included (i.e., the A and S matrices are not of the same dimension as the data matrix), then the 'F' argument should consist of a horizontal adhesion of an identity matrix and a matrix of zeros.

The 'M' argument refers to the M or means matrix in the RAM approach. It is a 1 x n matrix, where n is the number of manifest variables + the number of latent variables. The M matrix must be specified if either the mxData type is "cov" or "cor" and a means vector is provided, or if the mxData type is "raw". Otherwise the M matrix is ignored.

The [MxMatrix](#) objects included as arguments may be of any type, but should have the properties described above. The mxRAMObjective will not return an error for incorrect specification, but incorrect specification will likely lead to estimation problems or errors in the [mxRun](#) function.

mxRAMObjective evaluates with respect to an [MxData](#) object. The [MxData](#) object need not be referenced in the mxRAMObjective function, but must be included in the [MxModel](#) object. mxRAMObjective requires that the 'type' argument in the associated [MxData](#) object be equal to 'cov' or 'cor'.

To evaluate, place MxRAMObjective objects, the [mxData](#) object for which the expected covariance approximates, referenced [MxAlgebra](#) and [MxMatrix](#) objects, and optional [MxBounds](#) and [MxConstraint](#) objects in an [MxModel](#) object. This model may then be evaluated using the [mxRun](#) function. The results of the optimization can be found in the 'output' slot of the resulting model, and may be obtained using the [mxEval](#) function..

Value

Returns a list containing an MxExpectationRAM object and an MxFitFunctionML object.

References

McArdle, J. J. and MacDonald, R. P. (1984). Some algebraic properties of the Reticular Action Model for moment structures. *British Journal of Mathematical and Statistical Psychology*, 37, 234-251.

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```
# Create and fit a model using mxMatrix, mxAlgebra,
```

```

# mxExpectationNormal, and mxFitFunctionML

library(OpenMx)

# Simulate some data

x=rnorm(1000, mean=0, sd=1)
y= 0.5*x + rnorm(1000, mean=0, sd=1)
tmpFrame <- data.frame(x, y)
tmpNames <- names(tmpFrame)

# Define the matrices

matrixS <- mxMatrix(type = "Full", nrow = 2, ncol = 2, values=c(1,0,0,1),
                    free=c(TRUE,FALSE,FALSE,TRUE), labels=c("Vx", NA, NA, "Vy"),
                    name = "S")
matrixA <- mxMatrix(type = "Full", nrow = 2, ncol = 2, values=c(0,1,0,0),
                    free=c(FALSE,TRUE,FALSE,FALSE), labels=c(NA, "b", NA, NA),
                    name = "A")
matrixF <- mxMatrix(type="Iden", nrow=2, ncol=2, name="F")
matrixM <- mxMatrix(type = "Full", nrow = 1, ncol = 2, values=c(0,0),
                    free=c(TRUE,TRUE), labels=c("Mx", "My"), name = "M")

# Define the expectation

expFunction <- mxExpectationRAM(M="M", dimnames = tmpNames)

# Choose a fit function

fitFunction <- mxFitFunctionML()

# Define the model

tmpModel <- mxModel(model="exampleRAMModel",
                    matrixA, matrixS, matrixF, matrixM,
                    expFunction, fitFunction,
                    mxData(observed=cov(tmpFrame), type="cov", numObs=nrow(tmpFrame),
                            means = colMeans(tmpFrame)))

# Fit the model and print a summary

tmpModelOut <- mxRun(tmpModel)
summary(tmpModelOut)

```

mxRename

Rename MxModel or a Submodel

Description

This functions renames either the top model or a submodel to a new name. All internal references to the old model name are replaced with references to the new name.

Usage

```
mxRename(model, newname, oldname = NA)
```

Arguments

model a MxModel object.
 newname the new name of the model.
 oldname the name of the target model to rename. If NA then rename top model.

Value

Return a `mxModel` object with the target model renamed.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```
library(OpenMx)

# create two empty models
modelA <- mxModel(model='modelA')
modelB <- mxModel(model='modelB')

# create a parent model with two submodels
modelC <- mxModel(model='modelC', modelA, modelB)

# Rename modelC to model1
model1 <- mxRename(modelC, 'model1')

# Rename submodel modelB to model2
model1 <- mxRename(model1, oldname = 'modelB', newname = 'model2')

model1
```

 mxRestore

Restore From Checkpoint File

Description

The function loads the last saved state from a checkpoint file.

Usage

```
mxRestore(model, chkpt.directory = ".", chkpt.prefix = "", line=NULL, strict=FALSE)
```

Arguments

model	MxModel object to be loaded.
chkpt.directory	character. Directory where the checkpoint file is located.
chkpt.prefix	character. Prefix of the checkpoint file.
line	integer. Which line from the checkpoint file to restore (defaults to the last line)
strict	logical. Require that the checkpoint name and model name match.

Details

In general, the arguments ‘chkpt.directory’ and ‘chkpt.prefix’ should be identical to the [mxOption](#): ‘Checkpoint Directory’ and ‘Checkpoint Prefix’ that were specified on the model before execution.

Alternatively, the checkpoint file can be manually loaded as a data.frame in R. Use [read.table](#) with the options header=TRUE, sep="\t", stringsAsFactors=FALSE, check.names=FALSE.

Value

Returns an MxModel object with free parameters updated to the last saved values. When ‘line’ is provided, the MxModel is updated to the values on that line within the checkpoint file.

References

The OpenMx User’s guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```
library(OpenMx)

# Simulate some data

x=rnorm(1000, mean=0, sd=1)
y= 0.5*x + rnorm(1000, mean=0, sd=1)
tmpFrame <- data.frame(x, y)
tmpNames <- names(tmpFrame)

# Create a model that includes an expected covariance matrix,
# an expectation function, a fit function, and an observed covariance matrix

data <- mxData(cov(tmpFrame), type="cov", numObs = 1000)
expCov <- mxMatrix(type="Symm", nrow=2, ncol=2, values=c(.2,.1,.2), free=TRUE, name="expCov")
expFunction <- mxExpectationNormal(covariance="expCov", dimnames=tmpNames)
fitFunction <- mxFitFunctionML()
testModel <- mxModel(model="testModel", expCov, data, expFunction, fitFunction)

#Use mxRun to optimize the free parameters in the expected covariance matrix
modelOut <- mxRun(testModel, checkpoint = TRUE)
modelOut$expCov
```



```
#Use mxRestore to load the last checkpoint saved state of the model
modelRestore <- mxRestore(testModel)
modelRestore$expCov
```

mxRObjective

DEPRECATED: Create MxRObjective Object

Description

WARNING: Objective functions have been deprecated as of OpenMx 2.0.

Please use `mxFitFunctionR()` instead. As a temporary workaround, `mxRObjective` returns a list containing a NULL `MxExpectation` object and an `MxFitFunctionR` object.

All occurrences of

```
mxRObjective(fitfun, ...)
```

Should be changed to

```
mxFitFunctionR(fitfun, ...)
```

Arguments

`objfun` A function that accepts two arguments.

`...` The initial state information to the objective function.

Details

NOTE: THIS DESCRIPTION IS DEPRECATED. Please change to using [mxExpectationNormal](#) and [mxFitFunctionML](#) as shown in the example below.

The `fitfun` argument must be a function that accepts two arguments. The first argument is the `mxModel` that should be evaluated, and the second argument is some persistent state information that can be stored between one iteration of optimization to the next iteration. It is valid for the function to simply ignore the second argument.

The function must return either a single numeric value, or a list of exactly two elements. If the function returns a list, the first argument must be a single numeric value and the second element will be the new persistent state information to be passed into this function at the next iteration. The single numeric value will be used by the optimizer to perform optimization.

The initial default value for the persistent state information is NA.

Throwing an exception (via `stop`) from inside `fitfun` may result in unpredictable behavior. You may want to wrap your code in `tryCatch` while experimenting.

Value

Returns a list containing a NULL `mxExpectation` object and an `MxFitFunctionR` object.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```
# Create and fit a model using mxFitFunctionR

library(OpenMx)

A <- mxMatrix(nrow = 2, ncol = 2, values = c(1:4), free = TRUE, name = 'A')
squared <- function(x) { x ^ 2 }

# Define the objective function in R

objFunction <- function(model, state) {
  values <- model$A$values
  return(squared(values[1,1] - 4) + squared(values[1,2] - 3) +
    squared(values[2,1] - 2) + squared(values[2,2] - 1))
}

# Define the expectation function

fitFunction <- mxFitFunctionR(objFunction)

# Define the model

tmpModel <- mxModel(model="exampleModel", A, fitFunction)

# Fit the model and print a summary

tmpModelOut <- mxRun(tmpModel)
summary(tmpModelOut)
```

mxRowObjective

DEPRECATED: Create MxRowObjective Object

Description

WARNING: Objective functions have been deprecated as of OpenMx 2.0.

Please use `mxFitFunctionRow()` instead. As a temporary workaround, `mxRowObjective` returns a list containing a NULL `MxExpectation` object and an `MxFitFunctionRow` object.

All occurrences of

```
mxRowObjective(rowAlgebra, reduceAlgebra, dimnames, rowResults = "rowResults", filteredDataRow = "filteredDataRow", existenceVector = "existenceVector")
```

Should be changed to

```
mxFitFunctionRow(rowAlgebra, reduceAlgebra, dimnames, rowResults = "rowResults", filteredDataRow = "filteredDataRow", existenceVector = "existenceVector")
```

Arguments

rowAlgebra	A character string indicating the name of the algebra to be evaluated row-wise.
reduceAlgebra	A character string indicating the name of the algebra that collapses the row results into a single number which is then optimized.
dimnames	A character vector of names corresponding to columns be extracted from the data set.
rowResults	The name of the auto-generated "rowResults" matrix. See details.
filteredDataRow	The name of the auto-generated "filteredDataRow" matrix. See details.
existenceVector	The name of the auto-generated "existenceVector" matrix. See details.

Details

Objective functions are functions for which free parameter values are chosen such that the value of the objective function is minimized. The `mxRowObjective` function evaluates a user-defined `MxAlgebra` object called the 'rowAlgebra' in a row-wise fashion. It then stores results of the row-wise evaluation in another `MxAlgebra` object called the 'rowResults'. Finally, the `mxRowObjective` function collapses the row results into a single number which is then used for optimization. The `MxAlgebra` object named by the 'reduceAlgebra' collapses the row results into a single number.

The 'filteredDataRow' is populated in a row-by-row fashion with all the non-missing data from the current row. You cannot assume that the length of the filteredDataRow matrix remains constant (unless you have no missing data). The 'existenceVector' is populated in a row-by-row fashion with a value of 1.0 in column j if a non-missing value is present in the data set in column j, and a value of 0.0 otherwise. Use the functions `omxSelectRows`, `omxSelectCols`, and `omxSelectRowsAndCols` to shrink other matrices so that their dimensions will be conformable to the size of 'filteredDataRow'.

Value

Please use `mxFitFunctionRow()` instead. As a temporary workaround, `mxRowObjective` returns a list containing a NULL `MxExpectation` object and an `MxFitFunctionRow` object.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```
# Model that adds two data columns row-wise, then sums that column
# Notice no optimization is performed here.

library(OpenMx)

xdat <- data.frame(a=rnorm(10), b=1:10) # Make data set
amod <- mxModel(model="example1",
  mxData(observed=xdat, type='raw'),
  mxAlgebra(sum(filteredDataRow), name = 'rowAlgebra'),
  mxAlgebra(sum(rowResults), name = 'reduceAlgebra'),
```

```

        mxFitFunctionRow(
            rowAlgebra='rowAlgebra',
            reduceAlgebra='reduceAlgebra',
            dimnames=c('a','b'))
    )
    amodOut <- mxRun(amod)
    mxEval(rowResults, model=amodOut)
    mxEval(reduceAlgebra, model=amodOut)

# Model that find the parameter that minimizes the sum of the
# squared difference between the parameter and a data row.

bmod <- mxModel(model="example2",
    mxData(observed=xdat, type='raw'),
    mxMatrix(values=.75, ncol=1, nrow=1, free=TRUE, name='B'),
    mxAlgebra((filteredDataRow - B) ^ 2, name='rowAlgebra'),
    mxAlgebra(sum(rowResults), name='reduceAlgebra'),
    mxFitFunctionRow(
        rowAlgebra='rowAlgebra',
        reduceAlgebra='reduceAlgebra',
        dimnames=c('a'))
    )
    bmodOut <- mxRun(bmod)
    mxEval(B, model=bmodOut)
    mxEval(reduceAlgebra, model=bmodOut)
    mxEval(rowResults, model=bmodOut)

```

mxRun

Send a Model to the Optimizer

Description

This function begins optimization on the top-level model.

Usage

```

mxRun(model, ..., intervals = NULL, silent = FALSE, suppressWarnings = FALSE,
    unsafe = FALSE, checkpoint = FALSE, useSocket = FALSE, onlyFrontend = FALSE,
    useOptimizer = TRUE)

```

Arguments

model	A MxModel object to be optimized.
...	Not used. Forces remaining arguments to be specified by name.
intervals	A boolean indicating whether to compute the specified confidence intervals.
silent	A boolean indicating whether to print status to terminal.
suppressWarnings	A boolean indicating whether to suppress warnings.

unsafe	A boolean indicating whether to ignore errors.
checkpoint	A boolean indicating whether to periodically write parameter values to a file.
useSocket	A boolean indicating whether to periodically write parameter values to a socket.
onlyFrontend	A boolean indicating whether to run only front-end model transformations.
useOptimizer	A boolean indicating whether to run only the log-likelihood of the current free parameter values but not move any of the free parameters.

Details

The mxRun function is used to optimize free parameters in [MxModel](#) objects based on an expectation function and fit function. MxModel objects included in the mxRun function must include an appropriate expectation and fit functions.

If the 'silent' flag is TRUE, then model execution will not print any status messages to the terminal.

If the 'suppressWarnings' flag is TRUE, then model execution will not issue a warning if NPSOL returns a non-zero status code.

If the 'unsafe' flag is TRUE, then any error conditions will throw a warning instead of an error. It is strongly recommended to use this feature only for debugging purposes.

Free parameters are estimated or updated based on the expectation and fit functions. These estimated values, along with estimation information and model fit, can be found in the 'output' slot of MxModel objects after mxRun has been used.

If a model is dependent on or shares parameters with another model, both models must be included as arguments in another MxModel object. This top-level MxModel object must include expectation and fit functions in both submodels, as well as an additional fit function describing how the results of the first two should be combined.

Value

Returns an MxModel object with free parameters updated to their final values. The return value contains an "output" slot with the results of optimization.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```
# Create and run the 1-factor CFA on the openmx.psyc.virginia.edu front page

library(OpenMx)

data(demoOneFactor) # load the demoOneFactor dataframe

manifests <- names(demoOneFactor) # set the manifest to the 5 demo variables
latents  <- c("G") # define 1 latent variable
model <- mxModel(model="One Factor", type="RAM",
  manifestVars = manifests,
  latentVars  = latents,
```

```

    mxPath(from=latents, to=manifests, labels=paste("b", 1:5, sep="")),
    mxPath(from=manifests, arrows=2, labels=paste("u", 1:5, sep="")),
    mxPath(from=latents, arrows=2, free=FALSE, values=1.0),
    mxData(cov(demoOneFactor), type="cov", numObs=500)
  )
  model <- mxRun(model) # Run the model, returning the result into model
  summary(model) # Show summary of the fitted model

```

 mxSave

Save End State to Checkpoint File

Description

The function saves the last state of a model to a checkpoint file.

Usage

```
mxSave(model, chkpt.directory = ".", chkpt.prefix = "")
```

Arguments

`model` [MxModel](#) object to be loaded.

`chkpt.directory` character. Directory where the checkpoint file is located.

`chkpt.prefix` character. Prefix of the checkpoint file.

Details

In general, the arguments ‘`chkpt.directory`’ and ‘`chkpt.prefix`’ should be identical to the [mxOption](#): ‘Checkpoint Directory’ and ‘Checkpoint Prefix’ that were specified on the model before execution.

Alternatively, the checkpoint file can be manually loaded as a data.frame in R. Use [read.table](#) with the options `header=TRUE`, `sep="\t"`, `stringsAsFactors=FALSE`, `check.names=FALSE`.

Value

Returns a logical indicating the succes of writing the checkpoint file to the checkpoint directory.

References

The OpenMx User’s guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```

library(OpenMx)

# Simulate some data

x=rnorm(1000, mean=0, sd=1)
y= 0.5*x + rnorm(1000, mean=0, sd=1)
tmpFrame <- data.frame(x, y)
tmpNames <- names(tmpFrame)

# Create a model that includes an expected covariance matrix,
# an expectation function, a fit function, and an observed covariance matrix

data <- mxData(cov(tmpFrame), type="cov", numObs = 1000)
expCov <- mxMatrix(type="Symm", nrow=2, ncol=2, values=c(.2,.1,.2), free=TRUE, name="expCov")
expFunction <- mxExpectationNormal(covariance="expCov", dimnames=tmpNames)
fitFunction <- mxFitFunctionML()
testModel <- mxModel(model="testModel", expCov, data, expFunction, fitFunction)

#Use mxRun to optimize the free parameters in the expected covariance matrix
modelOut <- mxRun(testModel)
modelOut$expCov

# Save the ending state of modelOut in a checkpoint file
mxSave(modelOut)

# Restore the saved model from the checkpoint file
modelSaved <- mxRestore(testModel)
modelSaved$expCov

# Imagine how much time you saved by not having to re-run the
# model that took hours or days to run.

```

 mxSE

Compute standard errors in OpenMx

Description

This function allows you to obtain standard errors for arbitrary expressions, named entities, and algebras.

Usage

```
mxSE(x, model, details = FALSE, ...)
```

Arguments

x the parameter to get SEs on (reference or expression)

model	the <code>mxModel</code> to use.
details	logical. Whether to provide further details, e.g. the full sampling covariance matrix of x.
...	further named arguments passed to <code>mxEval</code>

Details

x can be the name of an algebra, a bracket address, named entity or arbitrary expression. It is a frontend-only file that works much like `mxEval`. When the `details` argument is `TRUE`, the full sampling covariance matrix of x is also returned as part of a list. The square root of the diagonals of this sampling covariance matrix are the standard errors.

Value

SE value(s) returned as a matrix when `details` is `FALSE`. When `details` is `TRUE`, a list of the SE value(s) and the full sampling covariance matrix.

References

- https://en.wikipedia.org/wiki/Standard_error

See Also

- `mxCI`

Examples

```
library(OpenMx)
data(demoOneFactor)
# =====
# = Make and run a 1-factor CFA =
# =====

latents = c("G") # the latent factor
manifests = names(demoOneFactor) # manifest variables to be modeled
# =====
# = Make and run the model! =
# =====
m1 <- mxModel("One Factor", type = "RAM",
  manifestVars = manifests, latentVars = latents,
  mxPath(from = latents, to = manifests),
  mxPath(from = manifests, arrows = 2),
  mxPath(from = latents, arrows = 2, free = FALSE, values = 1),
  mxData(cov(demoOneFactor), type = "cov", numObs = 500)
)
m1 = mxRun(m1)
mxSE('A', model = m1)
mxSE((A + A) %*% S, model = m1)
mxSE(S, model = m1)
mxSE(A[1,2], model = m1)
mxSE(A[1,6]^2, model = m1)
```



```
mxSE(A[,6]%%2, model = m1, details = TRUE)
```

```
mxSetDefaultOptions     Reset global options to the default
```

Description

Reset global options to the default

Usage

```
mxSetDefaultOptions()
```

```
mxSimplify2Array        Like simplify2array but works with vectors of different lengths
```

Description

Vectors are filled column-by-column into a matrix. Shorter vectors are padded with NAs to fill whole columns.

Usage

```
mxSimplify2Array(x, higher = FALSE)
```

Arguments

x	a list of vectors
higher	whether to produce a higher rank array (defaults to FALSE)

Examples

```
v1 <- 1:3
v2 <- 4:5
v3 <- 6:10
mxSimplify2Array(list(v1,v2,v3))

#      [,1] [,2] [,3]
# [1,]  1   4   6
# [2,]  2   5   7
# [3,]  3  NA   8
# [4,] NA  NA   9
# [5,] NA  NA  10
```

mxStandardizeRAMpaths *Standardize RAM models' path coefficients*

Description

Provides a dataframe containing the standardized values of all nonzero path coefficients appearing in the A and S matrices of models that use RAM expectation (either of type="RAM" or containing an explicit `mxExpectationRAM()` statement). These standardized values are what the path coefficients would be if all variables in the analysis—both manifest and latent—were standardized to unit variance. Can optionally include asymptotic standard errors for those standardized coefficients, computed via the delta method.

Usage

```
mxStandardizeRAMpaths(model, SE=FALSE)
```

Arguments

model	An <code>mxModel</code> object, that either uses RAM expectation or contains at least one submodel that does.
SE	Logical. Should standard errors be included with the standardized point estimates? Defaults to FALSE. Certain conditions are required for use of SE=TRUE; see "Details" below.

Details

Matrix A contains the Asymmetric paths, i.e. the single-headed arrows. Matrix S contains the Symmetric paths, i.e. the double-headed arrows. The function will work even if `mxMatrix` objects named "A" and "S" are absent from the model, since it identifies which matrices in the model have been assigned the roles of A and S in the `mxExpectationRAM` statement. Note that, in models of type="RAM", the necessary matrices and expectation statement are automatically assembled from the `mxPath` objects.

If model contains any submodels with `independent=TRUE` that use RAM expectation, `mxStandardizeRAMpaths()` automatically applies itself recursively over those submodels.

Use of SE=TRUE requires that package `numDeriv` be installed. It also requires that model contain no `mxConstraint` statements, and have a nonempty hessian element in its output slot. There are three common reasons why the latter condition may not be met. First, the model may not have been run yet, i.e. it was not output by `mxRun()`. Second, `mxOption` "Hessian" might be set to "No". Third, computing the Hessian matrix might possibly have been skipped per a user-defined `mxCompute*` statement (if any are present in the model). If model contains RAM-expectation submodels with `independent=TRUE`, these conditions are checked separately for each such submodel.

In any event, using these standard errors for hypothesis-testing or forming confidence intervals is *not* generally advised. Instead, it is considered best practice to conduct likelihood-ratio tests or compute likelihood-based confidence intervals (from `mxCI()`), as in examples below.

The user should note that `mxStandardizeRAMpaths()` only cares whether an element of A or S is nonzero, and not whether it is a fixed or free parameter. So, for instance, if the function is used on a

model not yet run, any free parameters in A or S initialized at zero will not appear in the function's output.

The user is warned to interpret the output of `mxStandardizeRAMpaths()` cautiously if any elements of A or S depend upon definition variables.

Value

If argument `model` is a single-group model that uses RAM expectation, then `mxStandardizeRAMpaths()` returns a dataframe, with one row for each nonzero path coefficient in A and S, and with the following columns:

<code>name</code>	Character strings that uniquely identify each nonzero path coefficient in terms of the model name, the matrix ("A" or "S"), the row number, and the column number.
<code>label</code>	Character labels for those path coefficients that are labeled elements of an <code>mxMatrix</code> object, and NA for those that are not. Note that path coefficients having the same label (and therefore the same UNstandardized value) can have different standardized values, and therefore the same label may appear more than once in this dataframe.
<code>matrix</code>	Character strings of "A" or "S", depending on which matrix contains the given path coefficient.
<code>row</code>	Character. The rownames of the matrix containing each path coefficient; row numbers are used instead if the matrix has no rownames.
<code>col</code>	Character. The colnames of the matrix containing each path coefficient; column numbers are used instead if the matrix has no colnames.
<code>Raw.Value</code>	Numeric values of the raw (i.e., UNstandardized) path coefficients.
<code>Raw.SE</code>	Numeric values of the asymptotic standard errors of the raw path coefficients if <code>SE=TRUE</code> , or NA otherwise.
<code>Std.Value</code>	Numeric values of the standardized path coefficients.
<code>Std.SE</code>	Numeric values of the asymptotic standard errors of the standardized path coefficients if <code>SE=TRUE</code> , or NA otherwise.

If `model` is a multi-group model containing at least one submodel with RAM expectation, then `mxStandardizeRAMpaths()` returns a list. The list has a number of elements equal to the number of submodels that either have RAM expectation or contain a submodel that does. List elements corresponding to RAM-expectation submodels contain a dataframe, as described above. List elements corresponding to "container" submodels are themselves lists, of the kind described here.

Examples

```
library(OpenMx)
data(demoOneFactor)
manifests <- names(demoOneFactor)
latents   <- c("G")
factorModel <- mxModel(model="One Factor", type="RAM",
  manifestVars = manifests,
  latentVars   = latents,
```

```

    mxPath(from=latents, to=manifests),
    mxPath(from=manifests, arrows=2, values=0.1),
    mxPath(from=latents, arrows=2, free=FALSE, values=1.0),
    mxData(cov(demoOneFactor), type="cov", numObs=500)
)
factorFit <- mxRun(factorModel)
summary(factorFit)$parameters
mxStandardizeRAMpaths(model=factorFit, SE=FALSE)

## Likelihood ratio test of variable x1's factor loading:
factorModelNull <- omxSetParameters(factorModel, labels="One Factor.A[1,6]",
    values=0, free=FALSE)
factorFitNull <- mxRun(factorModelNull)
mxCompare(factorFit, factorFitNull)[2, "p"] #<--p-value

## Confidence intervals for all standardized paths:
factorModel2 <- mxModel(model=factorModel,
    mxMatrix(type="Iden", nrow=nrow(factorModel$A), name="I"),
    mxAlgebra( vec2diag(diag2vec( solve(I-A)%%S%%t(solve(I-A)) )%^-0.5) ,
        name="InvSD"),
    mxAlgebra( InvSD %% A %% solve(InvSD),
        name="Az", dimnames=dimnames(factorModel$A)),
    mxAlgebra( InvSD %% S %% InvSD,
        name="Sz", dimnames=dimnames(factorModel$S)),
    mxCI(c("Az", "Sz"))
)
## Not run:
factorFit2 <- mxRun(factorModel2, intervals=TRUE)
## Contains point values and confidence limits for all paths:
summary(factorFit2)$CI

## End(Not run)

```

mxThreshold

Create List of Thresholds

Description

This function creates a list of thresholds which mxModel can use to set up a thresholds matrix for a RAM model.

Usage

```

mxThreshold(vars, nThresh=NA,
    free=FALSE, values=NA, labels=NA,
    lbound=NA, ubound=NA)

```

Arguments

vars	character vector. These are the variables for which thresholds are to be specified.
nThresh	numeric vector. These are the number of thresholds for each variables listed in 'vars'.
free	boolean vector. Indicates whether threshold parameters are free or fixed.
values	numeric vector. The starting values of the parameters.
labels	character vector. The names of the parameters.
lbound	numeric vector. The lower bounds of free parameters.
ubound	numeric vector. The upper bounds of free parameters.

Details

If you are new to ordinal data modeling and just want something quick to make your ordinal data work, we recommend you try the `umxThresholdMatrix` function in the `umx` package.

The `mxPath` function creates `MxThreshold` objects. These consist of a list of ordinal variables and the thresholds that define the relationship between the observed ordinal variable and the continuous latent variable assumed to underly it. This function directly mirrors the usage of `mxPath`, but is used to specify thresholds rather than means, variances and bivariate relationships.

The 'vars' argument specifies which variables you wish to specify thresholds for. Variables are referenced by name, and these names must appear in the 'manifestVar' argument of the `mxModel` function if thresholds are to be correctly processed. Additionally, variables for which thresholds are specified must be specified as ordinal factors in whatever data is included in the model.

The 'nThresh' argument specifies how many thresholds are to be specified for the variable or variables included in the 'vars' argument. The number of thresholds for a particular variable should be one fewer than the number of categories specified for that variable.

The 'free' argument specifies whether the thresholds created by the `mxThreshold` function are free or fixed parameters. This argument may take either TRUE for free parameters, FALSE for fixed parameters, or a vector of TRUEs and FALSEs to be applied in order to the created thresholds.

'values' is a numeric vector containing the starting values of the created thresholds. This gives a starting point for estimation. The 'labels' argument specifies the names of the parameters in the resulting `MxThreshold` object. The 'lbound' and 'ubound' arguments specify lower and upper bounds for the created threshold parameters.

Thresholds for multiple variables may be specified simultaneously by including a vector of variable names to the 'vars' argument. When multiple variables are included in the 'vars' argument, the length of the 'vars' argument must be evenly divisible by the length of the 'nThresh' argument. All subsequent arguments ('free' through 'ubound') should have their lengths be a factor of the total number of thresholds specified for all variables.

If four variables are included in the 'vars' argument, then the 'nThresh' argument should contain either one, two or four elements. If the 'nThresh' argument specifies two thresholds for each variable, then 'free', 'values', and all subsequent arguments should specify eight values by including one, two, four or eight elements. Whenever fewer values are specified than are required (e.g., specify two values for eight thresholds), then the entire vector of values is repeated until the required number of values is reached, and will return an error if the correct number of values cannot be achieved by repeating the entire vector.

Value

Returns a list of thresholds.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

`umxThresholdMatrix` `demo("mxThreshold")` `mxPath` for comparable specification of paths. `mxMatrix` for a matrix-based approach to thresholds specification; `mxModel` for the container in which `mxThresholds` are embedded. More information about the OpenMx package may be found [here](#).

Examples

```
library(OpenMx)
# threshold objects for three variables: 2 binary, and one ordinal.
mxThreshold(vars = c("z1", "z2", "z3"), nThresh = c(1,1,2),
  free = TRUE, values = c(-1, 0, -.5, 1.2) )
```

 mxTryHard

Make multiple attempts to run a model

Description

Makes multiple attempts to fit an `MxModel` object with `mxRun()` until the optimizer yields an acceptable solution or the maximum number of attempts is reached. Each attempt uses the parameter estimates of the previous attempt as start values, but they are each perturbed by random numbers, and optimization-control parameters may be altered. From among its attempts, the function returns the fitted, post-`mxRun()` model with the smallest fit-function value, and can print to the console the start values it used for that model.

Usage

```
mxTryHard(model, extraTries = 10, greenOK = FALSE, loc = 1, scale = 0.25,
  initialGradientStepSize = imxAutoOptionValue("Gradient step size"),
  initialGradientIterations = imxAutoOptionValue('Gradient iterations'),
  initialTolerance=as.numeric(mxOption(NULL, 'Optimality tolerance')),
  checkHess = TRUE, fit2beat = Inf, paste = TRUE, iterationSummary=FALSE,
  bestInitsOutput=TRUE, showInits=FALSE, verbose=0, intervals = FALSE,
  finetuneGradient=TRUE, jitterDistrib=c("runif", "rnorm", "rcauchy"), exhaustive=FALSE,
  maxMajorIter=3000, OKstatuscodes, wtgcsv=c("prev", "best", "initial"))

mxTryHardOrig(model, finetuneGradient=FALSE, maxMajorIter=NA,
  wtgcsv=c("prev", "best"), ...)

mxTryHardctsem(model, initialGradientStepSize = .00001,
```

```

initialGradientIterations = 1,
initialTolerance=1e-12,jitterDistrib="rnorm", ...)

mxTryHardWideSearch(model, finetuneGradient=FALSE, jitterDistrib="rcauchy",
exhaustive=TRUE, wtgcsv="prev", ...)

mxTryHardOrdinal(model, greenOK = TRUE,checkHess = FALSE,
finetuneGradient=FALSE, exhaustive=TRUE,
OKstatuscodes=c(0,1,5,6), wtgcsv=c("prev","best"), ...)

```

Arguments

model	The MxModel to be run.
extraTries	The number of attempts to run the model <i>in addition to the first</i> . In effect, is the maximum number of attempts mxTryHard() will make, since the function will stop once an acceptable solution is reached. Defaults to 10 (for mxTryHard()), in which case a maximum of 11 total attempts will be made.
greenOK	Logical; is a solution with Mx status GREEN (optimizer status code 1) acceptable? Defaults to FALSE (for mxTryHard()). Ignored if a value is provided for OKstatuscodes.
loc, scale	Numeric. The location and scale parameters of the distribution from which random values are drawn to perturb start values between attempts, defaulting respectively to 1 and 0.25. See below, under "Details," for additional information.
initialGradientStepSize, initialGradientIterations, initialTolerance	Numeric. Initial values of optimization-control parameters passed to mxComputeGradientDescent() if model is using the default compute plan.
checkHess	Logical; is a positive-definite Hessian a requirement for an acceptable solution? Defaults to TRUE (for mxTryHard()). If TRUE, the Hessian and standard errors are calculated with each fit attempt, irrespective of the value of relevant options . The exception is if model or any of its submodels contains MxConstraints , in which case checkHess is coerced to TRUE.
fit2beat	Numeric upper limit to the fitfunction value that an acceptable solution may have. Useful if a nested submodel of model has already been fitted, since model, with its additional free parameters, should not yield a fitfunction value any greater than that of the submodel.
paste	Logical. If TRUE (default), start values for the returned fitted model are printed to console as a comma-separated string. This is useful if the user wants to copy-paste these values into an R script, say, in an omxSetParameters() statement. If FALSE, the vector of start values is printed as-is. Note that this vector, from omxGetParameters() , has names corresponding to the free parameters; these names are not displayed when paste=TRUE.
iterationSummary	Logical. If TRUE, displays parameter estimates and fit values for every fit attempt. Defaults to FALSE.
bestInitsOutput	Logical. If TRUE, displays starting values that resulted in best fit, according to format specified by paste argument. Defaults to TRUE.

showInits	Logical. If TRUE, displays starting values for every fit attempt. Defaults to FALSE.
verbose	If model is using the default compute plan, is passed to <code>mxComputeGradientDescent()</code> to specify level of output printed to console during optimization.
intervals	Logical. If TRUE, OpenMx will estimate any specified confidence intervals.
finetuneGradient	Logical. If TRUE (default for <code>mxTryHard()</code>), then as repeated fit attempts appear to be improving, <code>mxTryHard()</code> will adjust optimization-control parameters <code>gradientStepSize</code> , <code>gradientIterations</code> , and <code>tolerance</code> , as well as argument scale, to "fine-tune" its convergence toward an optimal solution. <code>finetuneGradient=FALSE</code> is recommended for analyses involving thresholds.
jitterDistrib	Character string naming which random-number distribution—either <code>uniform (rectangular)</code> , <code>normal (Gaussian)</code> , or <code>Cauchy</code> —to be used to perturb start values. Defaults to the uniform distribution (for <code>mxTryHard()</code>). See below, under "Details," for additional information.
exhaustive	Logical. If FALSE (default for <code>mxTryHard()</code>), <code>mxTryHard()</code> stops making additional attempts once it reaches an acceptable solution. If TRUE, the function instead continues until it reaches its maximum number of attempts (as per <code>extraTries</code>), and returns the best solution it found.
maxMajorIter	Integer; passed to <code>mxComputeGradientDescent()</code> . Defaults to 3000, which was the internally hardcoded value <code>mxTryHard()</code> used in at least one prior version of OpenMx. Value of NA is permitted, in which case <code>mxTryHard()</code> will calculate a value via the on-load default formula for the "Major iterations" option.
OKstatuscodes	Optional integer vector containing optimizer status codes that an acceptable solution is permitted to have. <code>mxTryHard()</code> always considers a status code of 0 to be acceptable, this argument notwithstanding. By default, <code>mxTryHard()</code> will consider status code 0 acceptable, and, if <code>greenOK=TRUE</code> , status code 1 as well. If a value is supplied for <code>OKstatuscodes</code> that conflicts with <code>greenOK</code> , <code>OKstatuscodes</code> controls.
wtgcsv	Character vector. "Where to get current start values." See below, under "Details," for additional information.
...	Additional arguments to be passed to <code>mxTryHard()</code> .

Details

`mxTryHardOrig()`, `mxTryHardctsem()`, `mxTryHardWideSearch()`, and `mxTryHardOrdinal()` are wrapper functions to the main workhorse function `mxTryHard()`. Each wrapper function has default values for certain arguments that are tailored toward a specific purpose. `mxTryHardOrig()` imitates the functionality of the earliest implementations of `mxTryHard()` in OpenMx's history; its chief purpose is to find good start values that lead to an acceptable solution. `mxTryHardctsem()` uses `mxTryHard()` to "zero in" on an acceptable solution with models that can be difficult to optimize, such as continuous-time state-space models. `mxTryHardWideSearch()` uses `mxTryHard()` to search a wide region of the parameter space, in hope of avoiding local fitfunction minima. `mxTryHardOrdinal()` attempts to use `mxTryHard()` as well as it can be used with models involving ordinal data.

Argument `wtgcsv` dictates where `mxTryHard()` is permitted to find free-parameter values, at the start of each fit attempt after the first, before randomly perturbing them to create the current fit attempt's start values. If `"prev"` is included, then `mxTryHard()` is permitted to use the parameter estimates of the most recent non-error fit attempt. If `"best"` is included, then `mxTryHard()` is permitted to use the parameter estimates at the best solution so far. If `"initial"` is included, then `mxTryHard()` is permitted to use the initial start values in `model`, as provided by the user. The default is to permit all three, in which case `mxTryHard()` is written to use the best solution's values if available, and otherwise to use the most recent solution's values, but to periodically revert to the initial values if recent fit attempts have not improved on the best solution.

Once the start values are located for the current fit attempt, they are randomly perturbed before being assigned to the `MxModel`. The distributional family from which the perturbations are randomly generated is dictated by argument `jitterDistrib`. The distribution is parametrized by arguments `loc` and `scale`, respectively the location and scale parameters. The location parameter is the distribution's median. For the uniform distribution, `scale` is the absolute difference between its median and extrema (i.e., half the width of the rectangle); for the normal distribution, `scale` is its standard deviation; and for the Cauchy, `scale` is one-half its interquartile range. Start values are first multiplied by random draws from a distribution with the provided `loc` and `scale`, then added to random draws from a distribution with the same `scale` but with a median of zero.

Value

Usually, `mxTryHard()` returns a post-`mxRun()` `MxModel` object. Specifically, this will be the fitted model having the smallest fit-function value found by `mxTryHard()` during its attempts. The start values used to obtain this fitted model are printed to console if `bestInitsOutput=TRUE`.

If every attempt at running `model` fails, `mxTryHard()` returns an object of class `'try-error'`.

`mxTryHard()` throws a warning if the returned `MxModel` object has a nonzero status code (unless nonzero status codes are considered acceptable per argument `greenOK` or `OKstatuscodes`).

See Also

[mxRun\(\)](#), [mxComputeTryHard](#)

Examples

```
library(OpenMx)

data(demoOneFactor) # load the demoOneFactor dataframe

manifests <- names(demoOneFactor) # set the manifest to the 5 demo variables
latents <- c("G") # define 1 latent variable
model <- mxModel(model="One Factor", type="RAM",
  manifestVars = manifests,
  latentVars = latents,
  mxPath(from=latents, to=manifests, labels=paste("b", 1:5, sep="")),
  mxPath(from=manifests, arrows=2, labels=paste("u", 1:5, sep="")),
  mxPath(from=latents , arrows=2, free=FALSE, values=1.0),
  mxData(cov(demoOneFactor), type="cov", numObs=500)
)
```

```
model <- mxTryHard(model) # Run the model, returning the result into model
summary(model) # Show summary of the fitted model
```

 mxTypes

List Currently Available Model Types

Description

This function returns a vector of the currently available type names.

Usage

```
mxTypes()
```

Value

Returns a character vector of type names.

Examples

```
mxTypes()
```

 mxVersion

Returns Current Version String

Description

This function returns a string with the current version number of OpenMx. Optionally (with `verbose = TRUE` (the default)), it prints a message containing the version of R, the platform, and the optimiser.

Usage

```
mxVersion(model = NULL, verbose = TRUE)
```

Arguments

model	optional MxModel to request optimizer from (default = NULL)
verbose	Whether to print version information to the console (default = TRUE)

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```

# Print useful version information.
mxVersion()
# If you just want the version, use this call.
x = mxVersion(verbose=FALSE)

library(OpenMx)
data(demoOneFactor) # load the demoOneFactor dataframe
manifests <- names(demoOneFactor) # set the manifest to the 5 demo variables
latents <- c("G") # define 1 latent variable
model <- mxModel(model = "One Factor", type = "RAM",
  manifestVars = manifests,
  latentVars = latents,
  mxPath(from = latents, to = manifests, labels = paste("b", 1:5, sep = "")),
  mxPath(from = manifests, arrows = 2, labels = paste("u", 1:5, sep = "")),
  mxPath(from = latents, arrows = 2, free = FALSE, values = 1.0),
  mxData(cov(demoOneFactor), type = "cov", numObs = 500)
)
mxVersion(model, verbose = TRUE)

```

myAutoregressiveData *Example data with autoregressively related columns*

Description

Data set used in some of OpenMx's examples.

Usage

```
data("myAutoregressiveData")
```

Format

A data frame with 100 observations on the following variables.

```

x1 x variable and time 1
x2 x variable and time 2
x3 x variable and time 3
x4 x variable and time 4
x5 x variable and time 5

```

Details

The rows are independently and identically distributed, but the columns are and auto-correlation structure.

Source

Simulated.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```
data(myAutoregressiveData)
round(cor(myAutoregressiveData), 2)
# note the sub-diagonal correlations (lag 1)
# x1-x2, x2-x3, x3-x4, x4-x5
# and the second sub-diagonal correlations (lag 2)
# x1-x3, x2-x4, x3-x5
```

myFADDataRaw

Example 500-row dataset with 12 generated variables

Description

Twelve columns of generated numeric data: x1 x2 x3 x4 x5 x6 y1 y2 y3 z1 z2 z3.

Usage

```
data(myFADDataRaw)
```

Details

The x variables intercorrelate around .6 with each other.

The y variables intercorrelate around .5 with each other, and correlate around .3 with the X vars.

There are three ordinal variables, z1, z2, and z3.

The data are used in some OpenMx examples, especially confirmatory factor analysis.

There are no missing data.

Examples

```
data(myFADDataRaw)
str(myFADDataRaw)
```

`myGrowthKnownClassData`*Data for a growth mixture model with the true class membership*

Description

Data set used in some of OpenMx's examples.

Usage

```
data("myGrowthKnownClassData")
```

Format

A data frame with 500 observations on the following variables.

x1 x variable and time 1

x2 x variable and time 2

x3 x variable and time 3

x4 x variable and time 4

x5 x variable and time 5

c Known class membership variable

Details

The same as [myGrowthMixtureData](#), but with the class membership variable.

Source

Simulated.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```
data(myGrowthKnownClassData)

#plot the observed trajectories
# blue lines are class 1, green lines are class 2
colSel <-c('blue', 'green')[myGrowthKnownClassData$c]
matplot(t(myGrowthKnownClassData[,-6]), type='l', lty=1, col=colSel)
```

myGrowthMixtureData *Data for a growth mixture model*

Description

Data set used in some of OpenMx's examples.

Usage

```
data("myGrowthMixtureData")
```

Format

A data frame with 500 observations on the following variables.

x1 x variable and time 1

x2 x variable and time 2

x3 x variable and time 3

x4 x variable and time 4

x5 x variable and time 5

Details

The same as [myGrowthKnownClassData](#), but without the class membership variable.

Source

Simulated.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```
data(myGrowthMixtureData)

matplot(t(myGrowthMixtureData), type='l', lty=1)

data(myGrowthKnownClassData)
all(myGrowthKnownClassData[,-6]==myGrowthMixtureData)
```

myLongitudinalData *Data for a linear latent growth curve model*

Description

Data set used in some of OpenMx's examples.

Usage

```
data("myLongitudinalData")
```

Format

A data frame with 500 observations on the following variables.

x1 x variable and time 1

x2 x variable and time 2

x3 x variable and time 3

x4 x variable and time 4

x5 x variable and time 5

Details

Linear growth model with mean intercept around 10, and slope of about 1.5.

Source

Simulated.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```
data(myLongitudinalData)
```

```
matplot(t(myLongitudinalData), type='l', lty=1)
```

`myRegData`*Example regression data with correlated predictors*

Description

Data set used in some of OpenMx's examples.

Usage

```
data("myRegData")
```

Format

A data frame with 100 observations on the following variables.

w Predictor variable

x Predictor variable

y Predictor variable

z Outcome variable

Details

w, x, and y are predictors of z. x and y are correlated.

Source

Simulated.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```
data(myRegData)
summary(lm(z ~ ., data=myRegData))
```

`myRegDataRaw`*Example regression data with correlated predictors*

Description

Data set used in some of OpenMx's examples.

Usage

```
data("myRegDataRaw")
```

Format

A data frame with 100 observations on the following variables.

w Predictor variable

x Predictor variable

y Predictor variable

z Outcome variable

Details

w, x, and y are predictors of z. x and y are correlated. Equal to [myRegData](#).

Source

Simulated.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```
data(myRegData)
```

```
data(myRegDataRaw)
```

```
all(myRegDataRaw == myRegData)
```

myTwinData

Twin data on weight and height

Description

Data set used in some of OpenMx's examples.

Usage

```
data("myTwinData")
```

Format

A data frame with 3808 observations on the following variables.

fam Family ID variable

age Age of the twin pair. Range: 17 to 88.

zyg Integer codes for zygosity and gender combinations

part

wt1 Weight in kilograms for twin 1

wt2 Weight in kilograms for twin 2

ht1 Height in meters for twin 1

ht2 Height in meters for twin 2

htwt1 Product of ht and wt for twin 1

htwt2 Product of ht and wt for twin 2

bmi1 Body Mass Index for twin 1

bmi2 Body Mass Index for twin 2

Details

Height and weight are highly correlated, and each individually highly heritable. These data present and opportunity for multivariate behavior genetics modeling.

Source

Timothy Bates

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```
data(myTwinData)
```

```
plot( ht1 ~ wt1, myTwinData)
```

mzfData	<i>MZ female example twin data</i>
---------	------------------------------------

Description

Data for extended twin example ETC88.R

Usage

```
data("mzfData")
```

Format

A data frame with 3099 observations on the following 37 variables.

famid a numeric vector

e1 a numeric vector

e2 a numeric vector

e3 a numeric vector

e4 a numeric vector

e5 a numeric vector

e6 a numeric vector

e7 a numeric vector

e8 a numeric vector

e9 a numeric vector

e10 a numeric vector

e11 a numeric vector

e12 a numeric vector

e13 a numeric vector

e14 a numeric vector

e15 a numeric vector

e16 a numeric vector

e17 a numeric vector

e18 a numeric vector

a1 a numeric vector

a2 a numeric vector

a3 a numeric vector

a4 a numeric vector

a5 a numeric vector

a6 a numeric vector

a7 a numeric vector
a8 a numeric vector
a9 a numeric vector
a10 a numeric vector
a11 a numeric vector
a12 a numeric vector
a13 a numeric vector
a14 a numeric vector
a15 a numeric vector
a16 a numeric vector
a17 a numeric vector
a18 a numeric vector

Examples

```
data(mzfData)  
str(mzfData)
```

mzmData

MZ Male example data

Description

Data for extended twin example ETC88.R

Usage

```
data("mzmData")
```

Format

A data frame with 3019 observations on the following 37 variables.

famid a numeric vector
e1 a numeric vector
e2 a numeric vector
e3 a numeric vector
e4 a numeric vector
e5 a numeric vector
e6 a numeric vector
e7 a numeric vector
e8 a numeric vector

e9 a numeric vector
e10 a numeric vector
e11 a numeric vector
e12 a numeric vector
e13 a numeric vector
e14 a numeric vector
e15 a numeric vector
e16 a numeric vector
e17 a numeric vector
e18 a numeric vector
a1 a numeric vector
a2 a numeric vector
a3 a numeric vector
a4 a numeric vector
a5 a numeric vector
a6 a numeric vector
a7 a numeric vector
a8 a numeric vector
a9 a numeric vector
a10 a numeric vector
a11 a numeric vector
a12 a numeric vector
a13 a numeric vector
a14 a numeric vector
a15 a numeric vector
a16 a numeric vector
a17 a numeric vector
a18 a numeric vector

Examples

```
data(mzmData)  
str(mzmData)
```

 Named-entity

Named Entities

Description

A named entity is an S4 object that can be referenced by name.

Details

Every named entity is guaranteed to have a slot called "name". Within a model, the named entities of that model can be accessed using the \$ operator. Access is limited to one nesting depth, such that if 'B' is a submodel of 'A', and 'C' is a matrix of 'B', then 'C' must be accessed using A\$B\$C.

The following S4 classes are named entities in the OpenMx library: [MxAlgebra](#), [MxConstraint](#), [MxMatrix](#), [MxModel](#), [MxData](#), and [MxObjective](#).

Examples

```
library(OpenMx)

# Create a model, add a matrix to it, and then access the matrix by name.

testModel <- mxModel(model="anEmptyModel")

testMatrix <- mxMatrix(type="Full", nrow=2, ncol=2, values=c(1,2,3,4), name="yourMatrix")

yourModel <- mxModel(testModel, testMatrix, name="noLongerEmpty")

yourModel$yourMatrix
```

 nuclear_twin_design_data

Twin data from a nuclear family design

Description

Data set used in some of OpenMx's examples.

Usage

```
data("nuclear_twin_design_data")
```

Format

A data frame with 1743 observations on the following variables.

Twin1
Twin2
Father
Mother
zyg Zygoty of the twin pair

Details

This is a wide format data set. A single variable has values for different member of the same nuclear family.

Source

Likely simulated.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```
data(nuclear_twin_design_data)
cor(nuclear_twin_design_data[, -5], use="pairwise.complete.obs")
```

numHess1	<i>numeric Hessian data 1</i>
----------	-------------------------------

Description

data file used by the HessianTest.R script

Usage

```
data("numHess1")
```

Format

A 12 by 12 data frame containing Hessian (numeric variables a-1)

Examples

```
data(numHess1)
str(numHess1)
```

numHess2	<i>numeric Hessian data 2</i>
----------	-------------------------------

Description

data file used by the HessianTest.R script

Usage

```
data("numHess2")
```

Format

A 12 by 12 data frame containing Hessian matrix (numeric variables a-l)

Examples

```
data(numHess2)
str(numHess2)
```

omxAllInt	<i>All Interval Multivariate Normal Integration</i>
-----------	-----------------------------------------------------

Description

omxAllInt computes the probabilities of a large number of cells of a multivariate normal distribution that has been sliced by a varying number of thresholds in each dimension. While the same functionality can be achieved by repeated calls to [omxMnor](#), omxAllInt is more efficient for repeated operations on a single covariance matrix. omxAllInt returns an nx1 matrix of probabilities cycling from lowest to highest thresholds in each column with the rightmost variable in *covariance* changing most rapidly.

Usage

```
omxAllInt(covariance, means, ...)
```

Arguments

covariance	the covariance matrix describing the multivariate normal distribution.
means	a row vector containing means of the variables of the underlying distribution.
...	a matrix or set of matrices containing one column of thresholds for each column of covariance. Each column must contain a strictly increasing set of thresholds for the corresponding variable of the underlying distribution. NA values in these thresholds indicate that the list of thresholds in that column has ended.

Details

covariance and *means* contain the covariances and means of the multivariate distribution from which probabilities are to be calculated.

covariance must be a square covariance or correlation matrix with one row and column for each variable.

means must be a vector of length `nrows(covariance)` that contains the mean for each corresponding variable.

All further arguments are considered threshold matrices.

Threshold matrices contain locations of the hyperplanes delineating the intervals to be calculated. The first column of the first matrix corresponds to the thresholds for the first variable represented by the covariance matrix. Subsequent columns of the same matrix correspond to thresholds for subsequent variables in the covariance matrix. If more variables exist in the covariance matrix than in the first threshold matrix, the first column of the second threshold matrix will be used, and so on. That is, if *covariance* is a 4x4 matrix, and the three threshold matrices are specified, one with a single column and the others with two columns each, the first column of the first matrix will contain thresholds for the first variable in *covariance*, the two columns of the second matrix will correspond to the second and third variables of *covariance*, respectively, and the first column of the third threshold matrix will correspond to the fourth variable. Any extra columns will be ignored.

Each column in the threshold matrices must contain some number of strictly increasing thresholds, delineating the boundaries of a cell of integration. That is, if the integral from -1 to 0 and 0 to 1 are required for a given variable, the corresponding threshold column should contain the values -1, 0, and 1, in that order. Thresholds may be set to `Inf` or `-Inf` if a boundary at positive or negative infinity is desired.

Within a threshold column, a value of `+Inf`, if it exists, is assumed to be the largest threshold, and any rows after it are ignored in that column. A value of `NA`, if it exists, indicates that there are no further thresholds in that column, and is otherwise ignored. A threshold column consisting of only `+Inf` or `NA` values will cause an error.

For all $i > 1$, the value in row i must be strictly larger than the value in row $i-1$ in the same column.

The return value of `omxAllInt` is a matrix consisting of a single column with one row for each combination of threshold levels.

See Also

[omxMnor](#)

Examples

```
data(myFADataRaw)

covariance <- cov(myFADataRaw[,1:5])
means <- colMeans(myFADataRaw[,1:5])

# Integrate from -Infinity to 0 and 0 to 1 on first variable
thresholdForColumn1 <- cbind(c(-Inf, 0, 1))
# Note: The first variable will never be calculated from 1 to +Infinity.
```

```

# These columns will be integrated from -Inf to -1, -1 to 0, etc.
thresholdsForColumn2 <- cbind(c(-Inf, -1, 0, 1, Inf))
thresholdsForColumns3and4 <- cbind(c(-Inf, 1.96, 2.326, Inf),
                                   c(-Inf, -1.96, 2.326, Inf))

# The integration
omxAllInt(covariance, means,
          thresholdForColumn1, thresholdsForColumn2,
          thresholdsForColumns3and4, thresholdsForColumn2)
# Notice that columns 2 and 5 are assigned identical thresholds.

#-----
# An alternative specification of the same calculation follows
covariance <- cov(myFADDataRaw[,1:5])
means <- colMeans(myFADDataRaw[,1:5])

# Note NAs to indicate the end of the sequence of thresholds.
thresholds <- cbind(c(-Inf, 0, 1, NA, NA),
                   c(-Inf, -1, 0, 1, Inf),
                   c(-Inf, 1.96, 2.32, Inf, NA),
                   c(-Inf, -1.96, 2.32, Inf, NA),
                   c(-Inf, -1, 0, 1, Inf))
omxAllInt(covariance, means, thresholds)

```

omxApply

On-Demand Parallel Apply

Description

If the snowfall library is loaded, then this function calls [sfApply](#). Otherwise it invokes [apply](#).

Usage

```
omxApply(x, margin, fun, ...)
```

Arguments

x	a vector (atomic or list) or an expressions vector. Other objects (including classed objects) will be coerced by as.list .
margin	a vector giving the subscripts which the function will be applied over.
fun	the function to be applied to each element of x.
...	optional arguments to fun.

See Also

[omxLapply](#), [omxSapply](#)

Examples

```
x <- cbind(x1 = 3, x2 = c(4:1, 2:5))
dimnames(x)[[1]] <- letters[1:8]
omxApply(x, 2, mean, trim = .2)
```

```
omxAssignFirstParameters
```

Assign First Available Values to Model Parameters

Description

Sometimes you may have a free parameter with two different starting values in your model. OpenMx will not run a model until all instances of a free parameter have the same starting value. It is often sufficient to arbitrarily select one of those starting values for optimization.

This function accomplishes that task of assigning valid starting values to the free parameters of a model. It selects an arbitrary current value (the "first" value it finds, where "first" is not defined) for each free parameter and uses that value for all instances of that parameter in the model.

Usage

```
omxAssignFirstParameters(model, indep = FALSE)
```

Arguments

model	a MxModel object.
indep	assign parameters to independent submodels.

See Also

[omxGetParameters](#), [omxSetParameters](#)

Examples

```
A <- mxMatrix('Full', 3, 3, values = c(1:9), labels = c('a','b', NA),
              free = TRUE, name = 'A')
model <- mxModel(model=A, name = 'model')
model <- omxAssignFirstParameters(model)

# Note: All cells with the same label now have the same start value.
# Note also that NAs are untouched.

model$matrices$A

# $labels
#      [,1] [,2] [,3]
```

```
# [1,] "a"  "a"  "a"
# [2,] "b"  "b"  "b"
# [3,] NA   NA   NA
#
# $values
#      [,1] [,2] [,3]
# [1,]   1   1   1
# [2,]   2   2   2
# [3,]   3   6   9
```

omxBrownie

Make Brownies in OpenMx

Description

This function returns a brownie recipe.

Usage

```
omxBrownie(quantity=1, walnuts=TRUE)
```

Arguments

quantity	Number of batches of brownies desired. Defaults to one.
walnuts	Logical. Indicates whether walnuts are to be included in the brownies. Defaults to TRUE.

Details

Returns a brownie recipe. Alter the ‘quantity’ variable to make more pans of brownies. Ingredients, equipment and procedure are listed, but neither ingredients nor equipment are provided.

Value

Returns a brownie recipe.

References

The OpenMx User’s guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

More information about the OpenMx package may be found [here](#).

Examples

```
# Return a brownie recipe
omxBrownie()
```

omxCheckCloseEnough *Approximate Equality Testing Function*

Description

This function tests whether two numeric vectors or matrixes are approximately equal to one another, within a specified threshold.

Usage

```
omxCheckCloseEnough(a, b, epsilon = 10-15, na.action = na.fail)
```

Arguments

a	a numeric vector or matrix
b	a numeric vector or matrix
epsilon	a non-negative tolerance threshold
na.action	either na.fail (default) or na.pass. Use of na.omit or na.exclude is not recommended.

Details

Arguments ‘a’ and ‘b’ must be of the same type, ie. they must be either vectors of equal dimension or matrices of equal dimension. The two arguments are compared element-wise for approximate equality. If the absolute value of the difference of any two values is greater than the threshold, then an error will be thrown. If ‘a’ and ‘b’ are approximately equal to each other, by default the function will print a statement informing the user the test has passed. To turn off these print statements use `options("mxPrintUnitTests" = FALSE)`.

When na.action is set to na.pass, a and b are expected to have identical missingness patterns.

References

The OpenMx User’s guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

[omxCheckWithinPercentError](#), [omxCheckIdentical](#), [omxCheckSetEquals](#), [omxCheckTrue](#), [omxCheckEquals](#)

Examples

```
omxCheckCloseEnough(c(1, 2, 3), c(1.1, 1.9, 3.0), epsilon = 0.5)
omxCheckCloseEnough(matrix(3, 3, 3), matrix(4, 3, 3), epsilon = 2)
# Throws an error
try(omxCheckCloseEnough(c(1, 2, 3), c(1.1, 1.9, 3.0), epsilon = 0.01))
```

omxCheckEquals *Equality Testing Function*

Description

This function tests whether two objects are equal using the '==' operator.

Usage

```
omxCheckEquals(a, b)
```

Arguments

a the first value to compare.
b the second value to compare.

Details

Performs the '==' comparison on the two arguments. If the two arguments are not equal, then an error will be thrown. If 'a' and 'b' are equal to each other, by default the function will print a statement informing the user the test has passed. To turn off these print statements use `options("mxPrintUnitTests" = FALSE)`.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

[omxCheckCloseEnough](#), [omxCheckWithinPercentError](#), [omxCheckSetEquals](#), [omxCheckTrue](#), [omxCheckIdentical](#)

Examples

```
omxCheckEquals(c(1, 2, 3), c(1, 2, 3))  
  
omxCheckEquals(FALSE, FALSE)  
  
# Throws an error  
try(omxCheckEquals(c(1, 2, 3), c(2, 1, 3)))
```

omxCheckError	<i>Correct Error Message Function</i>
---------------	---------------------------------------

Description

This function tests whether the correct error message is thrown.

Usage

```
omxCheckError(expression, message)
```

Arguments

expression	an R expression that produces an error
message	a character string with the desired error message

Details

Arguments ‘expression’ and ‘message’ give the expression that generates the error and the message that is supposed to be generated, respectively.

References

The OpenMx User’s guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

[omxCheckWarning](#), [omxCheckWithinPercentError](#), [omxCheckIdentical](#), [omxCheckSetEquals](#), [omxCheckTrue](#), [omxCheckEquals](#)

Examples

```
A <- mxMatrix('Full', 1, 1, labels = 'data.foo', free = TRUE, name = 'A')
model <- mxModel('model', A)
omxCheckError(mxRun(model),
  paste("The definition variable 'data.foo'",
    "has been assigned to a",
    "free parameter in matrix 'A'"))
omxCheckCloseEnough(matrix(3, 3, 3), matrix(4, 3, 3), epsilon = 2)
# Throws error, check the message
tmsg <- paste("In omxCheckCloseEnough(c(1, 2, 3), c(1.1, 1.9, 3), 0.01)",
  ": not equal to within 0.01 : '1 2 3' and '1.1 1.9 3'")
omxCheckError(omxCheckCloseEnough(c(1, 2, 3), c(1.1, 1.9, 3.0), .01), tmsg)
```

omxCheckIdentical *Exact Equality Testing Function*

Description

This function tests whether two objects are equal.

Usage

```
omxCheckIdentical(a, b)
```

Arguments

a	the first value to compare.
b	the second value to compare.

Details

Performs the 'identical' comparison on the two arguments. If the two arguments are not equal, then an error will be thrown. If 'a' and 'b' are equal to each other, by default the function will print a statement informing the user the test has passed. To turn off these print statements use `options("mxPrintUnitTests" = FALSE)`.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

[omxCheckCloseEnough](#), [omxCheckWithinPercentError](#), [omxCheckSetEquals](#), [omxCheckTrue](#), [omxCheckEquals](#)

Examples

```
omxCheckIdentical(c(1, 2, 3), c(1, 2, 3))  
  
omxCheckIdentical(FALSE, FALSE)  
  
# Throws an error  
try(omxCheckIdentical(c(1, 2, 3), c(2, 1, 3)))
```

omxCheckNamespace	<i>omxCheckNamespace</i>
-------------------	--------------------------

Description

This is an internal function exported for those people who know what they are doing.

Usage

```
omxCheckNamespace(model, namespace)
```

Arguments

model	model
namespace	namespace

Details

This function checks that the named entities in the model are valid.

omxCheckSetEquals	<i>Set Equality Testing Function</i>
-------------------	--------------------------------------

Description

This function tests whether two vectors contain the same elements.

Usage

```
omxCheckSetEquals(a, b)
```

Arguments

a	the first vector to compare.
b	the second vector to compare.

Details

Performs the 'setequal' function on the two arguments. If the two arguments do not contain the same elements, then an error will be thrown. If 'a' and 'b' contain the same elements, by default the function will print a statement informing the user the test has passed. To turn off these print statements use `options("mxPrintUnitTests" = FALSE)`.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

[omxCheckCloseEnough](#), [omxCheckWithinPercentError](#), [omxCheckIdentical](#), [omxCheckTrue](#), [omxCheckEquals](#)

Examples

```
omxCheckSetEquals(c(1, 1, 2, 2, 3), c(3, 2, 1))

omxCheckSetEquals(matrix(1, 1, 1), matrix(1, 3, 3))

# Throws an error
try(omxCheckSetEquals(c(1, 2, 3, 4), c(2, 1, 3)))
```

omxCheckTrue	<i>Boolean Equality Testing Function</i>
--------------	------------------------------------------

Description

This function tests whether an object is equal to TRUE.

Usage

```
omxCheckTrue(a)
```

Arguments

a the value to test.

Details

Checks element-wise whether an object is equal to TRUE. If any of the elements are false, then an error will be thrown. If 'a' is TRUE, by default the function will print a statement informing the user the test has passed. To turn off these print statements use `options("mxPrintUnitTests" = FALSE)`.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

[omxCheckCloseEnough](#), [omxCheckWithinPercentError](#), [omxCheckIdentical](#), [omxCheckSetEquals](#), [omxCheckEquals](#)

Examples

```
omxCheckTrue(1 + 1 == 2)

omxCheckTrue(matrix(TRUE, 3, 3))

# Throws an error
try(omxCheckTrue(FALSE))
```

omxCheckWarning	<i>Correct Warning Message Function</i>
-----------------	-----------------------------------------

Description

This function tests whether the correct warning message is thrown.

Usage

```
omxCheckWarning(expression, message)
```

Arguments

expression	an R expression that produces a warning
message	a character string with the desired warning message

Details

Arguments ‘expression’ and ‘message’ give the expression that generates the warning and the message that is supposed to be generated, respectively.

References

The OpenMx User’s guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

[omxCheckError](#) [omxCheckWithinPercentError](#), [omxCheckIdentical](#), [omxCheckSetEquals](#), [omxCheckTrue](#), [omxCheckEquals](#)

Examples

```
msg <- paste("Objective functions like mxFIMLObjective()",
"have been deprecated in favor of expectation and fit functions.\n",
"Please use mxExpectationNormal(covariance= , means = , ...) instead,",
"and add a call to mxFitFunctionML().",
"See examples at help(mxExpectationNormal)")
foo <- omxCheckWarning(mxFIMLObjective('cov', 'mean'), msg)
```

`omxCheckWithinPercentError`*Approximate Percent Equality Testing Function*

Description

This function tests whether two numeric vectors or matrixes are approximately equal to one another, within a specified percentage.

Usage

```
omxCheckWithinPercentError(a, b, percent = 0.1)
```

Arguments

<code>a</code>	a numeric vector or matrix.
<code>b</code>	a numeric vector or matrix.
<code>percent</code>	a non-negative percentage.

Details

Arguments ‘a’ and ‘b’ must be of the same type, ie. they must be either vectors of equal dimension or matrices of equal dimension. The two arguments are compared element-wise for approximate equality. If the absolute value of the difference of any two values is greater than the percentage difference of ‘a’, then an error will be thrown. If ‘a’ and ‘b’ are approximately equal to each other, by default the function will print a statement informing the user the test has passed. To turn off these print statements use `options("mxPrintUnitTests" = FALSE)`.

References

The OpenMx User’s guide can be found at <http://openmx.ssri.psu.edu/documentation>.

See Also

[omxCheckCloseEnough](#), [omxCheckIdentical](#), [omxCheckSetEquals](#), [omxCheckTrue](#), [omxCheckEquals](#)

Examples

```
omxCheckWithinPercentError(c(1, 2, 3), c(1.1, 1.9 ,3.0), percent = 50)

omxCheckWithinPercentError(matrix(3, 3, 3), matrix(4, 3, 3), percent = 150)

# Throws an error
try(omxCheckWithinPercentError(c(1, 2, 3), c(1.1, 1.9 ,3.0), percent = 0.01))
```

```
omxConstrainMLThresholds
      omxConstrainMLThresholds
```

Description

Add constraint to ML model to keep thresholds in order

Usage

```
omxConstrainMLThresholds(model, dist = 0.1)
```

Arguments

model	the MxModel to which constraints should be added
dist	unused

Details

This function adds a nonlinear constraint to an ML model. The constraint keeps the thresholds in order. Constraints often slow model estimation, however, keeping the thresholds in increasing order helps ensure the likelihood function is well-defined. If you're having problems with ordinal data, this is one of the things to try.

Value

a new MxModel object with the constraints added

See Also

```
demo("omxConstrainMLThresholds")
```

```
omxDefaultComputePlan Construct default compute plan
```

Description

This function generates a default compute plan, where "default compute plan" refers to an object of class [MxComputeSequence](#) which is appropriate for use in a wide variety of cases. The exact specification of the plan will depend upon the arguments provided to `omxDefaultComputePlan()`.

Usage

```
omxDefaultComputePlan(modelName=NULL, intervals=FALSE,
  useOptimizer=TRUE, optionList=options())$mxOption)
```

Arguments

modelName	Optional (defaults to NULL) character string, providing the name of the MxModel the fitfunction of which is to be evaluated, and usually, optimized.
intervals	Logical; will confidence intervals be computed? Defaults to FALSE.
useOptimizer	Logical; will a fitfunction be minimized? Defaults to TRUE.
optionList	List of mxOptions . Defaults to the current list of global mxOptions .

Details

At minimum, argument `optionList` must include “Gradient algorithm”, “Gradient iterations”, “Gradient step size”, “Calculate Hessian”, and “Standard Errors”. Users are advised to set “Calculate Hessian” and “Standard Errors” to “No” if the compute plan is to be used in an [MxModel](#) containing [MxConstraints](#).

Value

Returns an object of class [MxComputeSequence](#).

Examples

```
foo <- omxDefaultComputePlan(modelName="bar")
str(foo)
```

omxDetectCores

omxDetectCores

Description

Detects the number of cores on the local machine

Usage

```
omxDetectCores(...)
```

Arguments

```
...          unused
```

omxGetNPSOL

omxGetNPSOL

Description

Get the non-CRAN version of OpenMx from the OpenMx website.

Usage

```
omxGetNPSOL()
```

Details

This function

Value

Invisible NULL

Examples

```
## Not run: omxGetNPSOL()
```

omxGetParameters

Fetch Model Parameters

Description

Return a vector of the chosen parameters from the model.

Usage

```
omxGetParameters(model, indep = FALSE, free = c(TRUE, FALSE, NA),
  fetch = c('values', 'free', 'lbound', 'ubound', 'all'))
```

Arguments

model	a MxModel object
indep	fetch parameters from independent submodels.
free	fetch either free parameters (TRUE), or fixed parameters or both types. Default value is TRUE.
fetch	which attribute of the parameters to fetch. Default choice is 'values'.

Details

The argument ‘free’ dictates whether to return only free parameters or only fixed parameters or both free and fixed parameters. The function can return unlabelled free parameters (parameters with a label of NA). These anonymous free parameters will be identified as ‘modelname.matrixname[row,col]’. It will not return fixed parameters that have a label of NA. No distinction is made between ordinary labels, definition variables, and square bracket constraints. The function will return either a vector of parameter values, or free/fixed designations, or lower bounds, or upper bounds, depending on the ‘fetch’ argument. Using fetch with ‘all’ returns a data frame that is populated with all of the attributes.

See Also

[omxSetParameters](#), [omxLocateParameters](#), [omxAssignFirstParameters](#)

Examples

```
library(OpenMx)

A <- mxMatrix('Full', 2, 2, labels = c("A11", "A12", "A21", NA), values= 1:4,
  free = c(TRUE,TRUE,FALSE,TRUE), byrow=TRUE, name = 'A')
model <- mxModel(A, name = 'model')

# Request all free parameters in model
omxGetParameters(model)

# A11 A12 model.A[2,2]
# 1 2 4

# Request fixed parameters from model
omxGetParameters(model, free = FALSE)
# A21
# 3

A$labels
# [,1] [,2]
# [1,] "A11" "A12"
# [2,] "A21" NA

A$free
# [,1] [,2]
# [1,] TRUE TRUE
# [2,] FALSE TRUE

A$labels
# [,1] [,2]
# [1,] "A11" "A12"
# [2,] "A21" NA

# Example using un-labelled parameters
```



```

# Read in some demo data
data(demoOneFactor)
# Grab the names for manifestVars
manifestVars <- names(demoOneFactor)
nVar = length(manifestVars) # 5 variables
factorModel <- mxModel("One Factor",
  mxMatrix(name="A", type="Full", nrow=nVar, ncol=1, values=0.2, free=TRUE,
    lbound = 0.0, labels=letters[1:nVar]),
  mxMatrix(name="L", type="Symm", nrow=1, ncol=1, values=1, free=FALSE),
  # the "U" matrix has nVar (5) anonymous free parameters
  mxMatrix(name="U", type="Diag", nrow=nVar, ncol=nVar, values=1, free=TRUE),
  mxAlgebra(expression=A %&% L + U, name="R"),
  mxExpectationNormal(covariance="R", dimnames=manifestVars),
  mxFitFunctionML(),
  mxData(observed=cov(demoOneFactor), type="cov", numObs=500)
)

# Get all free parameters
params <- omxGetParameters(factorModel)
lbound <- omxGetParameters(factorModel, fetch="lbound")
# Set new values for these params, saving them in a new model
newFactorModel <- omxSetParameters(factorModel, names(params), values = 1:10)
# Read out the values from the new model
newParams <- omxGetParameters(newFactorModel)

```

omxGetRAMDepth

omxGetRAMDepth

Description

Get the potency of a matrix for inversion speed-up

Usage

```
omxGetRAMDepth(A, maxdepth = nrow(A) - 1)
```

Arguments

A	MxMatrix object
maxdepth	Numeric. maximum depth to check

Details

This function is used internally by the [mxExpectationRAM](#) function to determine how far to expand $(I - A)^{-1} = I + A + A^2 + A^3 + \dots$. It is similarly used by [mxExpectationLISREL](#) in expanding $(I - B)^{-1} = I + B + B^2 + B^3 + \dots$. In many situations A^2 is a zero matrix (nilpotent of order 2). So when A has large dimension it is much faster to compute $I + A$ than $(I - A)^{-1}$.

omxGraphviz	<i>Show RAM Model in Graphviz Format</i>
-------------	------------------------------------------

Description

The function accepts a RAM style model and outputs a visual representation of the model in Graphviz format. The function will output either to a file or to the console. The recommended file extension for an output file is ".dot".

Usage

```
omxGraphviz(model, dotFilename = "")
```

Arguments

model	An RAM-type model.
dotFilename	The name of the output file. Use "" to write to console.

Value

Invisibly returns a string containing the model description in graphviz format.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

omxLapply	<i>On-Demand Parallel Lapply</i>
-----------	----------------------------------

Description

If the snowfall library is loaded, then this function calls [sfLapply](#). Otherwise it invokes [lapply](#).

Usage

```
omxLapply(x, fun, ...)
```

Arguments

x	a vector (atomic or list) or an expressions vector. Other objects (including classed objects) will be coerced by as.list .
fun	the function to be applied to each element of x.
...	optional arguments to fun.

See Also

[omxApply](#), [omxSapply](#)

Examples

```
x <- list(a = 1:10, beta = exp(-3:3), logic = c(TRUE,FALSE,FALSE,TRUE))
# compute the list mean for each list element
omxLapply(x,mean)
```

omxLocateParameters *Summarize Model Parameters*

Description

Return a data.frame object summarizing the free parameters in the model.

Usage

```
omxLocateParameters(model, labels = NULL, indep = FALSE)
```

Arguments

model	a MxModel object
labels	optionally specify which free parameters to retrieve.
indep	fetch parameters from independent submodels.

Details

Invoking the function with the default value for the 'labels' argument retrieves all the free parameters. The 'labels' argument can be used to select a subset of the free parameters. Note that 'NA' is a valid possible input to the 'labels' argument.

See Also

[omxGetParameters](#), [omxSetParameters](#), [omxAssignFirstParameters](#)

Examples

```
A <- mxMatrix('Full', 2, 2, labels = c("A11", "A12", NA, NA), values= 1:4,
  free = TRUE, byrow = TRUE, name = 'A')

model <- mxModel(A, name = 'model')

# Request all free parameters in model
omxLocateParameters(model)
```

```
# Request free parameters "A11" and all NAs
omxLocateParameters(model, c("A11", NA))
```

omxLogical

Logical mxAlgebra() operators

Description

omxNot computes the unary negation of the values of a matrix. omxAnd computes the binary and of two matrices. omxOr computes the binary or of two matrices. omxGreaterThan computes a binary greater than of two matrices. omxLessThan computes the binary less than of two matrices. omxApproxEquals computes a binary equals within a specified epsilon of two matrices.

Usage

```
omxNot(x)
omxAnd(x, y)
omxOr(x, y)
omxGreaterThan(x, y)
omxLessThan(x, y)
omxApproxEquals(x, y, epsilon)
```

Arguments

x	the first argument, the matrix which the logical operation will be applied to.
y	the second argument, applicable to binary functions.
epsilon	the third argument, specifies the error threshold for omxApproxEquals. $\text{Abs}(x[i][j]-y[i][j])$ must be less than $\text{epsilon}[i][j]$.

Examples

```
A <- mxMatrix(values = runif(25), nrow = 5, ncol = 5, name = 'A')
B <- mxMatrix(values = runif(25), nrow = 5, ncol = 5, name = 'B')
EPSILON <- mxMatrix(values = 0.04*1:25, nrow = 5, ncol = 5, name = "EPSILON")

model <- mxModel(A, B, EPSILON, name = 'model')

mxEval(omxNot(A), model)
mxEval(omxGreaterThan(A,B), model)
mxEval(omxLessThan(B,A), model)
mxEval(omxOr(omxNot(A),B), model)
mxEval(omxAnd(omxNot(B), A), model)
mxEval(omxApproxEquals(A,B, EPSILON), model)
```

`omxManifestModelByParameterJacobian`*Estimate the Jacobian of manifest model with respect to parameters*

Description

The manifest model excludes any latent variables or processes. For RAM and LISREL models, the manifest model contains only the manifest variables with free means, covariance, and thresholds.

Usage

```
omxManifestModelByParameterJacobian(model, defvar.row = 1,  
  standardize = FALSE)
```

Arguments

<code>model</code>	an <code>mxModel</code>
<code>defvar.row</code>	which row to use for definition variables
<code>standardize</code>	logical, whether or not to standardize the parameters

Details

The Jacobian is estimated by the central finite difference.

If the `standardize` argument is `TRUE`, then the Jacobian is for the standardized model. For Normal expectations the standardized manifest model has the covariances returned as correlations, the variances returned as ones, the means returned as zeros, and the thresholds are returned as z-scores. For the thresholds the z-scores are computed by using the model-implied means and variances.

Value

a matrix with manifests in the rows and original parameters in the columns

See Also

[mxGetExpected](#)

omxMatrixOperations *MxMatrix operations*

Description

omxCbind columnwise binding of two or more MxMatrices. omxRbind rowwise binding of two or more MxMatrices. omxTranspose transpose of MxMatrix.

Usage

```
omxCbind(..., allowUnlabeled =
  getOption("mxOptions")[[ "Allow Unlabeled" ]],
  dimnames = NA, name = NA)
omxRbind(..., allowUnlabeled =
  getOption("mxOptions")[[ "Allow Unlabeled" ]],
  dimnames = NA, name = NA)
omxTranspose(matrix, allowUnlabeled =
  getOption("mxOptions")[[ "Allow Unlabeled" ]],
  dimnames = NA, name = NA)
```

Arguments

...	two or more MxMatrix objects
matrix	MxMatrix input
allowUnlabeled	whether or not to accept free parameters with NA labels
dimnames	list. The dimnames attribute for the matrix: a list of length 2 giving the row and column names respectively. An empty list is treated as NULL, and a list of length one as row names. The list can be named, and the list names will be used as names for the dimensions.
name	an optional character string indicating the name of the MxMatrix object

omxMnor *Multivariate Normal Integration*

Description

Given a covariance matrix, a means vector, and vectors of lower and upper bounds, returns the multivariate normal integral across the space between bounds.

Usage

```
omxMnor(covariance, means, lbound, ubound)
```

Arguments

covariance	the covariance matrix describing the multivariate normal distribution.
means	a row vector containing means of the variables of the underlying distribution.
lbound	a row vector containing the lower bounds of the integration in each variable.
ubound	a row vector containing the upper bounds of the integration in each variable.

Details

The order of columns in the ‘means’, ‘lbound’, and ‘ubound’ vectors are assumed to be the same as that of the covariance matrix. That is, means[i] is considered to be the mean of the variable whose variance is in covariance[i,i]. That variable will be integrated from lbound[i] to ubound[i] as part of the integration.

The value of ubound[i] or lbound[i] may be set to Inf or -Inf if a boundary at positive or negative infinity is desired.

For all i, ubound[i] must be strictly greater than lbound[i].

Examples

```
data(myFADDataRaw)

covariance <- cov(myFADDataRaw[,1:3])
means <- colMeans(myFADDataRaw[,1:3])
lbound <- c(-Inf, 0, 1) # Integrate from -Infinity to 0 on first variable
ubound <- c(0, Inf, 2.5) # From 0 to +Infinity on second, and from 1 to 2.5 on third
omxMnor(covariance, means, lbound, ubound)
# 0.0005995

# An alternative specification of the bounds follows
# Integrate from -Infinity to 0 on first variable
v1bound = c(-Inf, 0)
# From 0 to +Infinity on second
v2bound = c(0, Inf)
# and from 1 to 2.5 on third
v3bound = c(1, 2.5)
bounds <- cbind(v1bound, v2bound, v3bound)
lbound <- bounds[1,]
ubound <- bounds[2,]
omxMnor(covariance, means, lbound, ubound)
```

omxNameAnonymousParameters

omxNameAnonymousParameters

Description

Assign new names to the unnamed parameters

Usage

```
omxNameAnonymousParameters(model, indep = FALSE)
```

Arguments

model	the MxModel
indep	whether models are independent

Value

a list with components for the new MxModel with named parameters, and the new names.

omxParallelCI	<i>omxParallelCI</i>
---------------	----------------------

Description

Create parallel models for parallel confidence intervals

Usage

```
omxParallelCI(model, run = TRUE)
```

Arguments

model	an MxModel with confidence intervals in it
run	whether to run the model or just return the parallelized interval models

Value

an MxModel object

Examples

```
require(OpenMx)
data(demoOneFactor)
manifests <- names(demoOneFactor)
latents <- c("G")
factorModel <- mxModel("One Factor",
  type="RAM",
  manifestVars=manifests,
  latentVars=latents,
  mxPath(from=latents, to=manifests),
  mxPath(from=manifests, arrows=2),
  mxPath(from=latents, arrows=2, free=FALSE, values=1.0),
  mxData(observed=cov(demoOneFactor), type="cov",
    numObs=500),
  # add confidence intervals for free params in A and S matrices
```



```
          mxCI(c('A', 'S'))
factorRun <- mxRun(factorModel)
factorCI <- omxParallelCI(factorRun) # Run CIs in parallel
```

omxQuotes

omxQuotes

Description

Quote helper function, often for error messages.

Usage

```
omxQuotes(name)
```

Arguments

name a character vector

Details

This is a helper function for creating a nicely put together formatted string.

Value

a character string

Examples

```
omxQuotes(c("Oh", "blah", "dee", "Oh", "blah", "da"))
omxQuotes(c("A", "S", "F"))
omxQuotes("Hello World")
```

omxRAMtoML

omxRAMtoML

Description

Convert a RAM model to an ML model

Usage

```
omxRAMtoML(model)
```

Arguments

model the MxModel

Details

This is a legacy function that was once used to convert RAM models to ML models in the old (1.0 release of OpenMx) objective function style.

Value

an ML model with an ML objective

 omxRMSEA

Get the RMSEA with confidence intervals from model

Description

This function calculates the Root Mean Square Error of the Approximation (RMSEA) for a model and computes confidence intervals for that fit statistic.

Usage

```
omxRMSEA(model, lower=.025, upper=.975, null=.05, ...)
```

Arguments

model	An MxModel object for which the RMSEA is desired
lower	The lower confidence bound for the confidence interval
upper	The upper confidence bound for the confidence interval
null	Value of RMSEA used to test for close fit
...	Further named arguments passed to summary

Details

To help users obtain fit statistics related to the RMSEA, this function confidence intervals and a test for close fit. The user determines how close the fit is required to be by setting the null argument to the value desired for comparison.

Value

A named vector with elements lower, est.rmsea, upper, null, and 'Prob(x <= null)'.

References

Browne, M. W. & Cudeck, R. (1992). Alternative Ways of Assessing Model Fit. *Sociological Methods and Research*, 21, 230-258.

Examples

```

require(OpenMx)
data(demoOneFactor)
manifests <- names(demoOneFactor)
latents <- c("G")
factorModel <- mxModel("One Factor",
                        type="RAM",
                        manifestVars=manifests,
                        latentVars=latents,
                        mxPath(from=latents, to=manifests),
                        mxPath(from=manifests, arrows=2),
                        mxPath(from=latents, arrows=2, free=FALSE, values=1.0),
                        mxData(observed=cov(demoOneFactor), type="cov", numObs=500))
factorRun <- mxRun(factorModel)
factorSat <- mxRefModels(factorRun, run=TRUE)
summary(factorRun, refModels=factorSat)
# Gives RMSEA with 95% confidence interval

omxRMSEA(factorRun, .05, .95, refModels=factorSat)
# Gives RMSEA with 90% confidence interval
# and probability of 'close enough' fit

```

omxSapply

On-Demand Parallel Sapply

Description

If the snowfall library is loaded, then this function calls [sfSapply](#). Otherwise it invokes [sapply](#).

Usage

```
omxSapply(x, fun, ..., simplify = TRUE, USE.NAMES = TRUE)
```

Arguments

x	a vector (atomic or list) or an expressions vector. Other objects (including classed objects) will be coerced by as.list .
fun	the function to be applied to each element of x.
...	optional arguments to fun.
simplify	logical; should the result be simplified to a vector or matrix if possible?
USE.NAMES	logical; if TRUE and if x is a character, use x as names for the result unless it had names already.

See Also

[omxApply](#), [omxLapply](#)

Examples

```
x <- list(a = 1:10, beta = exp(-3:3), logic = c(TRUE,FALSE,FALSE,TRUE))
# compute the list mean for each list element
omxSapply(x, quantile)
```

omxSaturatedModel *Create Reference (Saturated and Independence) Models*

Description

This function creates and optionally runs saturated and independence (null) models of a base model or data set for use with [mxSummary](#) to obtain more fit indices.

Usage

```
mxRefModels(x, run=FALSE)
```

Arguments

x	A MxModel object, data frame, or matrix.
run	logical. If TRUE runs the models before returning; otherwise returns built models without running.

Details

For typical structural equation models the saturated model is the free-est possible model. All covariances and, when possible, all means are estimated. In the case of ordinal data, the ordinal means are fixed to zero and the thresholds are estimated. When the ordinal data are binary, those variances are also constrained to one. This is the free-est possible model, only constrained for model identification. The saturated model is used to create the RMSEA, and Chi-squared fit indices.

The independence model, sometimes called the null model, is a model of each variable being completely independent of every other variable. As such, all the variances and, when possible, all means are estimated. However, covariances are set to zero. Ordinal variables are handled the same for the independence and saturated models. The independence model is used, along with the saturated model, to create CFI and TLI fit indices.

The saturated and independence models could be used to create further fit indices. However, OpenMx does not recommend using GFI, AGFI, NFI (aka Bentler-Bonett), or SRMR. The page for [mxSummary](#) has information about why.

When the [mxFitFunctionMultigroup](#) fit function is used, `mxRefModels` creates the appropriate multigroup saturated and independence models. Saturated and independence models are created separately for each group. Each group has its own saturated and independence model. The multigroup saturated model is a multigroup model where each group has its own saturated model, and similarly for the independence model.

One potentially important limitation of the `mxRefModels` function is for behavioral genetics models. If variables 'x', 'y', and 'z' are measured on twins 1 and 2 creating the modeled variables 'x1', 'y1', 'z1', 'x2', 'y2', 'z2', then this function may not create the intended saturated or independence models. In particular, the means of 'x1' and 'x2' are estimated separately. Similarly, the covariance of 'x1' with 'y1' and 'x2' with 'y2' are allowed to be distinct: $cov(x1, y1) \neq cov(x2, y2)$. Moreover, the cross-twin covariances are estimated: e.g. $cov(x1, y2) \neq 0$.

Another potential misuse of this function is for models with definition variables. If definition variables are used, the saturated and independence model may not be correct because they do not account for the definition variables.

When an `MxModel` has been run, some effort is made to make the reference models for only the variables used in the model. For covariance data, all variables are modeled by default. For raw data when the model has been run, only the modeled variables are used in the reference models. This matches the behavior of `mxModel`.

In general, it is best practice to give `mxRefModels` a model that has already been run.

There are a few considerations specific to IFA models (`mxExpectationBA81`). The independence model preserves equality constraints among item parameters from the original model. The saturated model is a multinomial distribution with the proportions equal to the proportions in your data. For example, if you have 2 dichotomous items then there are 4 possible response patterns: 00, 01, 10, 11. A multinomial distribution for these 2 items is fully specified by 3 proportions or 3 parameters: $a, b, c, 1.0 - (a + b + c)$. Hence, there is no need to optimize the saturated model. When there is no missing data, the deviance is immediately known as $-2 * \text{sum}(\log \text{proportions})$. Typical Bayesian priors involve latent factors (various densities on the pseudo-guessing lower bound, log norm on loading, and uniqueness prior). These priors cannot be included in the independence model because there are no latent factors. Therefore, exercise caution when comparing the independence model to a model that includes Bayesian priors.

`mxRefModels()` is not compatible with `GREML expectation`, as there is no sensible general definition for a saturated GREML-type model.

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```
require(OpenMx)
data(demoOneFactor)
manifests <- names(demoOneFactor)
latents <- c("G")
factorModel <- mxModel("One Factor",
  type="RAM",
  manifestVars=manifests,
  latentVars=latents,
  mxPath(from=latents, to=manifests),
  mxPath(from=manifests, arrows=2),
  mxPath(from=latents, arrows=2, free=FALSE, values=1.0),
  mxData(observed=cov(demoOneFactor), type="cov", numObs=500))
summary(factorRun <- mxRun(factorModel))
factorSat <- mxRefModels(factorRun, run=TRUE)
summary(factorRun, refModels=factorSat)
```

omxSelectRowsAndCols *Filter rows and columns from an mxMatrix*

Description

This function filters rows and columns from a matrix using a single row or column R matrix as a selector.

Usage

```
omxSelectRowsAndCols(x, selector)
omxSelectRows(x, selector)
omxSelectCols(x, selector)
```

Arguments

x	the matrix to be filtered
selector	A single row or single column R matrix indicating which values should be filtered from the mxMatrix.

Details

omxSelectRowsAndCols, omxSelectRows, and omxSelectCols returns the filtered entries in a target matrix specified by a single row or single column selector matrix. Each entry in the selector matrix is treated as a logical data indicating if the corresponding entry in the target matrix should be excluded (0 or FALSE) or included (not 0 or TRUE). Typically the function is used to filter data from a target matrix using an existence vector which specifies what data entries are missing. This can be seen in the demo: RowObjectiveFIMLBivariateSaturated.

Value

Returns a new matrix with the filtered data.

References

The function is most often used when filtering data for missingness. This can be seen in the demo: RowObjectiveFIMLBivariateSaturated. The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>. The omxSelect* functions share some similarity to the Extract function in the R programming language.

Examples

```
loadings <- c(1, -0.625, 0.1953125, 1, -0.375, 0.0703125, 1, -0.375, 0.0703125)
loadings <- matrix(loadings, 3, 3, byrow= TRUE)
existenceList <- c(1, 0, 1)
existenceList <- matrix(existenceList, 1, 3, byrow= TRUE)
rowsAndCols <- omxSelectRowsAndCols(loadings, existenceList)
rows <- omxSelectRows(loadings, existenceList)
cols <- omxSelectCols(loadings, existenceList)
```

 omxSetParameters *Assign Model Parameters*

Description

Modify the attributes of parameters in a model. This function cannot modify parameters that have NA labels. Often you will want to call [omxAssignFirstParameters](#) after using this, to force the starting values of equated parameters to the same value (otherwise the model cannot begin to be evaluated)

Usage

```
omxSetParameters(model, labels, free = NULL, values = NULL,
  newlabels = NULL, lbound = NULL, ubound = NULL, indep = FALSE,
  strict = TRUE, name = NULL)
```

Arguments

model	an MxModel object.
labels	a character vector of target parameter names.
free	a boolean vector of parameter free/fixed designations.
values	a numeric vector of parameter values.
newlabels	a character vector of new parameter names.
lbound	a numeric vector of lower bound values.
ubound	a numeric vector of upper bound values.
indep	boolean. set parameters in independent submodels.
strict	boolean. If TRUE then throw an error when a label does not appear in the model.
name	character string. (optional) a new name for the model.

See Also

[omxGetParameters](#), [omxAssignFirstParameters](#)

Examples

```
A <- mxMatrix('Full', 3, 3, labels = c('a','b', NA), free = TRUE, name = 'A')
model <- mxModel(model="testModel", A, name = 'model')

# set value of cells labelled "a" and "b" to 1 and 2 respectively
model <- omxSetParameters(model, c('a', 'b'), values = c(1, 2))

# set label of cell labelled "a" to "b" and vice versa
model <- omxSetParameters(model, c('a', 'b'), newlabels = c('b', 'a'))
```

```
# set label of cells labelled "a" to "b"
model <- omxSetParameters(model, c('a'), newlabels = 'b')

# ensure initial values are the same for each instance of a labeled parameter
model <- omxAssignFirstParameters(model)
```

omxSymbolTable	<i>Internal OpenMx algebra operations</i>
----------------	-------------------------------------------

Description

This is an internal table used in the OpenMx backend.

OpenMx	<i>OpenMx: An package for Structural Equation Modeling and Matrix Algebra Optimization</i>
--------	--------------------------------------------------------------------------------------------

Description

OpenMx is a package for structural equation modeling, matrix algebra optimization and other statistical estimation problems. Try the example below. We try and have useful help files: for instance `help(mxRun)` to learn more. Also the reference manual

Details

OpenMx solves algebra optimization and statistical estimation problems using matrix algebra. Most users use it for Structural equation modeling.

The core function is `mxModel`, which makes a model. Models are containers for data, matrices, `mxPaths` algebras, bounds and constraints. Models most often have an expectation function (e.g., `mxExpectationNormal`) to calculate the expectations for the model. Models need a fit function. Several of these are built-in (e.g., `mxFitFunctionML`) OpenMx also allows user-defined fit functions for purposes not covered by the built-in functions. (e.g., `mxFitFunctionR` or `mxFitFunctionAlgebra`).

Once built, the resulting `mxModel` can be run (i.e., optimized) using `mxRun`. This returns the fitted model.

You can see the resulting parameter estimates, algebra evaluation etc using `summary(yourModel)`

The user's manual is online (see reference below), but functions `mxRun`, `mxModel`, `mxMatrix` all have working examples to get you started as well.

The main OpenMx functions are: `mxAlgebra`, `mxBounds`, `mxCI`, `mxConstraint`, `mxData`, `mxMatrix`, `mxModel`, and `mxPath`

Expectation functions include `mxExpectationNormal`, `mxExpectationRAM`, `mxExpectationLISREL`, and `mxExpectationStateSpace`;

Fit functions include `mxFitFunctionML`, `mxFitFunctionAlgebra`, `mxFitFunctionRow` and `mxFitFunctionR`.

OpenMx comes with several useful datasets built-in. Access them using `data(package="OpenMx")`

To cite package 'OpenMx' in publications use:

Michael C. Neale, Michael D. Hunter, Joshua N. Pritikin, Mahsa Zahery, Timothy R. Brick Robert M. Kickpatrick, Ryne Estabrook, Timothy C. Bates, Hermine H. Maes, Steven M. Boker. (in press). OpenMx 2.0: Extended structural equation and statistical modeling. *Psychometrika*. DOI: 10.1007/s11336-014-9435-8

Steven M. Boker, Michael C. Neale, Hermine H. Maes, Michael J. Wilde, Michael Spiegel, Timothy R. Brick, Jeffrey Spies, Ryne Estabrook, Sarah Kenny, Timothy C. Bates, Paras Mehta, and John Fox. (2011) OpenMx: An Open Source Extended Structural Equation Modeling Framework. *Psychometrika*, 306-317. DOI:10.1007/s11336-010-9200-6

Steven M. Boker, Michael C. Neale, Hermine H. Maes, Michael J. Wilde, Michael Spiegel, Timothy R. Brick, Ryne Estabrook, Timothy C. Bates, Paras Mehta, Timo von Oertzen, Ross J. Gore, Michael D. Hunter, Daniel C. Hackett, Julian Karch, Andreas M. Brandmaier, Joshua N. Pritikin, Mahsa Zahery, Robert M. Kirkpatrick, Yang Wang, and Charles Driver. (2016) OpenMx 2 User Guide. <http://openmx.psyc.virginia.edu/docs/OpenMx/latest/OpenMxUserGuide.pdf>

References

The OpenMx User's guide can be found at <http://openmx.psyc.virginia.edu/documentation>

Examples

```
library(OpenMx)
data(demoOneFactor)
# =====
# = Make and run a 1-factor CFA =
# =====

latents = c("G") # the latent factor
manifests = names(demoOneFactor) # manifest variables to be modeled
# =====
# = Make the MxModel =
# =====
m1 <- mxModel("One Factor", type = "RAM",
  manifestVars = manifests, latentVars = latents,
  mxPath(from = latents, to = manifests),
  mxPath(from = manifests, arrows = 2),
  mxPath(from = latents, arrows = 2, free = FALSE, values = 1.0),
  mxData(cov(demoOneFactor), type = "cov", numObs = 500)
)

# =====
# = mxRun it and get a summary! =
# =====

m1 = mxRun(m1)
summary(m1, show = "std")
```

ordinalTwinData	<i>Data for ordinal twin model</i>
-----------------	------------------------------------

Description

Example data for ordinal twin-data modelling. Three variables measured in each twin.

Usage

```
data("ordinalTwinData")
```

Format

A data frame with 139 observations on the following 7 variables.

zyg a numeric vector
var1_twin1 a numeric vector
var2_twin1 a numeric vector
var3_twin1 a numeric vector
var1_twin2 a numeric vector
var2_twin2 a numeric vector
var3_twin2 a numeric vector

Examples

```
data(ordinalTwinData)  
str(ordinalTwinData)
```

rvectorize	<i>Vectorize By Row</i>
------------	-------------------------

Description

This function returns the vectorization of an input matrix in a row by row traversal of the matrix. The output is returned as a column vector.

Usage

```
rvectorize(x)
```

Arguments

x an input matrix.

See Also

[cvectorize](#), [vech](#), [vechs](#)

Examples

```
rvectorize(matrix(1:9, 3, 3))
rvectorize(matrix(1:12, 3, 4))
```

summary.MxModel	<i>Model Summary</i>
-----------------	----------------------

Description

This function returns summary statistics of a model after it has been run

Usage

```
## S3 method for class 'MxModel'
summary(object, ..., verbose=FALSE)
```

Arguments

object	A MxModel object.
...	Any number of named arguments (see below).
verbose	Whether to include extra diagnostic information.

Details

mxSummary allows the user to set or override the following parameters of the model:

numObs Numeric. Specify the total number of observations for the model.

numStats Numeric. Specify the total number of observed statistics for the model.

refModels List of MxModel objects. Specify a saturated and independence likelihoods in single argument for testing.

SaturatedLikelihood Numeric or MxModel object. Specify a saturated likelihood for testing.

SaturatedDoF Numeric. Specify the degrees of freedom of the saturated likelihood for testing.

IndependenceLikelihood Numeric or MxModel object. Specify an independence likelihood for testing.

IndependenceDoF Numeric. Specify the degrees of freedom of the independence likelihood for testing.

indep Logical. Set to FALSE to ignore independent submodels in summary.

verbose logical. Changes the printing style for summary (see Details)

The verbose argument changes the printing style for the summary of a model. When verbose=FALSE, a relatively minimal amount of information is printed: the free parameters, the likelihood, and a few fit indices. When more information is available, more is printed. For example, when the model has a saturated likelihood, several additional fit indices are printed. On the other hand, when verbose=TRUE, the compute plan, the data summary, and additional timing information are always printed. Moreover, available fit indices are printed regardless of whether or not they are defined. The undefined fit indices are printed as NA. Running a saturated model and including it with the call to summary will define these fit indices and they will display meaningful values. It should be noted that the verbose argument only changes the printing style, all of the same information is calculated and exists in the output of summary. More information is displayed when verbose=TRUE, and less when verbose=FALSE.

The Information Criteria (AIC, BIC) are reported in a table. The table shows different versions of the information criteria. Each entry in the table is an AIC or BIC obtained using different penalties. In particular, the entries of the table do not show the values of different penalties, but rather different versions of AIC and BIC. For example the AIC is reported with both a Parameters Penalty and a Degrees of Freedom Penalty. AIC generally takes the form $Fit + 2 * k$. With the Parameters Penalty k is the number of free parameters: $AIC.param = Fit + 2 * param$. With the Degrees of Freedom Penalty, k is minus one times the model degrees of freedom. So, essentially the penalty is subtracted instead of added: $AIC.param = Fit - 2 * df$. The Degrees of Freedom penalty was used in Classic Mx. BIC is defined similarly: $Fit + k * log(N)$ where k is either the number of free parameters or minus one times the model degrees of freedom. The Sample-Size Adjusted BIC is only defined for the parameters penalty: $Fit + k * log((N + 2)/24)$. For raw data models, Fit is the minus 2 log likelihood, $-2LL$. For covariance data, Fit is the Chi-squared statistic. The $-2LL$ and saturated likelihood values reported under covariance data are not necessarily meaningful on their own, but their difference yields the Chi-squared value.

The refModels, SaturatedLikelihood, SaturatedDoF, IndependenceLikelihood, and IndependenceDoF arguments can be used to obtain further fit statistics (RMSEA, CFI, TLI, Chi-Squared). For covariance data, saturated and independence models are fitted automatically so all fit indices are reported. For raw data, these reference models are not estimated to save computational time. An easy way to make reference models for most cases is provided by the [mxRefModels](#) function. When the SaturatedLikelihood or IndependenceLikelihood arguments are used, the appropriate degrees of freedom are attempted to be calculated by OpenMx. However, depending on the model, it may sometimes behoove the user to also explicitly provide the corresponding SaturatedDoF and/or IndependenceDoF. Again, for the vast majority of cases, the [mxRefModels](#) function handles these situations effectively and conveniently.

The summary function can report Error codes as follows:

- 1: The final iterate satisfies the optimality conditions to the accuracy requested, but the sequence of iterates has not yet converged. NPSOL was terminated because no further improvement could be made in the merit function (Mx status GREEN)
- 2: The linear constraints and bounds could not be satisfied. The problem has no feasible solution.
- 3: The nonlinear constraints and bounds could not be satisfied. The problem may have no feasible solution.
- 4: The major iteration limit was reached (Mx status BLUE).
- 5: The Hessian at the solution does not appear to be convex (Mx status RED).

- 6: The model does not satisfy the first-order optimality conditions to the required accuracy, and no improved point for the merit function could be found during the final linesearch (Mx status RED)
- 7: The function derivatives returned by funcon or funobj appear to be incorrect.
- 9: An input parameter was invalid

When the information matrix is available, standard errors are reported. If the information matrix was estimated using finite differences then an additional diagnostic column 'A' is displayed. An exclamation point in the 'A' column indicates that the gradient appears to be asymmetric and the standard error may not accurately reflect the variability of that parameter. As a precaution, it is recommended that you compare the SEs with likelihood-based confidence intervals.

For many raw data models, OpenMx does not automatically report the absolute fit indices (Chi-Squared, CFI, TLI, and RMSEA). They are available once you fit reference models. See the example given in [mxRefModels](#).

With regard to RMSEA, it is important to note that OpenMx does not currently make a multigroup adjustment that some other structural equation modeling programs make. In particular, we do not multiply the single-group RMSEA by the square root of the number of groups as suggested by Steiger (1998). The RMSEA we use is based on the model likelihood (and degrees of freedom) as compared to the saturated model likelihood (and degrees of freedom), and we do not feel the adjustment is appropriate in this case.

OpenMx does not recommend using some fit indices. These are GFI, AGFI, NFI, and SRMR. The Goodness of Fit Index (GFI) and Adjusted Goodness of Fit Index (AGFI) are not recommended because they are strongly influenced by sample size and have rather high Type I error rates (Sharma, Mukherjee, Kumar, & Dillon, 2005). The Normed Fit Index (NFI) has no penalty for model complexity. That is, adding more parameters to a model always improves the NFI, regardless of how useful those parameters are. Because the Non-Normed Fit Index (NNFI), also known as the Tucker-Lewis Index (TLI), does adjust for model complexity it is used instead. Lastly, the Standardized Root Mean Square Residual (SRMR) is not reported because it (1) only applies to covariance models, having no direct extension to missing data, (2) has no penalty for model complexity, similar to the NFI, and (3) is positively biased (Hu & Bentler, 1999).

References

- The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.
- Hu, L., & Bentler, P. M. (1999). Cutoff criteria for fit indexes in covariance structure analysis: Conventional criteria versus new alternatives. *Structural Equation Modeling*, 6, 1-55.
- Savalei, V. (2012). The relationship between root mean square error of approximation and model misspecification in confirmatory factor analysis models. *Educational and Psychological Measurement*, 72(6), 910-932.
- Sharma, S., Mukherjee, S., Kumar, A., & Dillon, W.R. (2005). A simulation study to investigate the use of cutoff values for assessing model fit in covariance structure models. *Journal of Business Research*, 58, 935-43.
- Steiger, J. H. (1998). A note on multiple sample extensions of the RMSEA fit index. *Structural Equation Modeling: A Multidisciplinary Journal*, 5(4), 411-419. DOI: 10.1080/10705519809540115

Examples

```

library(OpenMx)
data(demoOneFactor) # load the demoOneFactor dataframe
manifests <- names(demoOneFactor) # set the manifest to the 5 demo variables
latents <- c("G") # define 1 latent variable
model <- mxModel(model="One Factor", type="RAM",
  manifestVars = manifests,
  latentVars = latents,
  mxPath(from = latents, to=manifests, labels = paste("b", 1:5, sep = "")),
  mxPath(from = manifests, arrows = 2, labels = paste("u", 1:5, sep = "")),
  mxPath(from = latents, arrows = 2, free = FALSE, values = 1.0),
  mxData(cov(demoOneFactor), type = "cov", numObs = 500)
)
model <- mxRun(model) # Run the model, returning the result into model

# Show summary of the fitted model
summary(model)

# Compute the summary and store in the variable "statistics"
statistics <- summary(model)

# Access components of the summary
statistics$parameters
statistics$SaturatedLikelihood

# Specify a saturated likelihood for testing
summary(model, SaturatedLikelihood = -3000)

# Add a CI and view it in the summary
model = mxRun(mxModel(model=model, mxCI("b5")), intervals = TRUE)
summary(model)

```

tr

trace

Description

This function returns the trace of an n-by-n square matrix x, defined to be the sum of the elements on the main diagonal (the diagonal from the upper left to the lower right).

Usage

```
tr(x)
```

Arguments

x an input matrix. Must be square

Details

The input matrix must be square.

See Also

[vech](#), [rvectorize](#), [cvectorize](#)

Examples

```
tr(matrix(1:9, 3, 3))
tr(matrix(1:12, 3, 4))
```

twinData

Australian twin sample biometric data.

Description

Australian twin data with 3,808 observations on the 12 variables including body mass index (BMI) assessed in both MZ and DZ twins.

Questionnaires were mailed to 5,967 pairs age 18 years and over. These data consist of completed questionnaires returned by both members of 3,808 (64 percent) pairs. There are two cohort blocks in the data: a younger group (zyg 1:5), and an older group (zyg 6:10)

It is a wide dataset, with two individuals per line. Families are identified by the variable “fam”.

Data include zygosity (zyg), along with heights in metres, weights in kg, and the derived variables BMI in kg/m² (stored as “htwt1” and “htwt2”), as well as the 7 times the log of this variable, stored here as bmi1 and bmi2. The logged values are more closely normally distributed and scaling by 7 put them into a similar range as the original variable.

For convenience, zyg is broken out into separate “zygosity” and “cohort” factors. “zygosity” is coded as a 5-level factor.

Usage

```
data(twinData)
```

Format

A data frame with 3808 observations on the following 12 variables.

fam The family ID

age Age in years (of both twins)

zyg Code for zygosity and cohort (see details)

part A numeric vector

wt1 Weight of twin 1 (kg)
 wt2 Weight of twin 2 (kg)
 ht1 Height of twin 1 (m)
 ht2 Height of twin 2 (m)
 htwt1 Raw BMI of twin 1 (kg/m²)
 htwt2 Raw BMI of twin 2 (kg/m²)
 bmi1 7*log(BMI) of twin 1
 bmi2 7*log(BMI) of twin 2
 cohort Either “younger” or “older”
 zygosity Zygosity factor with levels: MZFF, MZMM, DZFF, DZMM, DZOS
 age1 Age of Twin 1
 age2 Age of Twin 2

Details

“zyg” codes twin-zygosity as follows: 1 == MZFF (i.e MZ females) 2 == MZMM (i.e MZ males)
 3 == DZFF 4 == DZMM 5 == DZOS opposite sex pairs

Note: zyg 6:10 are for an older cohort in the sample. So: 6 == MZFF (i.e MZ females) 7 == MZMM
 (i.e MZ males) 8 == DZFF 9 == DZMM 10 == DZOS opposite sex pairs

The “zygosity” and “cohort” variables take care of this for you (conventions differ).

References

Martin, N. G. & Jardine, R. (1986). Eysenck’s contribution to behavior genetics. In S. Modgil & C. Modgil (Eds.), *Hans Eysenck: Consensus and Controversy*. Falmer Press: Lewes, Sussex.

Martin, N. G., Eaves, L. J., Heath, A. C., Jardine, R., Feingold, L. M., & Eysenck, H. J. (1986). Transmission of social attitudes. *Proceedings of the National Academy of Science*, **83**, 4364-4368.

Examples

```
data(twinData)
str(twinData)
plot(wt1 ~ wt2, data = twinData)
selVars = c("bmi1", "bmi2")
mzData <- subset(twinData, zyg == 1, selVars)
dzData <- subset(twinData, zyg == 3, selVars)

# equivalently
mzData <- subset(twinData, zygosity == "MZFF", selVars)

# Disregard sex, pick older cohort
mz <- subset(twinData, zygosity %in% c("MZFF", "MZMM") & cohort == "older", selVars)
```

twin_NA_dot	<i>Twin data on weight and height</i>
-------------	---------------------------------------

Description

Data set used in some of OpenMx's examples.

Usage

```
data("twin_NA_dot")
```

Format

A data frame with 3808 observations on the following variables.

fam Family ID variable
age Age of the twin pair. Range: 17 to 88.
zyg Integer codes for zygosity and gender combinations
part
wt1 Weight in kilograms for twin 1
wt2 Weight in kilograms for twin 2
ht1 Height in meters for twin 1
ht2 Height in meters for twin 2
htwt1 Product of ht and wt for twin 1
htwt2 Product of ht and wt for twin 2
bmi1 Body Mass Index for twin 1
bmi2 Body Mass Index for twin 2

Details

Same as [myTwinData](#) but has . as the missing data value instead of NA.

Source

Timothy Bates

References

The OpenMx User's guide can be found at <http://openmx.ssri.psu.edu/documentation>.

Examples

```
data(twin_NA_dot)
summary(twin_NA_dot)
# Note that all variables are treated as factors because of the missing data coding.
```

vec2diag	<i>Create Diagonal Matrix From Vector</i>
----------	-------------------------------------------

Description

Given an input row or column vector, `vec2diag` returns a diagonal matrix with the input argument along the diagonal.

Usage

```
vec2diag(x)
```

Arguments

`x` a row or column vector.

Details

Similar to the function [diag](#), except that the input argument is always treated as a vector of elements to place along the diagonal.

See Also

[diag2vec](#)

Examples

```
vec2diag(matrix(1:4, 1, 4))  
vec2diag(matrix(1:4, 4, 1))
```

vech	<i>Half-vectorization</i>
------	---------------------------

Description

This function returns the half-vectorization of an input matrix as a column vector.

Usage

```
vech(x)
```

Arguments

`x` an input matrix.

Details

The half-vectorization of an input matrix consists of the elements in the lower triangle of the matrix, including the elements along the diagonal of the matrix, as a column vector. The column vector is created by traversing the matrix in column-major order.

See Also

[vech2full](#), [vechs](#), [rvectorize](#), [cvectorize](#)

Examples

```
vech(matrix(1:9, 3, 3))
vech(matrix(1:12, 3, 4))
```

vech2full

Inverse Half-vectorization

Description

This function returns the symmetric matrix constructed from a half-vectorization.

Usage

```
vech2full(x)
```

Arguments

`x` an input single column or single row matrix.

Details

The half-vectorization of an input matrix consists of the elements in the lower triangle of the matrix, including the elements along the diagonal of the matrix, as a column vector. The column vector is created by traversing the matrix in column-major order. The inverse half-vectorization takes a vector and reconstructs a symmetric matrix such that `vech2full(vech(x))` is identical to `x` if `x` is symmetric.

Note that very few vectors have the correct number of elements to construct a symmetric matrix. For example, vectors with 1, 3, 6, 10, and 15 elements can be used to make a symmetric matrix, but none of the other numbers between 1 and 15 can. An error is thrown if the number of elements in `x` cannot be used to make a symmetric matrix.

See Also

[vechs2full](#), [vech](#), [vechs](#), [rvectorize](#), [cvectorize](#)

Examples

```
vech2full(1:10)

matrix(1:16, 4, 4)
vech(matrix(1:16, 4, 4))
vech2full(vech(matrix(1:16, 4, 4)))
```

vechs

Strict Half-vectorization

Description

This function returns the strict half-vectorization of an input matrix as a column vector.

Usage

```
vechs(x)
```

Arguments

x an input matrix.

Details

The half-vectorization of an input matrix consists of the elements in the lower triangle of the matrix, excluding the elements along the diagonal of the matrix, as a column vector. The column vector is created by traversing the matrix in column-major order.

See Also

[vech](#), [rvectorize](#), [cvectorize](#)

Examples

```
vechs(matrix(1:9, 3, 3))
vechs(matrix(1:12, 3, 4))
```

`vechs2full`*Inverse Strict Half-vectorization*

Description

This function returns the symmetric matrix constructed from a strict half-vectorization.

Usage

```
vechs2full(x)
```

Arguments

`x` an input single column or single row matrix.

Details

The strict half-vectorization of an input matrix consists of the elements in the lower triangle of the matrix, excluding the elements along the diagonal of the matrix, as a column vector. The column vector is created by traversing the matrix in column-major order. The inverse strict half-vectorization takes a vector and reconstructs a symmetric matrix such that `vechs2full(vechs(x))` is equal to `x` with zero along the diagonal if `x` is symmetric.

Note that very few vectors have the correct number of elements to construct a symmetric matrix. For example, vectors with 1, 3, 6, 10, and 15 elements can be used to make a symmetric matrix, but none of the other numbers between 1 and 15 can. An error is thrown if the number of elements in `x` cannot be used to make a symmetric matrix.

See Also

[vech2full](#), [vech](#), [vechs](#), [rvectorize](#), [cvectorize](#)

Examples

```
vechs2full(1:10)

matrix(1:16, 4, 4)
vechs(matrix(1:16, 4, 4))
vechs2full(vechs(matrix(1:16, 4, 4)))
```

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