Package ‘MplusAutomation’

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**Type** Package

**Title** An R Package for Facilitating Large-Scale Latent Variable Analyses in Mplus

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**Description** Leverages the R language to automate latent variable model estimation and interpretation using ‘Mplus’, a powerful latent variable modeling program developed by Muthen and Muthen (<http://www.statmodel.com>). Specifically, this package provides routines for creating related groups of models, running batches of models, and extracting and tabulating model parameters and fit statistics.

**License** LGPL-3

**URL** [https://github.com/michaelhallquist/MplusAutomation](https://github.com/michaelhallquist/MplusAutomation)

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**biocViews**

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.mplusMultinomial

Description

Internal Function for Multinomial Regression in Mplus

Usage

.mplusMultinomial(
  dv,
  iv,
  data,
  idvar = "",
  integration = 1000,
  processors = 2,
  OR = TRUE,
  pairwise = TRUE,
  ...
)

Arguments

dv A character string with the variable name for the dependent (outcome) variable.

iv A character vector with the variable name(s) for the independent (predictor/explanatory) variable(s).

data A dataset.

idvar Optional. A character string indicating the name of the ID variable. Not currently used but may be used in future.

integration An integer indicating the number of Monte Carlo integration points to use. Defaults to 1000.

processors An integer indicating the number of processors to use. Passed to Mplus. Defaults to 2.

OR A logical value whether odds ratios should be returned. Defaults to TRUE.

pairwise A logical value indicating whether all pairwise tests should be computed. Defaults to TRUE.

... Additional arguments passed to mplusModeler().

Value

A list of results and Mplus model object.
Author(s)

Joshua F. Wiley <jwiley.psych@gmail.com>

Examples

## Not run:

```r
set.seed(1234)
tmpd <- data.frame(
  x1 = rnorm(200),
  x2 = rnorm(200),
  x3 = cut(rnorm(200),
    breaks = c(-Inf, -.7, .7, Inf),
    labels = c("a", "b", "c"))
)
tmpd$y <- cut(rnorm(200, sd = 2) + tmpd$x1 + tmpd$x2 + I(tmpd$x3 == "b"),
  breaks = c(-Inf, -.5, 1, Inf),
  labels = c("L", "M", "H"))

tmpres <- MplusAutomation:::.mplusMultinomial(
  dv = "y",
  iv = c("x1", "x2"),
  data = tmpd,
  pairwise = TRUE)
tmpres2 <- MplusAutomation:::.mplusMultinomial(
  dv = "y",
  iv = c("x1", "x2"),
  data = tmpd,
  pairwise = FALSE)
tmpres3 <- MplusAutomation:::.mplusMultinomial(
  dv = "y",
  iv = c("x1@0", "x2@0"),
  data = tmpd,
  pairwise = FALSE)
```

## End(Not run)

---

**cd**

**Change directory**

Description

The function takes a path and changes the current working directory to the path. If the directory specified in the path does not currently exist, it will be created.

Usage

```
cd(base, pre, num)
```
Arguments

base a character string with the base path to the directory. This is required.
pre an optional character string with the prefix to add to the base path. Non character strings will be coerced to character class.
num an optional character string, prefixed by pre. Non character strings will be coerced to character class.

Details

The function has been designed to be platform independent, although it has had limited testing. Path creation is done using file.path, the existence of the directory is checked using file.exists and the directory created with dir.create. Only the first argument, is required. The other optional arguments are handy when one wants to create many similar directories with a common base.

Value

NULL, changes the current working directory

Author(s)

Joshua F. Wiley <jwiley.psych@gmail.com>

Examples

## Not run:
# an example just using the base
cd("~/testdir")

# an example using the optional arguments
base <- "~/testdir"
pre <- "test_"
cd(base, pre, 1)
cd(base, pre, 2)

## End(Not run)

---

coefficients for an mplus.model object

Description

This is a method for returning the coefficients of an mplus.model object. It works directly on an object stored from readModels such as: object <- readModels("/path/to/model/model.out"). Method that calls coef.mplus.model. See further documentation there.
Usage

```r
## S3 method for class 'mplus.model'
coef(
  object,
  type = c("un", "std", "stdy", "stdyx"),
  params = c("regression", "loading", "undirected", "expectation", "variability",
             "new"),
  ...
)
```

```r
## S3 method for class 'mplusObject'
coef(object, ...)
```

Arguments

- **object**: An object of class mplusObject
- **type**: A character vector indicating the type of coefficients to return. One of “un”, “std”, “stdy”, or “stdyx”.
- **params**: A character vector indicating what type of parameters to extract. Any combination of “regression”, “loading”, “undirected”, “expectation”, “variability”, and “new”. A single one can be passed or multiple. By default, all are used and all parameters are returned.
- **...**: Additional arguments to pass on (not currently used)
- **raw**: A logical defaulting to `FALSE` indicating whether to parse and return coefficients based on the type (regression, etc.) and relabel using an arrow notation, or to return the raw coefficients in a named vector.

Value

Either a data frame of class ‘mplus.model.coefs’, or in the case of multiple group models, a list of class ‘mplus.model.coefs’, where each element of the list is a data frame of class ‘mplus.model.coefs’, or a named vector of coefficients, if `raw=TRUE`.

Author(s)

Joshua F. Wiley <jwiley.psych@gmail.com>

See Also

`readModels`

Other Mplus-Formatting: `confint.mplus.model()`, `extract()`, `print.MplusRstructure()`, `summary.mplusObject()`

Examples

```r
## Not run:
# simple example of a model using builtin data
# demonstrates use
```
compareModels  

### Description

The `compareModels` function compares the output of two Mplus files and prints similarities and differences in the model summary statistics and parameter estimates. Options are provided for filtering out fixed parameters and nonsignificant parameters. When requested, `compareModels` will compute the chi-square difference test for nested models (does not apply to MLMV, WLSM, and WLSMV estimators, where DIFFTEST in Mplus is needed). Model outputs to be compared can be full summaries and parameters (generated by `readModels()`), summary statistics only (`extractModelSummaries`), or parameters only (`extractModelParameters`).

### Usage

```r
compareModels(
  m1,  
m2,  
  show = "all",  
equalityMargin = c(param = 1e-04, pvalue = 1e-04),
)```
compare = "unstandardized",
sort = "none",
showFixed = FALSE,
showNS = TRUE,
diffTest = FALSE
)

Arguments

m1
The first Mplus model to be compared. Generated by readModels, extractModelSummaries, or extractModelParameters.

m2
The second Mplus model to be compared.

show
What aspects of the models should be compared. Options are "all", "summaries", "equal", "diff", "pdiff", and "unique". See below for details.

equalityMargin
Defines the discrepancy between models that is considered equal. Different margins can be specified for p-value equality versus parameter equality. Defaults to .0001 for both.

compare
Which parameter estimates should be compared. Options are "unstandardized", "stdyx.standardized" "stdy.standardized", and "std.standardized".

sort
How to sort the output of parameter comparisons. Options are "none", "type", "alphabetical", and "maxDiff". See below for details.

showFixed
Whether to display fixed parameters in the output (identified where the est/se = 999.000, per Mplus convention). Default to FALSE.

showNS
Whether to display non-significant parameter estimates. Can be TRUE or FALSE, or a numeric value (e.g., .10) that defines what p-value is filtered as non-significant.

diffTest
Whether to compute a chi-square difference test between the models. Assumes that the models are nested. Not available for MLMV, WLSMV, and ULSMV estimators. Use DIFFTEST in Mplus instead.

Details

The show parameter can be one or more of the following, which can be passed as a vector, such as c("equal", "pdiff").

show "all" Display all available model comparison. Equivalent to c("summaries", "equal", "diff", "pdiff", "unique").


"allsummaries" Prints a comparison of all summary statistics available in each model. May generate a lot of output.

"equal" Print parameter estimates that are equal between models (i.e., <= equalityMargin["param"]).

"diff" Print parameter estimates that are different between models (i.e., > equalityMargin["param"]).

"pdiff" Print parameter estimates where the p-values differ between models (i.e., > equalityMargin["pvalue"]).

"unique" Print parameter estimates that are unique to each model.
The `sort` parameter determines the order in which parameter estimates are displayed. The following options are available:

- **sort "none"**  
  No sorting is performed, so parameters are output in the order presented in Mplus. *(Default)*

- **"type"**  
  Sort parameters by their role in the model. This groups output by regression coefficient (ON), factor loadings (BY), covariances (WITH), and so on. Within each type, output is alphabetical.

- **"alphabetical"**  
  Sort parameters in alphabetical order.

- **"maxDiff"**  
  Sort parameter output by the largest differences between models (high to low).

**Value**

No value is returned by this function. It is used to print model differences to the R console.

**Author(s)**

Michael Hallquist

**Examples**

```r
# make me!!!
```

---

**confint.mplus.model**  
*Return confidence intervals for an mplus.model object*

**Description**

This is a method for returning the confidence of an mplus.model object. It works directly on an object stored from `readModels` such as:

```r
object <- readModels("/path/to/model/model.out")
```

Method that calls `confint.mplus.model`. See further documentation there.

**Usage**

```r
## S3 method for class 'mplus.model'
confint(
  object,
  parm,
  level = 0.95,
  type = c("un", "std", "stdy", "stdyx"),
  params = c("regression", "loading", "undirected", "expectation", "variability", "new"),
  ...
)
```

```r
## S3 method for class 'mplusObject'
confint(object, ...)
```
confint.mplus.model

Arguments

object  An object of class mplusObject
parm    Included as all confint() methods must include it. Not used currently for Mplus.
level   A numeric vector indicating the level of confidence interval to extract. Options are .95, .90, or .99 as those are all Mplus provides.
type    A character vector indicating the type of confidence intervals to return. One of “un”, “std”, “stdy”, or “stdyx”.
params  A character vector indicating what type of parameters to extract. Any combination of “regression”, “loading”, “undirected”, “expectation”, “variability”, and “new”. A single one can be passed or multiple. By default, all are used and all parameters are returned.
...     Additional arguments to pass on (not currently used)

Value

A data frame of class ‘mplus.model.cis’, or in the case of multiple group models, a list of class ‘mplus.model.cis’, where each element of the list is a data frame of class ‘mplus.model.cis’.

Author(s)

Joshua F. Wiley <jwiley.psych@gmail.com>

See Also

readModels

Other Mplus-Formatting: coef.mplus.model(), extract(), print.MplusRstructure(), summary.mplusObject()

Examples

```r
## Not run:
# simple example of a model using builtin data
# demonstrates use
test <- mplusObject(
  TITLE = "test the MplusAutomation Package;",
  MODEL = "
    mpg ON wt hp;
    wt WITH hp;",
  OUTPUT = "STANDARDIZED; CINTERVAL;",
  usevariables = c("mpg", "wt", "hp"),
  rdata = mtcars)
res <- mplusModeler(test, "mtcars.dat", modelout = "modell.inp", run = 1L)

# example of the confint method on an mplus.model object
# note that res$results holds the results of readModels()
confint(res$results)
confint(res$results, type = "std")
confint(res$results, type = "stdy")
```
confint(res$results, type = "stdyx", level = .99)

# there is also a method for mplusObject class
confint(res)
screenreg(res, cis = TRUE, single.row = TRUE)

# remove files
unlink("mtcars.dat")
unlink("model1.inp")
unlink("model1.out")
unlink("Mplus Run Models.log")

## End(Not run)

createMixtures

Create syntax for a batch of mixture models

Description

Dynamically creates syntax for a batch of mixture models, with intelligent defaults. This function is a wrapper around mplusObject, and additional arguments can be passed to this function using .... In all arguments to mplusObject, a double space (" ") is replaced with a newline character. This can be used to obtain nicely formatted Mplus syntax. In the arguments model_class_specific and SAVEDATA, the character string "{C}" is substituted with the correct class number. The character string "{filename_stem}" is substituted with the filename stem, for example, to name savedata in line with the input files.

Usage

createMixtures(
classes = 1L,
filename_stem = NULL,
model_overall = NULL,
model_class_specific = NULL,
rdata = NULL,
usevariables = NULL,
OUTPUT = "TECH11 TECH14;",
SAVEDATA = "FILE IS {filename_stem}_{C}.dat; SAVE = cprobabilities;",
...
)

Arguments

classes A vector of integers, indicating which class solutions to generate. Defaults to 1L. E.g., classes = 1:6, classes = c(1:4, 6:8).
filename_stem Character. A stem for the automatically generated filenames of the syntax and data files.
model_overall Character. Mplus syntax for the overall model (across classes).
model_class_specific
Character vector. Mplus syntax for the class-specific model(s) of one or more
categorical latent variables. Each element of model_class_specific is used
as the class-specific syntax of a different categorical latent variable. This allows
one to easily specify latent transition analyses (see second example). The char-
acter string "{C}" is substituted with the correct class number, for example to
set unique parameter labels for each class, or to specify equality constraints.

rdata
Data.frame. An R dataset to be used for the model.

usevariables
Character vector, specifying the names of variables in the rdata object which
should be included in the Mplus data file and model.

OUTPUT
Character. Syntax for Mplus' OUTPUT option. Highly recommended when
determining the appropriate number of latent classes. TECH11 is required to
obtain the VLMR-test; TECH14 is required for the BLR-test.

SAVEDATA
Character. Syntax for Mplus' savedata option. Highly recommended when con-
ducting mixture models. The default option will often be adequate.

... Additional arguments, passed to mplusObject, such as syntax for other Mplus
options.

Value
None. Function is used for its side effects (generating syntax).

Author(s)
Caspar J. van Lissa

See Also
mplusObject, mplusModeler

Examples

## Not run:
createMixtures(classes = 1:3, filename_stem = "iris", rdata = iris)

## End(Not run)
## Not run:
data <- read.table("http://statmodel.com/usersguide/chap8/ex8.13.dat")[,c(1:10)]
names(data) <- c("u11", "u12", "u13", "u14", "u15", "u21", "u22", "u23", "u24", "u25")
createMixtures(
classes = 2,
filename_stem = "dating",
model_overall = "c2 ON c1;",
model_class_specific = c(
  "[u11$1] (a{C}); [u12$1] (b{C}); [u13$1] (c{C}); [u14$1] (d{C}); [u15$1] (e{C});",
  "[u21$1] (a{C}); [u22$1] (b{C}); [u23$1] (c{C}); [u24$1] (d{C}); [u25$1] (e{C});"
),
rdata = data,
ANALYSIS = "PROCESSORS IS 2; LRTSTARTS (0 0 40 20); PARAMETERIZATION = PROBABILITY;",
VARIABLE = "CATEGORICAL = u11-u15 u21-u25;"
)
createModels

Create Mplus Input Files from Template

Description

The `createModels` function processes a single Mplus template file and creates a group of related model input files. Definitions and examples for the template language are provided in the MplusAutomation vignette and are not duplicated here at the moment. See this documentation: `vignette("Vignette",package="MplusAutomation")`

Usage

```r
createModels(templatefile)
```

Arguments

- `templatefile`: The filename (absolute or relative path) of an Mplus template file to be processed. Example “C:/MplusTemplate.txt”

Value

No value is returned by this function. It is solely used to process an Mplus template file.

Author(s)

Michael Hallquist

Examples

```r
## Not run:
createModels("L2 Multimodel Template No iter.txt")

## End(Not run)
```
createSyntax  

Create the Mplus input text for an mplusObject

Description

This function takes an object of class mplusObject and creates the Mplus input text corresponding to it, including data link and variable names.

Usage

createSyntax(object, filename, check = TRUE, add = FALSE, imputed = FALSE)

Arguments

- object: An object of class mplusObject
- filename: The name of the data file as a character vector
- check: A logical indicating whether or not to run parseMplus on the created input file. Checks for errors like lines that are too long, or for missing semi-colons and gives notes.
- add: A logical passed on to parseMplus whether to add semi colons to line ends. Defaults to FALSE.
- imputed: A logical whether the data are multiply imputed. Defaults to FALSE.

Value

A character string containing all the text for the Mplus input file.

Author(s)

Joshua F. Wiley <jwiley.psych@gmail.com>

See Also

prepareMplusData, mplusModeler

Examples

# example mplusObject
example1 <- mplusObject(MODEL = "mpg ON wt;",
    usevariables = c("mpg", "hp"), rdata = mtcars)

# create the Mplus input text
cat(createSyntax(example1, "example1.dat"), file=stdout(), fill=TRUE)

# update the object, then create input text
cat(createSyntax(update(example1,
    TITLE = ~ "This is my title;"),
    file=stdout(), fill=TRUE)
detectVariables

Automatically detect variables from an Mplus model object

Description
This is a function to automatically detect the variables used in an Mplus model object.

Usage
detectVariables(object)

Arguments
object: An Mplus model object from mplusObject.

Value
A vector of variables from the R dataset to use.

Author(s)
Joshua F. Wiley <jwiley.psych@gmail.com>

See Also
mplusModeler, mplusObject

Examples
example1 <- mplusObject(MODEL = "mpg ON wt;",
                           rdata = mtcars, autov = FALSE)
example1$usevariables
MplusAutomation:::detectVariables(example1)

example2 <- mplusObject(MODEL = "mpg ON wt;",
                           rdata = mtcars, autov = TRUE)
example2$usevariables
example3 <- update(example2,
                   MODEL = ~ . + "mpg ON qsec; wt WITH qsec;",
                   autov = TRUE)
example3$usevariables
rm(example1, example2, example3)
extract

Extract function to make Mplus output work with the \texttt{texreg} package

Description

This is a method for extracting output in a format suitable for the \texttt{texreg} package. Uses \texttt{coef} for most the work.

Usage

\begin{verbatim}
extract.mplus.model(
    model,
    summaries = "none",
    cis = FALSE,
    escape.latex = FALSE,
    ...
)
\end{verbatim}

\begin{verbatim}
extract.mplusObject(model, summaries = "none", cis = FALSE, ...)
\end{verbatim}

## S4 method for signature 'mplus.model'
extract(model, summaries = "none", cis = FALSE, escape.latex = FALSE, ...)

## S4 method for signature 'mplusObject'
extract(model, summaries = "none", cis = FALSE, ...)

Arguments

- \texttt{model} An Mplus model object. This typically comes either from \texttt{readModels} directly, or indirectly via \texttt{mplusModeler}. The results will have different classes, but extract methods are defined for both.
- \texttt{summaries} A character vector which summaries to include. Defaults to “none”.
- \texttt{cis} A logical whether to extract confidence intervals.
- \texttt{escape.latex} A logical value whether to escape dollar signs in coefficient names for LaTeX. Defaults to FALSE.
- ... Additional arguments passed to \texttt{coef.mplus.model}.

Value

A \texttt{texreg} object, or for multiple group models, a list of \texttt{texreg} objects.

Author(s)

Joshua F. Wiley <jwiley.psych@gmail.com>
extractEFAparameters

Extract the model parameters from an EFA Mplus model output

See Also

readModels

Other Mplus-Formatting: coef.mplus.model(), confint.mplus.model(), print.MplusRstructure(), summary.mplusObject()

Examples

```r
## Not run:
# simple example of a model using builtin data
# demonstrates use
test <- mplusObject(
    TITLE = "test the MplusAutomation Package;",
    MODEL = 
        mpg ON wt hp;
        wt WITH hp;",
    OUTPUT = "STANDARDIZED;",
    usevariables = c("mpg", "wt", "hp"),
    rdata = mtcars)

res <- mplusModeler(test, "mtcars.dat", modelout = "model1.inp", run = 1L)

extract(res$results)
# there is also a method for mplusObject class
extract(res)

# load the texreg package
# to use pretty printing via screenreg
# uncomment to run these examples
# library(texreg)
# screenreg(res)
# screenreg(res, type = 'stdyx')

# screenreg(res, type = 'un', params = 'regression',
# single.row=TRUE)
# screenreg(res, type = 'un', params = 'regression', summaries = 'CFI',
# single.row=TRUE)

# remove files
unlink("mtcars.dat")
unlink("model1.inp")
unlink("model1.out")
unlink("Mplus Run Models.log")

## End(Not run)
```
Description

Extract the model parameters from an EFA Mplus model output

Usage

extractEFAparameters(outfiletext, filename)

Arguments

outfiletext character vector of Mplus output file being processed
filename name of the output file

Value

list of parsed EFA parameters

descrition

Extract model parameters from MODEL RESULTS section.

Usage

extractModelParameters(
  target = getwd(),
  recursive = FALSE,
  filefilter,
  dropDimensions = FALSE,
  resultType
)

Arguments

target the directory containing Mplus output files (.out) to parse OR the single output file to be parsed. May be a full path, relative path, or a filename within the working directory. Defaults to the current working directory. Example: “C:/Users/Michael/Mplus Runs”

recursive optional. If TRUE, parse all models nested in subdirectories within target. Defaults to FALSE.
extractModelParameters

filefilter a Perl regular expression (PCRE-compatible) specifying particular output files to
be parsed within directory. See regex or http://www.pcre.org/pcre.txt
for details about regular expression syntax.

dropDimensions Relevant only for multi-file parsing. If TRUE, then if only one output section
(usually unstandardized) is present for all files in the parsed list, then eliminate
the second-level list (which contains elements for each output section). The
result is that the elements of the returned list are data.frame objects with the
relevant parameters.

resultType N.B.: this parameter is deprecated and will be removed in a future version. The
new default is to extract all results that are present and return a list (see below
for details). resultType specified the results section to extract. If raw, the un-
standardized estimates will be returned. “stdyx”, “stdy”, and “std” are the other
options, which extract different standardized solutions. See the Mplus User’s
Guide for additional details about the differences in these standardizations.

Value

If target is a single file, a list containing unstandardized and standardized results will be re-
turned. If all standardized solutions are available, the list element will be named: unstandardized,
stdyx.standardized, stdy.standardized, and std.standardized. If confidence intervals are
output using OUTPUT:CINTERVAL, then a list element named ci.unstandardized will be in-
cluded. Each of these list elements is a data.frame containing relevant model parameters.

If target is a directory, a list will be returned, where each element contains the results for a single
file, and the top-level elements are named after the corresponding output file name. Each element
within this list is itself a list, with elements as in the single file case above.

The core data.frame for each MODEL RESULTS section typically has the following structure:

paramHeader The header that begins a given parameter set. Example: "FACTOR1 BY"
param The particular parameter being measured (within paramHeader). Example: "ITEM1"
est Parameter estimate value.
se Standard error of the estimate
est_se Quotient of est/se, representing z-test/t-test in large samples
pval Two-tailed p-value for the est_se quotient.

In the case of output from Bayesian estimation (ESTIMATOR=BAYES), the data.frame will con-
tain a different set of variables, including some of the above, as well as

posterior_sd Posterior standard deviation of the estimate.
lower_2.5ci Lower 2.5 percentile of the estimate.
upper_2.5ci Upper 2.5 percentile (aka 97.5 percentile) of the estimate.

Also note that the pval column for Bayesian output represents a one-tailed estimate.

In the case of output from a Monte Carlo study (MONTECARLO: and MODEL POPULATION:),
the data.frame will contain a different set of variables, including some of the above, as well as

population Population parameter value.
extractModelParameters

<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>average</td>
<td>Average parameter estimate across replications.</td>
</tr>
<tr>
<td>population_sd</td>
<td>Standard deviation of parameter value in population across replications.</td>
</tr>
<tr>
<td>average_se</td>
<td>Average standard error of estimated parameter value across replications.</td>
</tr>
<tr>
<td>mse</td>
<td>Mean squared error.</td>
</tr>
<tr>
<td>cover_95</td>
<td>Proportion of replications whose 95% confidence interval for the parameter includes the population value.</td>
</tr>
<tr>
<td>pct sig coef</td>
<td>Proportion of replications for which the two-tailed significance test of the parameter is significant (p &lt; .05).</td>
</tr>
</tbody>
</table>

In the case of confidence interval output (OUTPUT:CINTERVAL), the list element ci.unstandardized will contain a different set of variables, including some of the above, as well as

- low.5: Lower 0.5% CI estimate.
- low2.5: Lower 2.5% CI estimate.
- low5: Lower 5% CI estimate.
- est: Parameter estimate value.
- up5: Upper 5% (i.e., 95%) CI estimate.
- up2.5: Upper 2.5% (i.e., 97.5%) CI estimate.
- up.5: Upper 0.5% (i.e., 99.5%) CI estimate.

If the model contains multiple latent classes, an additional variable, LatentClass, will be included, specifying the latent class number. Also, the Categorical Latent Variables section will be included as LatentClass "Categorical.Latent.Variables."

If the model contains multiple groups, Group will be included.

If the model contains two-level output (between/within), BetweenWithin will be included.

Author(s)

Michael Hallquist

See Also

extractModelSummaries

Examples

```r
## Not run:
ex3.14 <- extractModelParameters(

## End(Not run)
```
extractModelSummaries

Extract summary statistics from a single output file or from a group of Mplus models within a directory

Description

Parses a group of Mplus model output files (.out extension) for model fit statistics. At this time, the details extracted are fixed and include: Filename, InputInstructions, Title, Estimator, LL, BIC, aBIC, AIC, AICC, Parameters, Observations, CFI, TLI, RMSEA_Estimate, RMSEA_90CI_LB, RMSEA_90CI_UB, RMSEA_pLT05, ChiSqM_Value, ChiSqM_DF, ChiSq_PValue, BLRT_KM1LL, BLRT_PValue, BLRT_Numdraws. The infrastructure is in place to allow for user-specified selection of summary statistics in future versions.

Usage

extractModelSummaries(target = getwd(), recursive = FALSE, filefilter)

Arguments

target the directory containing Mplus output files (.out) to parse OR the single output file to be parsed. Defaults to the current working directory. Example: "C:/Users/Michael/Mplus Runs"

recursive optional. If TRUE, parse all models nested in subdirectories within directory. Defaults to FALSE.

filefilter a Perl regular expression (PCRE-compatible) specifying particular output files to be parsed within directory. See regex or http://www.pcre.org/pcre.txt for details about regular expression syntax.

Value

Returns a data.frame containing model fit statistics for all output files within directory. The data.frame contains some of the following variables (depends on model type):

Title Title for the model, specified by the TITLE: command
Filename Filename of the output file
Estimator Estimator used for the model (e.g., ML, MLR, WLSMV, etc.)
LL Log-likelihood of the model
BIC Bayesian Information Criterion
aBIC Sample-Size-Adjusted BIC (Sclove, 1987)
AIC Akaike’s Information Criterion
AICC Corrected AIC, based on Sugiura (1978) and recommended by Burnham & Anderson (2002)
DIC Deviance Information Criterion. Available in ESTIMATOR=BAYES output.
Parameters Number of parameters estimated by the model
pD Estimated number of parameters in Bayesian output
<table>
<thead>
<tr>
<th>Metric</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Observations</td>
<td>The number of observations for the model (does not support multiple-groups analysis at this time)</td>
</tr>
<tr>
<td>CFI</td>
<td>Confirmatory Fit Index</td>
</tr>
<tr>
<td>TLI</td>
<td>Tucker-Lewis Index</td>
</tr>
<tr>
<td>RMSEA_Estimate</td>
<td>Point estimate of root mean squared error of approximation</td>
</tr>
<tr>
<td>RMSEA_90CI_LB</td>
<td>Lower bound of the 90% Confidence Interval around the RMSEA estimate.</td>
</tr>
<tr>
<td>RMSEA_90CI_UB</td>
<td>Upper bound of the 90% Confidence Interval around the RMSEA estimate.</td>
</tr>
<tr>
<td>RMSEA_pLT05</td>
<td>Probability that the RMSEA estimate falls below .05, indicating good fit.</td>
</tr>
<tr>
<td>ChiSQM_Value</td>
<td>Model chi-squared value</td>
</tr>
<tr>
<td>ChiSQM_DF</td>
<td>Model chi-squared degrees of freedom</td>
</tr>
<tr>
<td>ChiSQM_PValue</td>
<td>Model chi-squared p value</td>
</tr>
<tr>
<td>ChiSQM_ScalingCorrection</td>
<td>H0 Scaling Correction Factor</td>
</tr>
<tr>
<td>ObsRepChiSqDiff_95CI_LB</td>
<td>Lower bound of 95% confidence interval for the difference between observed and replicated chi-square values</td>
</tr>
<tr>
<td>ObsRepChiSqDiff_95CI_UB</td>
<td>Upper bound of 95% confidence interval for the difference between observed and replicated chi-square values</td>
</tr>
<tr>
<td>PostPred_PValue</td>
<td>Posterior predictive p-value</td>
</tr>
<tr>
<td>PriorPostPred_PValue</td>
<td>Prior Posterior Predictive P-Value</td>
</tr>
<tr>
<td>BLRT_RequestedDraws</td>
<td>Number of requested bootstrap draws for TECH14.</td>
</tr>
<tr>
<td>BLRT_KM1LL</td>
<td>Log-likelihood of the K-1 model (one less class) for the Bootstrapped Likelihood Ratio Test (TECH14).</td>
</tr>
<tr>
<td>BLRT_2xLLDiff</td>
<td>Two times the log-likelihood difference of the models with K and K-1 classes (TECH14).</td>
</tr>
<tr>
<td>BLRT_ParamDiff</td>
<td>Difference in the number of parameters for models with K and K-1 classes (TECH14).</td>
</tr>
<tr>
<td>BLRT_PValue</td>
<td>P-value of the Bootstrapped Likelihood Ratio Test (TECH14) testing whether the K class model is significantly better than K-1</td>
</tr>
<tr>
<td>BLRT_SuccessfulDraws</td>
<td>The number of successful bootstrapped samples used in the Bootstrapped Likelihood Ratio Test</td>
</tr>
<tr>
<td>SRMR</td>
<td>Standardized root mean square residual</td>
</tr>
<tr>
<td>SRMR_Between</td>
<td>For TYPE=TWOLEVEL output, standardized root mean square residual for between level</td>
</tr>
<tr>
<td>SRMR_Within</td>
<td>For TYPE=TWOLEVEL output, standardized root mean square residual for within level</td>
</tr>
<tr>
<td>WRMR</td>
<td>Weighted root mean square residual</td>
</tr>
</tbody>
</table>
**extractModelSummaries**

ChiSqBaseline_Value  
Baseline (unstructured) chi-squared value

ChiSqBaseline_DF  
Baseline (unstructured) chi-squared degrees of freedom

ChiSqBaseline_PValue  
Baseline (unstructured) chi-squared p value

NumFactors  
For TYPE=EFA output, the number of factors

T11_KM1Starts  
TECH11: Number of initial stage random starts for k-1 model

T11_KM1Final  
TECH11: Number of final stage optimizations for k-1 model

T11_KM1LL  
TECH11: Log-likelihood of the K-1 model used for the Vuong-Lo-Mendell-Rubin LRT

T11_VLMR_2xLLDiff  
TECH11: 2 * Log-likelihood Difference of K-class vs. K-1-class model for the Vuong-Lo-Mendell-Rubin LRT

T11_VLMR_ParamDiff  
TECH11: Difference in number of parameters between K-class and K-1-class model for the Vuong-Lo-Mendell-Rubin LRT

T11_VLMR_Mean  
TECH11: Vuong-Lo-Mendell-Rubin LRT mean

T11_VLMR_SD  
TECH11: Vuong-Lo-Mendell-Rubin LRT standard deviation

T11_VLMR_PValue  
TECH11: Vuong-Lo-Mendell-Rubin LRT p-value

T11_LMR_Value  
TECH11: Lo-Mendell-Rubin Adjusted LRT value

T11_LMR_PValue  
TECH11: Lo-Mendell-Rubin Adjusted LRT p-value

**Author(s)**

Michael Hallquist

**See Also**

`regex`, `runModels`, `readModels`

**Examples**

```r
## Not run:
allExamples <- extractModelSummaries("C:/Program Files/Mplus/Mplus Examples/User's Guide Examples")

## End(Not run)
```
extractModIndices  

**Extract model modification indices.**

**Description**

Extracts the model modification indices from the MODEL MODIFICATION INDICES section of one or more Mplus output files. If the target is a directory, all .out files therein will be parsed and a single list will be returned, where the list elements are named by the output file name. Returned parameters typically include the pairwise relationships between variables to be freed, the change in model chi-square (M.I.), and the expected parameter change (E.P.C.).

**Usage**

```
extractModIndices(target = getwd(), recursive = FALSE, filefilter)
```

**Arguments**

- `target`  
  the directory containing Mplus output files (.out) to parse OR the single output file to be parsed. May be a full path, relative path, or a filename within the working directory. Defaults to the current working directory. Example: `"C:/Users/Michael/Mplus Runs"`

- `recursive`  
  optional. If TRUE, parse all models nested in subdirectories within target. Defaults to FALSE.

- `filefilter`  
  a Perl regular expression (PCRE-compatible) specifying particular output files to be parsed within directory. See regex or [http://www.pcre.org/pcre.txt](http://www.pcre.org/pcre.txt) for details about regular expression syntax.

**Value**

If `target` is a single file, a data.frame containing modification results for the target output file will be returned. If `target` is a directory, a list will be returned, where each element contains a data.frame of the modification indices for a single file, and the top-level elements are named after the corresponding output file name. The basic data.frame containing the MODEL MODIFICATION INDICES section of outfile. Variables include

- `modV1`  
  The first variable in the pair to be freed according to the M.I.

- `operator`  
  The suggested relationship between modV1 and modV2 (e.g., WITH for freeing the covariance between modV1 and modV2)

- `modV2`  
  The first variable in the pair to be freed according to the M.I.

- `MI`  
  The decrease in model chi-square if the specified relationship is freely estimated

- `EPC`  
  The expected parameter estimate between modV1 and modV2 if freed.

- `Std_EPC`  
  The EPC value standardized using the variances of the continuous latent variables.

- `StdYX_EPC`  
  The EPC value standardized using the variances of the continuous latent variables as well as the variances of the background and/or outcome variables.
**getSavedata_Bparams**

**Author(s)**

Michael Hallquist

**See Also**

readModels, extractModelSummaries, extractModelParameters

**Examples**

```r
## Not run:
ex3.14 <- extractModIndices(
## End(Not run)
```

---

**getSavedata_Bparams**

*Load the draws from the Bayesian model posterior distribution (SAVE-DATA BPARAMETERS) command into an R data.frame*

**Description**

This function reads a the BPARAMETERS output file from the Mplus SAVEDATA BPARAMETERS command and returns an R data.frame object.

**Usage**

```r
getSavedata_Bparams(outfile, discardBurnin = TRUE)
```

**Arguments**

- **outfile**
  - Required. The name of the Mplus output file to read. Can be an absolute or relative path. If `outfile` is a relative path or just the filename, then it is assumed that the file resides in the working directory `getwd()`.

- **discardBurnin**
  - Optional. Whether to discard the burn-in phase of each MCMC chain (i.e., the first half).

**Value**

A list containing the draws from the MCMC chains for a Bayesian model that uses the SAVEDATA BPARAMETERS command. Each list element corresponds to a single MCMC chain, as specified by the ANALYSIS: CHAINS syntax in Mplus. If `discardBurnin` is FALSE, then a superordinate list is provided that divides output in terms of burn-in versus valid draw halves of the MCMC chains. For documentation of how Mplus implements chain convergence checks and MCMC draws, see here: [http://www.statmodel.com/download/Bayes3.pdf](http://www.statmodel.com/download/Bayes3.pdf).
getSavedata_Data

Note

Note that the outfile parameter should refer to the Mplus output file (.out extension), not the actual dataset generated by SAVEDATA. This function reads information about the dataset from the .out file and loads the dataset accordingly.

Author(s)

Michael Hallquist, Florian Boeing-Messing

References


See Also

getsavedata_Fileinfo, getsavedata_Data

Examples

```r
## Not run:
fileInfo <- getsavedata_Data("C:/Program Files/Mplus/Test Output.out")
## End(Not run)
```

getSavedata_Data

Load an analysis dataset from the SAVEDATA command into an R data.frame

Description

This function reads an analysis dataset generated by the Mplus SAVEDATA command and returns an R data.frame object.

Usage

getSavedata_Data(outfile)

Arguments

outfile Required. The name of the Mplus output file to read. Can be an absolute or relative path. If outfile is a relative path or just the filename, then it is assumed that the file resides in the working directory getwd().

Value

A data.frame containing the analysis dataset generated by the SAVEDATA command.
Note

Note that the outfile parameter should refer to the Mplus output file (.out extension), not the actual dataset generated by SAVEDATA. This function reads information about the dataset from the .out file and loads the dataset accordingly.

Author(s)

Michael Hallquist

See Also

getsavedata_Fileinfo

Examples

```r
## Not run:
savedat <- getsavedata_Data("C:/Program Files/Mplus/Test Output.out")
## End(Not run)
```

getsavedata_Fileinfo

Read Variable Names, Formats, and Widths from data generated by the SAVEDATA Command

Description

This function reads the SAVEDATA INFORMATION section from an Mplus output file that used the SAVEDATA command, and it returns a list with the filename, variable names, variable formats, and variable widths of the SAVEDATA file. If present, the function also parses information about the Bayesian Parameters (BPARAMETERS) file.

Usage

getsavedata_Fileinfo(outfile)

Arguments

outfile  
required. The name of the Mplus output file to read. Can be an absolute or relative path. If outfile is a relative path or just the filename, then it is assumed that the file resides in the working directory getwd().

Value

Returns a list of SAVEDATA file information that includes:

- fileName: The name of the file containing the analysis dataset created by the Mplus SAVEDATA command.
- fileVarNames: A character vector containing the names of variables in the dataset.
fileVarFormats  A character vector containing the Fortran-style formats of variables in the dataset.
fileVarWidths  A numeric vector containing the widths of variables in the dataset (which is stored in fixed-width format).
bayesFile  The name of the BPARAMETERS file containing draws from the posterior distribution created by the Mplus SAVEDATA BPARAMETERS command.
bayesVarNames  A character vector containing the names of variables in the BPARAMETERS dataset.
techn3File  A character vector of the tech 3 output.
techn4File  A character vector of the tech 4 output.

Author(s)
Michael Hallquist

See Also
getSavedata_Data

Examples
```r
## Not run:
fileInfo <- getSavedata_Fileinfo("C:/Program Files/Mplus/Test Output.out")
## End(Not run)
```

---

**HTMLSummaryTable**

Create an HTML file containing a summary table of Mplus model statistics

**Description**

Creates an HTML file containing a summary table of model fit statistics extracted using the extractModelSummaries function. By default, the following summary statistics are included: Title,LL,Parameters,AIC,AICC,BIC,RMSEA_Estimate, but these are customizable using the keepCols and dropCols parameters.

**Usage**

```r
HTMLSummaryTable(
    modelList,
    filename = file.path(getwd(), "Model Comparison.html"),
    keepCols,
    dropCols,
    sortBy,
    display = FALSE
)
```
Arguments

- **modelList**: A list of models (as a data.frame) returned from the `extractModelSummaries` function.
- **filename**: The name of the HTML file to be created. Can be an absolute or relative path. If `filename` is a relative path or just the filename, then it is assumed that the file resides in the working directory `getwd()`. Example: "Mplus Summary.html"
- **keepCols**: A vector of character strings indicating which columns/variables to display in the summary. Only columns included in this list will be displayed (all others excluded). By default, `keepCols` is: c("Title","LL","Parameters","AIC","AICC","BIC","RMSEA_Estimate") Example: c("Title","LL","AIC","CFI")
- **dropCols**: A vector of character strings indicating which columns/variables to omit from the summary. Any column not included in this list will be displayed. By default, `dropCols` is NULL. Example: c("InputInstructions","TLI")
- **sortBy**: Optional. Field name (as character string) by which to sort the table. Typically an information criterion (e.g., "AIC" or "BIC") is used to sort the table. Defaults to "AICC".
- **display**: Optional. This parameter specifies whether to display the table in a web browser upon creation (TRUE or FALSE).

Value

No value is returned by this function. It is solely used to create an HTML file containing summary statistics.

Note

You must choose between `keepCols` and `dropCols` because it is not sensible to use these together to include and exclude columns. The function will error if you include both parameters.

Author(s)

Michael Hallquist

See Also

- `extractModelSummaries`
- `showSummaryTable`
- `LatexSummaryTable`

Examples

# make me!!!
**Description**

Creates a LaTeX-formatted summary table of model fit statistics extracted using the `extractModelSummaries` function. The table syntax is returned by the function, which is useful for embedding LaTeX tables using Sweave. By default, the following summary statistics are included: `Title`, `LL`, `Parameters`, `AIC`, `AICC`, `BIC`, `RMSEA_Estimate`, but these are customizable using the `keepCols` and `dropCols` parameters.

**Usage**

```r
LatexSummaryTable(
  modelList,
  keepCols,
  dropCols,
  sortBy,
  label = NULL,
  caption = NULL
)
```

**Arguments**

- `modelList`: A list of models (as a data.frame) returned from the `extractModelSummaries` function.
- `keepCols`: A vector of character strings indicating which columns/variables to display in the summary. Only columns included in this list will be displayed (all others excluded). By default, `keepCols` is: `c("Title","LL","Parameters","AIC","AICC","BIC","RMSEA_Estimate")`. Example: `c("Title","LL","AIC", "CFI")`
- `dropCols`: A vector of character strings indicating which columns/variables to omit from the summary. Any column not included in this list will be displayed. By default, `dropCols` is `NULL`. Example: `c("InputInstructions","TLI")`
- `sortBy`: optional. Field name (as character string) by which to sort the table. Typically an information criterion (e.g., "AIC" or "BIC") is used to sort the table. Defaults to "AICC"
- `label`: optional. A character string specifying the label for the LaTeX table, which can be used for referencing the table.
- `caption`: optional. A character string specifying the caption for the LaTeX table.

**Value**

A LaTeX-formatted table summarizing the `modelList` is returned (created by `xtable`).

**Note**

You must choose between `keepCols` and `dropCols` because it is not sensible to use these together to include and exclude columns. The function will error if you include both parameters.
Author(s)

Michael Hallquist

See Also

extractModelSummaries, HTMLSummaryTable, showSummaryTable, Sweave

Examples

# make me!!!
long2LGMM

Long data to wide latent growth mixture model

Description

This function streamlines the process of converting long data into a format that Mplus can use for latent growth mixture models in wide form. It makes use of continuous time scores, and these time scores must be supplied as variables in the R dataset. For the conversion to wide form, it is assumed that although assessments may have happened in continuous time, a discrete number of assessments (likely similar for all participants) were collected.

Usage

long2LGMM(
  data,
  idvar,
  assessmentvar,
  dv,
  timevars,
  misstrick = TRUE,
  k = 1L,
  title = "Trajectory Model",
  base = "trajmodel_",
  run = FALSE,
  processors = 1L,
  starts = "500 100",
  newdata,
  cov = c("un", "independent", "intercept", "zero"),
  model
)

Arguments

data A data frame in long format (i.e., multiple rows per ID).
idvar A character string of the variable name in the dataset that is the ID variable.
assessmentvar A character string of the variable name in the dataset that indicates the particular assessment point for each timepoint.
v A character string of the dependent variable name.
timevars A character vector of the time variables. Can be a single variable or more than one. By allowing more than one variable, it is easy to include linear; linear and quadratic; it is also possible to calculate splines in R and pass these. The variable names should be 7 characters or fewer, each.
misstrick A logical value whether to set values of the DV where a time variable is missing to missing as well. Defaults to TRUE.
k An integer indicating the number of distinct classes to test. Currently must be greater than 0 and less than 10.
title A character string giving a title for the model
base A character string providing a base name for model outputs, that is combined with the number of classes.
run A logical value whether or not to run the models or only create the data and input files, but not run them.
processors An integer value indicating the number of processors to use.
starts A character string passed to Mplus providing the number of random starts and iterations
newdata A data frame of new values to use for generating predicted trajectories by class.
cov A character string indicating the random covariance structure to use
model An optional argument, can pass an existing model, the output from mplusModeler().

Details
One valuable feature of this function is that it makes it possible to feed any continuous time scores to Mplus for mixture modelling. For example, continuous linear time is straightforward, but so to are quadratic time models or piecewise models. Using facilities in R, spline models are also comparatively easy to specify.

Examples
## Not run:
## Simulate Some Data from 3 classes
library(MASS)
set.seed(1234)
allcoef <- rbind(
  cbind(1, mvrnorm(n = 200, mu = c(0, 2, 0),
      Sigma = diag(c(.2, .1, .01)), empirical = TRUE)),
  cbind(2, mvrnorm(n = 200, mu = c(-3.35, 2, 2),
      Sigma = diag(c(.2, .1, .1)), empirical = TRUE)),
  cbind(3, mvrnorm(n = 200, mu = c(3.35, 2, -2),
      Sigma = diag(c(.2, .1, .1)), empirical = TRUE)))
allcoef <- as.data.frame(allcoef)
names(allcoef) <- c("Class", "I", "L", "Q")
allcoef$ID <- 1:nrow(allcoef)
d <- do.call(rbind, lapply(1:nrow(allcoef), function(i) {
  out <- data.frame(
    ID = allcoef$ID[i],
    Class = allcoef$Class[i],
    Assess = 1:11,
    x = sort(runif(n = 11, min = -2, max = 2)))
  out$y <- rnorm(11,
```r
mean = allcoef$I[i] + allcoef$L[i] * out$x + allcoef$Q[i] * out$x^2,
sd = .1)
return(out)
))

## create splines
library(splines)
time_splines <- ns(d$x, df = 3, Boundary.knots = quantile(d$x, probs = c(.02, .98)))
d$t1 <- time_splines[, 1]
d$t2 <- time_splines[, 2]
d$t3 <- time_splines[, 3]
d$xq <- d$x^2

## create new data to be used for predictions
nd <- data.frame(ID = 1,
x = seq(from = -2, to = 2, by = .1))
nd.splines <- with(attributes(time_splines),
n(snd$x, df = degree, knots = knots,
   Boundary.knots = Boundary.knots))
nd$t1 <- nd.splines[, 1]
d$t2 <- nd.splines[, 2]
d$t3 <- nd.splines[, 3]
d$xq <- nd$x^2

## create a tuning grid of models to try
## all possible combinations are created of different time trends
## different covariance structures of the random effects
## and different number of classes

tuneGrid <- expand.grid(
  dv = "y",
  timevars = list(c("t1", "t2", "t3"), "x", c("x", "xq")),
  starts = "2 1",
  cov = c("independent", "zero"),
  k = c(1L, 3L),
  processors = 1L, run = TRUE,
  misstrick = TRUE, stringsAsFactors = FALSE)
tuneGrid$title <- paste0(
  c("linear", "quad", "spline")[sapply(tuneGrid$timevars, length)],
  "_",
sapply(tuneGrid$cov, function(x) if(nchar(x)==4) substr(x, 1, 4) else substr(x, 1, 3)),
  "_",
tuneGrid$k)
tuneGrid$base <- paste0(
  c("linear", "quad", "spline")[sapply(tuneGrid$timevars, length)],
  "_",
sapply(tuneGrid$cov, function(x) if(nchar(x)==4) substr(x, 1, 4) else substr(x, 1, 3)))

## example using long2LGMM to fit one model at a time
mres <- long2LGMM(
data = d,
idvar = "ID",
assessmentvar = "Assess",
dv = tuneGrid$dv[1],

   data = d,
idvar = "ID",
assessmentvar = "Assess",
dv = tuneGrid$dv[1],
```

lookupTech1Parameter

Description

The `lookupTech1Parameter` function identifies the position in the Mplus model matrices corresponding to a given parameter defined in the TECHNICAL 1 PARAMETER SPECIFICATION OUTPUT. The goal of this function is to aid in identifying problematic parameters often printed in the warnings and errors section of Mplus output.

Usage

`lookupTech1Parameter(tech1Output, paramNumber)`

Arguments

- `tech1Output`: The object corresponding to the TECH1 parameter specification from readModels.
- `paramNumber`: The parameter number to lookup

Value

A data.frame containing the row(s) and column(s) of TECH1 parameter specification matching the requested `paramNumber`.

Author(s)

Michael Hallquist

See Also

`readModels`
mixtureSummaryTable

Create a summary table of Mplus mixture models

Description

Creates a summary table of model fit statistics and relevant diagnostic information for a list of mixture models. Default statistics reported are in line with published guidelines (see Jung & Wickrama, 2008; Nylund et al., 2007): c("Title", "Classes", "Warnings", "AIC", "BIC", "aBIC", "Entropy", "T11_VLMR_PValue", "T11_LMR_PValue", "BLRT_PValue", "min_N", "max_N", "min_prob", "max_prob"). The table is customizable using the keepCols parameter, which is passed through to SummaryTable.

Usage

mixtureSummaryTable(
  modelList,
)

Arguments

modelList A list of models returned from the extractModelSummaries function.

keepCols A vector of character strings indicating which columns/variables to display in the summary. Only columns included in this list will be displayed (all others excluded). By default, keepCols is: c("Title", "Classes", "Warnings", "AIC", "BIC", "aBIC", "Entropy", "T11_VLMR_PValue", "T11_LMR_PValue", "BLRT_PValue", "min_N", "max_N", "min_prob", "max_prob")

Value

An object of class data.frame.

Note

This function is partially a wrapper around SummaryTable, with enhancements for summarizing mixture models.

Author(s)

Caspar J. van Lissa
### mplus.traceplot

Plot the samples for each MCMC chain as a function of iterations

---

#### Description

Displays a traceplot of the MCMC draws from the poster distribution of each parameter estimate for a Bayesian Mplus model. This function requires that 1) `PLOT: TYPE=PLOT2;` be included in the Mplus input file, 2) a gh5 file be present corresponding to the Mplus output file (and containing a bayesian_data section), and 3) that the rhdf5 package be installed to allow the gh5 file to be imported.

#### Usage

```r
mplus.traceplot(mplus.model, rows = 4, cols = 4, parameters_only = TRUE)
```

#### Arguments

- `mplus.model`: An Mplus model extracted by the `readModels` function.
- `rows`: Number of rows to display per plot.
- `cols`: Optional. Number of columns to display per plot.
- `parameters_only`: Optional. If TRUE, only the unstandardized parameter estimates from the MCMC draws will be displayed (as opposed to standardized estimates, r-square estimates, etc.). The unstandardized estimates all begin with "Parameter" in the Mplus gh5 output.

#### Details

A multi-panel plot is drawn to the screen and the user is prompted to display the next plot if more than rows x columns estimates are in the model.
Value

No value is returned by this function. Called for the side effect of displaying an MCMC chains traceplot.

Note

Trace and density plots can also be obtained using the coda package and the bparameters element of the mplus.model object. This requires that the posterior draws be saved using SAVEDATA: BPARAMETERS syntax. See example below.

Author(s)

Joseph Glass, Michael Hallquist

See Also

plot.mcmc

Examples

```r
## Not run:
myModel <- readModels("BayesModel_WithGH5MCMC.out")
mplus.traceplot(myModel, rows=2, cols=3)

#alternative using the coda package
library(coda)
plot(myModel$bparameters$valid_draw)

## End(Not run)
```

Description

The MplusAutomation package leverages the flexibility of the R language to automate latent variable model estimation and interpretation using 'Mplus', a powerful latent variable modeling program developed by Muthen and Muthen (http://www.statmodel.com). Specifically, MplusAutomation provides routines for creating related groups of models, running batches of models, and extracting and tabulating model parameters and fit statistics.

Details

The MplusAutomation package has four primary purposes:

1. To automatically run groups/batches of models.
2. To provide routines to extract model fit statistics, parameter estimates, and raw data from 'Mplus' output files.
3. To facilitate comparisons among models
4. To provide a template language that allows for the creation of related input files.

The core routine for running batches of models is `runModels`, with an easy-to-use GUI wrapper, `runModels_Interactive`.

The core routine for extracting information from 'Mplus' outputs is `readModels`, which returns a list containing all output sections that the package can extract.

To extract summaries, parameters, modification indices, SAVEDATA output, and all other sections that the package can understand, use the `readModels` function. This is the recommended way to extract 'Mplus’ output with this package. If the target argument to `readModels` is a single .out file, an `mplus.model` (that is also a list) will be returned containing all output sections that the package can extract. If target is a directory, a list of `mplus.model` objects will be returned, named according to the output filenames.

Note: `extractModelSummaries` is deprecated and `readModels` should be preferred. To extract model summary statistics from one or more output files, see `extractModelSummaries`, which returns a `data.frame` of fit statistics for models located within a directory. Model fit results can be summarized in tabular form (for comparing among models) using `showSummaryTable` (displays table in separate window), `HTMLSummaryTable` (creates HTML file containing summary table), or `LatexSummaryTable` (returns a LaTeX-formatted table of summary statistics).

Deprecated: To extract raw data created by the SAVEDATA command (e.g., class membership probabilities or factor scores), see `getSavedata_Data`.

Deprecated: To extract unstandardized or standardized parameter estimates from a single output file, see `extractModelParameters`.

Detailed model fit and parameter comparisons between two models can be obtained using `compareModels`.

To create a group of related models from a single template, see `createModels`. Please read the MplusAutomation vignette provided along with the package (and on the CRAN website) in order to understand the template language: vignette("Vignette", package="MplusAutomation").

In addition to the major functions above, a function for converting an R data.frame for use with 'Mplus' is provided: `prepareMplusData`. This converts the data.frame to a tab-delimited file and provides an 'Mplus' syntax stub for variable names.

```
Package: MplusAutomation
Type: Package
Version: 0.8
Date: 2020-09-28
License: LGPL-3
LazyLoad: yes
```

**Author(s)**

Michael Hallquist `<michael.hallquist@gmail.com>`, Joshua F. Wiley `<jwiley.psych@gmail.com>`

Maintainer: Michael Hallquist `<michael.hallquist@gmail.com>`
References


See Also

See runModels for an example running a model.

---

mplusAvailable

Check whether Mplus can be found

Description

This is a simple utility to check whether Mplus can be found. Returns 0 if Mplus command can be found by the system. If silent = FALSE, prints a message to the user to help suggest what to do.

Usage

mplusAvailable(silent = TRUE)

Arguments

silent

A logical whether to print a message or not. Defaults to TRUE for silent operation.

Value

The status of finding Mplus. Per unix conventions, status 0 indicates Mplus was found (0 problems) and status 1 indicates that Mplus was not found.

Author(s)

Joshua Wiley

Examples

mplusAvailable(silent = TRUE)
mplusAvailable(silent = FALSE)
The purpose of this function is to make it (relatively) easy to fit (most) generalized linear models in Mplus. Fitting GLMs in Mplus offers advantages such as using full information maximum likelihood for missing data, robust estimators (default used is MLR), and standard errors adjusted for clustering (planned; not currently available via \texttt{mplusGLM}). The overarching aim of this function is to make most GLMs as easy to fit in Mplus as they are in R.

**Usage**

\texttt{mplusGLM(formula, data, idvar = "", ...)}

**Arguments**

- **formula**: An R formula class object as used in \texttt{glm}. Note that currently, only basic formula are accepted. On the fly recoding, arithmetic, and on the fly interactions do not currently work.
- **data**: A dataset.
- **idvar**: Optional. A character string indicating the name of the ID variable. Not currently used but may be used in future.
- **...**: Additional arguments passed to helper functions. For example \texttt{.mplusMultinomial}.

**Details**

Note that although there are benefits to fitting GLMs in Mplus. Caution also is warranted. Using full information maximum likelihood for missing data requires a number of assumptions. These may be (badly) violated. \texttt{mplusGLM} requires the analyst to check these as appropriate.

Currently, \texttt{mplusGLM} only supports multinomial outcomes. More outcomes are planned in the future including binary, continuous/normal, and count outcomes.

**Value**

A list of results and Mplus model object.

**Author(s)**

Joshua F. Wiley <jwiley.psych@gmail.com>
mplusModeler

Create, run, and read Mplus models.

Description

This is a convenience wrapper to automate many of the usual steps required to run an Mplus model. It relies in part on functions from the MplusAutomation package.

Usage

mplusModeler(
  object,
  dataout,
  modelout,
  run = 0L,
  check = FALSE,
  varwarnings = TRUE,
  Mplus_command = "Mplus",
  writeData = c("ifmissing", "always", "never"),
  hashfilename = TRUE,
  killOnFail = TRUE,
  ...
)

Arguments

object An object of class mplusObject
dataout the name of the file to output the data to for Mplus. If missing, defaults to modelout changing .inp to .dat.
modelout the name of the output file for the model. This is the file all the syntax is written to, which becomes the Mplus input file. It should end in .inp. If missing, defaults to dataout changing the extension to .inp.

Examples

## Not run:
set.seed(1234)
tmpd <- data.frame(
  x1 = rnorm(200),
  x2 = rnorm(200),
  x3 = cut(rnorm(200),
    breaks = c(-Inf, -.7, .7, Inf),
    labels = c("a", "b", "c")))
tmpd$y <- cut(rnorm(200, sd = 2) + tmpd$x1 + tmpd$x2 + I(tmpd$x3 == "b"),
  breaks = c(-Inf, -.5, 1, Inf),
  labels = c("L", "M", "H"))
test <- mplusGLM(y ~ x1 + x2 + x3, data = tmpd)
## End(Not run)
run

an integer indicating how many models should be run. Defaults to zero. If zero, the data and model input files are all created, but the model is not run. This can be useful for seeing how the function works and what setup is done. If one, a basic model is run. If greater than one, the model is bootstrapped with run replications as well as the basic model.

check

logical whether the body of the Mplus syntax should be checked for missing semicolons using the `parseMplus` function. Defaults to `FALSE`.

varwarnings

A logical whether warnings about variable length should be left, the default, or removed from the output file.

Mplus_command

optional. N.B.: No need to pass this parameter for most users (has intelligent defaults). Allows the user to specify the name/path of the Mplus executable to be used for running models. This covers situations where Mplus is not in the system’s path, or where one wants to test different versions of the Mplus program.

writeData

A character vector, one of ‘ifmissing’, ‘always’, ‘never’ indicating whether the data files (*.dat) should be written to disk. This is passed on to `prepareMplusData`. Note that previously, `mplusModeler` always (re)wrote the data to disk. However, now the default is to write the data to disk only if it is missing (i.e., ‘ifmissing’). See details for further information.

hashfilename

A logical whether or not to add a hash of the raw data to the data file name. Defaults to `TRUE` in `mplusModeler`. Note that this behavior is a change from previous versions and differs from `prepareMplusData` which maintains the old behavior by default of `FALSE`.

killOnFail

A logical whether or not to kill any mplus processes on failure. Passed on to control behavior of `runModels`. Defaults to `TRUE`.

... additional arguments passed to the `prepareMplusData` function.

Details

Combined with functions from the MplusAutomation package, this function is designed to make it easy to fit Mplus models from R and to ease many of the usual frustrations with Mplus. For example, Mplus has very specific formats it accepts data in, but also very little data management facilities. Using R data management is easy. This function is designed to make using data from R in Mplus models easy. It is also common to want to fit many different models that are slight variants. This can be tedious in Mplus, but using R you can create one basic set of input, store it in a vector, and then just modify that (e.g., using regular expressions) and pass it to Mplus. You can even use loops or the `*apply` constructs to fit the same sort of model with little variants.

The `writeData` argument is new and can be used to reduce overhead from repeatedly writing the same data from R to the disk. When using the ‘always’ option, `mplusModeler` behaves as before, always writing data from R to the disk. This remains the default for the `prepareMplusData` function to avoid confusion or breaking old code. However, for `mplusModeler`, the default has been set to ‘ifmissing’. In this case, R generates an md5 hash of the data prior to writing it out to the disk. The md5 hash is based on: (1) the dimensions of the dataset, (2) the variable names, (3) the class of every variable, and (4) the raw data from the first and last rows. This combination ensures that under most all circumstances, if the data changes, the hash will change. The hash is appended to the specified data file name (which is controlled by the logical `hashfilename` argument). Next
R checks in the directory where the data would normally be written. If a data file exists in that directory that matches the hash generated from the data, R will use that existing data file instead of writing out the data again. A final option is ‘never’. If this option is used, R will not write the data out even if no file matching the hash is found.

Value

An Mplus model object, with results. If run = 1, returns an invisible list of results from the run of the Mplus model (see readModels from the MplusAutomation package). If run = 0, the function returns a list with two elements, ‘model’ and ‘boot’ that are both NULL, if run >= 1, returns a list with two elements, ‘model’ and ‘boot’ containing the regular Mplus model output and the boot object, respectively. In all cases, the Mplus data file and input files are created.

Author(s)

Joshua F. Wiley <jwiley.psych@gmail.com>

See Also

runModels and readModels

Examples

```r
## Not run:
# minimal example of a model using builtin data, allowing R
# to automatically guess the correct variables to use
test <- mplusObject(MODEL = "mpg ON wt hp;
   wt WITH hp;", rdata = mtcars)

# estimate the model in Mplus and read results back into R
res <- mplusModeler(test, modelout = "model1.inp", run = 1L)

# when forcing writeData = "always" data gets overwritten (with a warning)
resb <- mplusModeler(test, modelout = "model1.inp", run = 1L,
   writeData = "always")

# using writeData = "ifmissing", the default, no data re-written
resc <- mplusModeler(test, modelout = "model1.inp", run = 1L)

# using writeData = "ifmissing", the default, data ARE written
# if data changes
test <- mplusObject(MODEL = "mpg ON wt hp;
   wt WITH hp;", rdata = mtcars[-10, ])
resd <- mplusModeler(test, modelout = "model1.inp", run = 1L)

# show summary
summary(resd)

# show coefficients
coef(resd)

# what if you wanted confidence intervals
```
# and standardized values?
# first update to tell Mplus you want them, re-run and print
test <- update(test, OUTPUT = ~ "CINTERVAL; STDYX;")
resd <- mplusModeler(test, modelout = "model1.inp", run = 1L)

coef(resd)
confint(resd)

# now standardized
coef(resd, type = "stdyx")
confint(resd, type = "stdyx")

# put together in one data frame if desired
merge(
  coef(resd, type = "stdyx"),
  confint(resd, type = "stdyx"),
  by = "Label")

# remove files
unlink(resc$results$input$data$file)
unlink(resd$results$input$data$file)
unlink("model1.inp")
unlink("model1.out")

# simple example of a model using builtin data
# demonstrates use with a few more sections
test2 <- mplusObject(
  TITLE = "test the MplusAutomation Package and mplusModeler wrapper;",
  MODEL = "
  mpg ON wt hp;
  wt WITH hp;",
  usevariables = c("mpg", "wt", "hp"),
  rdata = mtcars)
res2 <- mplusModeler(test2, modelout = "model2.inp", run = 1L)

# remove files
unlink(res2$results$input$data$file)
unlink("model2.inp")
unlink("model2.out")

# similar example using a robust estimator for standard errors
# and showing how an existing model can be easily updated and reused
test3 <- update(test2, ANALYSIS = ~ "ESTIMATOR = MLR;"
res3 <- mplusModeler(test3, modelout = "model3.inp", run = 1L)
unlink(res3$results$input$data$file)
unlink("model3.inp")
unlink("model3.out")

# now use the built in bootstrapping methods
# note that these work, even when Mplus will not bootstrap
# also note how categorical variables and weights are declared
# in particular, the usevariables for Mplus must be specified
# because mroe variables are included in the data than are in the
# model. Note the R usevariables includes all variables for both
# model and weights. The same is true for clustering.
test4 <- mplusObject(
  TITLE = "test bootstrapping;",
  VARIABLE = "
    CATEGORICAL = cyl;
    WEIGHT = wt;
    USEVARIABLES = cyl mpg;",
  ANALYSIS = "ESTIMATOR = MLR;",
  MODEL = "
    cyl ON mpg;",
  usevariables = c("mpg", "wt", "cyl"),
  rdata = mtcars)

res4 <- mplusModeler(test4, "mtcars.dat", modelout = "model4.inp", run = 10L,
  hashfilename = FALSE)

# see the results
res4$results$boot

# remove files
unlink("mtcars.dat")
unlink("model4.inp")
unlink("model4.out")

# Monte Carlo Simulation Example
montecarlo <- mplusObject(
  TITLE = "Monte Carlo Example;",
  MONTECARLO = "
    NAMES ARE i1-i5;
    NOBSERVATIONS = 100;
    NREPS = 100;
    SEED = 1234;",
  MODELPOPULATION = "
    f BY i1-i5*1;
    f@1;
    i1-i5*1;",
  ANALYSIS = "
    ESTIMATOR = BAYES;
    PROC = 2;
    fbiter = 100;",
  MODEL = "
    f BY i1-i5*.8 (11-15);
    f@1;
    i1-i5*1;",
  MODELPRIORS = "
    i1-15 ~ N(.5 .1);",
  OUTPUT = "TECH9;"
)

fitMonteCarlo <- mplusModeler(montecarlo, modelout = "montecarlo.inp", run = 1L,
writeData = "always",
hashfilename = FALSE)

unlink("montecarlo.inp")
unlink("montecarlo.out")

# Example including ID variable and extracting factor scores
dat <- mtcars
dat$UID <- 1:nrow(mtcars)

testIDs <- mplusObject(
    TITLE = "test the mplusModeler wrapper with IDs;",
    VARIABLE = "IDVARIABLE = UID;",
    MODEL = "F BY mpg wt hp;",
    SAVEDATA = "FILE IS testid_fscores.dat;
SAVE IS fscores;
FORMAT IS free;",
    usevariables = c("UID", "mpg", "wt", "hp"),
    rdata = dat)

resIDs <- mplusModeler(testIDs, modelout = "testid.inp", run = 1L)

# view the saved data from Mplus, including factor scores
# the indicator variables, and the ID variable we specified
head(resIDs$results$savedata)

# merge the factor scores with the rest of the original data
# merge together by the ID column
dat <- merge(dat, resIDs$results$savedata[, c("F", "UID")],
by = "UID")

# correlate merged factor scores against some other new variable
with(dat, cor(F, qsec))

# can write multiply imputed data too
# here are three "imputed" datasets
idat <- list(
    data.frame(mpg = mtcars$mpg, hp = c(100, mtcars$hp[-1])),
    data.frame(mpg = mtcars$mpg, hp = c(110, mtcars$hp[-1])),
    data.frame(mpg = mtcars$mpg, hp = c(120, mtcars$hp[-1])))

# if we turn on hashing in the filename the first time,
# we can avoid overwriting notes the second time
testobjimp <- mplusObject(MODEL = "[mpg];", rdata = idat, imputed = TRUE)
testimp <- mplusModeler(testobjimp,
mplusObject

Create an Mplus model object

Description

This is a function to create an Mplus model object in R. The object holds all the sections of an Mplus input file, plus some extra R ones. Once created, the model can be run using other functions such as mplusModeler or updated using methods defined for the update function.

Usage

mplusObject(
  TITLE = NULL,
  DATA = NULL,
  VARIABLE = NULL,
  DEFINE = NULL,
  MONTECARLO = NULL,
  MODELPOPULATION = NULL,
  MODELMISSING = NULL,
mplusObject

ANALYSIS = NULL,
MODEL = NULL,
MODELINDIRECT = NULL,
MODELCONSTRAINT = NULL,
MODELTEST = NULL,
MODELPRIMORS = NULL,
OUTPUT = NULL,
SAVEDATA = NULL,
PLOT = NULL,
usevariables = NULL,
rdata = NULL,
autov = TRUE,
imputed = FALSE
)

Arguments

TITLE A character string of the title for Mplus.
DATA A character string of the data section for Mplus (note, do not define the filename
as this is generated automatically)
VARIABLE A character string of the variable section for Mplus (note, do not define the
variable names from the dataset as this is generated automatically)
DEFINE A character string of the define section for Mplus (optional)
MONTECARLO A character string of the montecarlo section for Mplus (optional). If used, autov
is defaults to FALSE instead of the usual default, TRUE, but may still be overwritten,
if desired.
MODELPOPULATION A character string of the MODEL POPULATION section for Mplus (optional).
MODELMISSING A character string of the MODEL MISSING section for Mplus (optional).
ANALYSIS A character string of the analysis section for Mplus (optional)
MODEL A character string of the model section for Mplus (optional, although typically
you want to define a model)
MODELINDIRECT A character string of the MODEL INDIRECT section for Mplus (optional).
MODELCONSTRAINT A character string of the MODEL CONSTRAINT section for Mplus (optional).
MODELTEST A character string of the MODEL TEST section for Mplus (optional).
MODELPRIMORS A character string of the MODEL PRIORS section for Mplus (optional).
OUTPUT A character string of the output section for Mplus (optional)
SAVEDATA A character string of the savedata section for Mplus (optional)
PLOT A character string of the plot section for Mplus (optional)
usevariables A character vector of the variables from the R dataset to use in the model.
rdata An R dataset to be used for the model.
autov A logical (defaults to TRUE) argument indicating whether R should attempt to
guess the correct variables to use from the R dataset, if usevariables is left
NULL.
imputed A logical whether the data are multiply imputed (a list). Defaults to FALSE.
Details

Mplus model objects allow a base model to be defined, and then flexibly update the data, change the precise model, etc. If a section does not vary between models, you can leave it the same. For example, suppose you are fitting a number of models, but in all cases, wish to use maximum likelihood estimator, “ANALYSIS: ESTIMATOR = ML;” and would like standardized output, “OUTPUT: STDYX;”. Rather than retype those in every model, they can be defined in one Mplus model object, and then that can simply be updated with different models, leaving the analysis and output sections untouched. This also means that if a reviewer comes back and asks for all analyses to be re-run say using the robust maximum likelihood estimator, all you have to do is change it in the model object once, and re run all your code.

Value

A list of class mplusObject with elements

- **TITLE**: The title in Mplus (if defined)
- **DATA**: The data section in Mplus (if defined)
- **VARIABLE**: The variable section in Mplus (if defined)
- **DEFINE**: The define section in Mplus (if defined)
- **MONTECARLO**: The montecarlo section in Mplus (if defined)
- **MODELPOPULATION**: The modelpopulation section in Mplus (if defined)
- **MODELMISSING**: The modelmissing section in Mplus (if defined)
- **ANALYSIS**: The analysis section in Mplus (if defined)
- **MODEL**: The model section in Mplus (if defined)
- **MODELINDIRECT**: The modelindirect section in Mplus (if defined)
- **MODELCONSTRAINT**: The modelconstraint section in Mplus (if defined)
- **MODELTEST**: The modeltest section in Mplus (if defined)
- **MODELPRIORS**: The modelpriors section in Mplus (if defined)
- **OUTPUT**: The output section in Mplus (if defined)
- **SAVEDATA**: The savedata section in Mplus (if defined)
- **PLOT**: The plot section in Mplus (if defined)
- **results**: NULL by default, but can be later updated to include the results from the model run.
- **usevariables**: A character vector of the variables from the R data set to be used.
- **rdata**: The R data set to use for the model.
- **imputed**: A logical whether the data are multiply imputed.
- **autov**: A logical whether the data should have the usevariables detected automatically or not

Author(s)

Joshua F. Wiley <jwiley.psych@gmail.com>
mplusRcov

Create Mplus code for various residual covariance structures.

Description

This function makes it easy to write the Mplus syntax for various residual covariance structure.

Usage

mplusRcov(
  x,
  type = c("homogenous", "heterogenous", "cs", "toeplitz", "ar", "un"),
  r = "rho",
  e = "e",
  collapse = FALSE
)
mplusRcov

Arguments

x
input character vector of variable names, ordered by time

type
A character string indicating the type of residual covariance structure to be used. Defaults to ‘homogenous’. Current options include ‘homogenous’, ‘heterogenous’, ‘cs’ for compound symmetric, ‘toeplitz’ for banded toeplitz, ‘ar’ for autoregressive, and ‘un’ for unstructured.

r
a character vector of the base label to name covariance parameters. Defaults to ‘rho’.

e
a character vector of the error variance of the variable. Used to create constraints on the covariance parameters. Defaults to ‘e’.

collapse
whether to collapse the covariance code using ‘PWITH’. Note that at the time of writing, Mplus does not allow more than 80 characters per row. Defaults to FALSE.

Details

The **homogenous** residual covariance structure estimates one parameter: the residual variance, $\sigma^2_e$. The residual variance is assumed to be identical for all variables and all covariances are assumed to be zero. The structure is represented in this table.

<table>
<thead>
<tr>
<th>t1</th>
<th>t2</th>
<th>t3</th>
<th>…</th>
<th>tn</th>
</tr>
</thead>
<tbody>
<tr>
<td>t1</td>
<td>$\sigma^2_e$</td>
<td>…</td>
<td></td>
<td></td>
</tr>
<tr>
<td>t2</td>
<td>0</td>
<td>$\sigma^2_e$</td>
<td>…</td>
<td></td>
</tr>
<tr>
<td>t3</td>
<td>0</td>
<td>0</td>
<td>$\sigma^2_e$</td>
<td>…</td>
</tr>
<tr>
<td>…</td>
<td>…</td>
<td>…</td>
<td>…</td>
<td>…</td>
</tr>
<tr>
<td>tn</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>…</td>
</tr>
</tbody>
</table>

The **heterogenous** residual covariance structure estimates \( n \) parameters, where \( n \) is the number of variables. A unique residual variance is estimated for every variable. All covariances are assumed to be zero. The structure is represented in this table.

<table>
<thead>
<tr>
<th>t1</th>
<th>t2</th>
<th>t3</th>
<th>…</th>
<th>tn</th>
</tr>
</thead>
<tbody>
<tr>
<td>t1</td>
<td>$\sigma^2_{e1}$</td>
<td>…</td>
<td></td>
<td></td>
</tr>
<tr>
<td>t2</td>
<td>0</td>
<td>$\sigma^2_{e2}$</td>
<td>…</td>
<td></td>
</tr>
<tr>
<td>t3</td>
<td>0</td>
<td>0</td>
<td>$\sigma^2_{e3}$</td>
<td>…</td>
</tr>
<tr>
<td>…</td>
<td>…</td>
<td>…</td>
<td>…</td>
<td>…</td>
</tr>
<tr>
<td>tn</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>…</td>
</tr>
</tbody>
</table>

The **compound symmetric** residual covariance structure estimates two parameters: one for the residual variance $\sigma^2_e$, and one for the covariance. The residual variance is assumed to be identical for all variables and all covariances are assumed to be identical. The structure is represented in this table.

<table>
<thead>
<tr>
<th>t1</th>
<th>t2</th>
<th>t3</th>
<th>…</th>
<th>tn</th>
</tr>
</thead>
<tbody>
<tr>
<td>t1</td>
<td>$\sigma^2_e$</td>
<td>…</td>
<td></td>
<td></td>
</tr>
<tr>
<td>t2</td>
<td>…</td>
<td>…</td>
<td>…</td>
<td>…</td>
</tr>
<tr>
<td>t3</td>
<td>…</td>
<td>…</td>
<td>…</td>
<td>…</td>
</tr>
<tr>
<td>…</td>
<td>…</td>
<td>…</td>
<td>…</td>
<td>…</td>
</tr>
<tr>
<td>tn</td>
<td>…</td>
<td>…</td>
<td>…</td>
<td>…</td>
</tr>
</tbody>
</table>

The *toeplitz* residual covariance structure estimates \( n \) parameters, one for every band of the matrix. The residual variance, \( \sigma^2_e \), is assumed to be identical for all variables. The covariances one step removed are all assumed identical. Likewise for all further bands. The structure is represented in this table.

\[
\begin{array}{cccccc}
  t_1 & t_2 & t_3 & \ldots & t_n \\
  t_1 & \sigma^2_e & & & \\
  t_2 & \rho & \sigma^2_e & & \\
  t_3 & \rho & \rho & \sigma^2_e & \\
  \vdots & \vdots & \vdots & \vdots & \vdots \\
  t_n & \rho & \rho & \rho & \cdots & \sigma^2_e \\
\end{array}
\]

The *autoregressive* residual covariance structure has two parameters: the residual variance, \( \sigma^2_e \), and the correlation between adjacent time points, \( \rho \). The variances are constrained to be equal for all time points. A single correlation parameter is estimated. The \( \rho \) is the correlation between adjacent time points such as 1 and 2 or 2 and 3. More distant relationships are assumed to have smaller correlations, decreasing exponentially. Thus between 1 and 3, the estimate is \( \rho^2 \). The structure is represented in this table.

\[
\begin{array}{cccccc}
  t_1 & t_2 & t_3 & \ldots & t_n \\
  t_1 & \sigma^2_e & & & \\
  t_2 & \rho & \sigma^2_e & & \\
  t_3 & \rho^2 & \rho & \sigma^2_e & \\
  \vdots & \vdots & \vdots & \vdots & \vdots \\
  t_n & \rho^{n-1} & \rho^{n-2} & \rho^{n-3} & \cdots & \sigma^2_e \\
\end{array}
\]

Because structural equation models generally model covariance structures, the autoregressive residual structure must be parameterized in terms of covariances. This is done in two parts. First, the function returns syntax to estimate all the pairwise covariances, labelling the parameters \( \rho, \rho^2, \) etc. so that they are constrained to be equal. Next, it returns the syntax for the necessary model constraints to constrain the different covariances, to decrease exponentially in their correlations. This is done via:

\[ \rho^2 = \left( \frac{\rho}{\sigma^2_e} \right)^2 \sigma^2_e \]

and likewise for all later time points.

The *unstructured* residual covariance structure estimates \( \frac{n(n+1)}{2} \) parameters. It is unstructured in that every variance and covariance is freely estimated with no constraints. However, in most cases, this results in an overparameterized model and is unestimable. The structure is represented in this table.
mplusRcov

<table>
<thead>
<tr>
<th>t1</th>
<th>t2</th>
<th>t3</th>
<th>...</th>
<th>tn</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\sigma^2_{e1}$</td>
<td>$\sigma^2_{e2}$</td>
<td>$\sigma^2_{e3}$</td>
<td>...</td>
<td></td>
</tr>
<tr>
<td>$\rho_1$</td>
<td>$\rho_2$</td>
<td>$\rho_3$</td>
<td>$\rho_4$</td>
<td>$\rho_5$</td>
</tr>
</tbody>
</table>

Value

A named character vector of class `MplusRstructure` with four elements:

- **all**: A character string collapsing all other sections.
- **Variances**: A character string containing all of the variances.
- **Covariances**: A character string containing all of the covariances, properly labelled to allow constraints and the autoregressive residual covariance structure.
- **Constraints**: A character string containing the `MODEL CONSTRAINT` section and code needed to parameterize the residual covariance structure as autoregressive.

Author(s)

Joshua F. Wiley <jwiley.psych@gmail.com>

Examples

# all five structures collapsing
mplusRcov(letters[1:4], "homogenous", "rho", "e", TRUE)
mplusRcov(letters[1:4], "heterogenous", "rho", "e", TRUE)
mplusRcov(letters[1:4], "cs", "rho", "e", TRUE)
mplusRcov(letters[1:4], "toeplitz", "rho", "e", TRUE)
mplusRcov(letters[1:4], "ar", "rho", "e", TRUE)
mplusRcov(letters[1:4], "un", "rho", "e", TRUE)

# all five structures without collapsing
# useful for long names or many variables
# where a line may cross 80 characters
mplusRcov(letters[1:4], "homogenous", "rho", "e", FALSE)
mplusRcov(letters[1:4], "heterogenous", "rho", "e", FALSE)
mplusRcov(letters[1:4], "cs", "rho", "e", FALSE)
mplusRcov(letters[1:4], "toeplitz", "rho", "e", FALSE)
mplusRcov(letters[1:4], "ar", "rho", "e", FALSE)
mplusRcov(letters[1:4], "un", "rho", "e", FALSE)
**paramExtract**

Extract parameters from a data frame of Mplus estimates

**Description**

This is a simple convenience function designed to facilitate looking at specific parameter types by easily return a subset of a data frame with those types only. It is designed to follow up the results returned from the `readModels` function.

**Usage**

```r
paramExtract(
  x,
  params = c("regression", "loading", "undirected", "expectation", "variability", "new")
)
```

**Arguments**

- `x` A data frame (specifically the type returned by `readModels`) containing parameters. Should be specific such as unstandardized and the data frame must have a column called `paramHeader`.

- `params` A character string indicating the types of parameters to be returned. Options currently include 'regression', 'loading', 'undirected', 'expectation', 'variability', and 'new' for new/additional parameters. Regressions include regression of one variable ON another. 'loading' include indicator variables (which are assumed caused by the underlying latent variable) and variables in latent growth models (BY or |). Undirected paths currently only include covariances, indicated by the WITH syntax in Mplus. Expectation paths are the unconditional or conditional expectations of variables. In other words those parameters related to the first moments. For independent variables, these are the means, \( E(X) \) and the conditional means or intercepts, \( E(X|f(\theta)) \) where \( f(\theta) \) is the model, some function of the parameters, \( \theta \). Finally 'variability' refers to both variances and residual variances, corresponding to the second moments. As with the expectations, variances are unconditional for variables that are not predicted or conditioned on any other variable in the model whereas residual variances are conditional on the model. Note that `R` uses fuzzy matching so that each of these can be called via shorthand, 'r', 'l', 'u', 'e', and 'v'.

**Value**

A subset data frame with the parameters of interest.

**Author(s)**

Joshua F. Wiley <jwiley.psych@gmail.com>
parseCatOutput

### Description
Helper function for parsing output with variables and categories.

### Usage
```r
parseCatOutput(text)
```

### Arguments
- **text** The output to parse.

### Value
The parsed output

### Author(s)
Michael Hallquist
Examples

Example:
UNIVARIATE PROPORTIONS AND COUNTS FOR CATEGORICAL VARIABLES

SOP2A
  Category 1 0.254 631.000
  Category 2 0.425 1056.000
  Category 3 0.174 432.000
  Category 4 0.147 365.000

Or Item Categories in IRT Parameterization

Item Categories
  U1
    Category 1 0.000 0.000 0.000 1.000
    Category 2 -0.247 0.045 -5.534 0.000
    Category 3 0.699 0.052 13.325 0.000
    Category 4 -0.743 0.057 -12.938 0.000
    Category 5 0.291 0.052 5.551 0.000

Description

The function parses a character string containing Mplus code and checks that every non blank line
ends in either a colon or a semicolon. In addition, it checks that every line is less than 90 characters,
because Mplus ignores everything after 90 characters on a line which can be a source of enigmatic
errors.

Usage

parseMplus(x, add = FALSE)

Arguments

x

a character string containing Mplus code.

add

logical indicating whether or not to add semicolons to lines that do not have
them. Defaults to FALSE.

Details

The function is fairly basic at the moment. It works by simply removing blank space (spaces, tabs,
etc.) and then if a line does not terminate in a colon or semicolon, it returns a note and the line
number. Optionally, it can add semicolons to any lines missing them and return the input with
added semicolons. To check for lines that are too long, all trailing (but not before) white space is
removed, and then the number of characters is checked.
Value

a character vector containing the input text and optionally added semicolons.

Author(s)

Joshua F. Wiley <jwiley.psych@gmail.com>

See Also

mplusModeler

Examples

# sample input
test <- "
MODEL:
  mpg ON wt hp;
  wt WITH hp
"
# check and return
cat(parseMplus(test), file=stdout(), fill=TRUE)
# add missing semicolons and return
cat(parseMplus(test, TRUE), file=stdout(), fill=TRUE)
# line that is too long for Mplus
test <- "
MODEL:
  mpg cyl disp hp drat wt qsec vs am gear PWITH cyl disp hp drat wt qsec vs am gear carb;
"
cat(parseMplus(test), file=stdout())
closeAllConnections()
plotMixtureDensities

Arguments

- **x**: An object of class mplusObject
- **y**: Not currently used
- **type**: A character vector indicating the type of coefficients to return. One of “un”, “std”, “stdy”, or “stdyx”. Defaults to “stdyx”.
- ...: Additional arguments to pass on (not currently used)

Value

Nothing. Called for its side effect of plotting the coefficients.

Author(s)

Joshua F. Wiley <jwiley.psych@gmail.com>

Examples

```r
## Not run:
# simple example of a model using builtin data
# demonstrates use
test <- mplusObject(
  TITLE = "test the MplusAutomation Package;",
  MODEL = "
    mpg ON wt hp;
    wt WITH hp;",
  OUTPUT = "STANDARDIZED;",
  usevariables = c("mpg", "wt", "hp"),
  rdata = mtcars)
res <- mplusModeler(test, "mtcars.dat", modelout = "model1.inp", run = 1L)
# example of the coef method
plot(res)

# remove files
unlink("mtcars.dat")
unlink("model1.inp")
unlink("model1.out")
unlink("Mplus Run Models.log")
## End(Not run)
```

plotMixtureDensities  Create density plots for mixture models
**Description**

Creates a density plot for a single object of class 'mplus.model', or a faceted plot of density plots for an object of class 'mplus.model.list'. For each variable, a Total density plot will be shown, along with separate density plots for each latent class, where cases are weighted by the posterior probability of being assigned to that class.

**Usage**

```r
plotMixtureDensities(
  modelList, 
  variables = NULL, 
  bw = FALSE, 
  conditional = FALSE, 
  alpha = 0.2, 
  facet_labels = NULL
)
```

**Arguments**

- `modelList`: A list object of Mplus models, or a single Mplus model.
- `variables`: Which variables to plot. If NULL, plots all variables that are present in all Mplus models.
- `bw`: Logical. Whether to make a black and white plot (for print) or a color plot. Defaults to FALSE, because these density plots are hard to read in black and white.
- `conditional`: Logical. Whether to show a conditional density plot (surface area is divided amongst the latent classes), or a classic density plot (surface area of the total density plot is equal to one, and is subdivided amongst the classes).
- `alpha`: Numeric (0-1). Only used when bw and conditional are FALSE. Sets the transparency of `geom_density`, so that classes with a small number of cases remain visible.
- `facet_labels`: Named character vector, the names of which should correspond to the facet labels one wishes to rename, and the values of which provide new names for these facets. For example, to rename variables, in the example with the 'iris' data below, one could specify: `facet_labels = c("Pet_leng" = "Petal length")`.

**Value**

An object of class 'ggplot'.

**Note**

This function returns warnings, indicating that sum(weights) != 1. These can be ignored. The sum of the "Total" density per variable per model is equal to 1, and the sum of all of the posterior probabilities is equal to 1. This results in a normal density plot for the "Total", which is subdivided by the latent classes, in proportion to the posterior probabilities of participants being assigned to those classes.
Author(s)

Caspar J. van Lissa

Examples

```r
## Not run:
createMixtures(classes = 1:3, filename_stem = "iris", rdata = iris)
runModels(filefilter = "iris")
results <- readModels(filefilter = "iris")
plotMixtureDensities(results)

## End(Not run)
## Not run:
plotMixtureDensities(results, variables = "PETAL_LE")

## End(Not run)
## Not run:
plotMixtureDensities(results, bw = TRUE)

## End(Not run)
## Not run:
plotMixtureDensities(results, bw = FALSE, conditional = TRUE)

## End(Not run)
## Not run:
plotMixtureDensities(results[[2]], variables = "PETAL_LE")

## End(Not run)
```

---

### plotMixtures

Create latent profile plots

**Description**

Creates a profile plot for a single object of class `mplus.model`, or a faceted plot of profile plots for an object of class `mplus.model.list`.

**Usage**

```r
plotMixtures(
  modelList,
  variables = NULL,
  coefficients = c("unstandardized", "stdy.x.standardized", "stdy.y.standardized",
    "stdy.z.standardized"),
  parameter = c("Means", "Intercepts"),
  ci = 0.95,
  bw = FALSE,
  rawdata = FALSE,
  alpha_range = c(0, 0.1)
)
```
Arguments

modellist A list of Mplus mixture models, or a single mixture model
variables A character vectors with the names of the variables (included in the Mplus output) to be plotted.
coefficients Which type of coefficients to plot on the y-axis; default is 'unstandardized'. Options include: c('stdyx.standardized', 'stdy.standardized', 'std.standardized')
parameter Which parameter to plot (from Mplus parameter estimate headings included in the output). Defaults to c('Means', 'Intercepts').
ci What confidence interval should the errorbars span? Defaults to a 95% confidence interval. Set to NULL to remove errorbars.
bw Logical. Should the plot be black and white (for print), or color?
rawdata Should raw data be plotted in the background? Setting this to TRUE might result in long plotting times. Requires including the Mplus syntax 'SAVEDATA: FILE IS "filename"; SAVE = cprobabilities' in the Mplus input.
alpha_range The minimum and maximum values of alpha (transparency) for the raw data. Minimum should be 0; lower maximum values of alpha can help reduce overplotting.

Value

An object of class 'ggplot'.

Author(s)

Caspar J. van Lissa

Examples

```
## Not run:
createMixtures(classes = 1:4, filename_stem = "cars",
    model_overall = "wt ON drat;",
    model_class_specific = "wt; qsec;",
    rdata = mtcars,
    usevariables = c("wt", "qsec", "drat"),
    OUTPUT = "standardized")
runModels(replaceOutfile = "modifiedDate")
cars_results <- readModels(filefilter = "cars")
plotMixtures(cars_results, rawdata = TRUE)
## End(Not run)

## Not run:
plotMixtures(cars_results, variables = "wt")
## End(Not run)

## Not run:
plotMixtures(cars_results, coefficients = "stdyx.standardized")
## End(Not run)
```
prepareMplusData  Create tab-delimited file and Mplus input syntax from R data.frame

Description

The `prepareMplusData` function converts an R data.frame (or a list of data frames), into a tab-delimited file (without header) to be used in an Mplus input file. The corresponding Mplus syntax, including the data file definition and variable names, is printed to the console or optionally to an input file.

Usage

```r
prepareMplusData(
  df, 
  filename, 
  keepCols, 
  dropCols, 
  inpfile = FALSE, 
  interactive = TRUE, 
  overwrite = TRUE, 
  imputed = FALSE, 
  writeData = c("always", "ifmissing", "never"), 
  hashfilename = FALSE
)
```

Arguments

- **df**: The R data.frame to be prepared for Mplus
- **filename**: The path and filename for the tab-delimited data file for use with Mplus. Example: "C:/Mplusdata/data1.dat"
- **keepCols**: A character vector specifying the variable names within `df` to be output to `filename` or a numeric vector of the column indices to be output or a logical vector corresponding to the same.
- **dropCols**: A character vector specifying the variable names within `df` to be omitted from the data output to `filename` or a numeric vector of the column indices not to be output or a logical vector corresponding to the same.
- **inpfile**: Logical value whether the Mplus syntax should be written to the console or to an input file. Defaults to FALSE. If TRUE, the file name will be the same as `filename` with the extension changed to .inp. Alternately, this can be a character string giving the file name to write the Mplus syntax to.
- **interactive**: Logical value indicating whether file names should be selected interactively. If `filename` is missing and `interactive=TRUE`, then a dialogue box will pop up to select a file or a console prompt if in a non interactive context. Defaults to TRUE.
- **overwrite**: Logical value indicating whether data and input (if present) files should be overwritten. Defaults to TRUE to be consistent with prior behavior. If FALSE and the file to write the data to already exists, it will throw an error.
prepareMplusData

- `imputed`: A logical whether data are multiply imputed. Defaults to `FALSE`. If `TRUE`, the data should be a list, where each element of the list is a multiply imputed dataset.

- `writeData`: A character vector, one of ‘always’, ‘ifmissing’, ‘never’ indicating whether the data files (*.dat) should be written to disk. Defaults to ‘always’ for consistency with previous behavior. See details for further information.

- `hashfilename`: A logical whether or not to add a hash of the raw data to the data file name. Defaults to `FALSE` for consistency with previous behavior where this feature was not available.

**Details**

The `writeData` argument is new and can be used to reduce overhead from repeatedly writing the same data from R to the disk. When using the ‘always’ option, `prepareMplusData` behaves as before, always writing data from R to the disk. When ‘ifmissing’, R generates an md5 hash of the data prior to writing it out to the disk. The md5 hash is based on: (1) the dimensions of the dataset, (2) the variable names, (3) the class of every variable, and (4) the raw data from the first and last rows. This combination ensures that under most all circumstances, if the data changes, the hash will change. The hash is appended to the specified data file name (which is controlled by the logical `hashfilename` argument). Next R checks in the directory where the data would normally be written. If a data file exists in that directory that matches the hash generated from the data, R will use that existing data file instead of writing out the data again. A final option is ‘never’. If this option is used, R will not write the data out even if no file matching the hash is found.

**Value**

Invisibly returns a character vector of the Mplus input syntax. Primarily called for its side effect of creating Mplus data files and optionally input files.

**Author(s)**

Michael Hallquist

**Examples**

```r
## Not run:
library(foreign)

study5 <- read.spss("reanalysis-study-5-mt-fall-08.sav", to.data.frame=TRUE)
ASData5 <- subset(study5, select=c("ppnum", paste("as", 1:33, sep="")))
prepareMplusData(ASData5, "study5.dat")

# basic example
test01 <- prepareMplusData(mtcars, "test01.dat")

# see that syntax was stored
test01
```
# example when there is a factor and logical
tmpd <- mtcars
tmpd$cyl <- factor(tmpd$cyl)
tmpd$am <- as.logical(tmpd$am)
prepareMplusData(tmpd, "test_type.dat")
rm(tmpd)

# by default, if re-run, data is re-written, with a note
test01b <- prepareMplusData(mtcars, "test01.dat")

# if we turn on hashing in the filename the first time,
# we can avoid overwriting notes the second time
# now that the filename was hashed in test01c, future calls do not re-write data
# as long as the hash matches
test01d <- prepareMplusData(mtcars, "test01c.dat", hashfilename=TRUE)

# tests for keeping and dropping variables
prepareMplusData(mtcars, "test02.dat", keepCols = c("mpg", "hp"))
prepareMplusData(mtcars, "test03.dat", keepCols = c(1, 2))
prepareMplusData(mtcars, "test04.dat", keepCols = c(TRUE, FALSE, FALSE, TRUE, FALSE, FALSE, FALSE, FALSE, FALSE, FALSE, FALSE, FALSE))
prepareMplusData(mtcars, "test05.dat", dropCols = c("mpg", "hp"))
prepareMplusData(mtcars, "test06.dat", dropCols = c(1, 2))
prepareMplusData(mtcars, "test07.dat", dropCols = c(TRUE, FALSE, FALSE, TRUE, FALSE, FALSE, FALSE, FALSE, FALSE, FALSE, FALSE, FALSE))

# interactive (test08.dat)
prepareMplusData(mtcars, interactive=TRUE)

# write syntax to input file, not stdout
prepareMplusData(mtcars, "test09.dat", inpfile=TRUE)

# write syntax to alternate input file, not stdout
prepareMplusData(mtcars, "test10.dat", inpfile="test10alt.inp")

# should be error, no file
prepareMplusData(mtcars, interactive=FALSE)

# new warnings if it is going to overwrite files
# (the default to be consistent with prior behavior)
prepareMplusData(mtcars, "test10.dat")

# new warnings if it is going to overwrite files
# (the default to be consistent with prior behavior)
prepareMplusData(mtcars, "test11.dat", inpfile="test10alt.inp")

# new errors if files exist and overwrite=FALSE
prepareMplusData(mtcars, "test10.dat",
                inpfile="test10alt.inp", overwrite=FALSE)

# can write multiply imputed data too
# here are three "imputed" datasets
idat <- list(
  data.frame(mpg = mtcars$mpg, hp = c(100, mtcars$hp[-1])),
  data.frame(mpg = mtcars$mpg, hp = c(110, mtcars$hp[-1])),
  data.frame(mpg = mtcars$mpg, hp = c(120, mtcars$hp[-1])))

# if we turn on hashing in the filename the first time,
# we can avoid overwriting notes the second time
testimp1 <- prepareMplusData(idat, "testi1.dat",
                            writeData = "ifmissing", hashfilename=TRUE,
                            imputed = TRUE)

# now that the filename was hashed, future calls do not re-write data
# as long as all the hashes match
testimp2 <- prepareMplusData(idat, "testi2.dat",
                            writeData = "ifmissing", hashfilename=TRUE,
                            imputed = TRUE)

# in fact, the number of imputations can decrease
# and they still will not be re-written
testimp3 <- prepareMplusData(idat[-3], "testi3.dat",
                            writeData = "ifmissing", hashfilename=TRUE,
                            imputed = TRUE)

# however, if the data changes, then all are re-written
# note that it warns for the two files that already exist
# as these two are overwritten
idat2 <- list(
  data.frame(mpg = mtcars$mpg, hp = c(100, mtcars$hp[-1])),
  data.frame(mpg = mtcars$mpg, hp = c(109, mtcars$hp[-1])),
  data.frame(mpg = mtcars$mpg, hp = c(120, mtcars$hp[-1])))
testimp4 <- prepareMplusData(idat2, "testi4.dat",
                            writeData = "ifmissing", hashfilename=TRUE,
                            imputed = TRUE)
print.MplusRstructure

## End(Not run)

### print.MplusRstructure

Print an Mplus Residual Structure object

#### Description

This is a method for printing an Mplus Residual Structure object.

#### Usage

```r
## S3 method for class 'MplusRstructure'
print(x, ...)
```

#### Arguments

- `x` An object of class MplusRstructure
- `...` Additional arguments to pass on (not currently used)

#### Value

NULL Called for its side effect of printing the object to the console

#### Author(s)

Joshua F. Wiley <jwiley.psych@gmail.com>

#### See Also

Other Mplus-Formatting: `coef.mplus.model()`, `confint.mplus.model()`, `extract()`, `summary.mplusObject()`

#### Examples

```r
# default 'show' uses printing
mplusRcov(c("a", "b", "c"), type = "ar")

# also if calling print explicitly
print(mplusRcov(c("a", "b", "c"), type = "ar"))

# to see all aspects of the raw/original object
str(mplusRcov(c("a", "b", "c"), type = "ar"))
```
readModels

*Read Parameters, Summary Statistics, and Savedata from Mplus Output*

**Description**
Extracts information from one or more Mplus output files, including fit statistics and parameters. Its is to parse all (supported) aspects of Mplus output and to combine these into a list object, with one element per output file identified.

**Usage**
```r
readModels(
  target = getwd(),
  recursive = FALSE,
  filefilter,
  what = "all",
  quiet = FALSE
)
```

**Arguments**
- **target**: the directory containing Mplus output files (.out) to parse OR the single output file to be parsed. May be a full path, relative path, or a filename within the working directory. Defaults to the current working directory. Example: "C:/Users/Michael/Mplus Runs"
- **recursive**: optional. If TRUE, parse all models nested in subdirectories within target. Defaults to FALSE.
- **filefilter**: a Perl regular expression (PCRE-compatible) specifying particular output files to be parsed within directory. See regex or [http://www.pcre.org/pcre.txt](http://www.pcre.org/pcre.txt) for details about regular expression syntax.
- **what**: a character vector denoting what aspects of Mplus output to extract. Defaults to "all", which will extract all supported output sections. See details for additional information.
- **quiet**: whether to suppress printing to the screen the file currently being processed. Defaults to FALSE.

**Details**
The what parameter defaults to "all", which extracts all supported output. If you would like to extract a reduced set of output sections (especially to speed up the function when reading many files), specify the sections as a character vector from the following options:
Value

A list with one mplus.model per file. Each mplus.model object is composed of elements containing major output sections, as detailed below. If target is a single file, then the top-level elements will be a single mplus.model object, not a list of files. Specific elements are:

- input: Mplus input syntax parsed into a list by major section
- warnings: Syntax and estimation warnings as a list
- errors: Syntax and estimation errors as a list
- data_summary: Output of SUMMARY OF DATA section, including cluster sizes and ICCs
- sampstat: Sample statistics provided by OUTPUT: SAMPSTAT, if specified
- covariance_coverage: Covariance coverage matrix for checking missingness patterns
- summaries: Summary statistics from extractModelSummaries, having structure as specified by that function
- parameters: Model parameters from extractModelParameters, having structure as specified by that function
- class_counts: Latent class counts and proportions for models that include a categorical latent variable
- indirect: Output of MODEL INDIRECT if available in output. Contains $overall and $specific data.frames for each indirect effect section
- mod_indices: Model modification indices from extractModIndices, having structure as specified by that function
- residuals: a list containing relevant information from OUTPUT: RESIDUALS
- savedata_info: File information about SAVEDATA files related to this output
- savedata: SAVEDATA file as an R data.frame, as described in getSavedata_Data
- bparameters: an mcmclist object containing the draws from the MCMC chains for a Bayesian model that uses the SAVEDATA: BPARAMETERS command
- tech1: a list containing parameter specification and starting values from OUTPUT: TECH1
- tech3: a list containing parameter covariance and correlation matrices from OUTPUT: TECH3
- tech4: a list containing means, covariances, and correlations for latent variables from OUTPUT: TECH4
- tech7: a list containing sample statistics for each latent class from OUTPUT: TECH7
- tech8: a list containing optimization history of the model. Currently only supports potential scale reduction in BAYES. OUTPUT: TECH8
- tech9: a list containing warnings/errors from replication runs for MONTECARLO analyses from OUTPUT: TECH9
- tech10: a list containing model fit information from OUTPUT: TECH10
runModels

Description

This function runs a group of Mplus models (.inp files) located within a single directory or nested within subdirectories.

Usage

runModels(
    target = getwd(),
    recursive = FALSE,
    filefilter = NULL,
    showOutput = FALSE,
    replaceOutfile = "always",
    logFile = "Mplus Run Models.log",
    Mplus_command = "Mplus",
    killOnFail = TRUE,
    local_tmpdir = FALSE
)
runModels

Arguments

target: a character vector where each element is a directory containing Mplus input files (.inp) to run OR a single .inp file to be run. Elements may be a full path, relative path, or a filename within the working directory. Defaults to the current working directory. Example: “C:/Users/Michael/Mplus Runs”

recursive: optional. If TRUE, run all models nested in subdirectories within directory. Defaults to FALSE. Not relevant if target is a single file.

filefilter: a Perl regular expression (PCRE-compatible) specifying particular input files to be run among those found in target. See regex or [http://www.pcre.org/pcre.txt](http://www.pcre.org/pcre.txt) for details about regular expression syntax.

showOutput: optional. If TRUE, show estimation output (TECH8) in the R console. Note that if run within Rgui, output will display within R, but if run via Rterm, a separate window will appear during estimation.

replaceOutfile: optional. Currently supports three settings: “always”, which runs all models, regardless of whether an output file for the model exists; “never”, which does not run any model that has an existing output file; and “modifiedDate”, which only runs a model if the modified date for the input file is more recent than the output file modified date (implying there have been updates to the model).

logFile: optional. If non-null, specifies a file (and optionally, directory) that records the settings passed into the function and the models run (or skipped) during the run.

Mplus_command: optional. N.B.: No need to pass this parameter for most users (has intelligent defaults). Allows the user to specify the name/path of the Mplus executable to be used for running models. This covers situations where Mplus is not in the system’s path, or where one wants to test different versions of the Mplus program.

killOnFail: optional. Windows only for now. If TRUE, kill all processes named mplus.exe when runModels does not terminate normally. Defaults to TRUE.

local_tmpdir: optional. Linux/Mac for now. If TRUE, set the TMPDIR environment variable to the location of the .inp file prior to execution. This is useful in Monte Carlo studies where many instances of Mplus may run in parallel and we wish to avoid collisions in temporary files among processes.

Value

None. Function is used for its side effects (running models).

Author(s)

Michael Hallquist

See Also

runModels_Interactive
runModels_Interactive

Examples

```r
## Not run:
runModels("C:/Users/Michael/Mplus Runs", recursive=TRUE, showOutput=TRUE,
replaceOutfile="modifiedDate", logFile="MH_RunLog.txt",
Mplus_command="C:\Users\Michael\Mplus Install\Mplus51.exe")
## End(Not run)
## Not run:
runModels(getwd(), filefilter = "ex8.*", logFile=NULL)
## End(Not run)
```

runModels_Interactive  Run Mplus Models Using Graphical Interface

Description

This function is provides a graphical user interface to the runModels function. It uses Tcl/Tk to
display a window in which the user can specify parameters for runModels, including the directory
for runs, recursing through subdirectories, displaying output on the console, and replacing existing
outfiles.

Usage

```r
runModels_Interactive(
  directory = getwd(),
  recursive = "0",
  showOutput = "1",
  replaceOutfile = "1",
  checkDate = "0",
  logFile = "1"
)
```

Arguments

directory  optional. The starting directory that will display in the dialog window. Defaults
to the current working directory.

recursive  optional. Whether the recursive checkbox should be checked when the window
opens. “0” for FALSE, “1” for TRUE.

showOutput  optional. Whether the show output checkbox should be checked when the win-
dow opens. “0” for FALSE, “1” for TRUE.

replaceOutfile  optional. Whether the replace outfile checkbox should be checked when the
window opens. “0” for FALSE, “1” for TRUE.

checkDate  optional. Whether the check modified date checkbox should be checked when the
window opens. “0” for FALSE, “1” for TRUE.

logFile  optional. Whether the log file checkbox should be checked when the window
opens. “0” for FALSE, “1” for TRUE.
separateHyphens

Details
This function exists as a GUI wrapper for runModels and does not provide any distinct functionality.

Value
None. Function is used to display user interface for running models.

Author(s)
Michael Hallquist

See Also
runModels

Examples

# interactive, none

-------
separateHyphens        Separate Hyphenated Variable Strings
-------

Description
This code is a simplified form of expandCmd from the lavaan package. It separates hyphenated variable strings into a list of vectors, while ignoring hyphens that may be used in numbers.

Usage
separateHyphens(cmd)

Arguments
cmd          A character string

Details
Note that this is an internal function only.

Value
The character string if no hyphens, or a list of vectors if there are hyphens.

Author(s)
Michael Hallquist revised by Joshua Wiley
showSummaryTable

Display summary table of Mplus model statistics in separate window

Description

Displays a summary table of model fit statistics extracted using the `extractModelSummaries` function. This function relies on the `showData` function from the relimp package, which displays data in a Tk-based window. By default, the following summary statistics are included: Title, LL, Parameters, AIC, AICC, BIC, RMSEA_Estimate, but these are customizable using the `keepCols` and `dropCols` parameters.

Usage

```r
showSummaryTable(modellist, keepCols, dropCols, sortBy, font = "Courier 9")
```

Arguments

- `modellist`: A list of models (as a `data.frame`) returned from the `extractModelSummaries` function.
- `keepCols`: A vector of character strings indicating which columns/variables to display in the summary. Only columns included in this list will be displayed (all others excluded). By default, `keepCols` is: c("Title","LL","Parameters","AIC","AICC","BIC","RMSEA_Estimate"). Example: c("Title","LL","AIC","CFI")
- `dropCols`: A vector of character strings indicating which columns/variables to omit from the summary. Any column not included in this list will be displayed. By default, `dropCols` is NULL. Example: c("InputInstructions","TLI")
- `sortBy`: Optional. Field name (as character string) by which to sort the table. Typically an information criterion (e.g., "AIC" or "BIC") is used to sort the table. Defaults to "AICC".
- `font`: Optional. The font to be used to display the summary table. Defaults to Courier 9.

Value

No value is returned by this function. It is solely used to display the summary table in a separate window.

Note

You must choose between `keepCols` and `dropCols` because it is not sensible to use these together to include and exclude columns. The function will error if you include both parameters.
summary.mplusObject

Author(s)
Michael Hallquist

See Also
extractModelSummaries HTMLSummaryTable LatexSummaryTable

Examples
# make me!!!

summary.mplusObject Summary an mplusObject

Description
This is a method for summarizing an mplusObject.

Usage
## S3 method for class 'mplusObject'
summary(object, verbose = FALSE, ...)

Arguments
object An object of class mplusObject
verbose Logical whether to print verbose output. Defaults to FALSE.
... Additional arguments to pass on (not currently used)

Value
NULL Called for its side effect of printing a model summary to the console

Author(s)
Joshua F. Wiley <jwiley.psych@gmail.com>

See Also
Other Mplus-Formatting: coef.mplus.model(), confint.mplus.model(), extract(), print.MplusRstructure()
Examples

```r
## Not run:
# simple example of a model using builtin data
# demonstrates use
test <- mplusObject(
  TITLE = "test the MplusAutomation Package;",
  MODEL = "
  mpg ON wt hp;
  wt WITH hp;",
  usevariables = c("mpg", "wt", "hp"),
  rdata = mtcars)

res <- mplusModeler(test, "mtcars.dat", modelout = "model1.inp", run = 1L)

# example of the summary method
summary(res)

# example of verbose output
summary(res, verbose=TRUE)

# remove files
unlink("mtcars.dat")
unlink("model1.inp")
unlink("model1.out")
unlink("Mplus Run Models.log")

## End(Not run)
```

**SummaryTable**

Create a summary table of Mplus model statistics

**Description**

Creates output (optionally sent to a file) containing a summary table of model fit statistics extracted using the `extractModelSummaries` function. By default, the following summary statistics are included: Title, LL, Parameters, AIC, AICC, BIC, RMSEA_Estimate, but these are customizable using the `keepCols` and `dropCols` parameters.

**Usage**

```r
SummaryTable(
  modelList,  # list of model objects
  type = c("screen", "popup", "html", "latex", "markdown", "none"),
  filename = "",  # name of file or "screen"
  keepCols,  # columns to keep
  dropCols,  # columns to drop
  sortBy,  # column to sort by
  caption = "",  # caption for table
  display = FALSE,  # if TRUE, display summary in console
)```
include.rownames = FALSE
)

Arguments

modelList  A list of models returned from the `extractModelSummaries` function.

type  A character vector indicating the type of output format to be generated. One of: "none", "screen", "popup", "html", "latex", or "markdown". Screen results in a simple summary table being sent to the R console.

filename  The name of the file to be created. Can be an absolute or relative path. If filename is a relative path or just the filename, then it is assumed that the file resides in the working directory `getwd()`. Example: "Mplus Summary.html". By default, no filename is given, which results in the output being sent to the console. Note that currently, filename only has an effect for "html" and "latex".

keepCols  A vector of character strings indicating which columns/variables to display in the summary. Only columns included in this list will be displayed (all others excluded). By default, keepCols is: c("Title", "LL", "Parameters", "AIC", "AICC", "BIC", "RMSEA_Estimate"). Example: c("Title", "LL", "AIC", "CFI")

dropCols  A vector of character strings indicating which columns/variables to omit from the summary. Any column not included in this list will be displayed. By default, dropCols is NULL. Example: c("InputInstructions", "TLI")

sortBy  optional. Field name (as character string) by which to sort the table. Typically an information criterion (e.g., "AIC" or "BIC") is used to sort the table. Defaults to "AICC".

caption  A character string, the caption to be given to the table. Currently only applies to types "html", "latex", and "markdown".

display  optional logical (defaults to FALSE). This parameter specifies whether to display the table upon creation (TRUE or FALSE).

include.rownames  optional logical whether to include rownames or not.

...  additional arguments passed on to specific formatting types.

Value

Invisibly returns the summary table, which can be used if the printing options available are not sufficient.

Note

You must choose between keepCols and dropCols because it is not sensible to use these together to include and exclude columns. The function will error if you include both parameters.

Author(s)

Joshua F. Wiley based on code by Michael Hallquist
testBParamCompoundConstraint

Test inequality-constrained hypothesis for two or more parameters based on iterations of MCMC chains

Description

Tests an inequality-constrained hypothesis (van de Schoot, Hoijtink, Hallquist, & Boelen, in press) based on draws from the posterior distribution of the model parameters, which provides information about the proportion of the distribution that is in agreement with a given hypothesis. This function is used for more complex hypotheses about three or more parameters, whereas testBParamConstraint tests a simple two-parameter hypothesis.

Usage

testBParamCompoundConstraint(bparams, test)
testBParamCompoundConstraint

Arguments

bparams        An object containing draws from the posterior distribution (class mplus.model
               or mplus.bparameters). Obtained by SAVEDATA:BPARAMETERS in Mplus
               and getSavedata_Bparams or readModels in MplusAutomation.

test           The R code defining the parameter test of three or more parameters. Example:
               "(STAITOT.ON.CG > STAITOT.ON.UCG) & (BDIM.ON.CG > BDIM.ON.UCG)".

Details

This function accepts a bparameters object containing iterations of the MCMC chains (rows) for
each model parameter (columns) and prints out the number and proportion of draws that are con-
sistent with the requested hypothesis test.

The test argument is evaluated directly as R code, with the bparams object attached so that variable
names are available directly in the environment. Because the goal is to evaluate the test for each
draw from the posterior distribution, remember to use vector-based logic operators, not boolean
operators. That is, stick to & or | for joining tests of parameters, rather than && or || since the latter
will return a single TRUE/FALSE, which is irrelevant.

An example test in R logic would be "(STAITOT.ON.CG > STAITOT.ON.UCG) & (BDIM.ON.CG >
BDIM.ON.UCG)".

Value

No value is returned by this function. Instead, two summary tables are printed to the screen con-
taining the number and proportion of draws consistent with the hypothesis.

Author(s)

Michael Hallquist

See Also

testBParamConstraint

Examples

## Not run:

#using bparameters directly
btest <- getSavedata_Bparams("model vbl_simpel_b.out")
testBParametersCompoundConstraint(btest,
"(STDYX_STAITOT.ON.CG > STDYX_STAITOT.ON.UCG) & (STDYX_BDIM.ON.CG > STDYX_BDIM.ON.UCG)"
)

#or using readModels
btest <- readModels("model vbl_simpel_b.out")
testBParametersCompoundConstraint(btest,
"(STDYX_STAITOT.ON.CG > STDYX_STAITOT.ON.UCG) & (STDYX_BDIM.ON.CG > STDYX_BDIM.ON.UCG)"
)

## End(Not run)
testBParamConstraint Test inequality-constrained hypothesis for two parameters based on iterations of MCMC chains

Description
Tests a simple inequality-constrained hypothesis (van de Schoot, Hoijtink, Hallquist, & Boelen, in press) based on draws from the posterior distribution of the model parameters, which provides information about the proportion of the distribution that is in agreement with a given hypothesis. This function is used for simple hypothesis for two parameters, whereas testBParamCompoundConstraint gives full access to multiple parameters and R’s logic syntax. This function accepts a bparameters object containing iterations of the MCMC chains (rows) for each model parameter (columns) and prints out the number and proportion of draws that are consistent with the requested hypothesis test. The coef1, operator, and coef2 arguments are appended in sequence, so that the hypothesis test is constructed from left-to-right. e.g., testBParamConstraint(bparamsDF,"MGM.TRT1",">","MGM.EX2").

Usage
testBParamConstraint(bparams, coef1, operator, coef2)

Arguments
- `bparams` An object containing draws from the posterior distribution (class mplus.model or mplus.bparameters). Obtained by SAVEDATA:BPARAMETERS in Mplus and getSavedata_Bparams or readModels in MplusAutomation.
- `coef1` The name of the first parameter to be compared. Example: "MGM.TRT1"
- `operator` A logical operator to compare the two parameters. Should be one of >=, >, <, or <=. Example: ">="
- `coef2` The name of the first parameter to be compared. Example: "MGM.EX2"

Value
No value is returned by this function. Instead, two summary tables are printed to the screen containing the number and proportion of draws consistent with the hypothesis.

Author(s)
Michael Hallquist

See Also
testBParamCompoundConstraint
trainLGMM

Train a variety of latent growth mixture model

Description

This function iterates through a grid of values to train LGMMs, optionally using a local or remote cluster.

Usage

```r
trainLGMM(
  data,
  idvar,
  assessmentvar,
  newdata = FALSE,
  tuneGrid,
  cl,
  ncores = 1L
)
```

Arguments

- **data**: A data frame or data table in long format (i.e., multiple rows per ID).
- **idvar**: A character string of the variable name in the dataset that is the ID variable.
- **assessmentvar**: A character string of the variable name in the dataset that indicates the particular assessment point for each timepoint.
- **newdata**: A data frame of new values to use for generating predicted trajectories by class or FALSE if no predictions to be made (the default).
- **tuneGrid**: A dataframe or list. It should have names for the needed arguments for `long2LGMM()`.
- **cl**: Optional. An existing cluster to be used to estimate models. Can be a local or remote cluster. In either case it needs MplusAUtomation and Mplus available.
- **ncores**: If a cluster is not passed to cl, specify the number of cores to use to create a local cluster. Must be an integer. Defaults to 1L.
Examples

## Not run:
## This example is not run by default because even with very limited number of
## random starts and iterations, it takes quite a few minutes
setwd(tempdir())

## Simulate Some Data from 3 classes
library(MASS)
set.seed(1234)
alldata <- rbind(
  cbind(1, mvrnorm(n = 200,
    mu = c(0, 2, 0),
    Sigma = diag(c(.2, .1, .01)),
    empirical = TRUE)),
  cbind(2, mvrnorm(n = 200,
    mu = c(-3.35, 2, 2),
    Sigma = diag(c(.2, .1, .1)),
    empirical = TRUE)),
  cbind(3, mvrnorm(n = 200,
    mu = c(3.35, 2, -2),
    Sigma = diag(c(.2, .1, .1)),
    empirical = TRUE)))
alldata <- as.data.frame(alldata)
names(alldata) <- c("Class", "I", "L", "Q")
alldata$ID <- 1:nrow(alldata)
d <- do.call(rbind, lapply(1:nrow(alldata), function(i) {
  out <- data.frame(
    ID = alldata$ID[i],
    Class = alldata$Class[i],
    Assess = 1:11,
    x = sort(runif(n = 11, min = -2, max = 2)))
  out$y <- rnorm(11,
    mean = alldata$I[i] + alldata$L[i] * out$x + alldata$Q[i] * out$x^2,
    sd = .1)
  return(out)
}))

## create splines
library(splines)
time_splines <- ns(d$x, df = 3, Boundary.knots = quantile(d$x, probs = c(.02, .98)))
d$t1 <- time_splines[, 1]
d$t2 <- time_splines[, 2]
d$t3 <- time_splines[, 3]
d$xq <- d$x^2

## create new data to be used for predictions
newdata <- data.frame(ID = 1,
  x = seq(from = -2, to = 2, by = .1))
new.splines <- with(attributes(time_splines),
  ns(newdata$x, df = degree, knots = knots,
    Boundary.knots = Boundary.knots))
newdata$t1 <- new.splines[, 1]
## create a tuning grid of models to try
## all possible combinations are created of different time trends
## different covariance structures of the random effects
## and different number of classes

```
tuneGrid <- expand.grid(
  dv = "y",
  timevars = list(c("t1", "t2", "t3"), "x", c("x", "xq")),
  starts = "2 1",
  cov = c("independent", "zero"),
  k = c(1L, 3L),
  processors = 1L, run = TRUE,
  misstrick = TRUE, stringsAsFactors = FALSE)
tuneGrid$title <- paste0(
  c("linear", "quad", "spline")[sapply(tuneGrid$timevars, length)],
  "_",
  sapply(tuneGrid$cov, function(x) if(nchar(x)==4) substr(x, 1, 4) else substr(x, 1, 3)),
  "_",
  tuneGrid$k)
tuneGrid$base <- paste0(
  c("linear", "quad", "spline")[sapply(tuneGrid$timevars, length)],
  "_",
  sapply(tuneGrid$cov, function(x) if(nchar(x)==4) substr(x, 1, 4) else substr(x, 1, 3)))

## example using long2LGMM to fit one model at a time
mres <- long2LGMM(
  data = d,
  idvar = "ID",
  assessmentvar = "Assess",
  dv = tuneGrid$dv[1],
  timevars = tuneGrid$timevars[[1]],
  misstrick = tuneGrid$misstrick[1],
  k = tuneGrid$k[1],
  title = paste0(tuneGrid$title[1], tuneGrid$k[1]),
  base = tuneGrid$base[1],
  run = tuneGrid$run[1],
  processors = tuneGrid$processors[1],
  starts = tuneGrid$starts[1],
  newdata = nd,
  cov = tuneGrid$cov[1])
```

## Example using trainLGMM to fit a whole set of models
## can be distributed across a local or remote cluster
## Defaults to creating a local cluster, but can also pass an
## existing cluster

```
AllRes <- trainLGMM(
  data = d,
  idvar = "ID",
  assessmentvar = "Assess",
  newdata = nd,
  nd$xq <- nd$x^2
```
tuneGrid = tuneGrid,
ncores = 2L)

tuneGridRes <- as.data.frame(cbind(tuneGrid,
  do.call(rbind, lapply(AllRes, function(x) {
    if (is.null(x$Model$results$summaries)) {
      NA
    } else {
      out <- x$Model$results$summaries
      ## deal with missing summary information for k = 1
      if (is.null(out$Entropy)) {
        out$Entropy <- 1
      }
      if (is.null(out$NCategoricalLatentVars)) {
        out$NCategoricalLatentVars <- 0
      }
      out[, sort(names(out)), drop = FALSE]
    }
  })))),

tuneGridRes$Type <- gsub("([a-z]+)_.*",$1, tuneGridRes$title)

tuneGridRes$MinClass <- sapply(AllRes, function(x) {
  n <- x$Model$results$class_counts$mostLikely$count
  if(is.null(n)) {
    length(unique(d$ID))
  } else {
    min(n, na.rm = TRUE)
  }
})

## when trying many models, some may not converge
## subset to omit any missing AICC and look only at those with some
## minimum number of participants per class,
## for demonstration only arbitrarily set at 30
subset(tuneGridRes, !is.na(AICC) & MinClass >= 30, 
  select = c(title, aBIC, AICC, Entropy, MinClass, LL))

## reshape data into long form which can make a very nice plot using ggplot2
reshape(tuneGridResL <- reshape(subset(tuneGridRes, select = c(Type, cov, k, Parameters, aBIC, AICC, AIC, BIC, Entropy)),
  varying = c("Parameters", "aBIC", "AICC", "AIC", "BIC", "Entropy"),
  v.names = "value",
  times = c("Parameters", "aBIC", "AICC", "AIC", "BIC", "Entropy"),
  timevar = "variable",
  idvar = c("Type", "cov", "k"),
  direction = "long")
tuneGridResL$cov <- factor(tuneGridResL$cov, levels = c("zero", "independent"))

## uncomment to run
## library(ggplot2)
## ggplot(tuneGridResL, aes(k, value, colour = Type, shape = Type)) +
## geom_point() +
## facet_grid(variable~cov, scales = "free")

## nice plot of the average trajectories in each class
## these are possible as trainLGM exports predicted values for the
## new data fed in
## uncomment to run
## ggplot(AllRes[[which(tuneGridRes$title=="quad_ind_3")]]$predictions, aes(x)) +
## geom_line(aes(y = y_1), colour = "black", size = 2) +
## geom_line(aes(y = y_2), colour = "red", size = 2) +
## geom_line(aes(y = y_3), colour = "blue", size = 2)
## End(Not run)

### update.mplusObject

**Update an Mplus model object**

**Description**

This is a method for updating an Mplus model object. It takes an Mplus model object as the first argument, and then optionally any sections to update. There are two ways to update a section using a formula interface. ~ "new stuff" will replace a given section with the new text. Alternately, you can add additional text using ~ + "additional stuff". Combined these let you replace or add to a section.

**Usage**

```r
## S3 method for class 'mplusObject'
update(object, ...)
```

**Arguments**

- `object` An object of class mplusObject
- `...` Additional arguments to pass on

**Value**

An (updated) Mplus model object

**Author(s)**

Joshua F. Wiley <jwiley.psych@gmail.com>
Examples

```r
example1 <- mplusObject(MODEL = "mpg ON wt;",
                        usevariables = c("mpg", "hp"), rdata = mtcars)
x <- "ESTIMATOR = ML;"
str(update(example1, rdata = iris))
str(update(example1, ANALYSIS = x))
str(update(example1, MODEL = ~ "wt ON hp;"))
str(update(example1, MODEL = ~ . + "wt ON hp;"))
str(update(example1, ANALYSIS = x, MODEL = ~ . + "wt ON hp;"))

## check that use variables can be updated & over ridden
str(update(example1, usevariables = c("mpg", "hp", "cyl")))

# test to make sure . in Mplus code does not cause problems
str(update(example1, ANALYSIS = x, MODEL = ~ . + "wt ON hp*.5;"))
rm(example1, x)
```
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