

# Package ‘eat’

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**Description** The package eat is designed to simplify data preparation and IRT modeling with the software ConQuest within the R programming environment. It includes routines for automation of data preprocessing and an interface to specify and run several IRT models.

**License** GPL

**LazyLoad** yes

**LazyData** yes

**OS\_type** windows

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---

aggregateData	<i>Aggregate Datasets with Missing Values</i>
---------------	---

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## Description

Aggregates datasets with constraints on missing values

## Usage

```
aggregateData(dat, subunits, units, aggregatemissings = "use.default", rename = FALSE, recodedData
```

## Arguments

dat	A data frame.
subunits	A data frame with subunit information. See 'Details'.
units	A data frame with unit information. See 'Details'.
aggregatemissings	Either the character string "use.default" or a $n \times n$ matrix with information on how missing values should be aggregated. See 'Details'.
rename	Should units with only one subunit be renamed to their unit name? Default is FALSE.
recodedData	Logical indicating whether colnames in dataset to aggregate are the subunit names (as in subunits\$subunit) or recoded subunit names (as in subunits\$subunitRecoded). Default is TRUE, meaning that colnames are recoded subitem names.

## Details

aggregateData aggregates units in data frames with special consideration of missing values. The aggregation of missing values is specified in argument aggregatemissings.

The results of aggregateData will be written to a protocol file with sunk.

Examples of data frames subunits and units can be found via data(inputList).

## Value

A data frame with aggregated units and, if rename = TRUE, renamed subunits.

**Warning**

Missings are only correctly aggregated if their values correspond to the values given in `aggregatemissings`. `aggregateData` does not check for value types or whether codes are valid. Use of `checkData` and `recodeData` before using `aggregateData` is therefore strongly recommended.

**Author(s)**

Nicole Haag, Anna Lenski

**References**

For missing types see <http://code.google.com/p/zkdlb/wiki/MissingHandling>

**See Also**

[recodeData](#), [checkData](#)

**Examples**

```
data(inputDat)
data(inputList)

dat1 <- inputDat[[1]] # get first dataset from inputDat
datRec <- recodeData(dat1, inputList$values, inputList$subunits) # recode Data first
datAggr <- aggregateData(datRec, inputList$subunits, inputList$units, rename = TRUE, recodedData = TRUE)
```

---

asNumericIfPossible	<i>Transform columns of a data.frame into numeric values if possible</i>
---------------------	--

---

**Description**

In contrast to `as.numeric`, Function transforms only "transformable" columns of a data.frame into numeric values (i.e. without creating NA when transformation fails. Non-transformable columns are maintained. Optionally, only a logical vector is given, indicating which columns are transformable.

**Usage**

```
asNumericIfPossible ( dat, set.numeric = TRUE, transform.factors = FALSE, maintain.factor.scores
```

**Arguments**

<code>dat</code>	A data.frame which columns should be transformed.
<code>set.numeric</code>	Logical: If TRUE, data.frame with transformed columns is returned. If FALSE, a logical vector is returned, indicating which columns are transformable.
<code>transform.factors</code>	Logical: Should columns of class factor transformed? If FALSE, columns of class factor are maintained. If TRUE, columns of class factor are attempted to transform.
<code>maintain.factor.scores</code>	Logical. Only relevant if <code>transform.factors = TRUE</code> . If TRUE, the nominal values of the factor are transformed if possible. If FALSE, the integer numbers representing the factors' nominal values are returned. See details.

verbose                      Logical: If TRUE, informations about the class of the columns in the data.frame are printed to the console.

## Details

In R, factors may represent ordered categories or nominal variables. Depending on the meaning of the variable, a transformation of the nominal values (of a factor variable) to numeric values may be desirable or not. The arguments `transform.factors` and `maintain.factor.scores` serve to specify if and how factor variables should be transformed. See examples.

## Value

Either a logic vector, indicating which columns in the data.frame are transformable according to the specified conditions, ora data.frame in which transformable columns are transformed.

## Author(s)

Sebastian Weirich

## Examples

```
( dat <- data.frame( X1 = c("1",NA,"0"), X2 = c("a",NA,"b"), X3 = c(TRUE,FALSE,FALSE), X4 = as.factor(
str(dat)
asNumericIfPossible(dat)
asNumericIfPossible(dat, transform.factors=TRUE, maintain.factor.scores=FALSE)
asNumericIfPossible(dat, transform.factors=TRUE, maintain.factor.scores=TRUE)
```

---

automateConquestModel    *automateConquestModel: Write all requirend Input for a single ConQuest Run.*

---

## Description

automateConquestModel facilitates data analysis using the software ConQuest. It automatically writes ConQuest syntax, label, anchor and data files for a single model specified by several arguments in R. Moreover, a batch file is created to start the analysis. For automatically specifying and running several models in a row, see `automateModels`.

## Usage

```
automateConquestModel(dat, ID, regression=NULL, DIF=NULL, group.var=NULL,
weight=NULL, items, na=list(items=NULL, DIF=NULL, HG=NULL, group=NULL,
weight=NULL), person.grouping=NULL, item.grouping=NULL, model.statement="item",
m.model="1p1", Title = NULL, jobName, jobFolder, subFolder=list(), dataName=NULL,
anchor=NULL, pathConquest, method=NULL, std.err=NULL ,distribution=NULL,
n.plausible=NULL, set.constraints=NULL, nodes=NULL, p.nodes=NULL, f.nodes=NULL,
n.iterations=NULL, converge=NULL, deviancechange=NULL, name.unidim=NULL,
equivalence.table="wle", use.letters=FALSE, checkLink=FALSE, verbose=TRUE,
export = list(logfile = TRUE, systemfile = TRUE, history = TRUE, covariance = TRUE, reg_coeffici
```

**Arguments**

<code>dat</code>	A data frame containing all variables necessary for analysis.
<code>ID</code>	Name or column number of the identifier (ID) variable.
<code>regression</code>	Names or column numbers of one or more context variables (e.g., sex, school). These variables will be used for latent regression in ConQuest.
<code>DIF</code>	Name or column number of one grouping variable for which differential item functioning analysis is to be done.
<code>group.var</code>	Names or column numbers of one or more grouping variables. Descriptive statistics for WLEs and Plausible Values will be computed separately for each group in ConQuest.
<code>weight</code>	Name or column number of one weighting variable.
<code>items</code>	Names or column numbers of variables with item responses.
<code>na</code>	A named list of numerical vectors indicating values to be considered as missing. Specific missing codes can be defined for each type of variable.
<code>item.grouping</code>	A named data frame indicating how items should be grouped to dimensions. The first column contains the names of all items and must be named <code>item</code> . The other columns contain dimension definitions and must be named with the respective dimension names. A value of 1 indicates that an item loads on this dimension, a value of 0 indicates that the respective item does not load on this dimension.
<code>person.grouping</code>	A named data frame indicating which persons should be grouped. The first column contains the identifier variable and must have the same name as the respective column in <code>dat</code> . The other columns contain grouping definitions and must be named with the respective group names. A value of 1 indicates that a person belongs to this group, a value of 0 indicates that the respective person does not belong to this group.
<code>model.statement</code>	A character string with the model statement to use in the ConQuest syntax. If <code>model.statement == NULL</code> , the model statement in the ConQuest syntax is set to <code>item</code> by default. When a DIF variable is specified, the model statement is set to <code>item - [name of DIF variable] + item*[name of DIF variable]</code> by default.
<code>m.model</code>	A character string specifying the IRT model used for analysis. At the time, only "1PL" is available.
<code>Title</code>	A character string with the analysis title for the ConQuest syntax. If <code>Title == NULL</code> , informations about computer and user name and R version are used as title.
<code>jobName</code>	A character string specifying the analysis name. All Conquest input and output files will named <code>jobName</code> with their corresponding extensions.
<code>jobFolder</code>	A character string specifying an already existing folder where all analysis files will be written to, for example "C:/programme/analysis"
<code>subFolder</code>	A named list of character strings specifying a maximum of two folders relative to <code>jobFolder</code> for data and output files. Character strings must be named <code>data</code> and <code>out</code> , for example <code>subFolder=list(data="../../dataset/analysis1", out="../../output/ar</code> . If <code>subFolder\$data == NULL</code> , the dataset is written to the folder specified by <code>jobFolder</code> . The same is true for <code>subFolder\$out == NULL</code> .
<code>dataName</code>	A character string specifying the dataset name if it is intended to be different from the name specified by <code>jobName</code> . If <code>dataName == NULL</code> , the dataset is named <code>[jobName].dat</code>

anchor	A named data frame with anchor parameters. The first column contains the names of all anchor items and must be named <code>item</code> . The second column contains anchor parameters. Anchor items can be a subset of the items in the dataset and vice versa.
pathConquest	A character string with path and name of the ConQuest console, for example "c:/programme/conquest/console_Feb2007.exe" if NULL the newest executable in <code>file.path(Library,"eat/winexe/conquest")</code> is used
method	A character string indicating which method should be used for analysis. Possible options are "gauss" (default), "quadrature" and "montecarlo". See ConQuest manual pp.225 for details on these methods.
std.err	A character string specifying which type of standard error should be estimated. Possible options are "full", "quick" (default) and "none". See ConQuest manual pp.167 for details on standard error estimation.
distribution	A character string indicating the a priori trait distribution. Possible options are "normal" (default) and "discrete". See ConQuest manual pp.167 for details on population distributions.
n.plausible	An integer value specifying the number of plausible values to draw. The default value is 5.
set.constraints	A character string specifying how the scale should be constrained. Possible options are "cases" (default), "items" and "none". When anchor parameter are specified in anchor, constraints will be set to "none".
nodes	An integer value specifying the number of nodes to be used in the analysis. The default value is 15.
p.nodes	An integer value specifying the number of nodes that are used in the approximation of the posterior distributions, which are used in the drawing of plausible values and in the calculation of EAP estimates. The default value is 2000.
f.nodes	An integer value specifying the number of nodes that are used in the approximation of the posterior distributions in the calculation of fit statistics. The default value is 2000.
n.iterations	An integer value specifying the maximum number of iterations for which estimation will proceed without improvement in the deviance. The minimum value permitted is 5. The default value is 20.
converge	An integer value specifying the convergence criterion for parameter estimates. The estimation will terminate when the largest change in any parameter estimate between successive iterations of the EM algorithm is less than converge. The default value is 0.0001.
deviancechange	An integer value specifying the convergence criterion for the deviance. The estimation will terminate when the change in the deviance between successive iterations of the EM algorithm is less than deviancechange. The default value is 0.0001.
name.unidim	A character string with the name of one latent dimension. Alternatively, the dimension name can be specified using the argument <code>item.grouping</code> .
equivalence.table	A character string specifying the type of equivalence table to print. Possible options are "wle" (default), "mle" and NULL.
use.letters	A logical value indicating whether item response values should be coded as letters. This option can be used in partial credit models comprising items with more than 10 categories to avoid response columns with width 2 in ConQuest.

checkLink	A logical value indicating whether the items in dataset are checked for being connected with each other via design. If TRUE, the function <a href="#">checkLink</a> is called.
verbose	A logical value indicating whether messages are printed on the R console.
export	A named or unnamed list or vector of logical elements indicating whether Conquest should create logfile, systemfile, history file, covariance file, file of regression coefficients and file of designmatrix.

## Details

If the folders specified in subFolder should be parent folders to jobFolder, they can be specified using double dots ... For example, if jobFolder is "C:/programme/analysis" and subFolder is list(data=" ../dataset/analysis1", out=" ../output/analysis1"), dataset is written to "C:/programme/dataset/analysis1" and output is written to "C:/output/analysis1".

## Value

No results are returned to console. Input files and batch string are written to disk in specified folder(s).

## Author(s)

Sebastian Weirich, Karoline Sachse, Martin Hecht

## References

Wu, M.L., Adams, R.J., Wilson, M.R., & Haldane, S.A. (2007). *ACER ConQuest Version 2.0. Generalised Item Response Modeling Software*. Camberwell, Victoria: ACER Press.

## See Also

[automateModels](#), [checkLink](#)

## Examples

```
## Not run:
#
# if software="conquest" (currently the only and default option) the path of the
# windows executable ConQuest console must be specified by setting
# conquestParameters = list ("pathConquest"="<path_to_your_conquest.exe>")
# e.g. conquestParameters = list ("pathConquest"="C:/ConQuest/console.exe")
# if not explicitly specified it is searched for in
# file.path(.Library,"eat/winexe/conquest")
# e.g. "C:/R/R-2.14.2/library/eat/winexe/conquest"
# you can put your ConQuest executable there
#
# load example data
# (these are simulated achievement test data)
# Note: all examples corresponding to examples in help file of 'automateModels'
data ( science1 )
#
### Example 1: create input files for a unidimensional Rasch model with all variables in dataset 'science1'
# only variables of 'science1' you want to use for analysis must be classified. In unidimensional Rasch model
# 'id' and 'items' have to be specified
# automateConquestModel needs data with collapsed missing
science1.collapsed <- collapseMissings(science1, items = science1.items)
```



```

dir.create("C:/temp")
ex1 <- automateConquestModel ( dat = science1.collapsed, ID = "id", items = science1.items,
  jobFolder = "C:/temp", jobName = "rasch_unidim")
#
### Example 2: create input files for a multidimensional Rasch model with DIF
# option 'item.grouping' specifies dimensions and mapping of items to dimensions
# 'item.grouping' is a data.frame with item names in first column ('item')
# and dimensions in further columns, mapping of items to dimension is
# indicated by 0 (item loads not on dimension) or 1 (item loads on dimension)
# (have a look at the example item.grouping 'science1.scales')
# since 6 dimensions are specified in 'science1.scales' input for a 6-dimensional Rasch model is run
# running this example may take some time + convergence is suboptimal. This is only for illustration.
# Note: in higher dimensional modes, number of nodes increased to 2^[number of dimensions]. If not explicitly
# specified by the user, automateModels automatically uses the estimator 'montecarlo', if nodes increased to
# Note: As DIF variable(s) have to be numeric in Conquest, factor variables (e.g. "sex" with male/female)
# will be expressed as numeric indicator variables.
science1.collapsed <- collapseMissings(science1, items = science1.items)
dir.create("C:/temp")
ex2 <- automateConquestModel ( item.grouping = science1.scales, dat = science1.collapsed, ID = "id", items
  DIF = "sex", jobFolder = "C:/temp", jobName = "rasch_multidim" )

### Example 3: create input files for a multidimensional multigroup Rasch model with latent regression
# Note: As regression and group variables have to be numeric, factor variables (e.g. "sex" with male/female)
# will be expressed as numeric indicator variables.
# Moreover, unless estimation method is not specified explicitly, automateConquestModel chooses 'montecarlo'
# estimation as 'gaussian quadrature' is not available due to latent regression model and 'Bock-Aitken' would
# 11390625 nodes. Note: As 'montecarlo' needs to fix all item parameter when latent regression is applied,
# parameters estimated in example 2 are used as anchor parameters here.
# Warning: This example may take a considerable amount of time. It's only for instruction.

science1.collapsed <- collapseMissings(science1, items = science1.items)
# in Conquest, latent regressors have to be numeric
dir.create("C:/temp")
# Run example 2 to gain item parameters
ex2 <- automateConquestModel ( item.grouping = science1.scales, dat = science1.collapsed, ID = "id", items
  DIF = "sex", jobFolder = "C:/temp", jobName = "rasch_multidim" )
setwd("C:/temp")
system ( "rasch_multidim.bat" , wait = TRUE , show.output.on.console = FALSE , invisible = FALSE )
### get ANCHOR parameters
prm <- get.shw("rasch_multidim.shw")[[1]][,2:3]
ex3 <- automateConquestModel ( item.grouping = science1.scales, dat = science1.collapsed, ID = "id", items
  anchor = prm, group = "track", regression = "grade", jobFolder = "C:/temp", jobName = "rasch_multidim_regression" )

## End(Not run)

```

---

automateDataPreparation

*automateDataPreparation*

---

## Description

prepare datasets for [automateModels](#)

## Usage

```
automateDataPreparation( datList = NULL, inputList, path = NULL, loadSav,
  checkData, mergeData, recodeData, aggregateData, scoreData, writeSpss,
  filedat = "zkddata.txt", filesps = "readZkdData.sps",
  aggregatemiissings = "use.default", rename = TRUE, recodedData = TRUE,
  correctDigits=FALSE, truncateSpaceChar = TRUE, newID = NULL, oldIDs = NULL,
  missing.rule = list(mvi=0, mnr=0, mci=0, mbd=NA, mir=0, mbi=0))
```

## Arguments

<code>datList</code>	A list of data frames if no .sav files shall be read in.
<code>inputList</code>	A list of data frames containing additional information (see Details).
<code>path</code>	A character string containing the path where the logfolder will be created. Also required by <a href="#">loadSav</a> (source of SPSS files) and <a href="#">writeSpss</a> . Default is the current R working directory.
<code>loadSav</code>	logical (whether function <a href="#">loadSav</a> shall be called).
<code>checkData</code>	logical (whether function <a href="#">checkData</a> shall be called).
<code>mergeData</code>	logical (whether function <a href="#">mergeData</a> shall be called).
<code>recodeData</code>	logical (whether function <a href="#">recodeData</a> shall be called for subunits).
<code>aggregateData</code>	logical (whether function <a href="#">aggregateData</a> shall be called).
<code>scoreData</code>	logical (whether function <a href="#">recodeData</a> shall be called for units).
<code>writeSpss</code>	logical (whether function <a href="#">writeSpss</a> shall be called).
<code>filedat</code>	A character string with the name of the output data file required by <a href="#">writeSpss</a> .
<code>filesps</code>	A character string with the name of the output syntax file required by <a href="#">writeSpss</a> .
<code>missing.rule</code>	A list containing recode information for character missings required by <a href="#">writeSpss</a> . See 'References' for description of default values.
<code>aggregatemiissings</code>	A character string. Either "use.default" or "seeInputList", if pattern was specified in <code>inputList\$aggrMiss</code> .
<code>rename</code>	logical. See <a href="#">aggregateData</a> .
<code>recodedData</code>	logical. See <a href="#">aggregateData</a> .
<code>correctDigits</code>	logical. See <a href="#">loadSav</a> .
<code>truncateSpaceChar</code>	logical. See <a href="#">loadSav</a> .
<code>newID</code>	A character string containing the case IDs name in the final data frame. Default is "ID" or a character string specified in <code>inputList</code> sheet 6 (see <a href="#">readDaemonXlsx</a> ).
<code>oldIDs</code>	A vector of character strings containing the IDs names in the original datasets. Default is as specified in <code>inputList\$savFiles</code> .

## Details

`inputList` is a list of data frames. It can be created either by ZKDaemon via [readDaemonXlsx](#) or by [makeInputLists](#). Compulsory: units, subunits, values. Optional: unitRecodings, savFiles, newID, aggregateMissings.

## Value

A single data frame in last transformation status.

## Author(s)

Karoline Sachse

## References

<http://code.google.com/p/zkdlb/wiki/MissingHandling>

## Examples

```
inpList <- inputList
inpDat <- inputDat
test <- automateDataPreparation (inputList=inpList, datList = inpDat,
                                path = "c:/temp/test_eat", loadSav = FALSE, checkData=TRUE,
                                mergeData = TRUE, recodeData=TRUE, aggregateData=TRUE, scoreData= TRUE,
                                writeSpss=TRUE)
```

---

automateModels

*automateModels*

---

## Description

specify and run several ConQuest models

## Usage

```
automateModels(dat, id = NULL, context.vars = NULL, items = NULL,
               item.grouping = NULL, select.item.group = NULL, person.grouping.vars = NULL,
               person.grouping.vars.include.all = FALSE, person.grouping = NULL,
               select.person.group = NULL, checkLink = FALSE, additional.item.props = NULL, folder,
               overwrite.folder = TRUE, analyse.name.prefix = NULL, analyse.name = NULL,
               analyse.name.elements = NULL, data.name = NULL, m.model = NULL, software = NULL,
               dif = NULL, weight = NULL, anchor = NULL, regression = NULL, adjust.for.regression = TRUE,
               q3 = FALSE, q3.p.est = c ( "wle" , "pv" , "eap" ), icc = FALSE, missing.rule = NULL, cross = NULL,
               subfolder.order = NULL, subfolder.mode = NULL, allNAdelete = TRUE, additionalSubFolder = NULL,
               run.mode = NULL, n.batches = NULL, run.timeout = 1440, run.status.refresh = 0.2,
               all.local.cores = TRUE, email = NULL, smtpServer = NULL, write.txt.dataset = FALSE,
               write.xls.results = TRUE,
               delete.folder.countdown = 5, conquestParameters = NULL )
```

## Arguments

<code>dat</code>	data.frame containing all variables type of variables ("id" , "context.vars" or "items") must be set using options id, context.vars, items
<code>id</code>	name or column number of 'id' variable in dat
<code>context.vars</code>	names or column numbers of 'context' variables ( e.g. sex, school , ... ) in dat
<code>items</code>	names or column numbers of 'item' variables in dat if omitted, all variables that are not classified as 'id' or 'context' variables are treated as 'items'
<code>item.grouping</code>	data.frame with grouping information of items, first column must be 'item' which includes item names, further columns contain scale definitions, 0 indicates that the respective item is NOT part of the scale, 1 indicates that this item is part of the scale, colnames of columns are the names of the scales

<code>select.item.group</code>	character vector of scale names chosen for analysis
<code>person.grouping.vars</code>	character vector of 'context' variables in dataset which are used to automatically generate 'person.grouping', each category is transformed into the 'person.grouping' format
<code>person.grouping.vars.include.all</code>	logical vector (along <code>person.grouping.vars</code> ), indicates whether to generate a variable 'all' for the specific variable
<code>person.grouping</code>	data.frame with grouping information of persons, first column must be the name of 'id' (e.g. <code>idstud</code> ), further columns contain group definitions, 0 indicates that the respective person is NOT part of the group, 1 indicates that this person is part of the group, colnames of columns are the names of the groups
<code>select.person.group</code>	character vector of group names chosen for analysis
<code>checkLink</code>	logical: If TRUE, items in dataset are checked for being connected with each other via design (function <a href="#">checkLink</a> is called) 23.02.2012: not yet implemented
<code>additional.item.props</code>	data.frame of additional item information to be merged to model results, first column must be 'item' and contain item names
<code>folder</code>	folder to write output into
<code>overwrite.folder</code>	logical, if TRUE (default), folder is completely emptied
<code>analyse.name.prefix</code>	prefix (e.g. "pilotStudy") to be attached to all analyses names
<code>analyse.name</code>	analyses names are usually automatically set, if you want to set them manually use this option
<code>analyse.name.elements</code>	analyses names are set automatically using these elements: <code>c("scale", "group", "dif", "regression", "anchor")</code> , use this option to change composition and order of the analyses names generation
<code>data.name</code>	optional: character string specifying name of dataset if intend to differ from name specified by <code>jobName</code> . When <code>dataName == NULL</code> , dataset is named <code>[jobName].dat</code>
<code>m.model</code>	measurement model, "1pl" (default), "2pl", "3pl", "4pl"
<code>software</code>	"conquest" (default) no other software implemented yet
<code>dif</code>	variable that is used for differential item functioning
<code>weight</code>	case weight variable
<code>anchor</code>	data.frame with anchor information
<code>regression</code>	variable(s) that is/are used
<code>adjust.for.regression</code>	center plausible values and items on grand mean
<code>q3</code>	Logical: If TRUE, Yen's Q3 statistic is computed.
<code>q3.p.est</code>	person estimates that are used in q3 calculation, default: <code>wle</code>
<code>icc</code>	Logical: If TRUE, pdfs of item icc are generated.
<code>missing.rule</code>	definition how to recode distinct missings in dataset

cross	scales in 'item.grouping' and groups in 'person.grouping' can be crossed to define distinct analyses "all": scales and groups are crossed "item.groups", scales are separately (unidimensional) run (instead of one multidimensional model) "person.groups", person groups are separately (single group) run (instead of one multigroup model)
subfolder.order	subfolders are automatically generated in this order c ( "i.model" , "p.model" , "m.model" , "software" , "dif" , "regression" , "anchor" )
subfolder.mode	"none": no subfolders are created "full": complete subfolders are created according to 'subfolder.order' "intelligent" (default): meaningful subfolders are created
allNAdelete	if TRUE all cases with complete missings on items are removed, if FALSE these cases are not deleted Note: this is a global option, that is set for all models
additionalSubFolder	specification for 'data' and 'out' subfolder (constant over all analyses)
run.mode	"serial": serial runs on local machine "parallel": batch files must be started manually (e.g. on several machines)
n.batches	number of batch files that are created, batch files contain one or more analyses
run.timeout	minutes to wait for analyses to finish, default: 1440 (24h)
run.status.refresh	time for console refresh of model run status, default: 0.2 (12sec)
all.local.cores	if TRUE and run.mode="serial" all cores of local machine are used for analysis
email	set email address to receive an email when analyses are finished or time's up
smtpServer	smtpServer for sending emails, default: "mailhost.cms.hu-berlin.de"
write.txt.dataset	write out datasets as ascii, default: FALSE
write.xls.results	if TRUE (default) results are written to Excel files
delete.folder.countdown	countdown for deletion of 'folder', default: 5 (seconds)
conquestParameters	Set ConQuest parameters as a named list. Available option are: "pathConquest", "method", "std.err", "distribution", "n.plausible", "set.constraints", "nodes", "p.nodes", "f.nodes", "n.iterations", "converge", "deviancechange", "equivalence.table", "use.letters", "na", "model.statement", "export" See <a href="#">automateConquestModel</a> documentation for details.

## Details

To run several models list parameters as corresponding lists Explicitly list NULL if parameter should not be set or be defaulted See examples

## Value

returns results in specific format

**Author(s)**

Martin Hecht, Karoline Sachse, Sebastian Weirich, Christiane Penk, Malte Jansen, Sebastian Wurster

**Examples**

```
## Not run:
# 'folder' must be specified, WARNING: this folder is deleted by automateModels!!!
#
# if software="conquest" (currently the only and default option) the path of the
# windows executable ConQuest console must be specified by setting
# conquestParameters = list ("pathConquest"="<path_to_your_conquest.exe>")
# e.g. conquestParameters = list ("pathConquest"="C:/ConQuest/console.exe")
# if not explicitly specified it is searched for in
# file.path(.Library,"eat/winexe/conquest")
# e.g. "C:/R/R-2.14.2/library/eat/winexe/conquest"
# you can put your ConQuest executable there
#
# load example data
# (these are simulated achievement test data)
data ( science1 )
#
### Example 1: running a unidimensional Rasch model with all variables in dataset 'science1'
# all variables in 'science1' must be classified as either 'id', 'context.vars' or 'items'
# 'items' may be omitted, then it is defaulted to variables that are not 'id' or 'context.vars'
ex1 <- automateModels ( dat = science1, id = "id", context.vars = science1.context.vars,
  folder = "C:/temp/automateModels/Example1" )
#
# item and person parameters can be obtained using \link{get.item.par} and \link{get.person.par}
item.par <- get.item.par ( ex1 )
person.par <- get.person.par ( ex1 )
#
### Example 2: running a multidimensional Rasch model
# option 'item.grouping' specifies dimensions and mapping of items to dimensions
# 'item.grouping' is a data.frame with item names in first column ('item')
# and dimensions in further columns, mapping of items to dimension is
# indicated by 0 (item loads not on dimension) or 1 (item loads on dimension)
# (have a look at the example item.grouping 'science1.scales')
# since 6 dimensions are specified in 'science1.scales' a 6-dimensional Rasch model is run
# this example runs some time + convergence is suboptimal
ex2 <- automateModels ( item.grouping = science1.scales, dat = science1, id = "id",
  context.vars = science1.context.vars, folder = "C:/temp/automateModels/Example2" )
#
### Example 3: running several unidimensional Rasch models in a row
# we use item.grouping = 'science1.scales' with 6 dimensions
# instead of running one 6-dimensional model we will run 6 unidimensional models
# by specifying cross = "item.groups"
ex3 <- automateModels ( cross = "item.groups", item.grouping = science1.scales, dat = science1,
  id = "id", context.vars = science1.context.vars,
  folder = "C:/temp/automateModels/Example3" )
#
### Example 4: running 15 2-dimensional models (every scale combined with every other)
# Option 'select.item.group' is used to specify various combinations of dimensions
# it is a list of 15 character vectors that incorporate scale names (from 'item.grouping' data)
ex4 <- automateModels ( select.item.group =
  list ( c("BioKno","BioPro"),c("BioKno","CheKno"),c("BioKno","ChePro"),
    c("BioKno","PhyKno"),c("BioKno","PhyPro"),c("BioPro","CheKno"),c("BioPro","ChePro"),
```

```

c("BioPro", "PhyKno"), c("BioPro", "PhyPro"), c("CheKno", "ChePro"), c("CheKno", "PhyKno"),
c("CheKno", "PhyPro"), c("ChePro", "PhyKno"), c("ChePro", "PhyPro"), c("PhyKno", "PhyPro") ),
item.grouping = science1.scales, dat = science1,
id = "id", context.vars = science1.context.vars,
folder = "C:/temp/automateModels/Example4" )
#
### Example 5: running Rasch models for several person subgroups
# we specify person.grouping.vars = "grade" to run separate analysis for every value of grade (9/10)
# to include the complete analysis (all grades) 'person.grouping.vars.include.all' is set to TRUE
# to trigger separate person subgroup analyses 'cross' must be set to "person.groups"
# with this specification 3 models are run: all grades (9 and 10), grade 9, grade 10
ex5 <- automateModels ( person.grouping.vars = "grade",
  person.grouping.vars.include.all = TRUE,
  cross = "person.groups",
  dat = science1, id = "id", context.vars = science1.context.vars,
  folder = "C:/temp/automateModels/Example5" )
#
### Example 6: running Rasch models for several person subgroups and scales
# cross = "all" triggers unidimensional models with the combination of scales and person subgroups
# in this example every scale is run with grade 9 and with grade 10 separately (=12 models)
ex6 <- automateModels ( person.grouping.vars = "grade",
  item.grouping = science1.scales,
  cross = "all",
  dat = science1, id = "id", context.vars = science1.context.vars,
  folder = "C:/temp/automateModels/Example6" )

## End(Not run)

```

---

bi.linking

*bi.linking*


---

## Description

Links results from several analysis. Each analysis is linked with each other.

## Usage

```
bi.linking ( results , folder=NULL , file.name=NULL , method = NULL , lower.triangle = TRUE , scales )
```

## Arguments

results	result list from automateModels run
folder	output folder, will be emptied!
file.name	file.name for output excel, default: "bi.linking.results.xlsx"
method	set linking method to either "Mean-Mean" , "Haebara" or "Stocking-Lord" (default)
lower.triangle	set reference groups for the linking
scales	Character vector of scales for which linking should separately done. If NULL, all analysis in the results list are linked. Note: due to suboptimalities in development process, analysis name must contain 'scale'! use this option with care!!

**Value**

writes linking results to excel file. returns linking results as list.

**Author(s)**

Martin Hecht

**Examples**

```
## Not run:
# 'folder' must be specified, WARNING: this folder is deleted by automateModels!!!
#
# load example data
# this is the results structure returned from running Example 5 of \link{automateModels}
# see there for details of analyses
#
data ( ex5 )
#
# ex5 contains the results of 3 analyses:
names(ex5)
# [1] "all.i__grade.10" "all.i__grade.9" "all.i__grade.all"
#
# each pair of these 3 analyses are linked together by bi.linking
# if not run together, you can easily combine analyses from separate \link{automateModels} runs by calling
# in this case make sure that analysis names are unique
#
# start linking, results are written to folder and are returned
ex5_linked <- bi.linking ( ex5 , folder = "C:/temp/automateModels/Example5/Linking" , file.name = "ex5_link" )
#
#
# if you want to link analyses for which no \code{automateModels} results structure is available
# you can use \link{make.link.dummy} to create a structure similar to \code{automateModels} results structure
# this can be used as input for \code{bi.linking}
#
# e.g. let's add an additional analysis for which only item difficulty and standard errors are available
# this information must be in a data.frame, see \link{make.link.dummy} for details
dfr <- data.frame (
  "item" = c ( "BioKno01" , "CheKno02" , "PhyKno03" ) ,
  "b"     = c ( -3.14      , -2.24      , -3.42      ) ,
  "b.se"  = c ( 0.612     , 0.453     , 0.783     )
)
#
# create a results object
add <- make.link.dummy ( dfr , "additional" )
#
# add this object to Example 5
ex5add <- c ( add , ex5 )
#
# start the linking procedure with the additional analysis
ex5add_linked <- bi.linking ( ex5add , folder = "C:/temp/automateModels/Example5/Linking2" , file.name = "ex5add_link" )
## End(Not run)
```



---

cat.pbc	<i>Calculate Item Discrimination for Each Category of Categorical Variables</i>
---------	---

---

## Description

cat.pbc calculates discrimination statistics for the categories of categorical variables. This information can be useful in determining which categories of an item are influencing the overall fit and discrimination and/or to find mistakes in recoding.

## Usage

```
cat.pbc(datRaw, datRec, idRaw, idRec, context.vars, values, subunits, xlsx = NULL)
```

## Arguments

datRaw	A merged unrecoded dataset
datRec	The same dataset as in datRaw, in recoded form
idRaw	Name or column number of the identifier (ID) variable in unrecoded dataset
idRec	Name or column number of the identifier (ID) variable in recoded dataset
context.vars	Names or column numbers of one or more context variables (e.g., sex, school). cat.pbc will ignore these variables.
values	Data frame with information about values, see <a href="#">inputList</a> for details.
subunits	Data frame with information about subunits, see <a href="#">inputList</a> for details.
xlsx	full path of excel to be written

## Details

The column names of datRaw and datRec must be consistent with the names provided by the columns subunit and subunitRecoded in data.frame subunits. Otherwise, cat.pbc will fail.

## Value

A data frame with the discrimination values for each category of categorical variables. The data frame contains the following columns:

item	Name of unrecoded item
cat	Name of category
n	Number of responses for this item
freq	Absolute frequency of the category
freq.rel	Relative frequency of the category
cat.pbc	Discrimination value for the category (correlation with total score)
recodevalue	Recode value for the category
subunitType	Type of subunit, see <a href="#">inputList</a> for details

## Author(s)

Nicole Haag

**Examples**

```

data(inputDat)
data(inputList)

datRaw <- mergeData(newID = "idstud", datList = inputDat, addMbd = TRUE)
datRec <- recodeData(datRaw, values = inputList$values, subunits=inputList$subunits)
pbcs   <- cat.pbc(datRaw, datRec, idRaw = "idstud", idRec = "idstud", context.vars = "hisei",
                  values = inputList$values, subunits = inputList$subunits)

```

checkData

*Check Datasets for Missing Values and Invalid Codes***Description**

Check data frames for missing or duplicated entries in the ID variable, persons and/or variables without valid codes, and invalid codes. Invalid codes are codes which are not specified in table values.

**Usage**

```
checkData (dat, values, subunits, units)
```

**Arguments**

dat	A data frame
values	A data frame with code information. See 'Details'.
subunits	A data frame with subunit information. See 'Details'.
units	A data frame with unit information. See 'Details'.

**Details**

The results of checkData will be written to a protocol file with sunk.

Examples of data frames values, subunits and units can be found via data(inputList).

**Value**

Used for its side effects. The return value is NULL.

**Author(s)**

Nicole Haag, Anna Lenski

**References**

For missing types see <http://code.google.com/p/zkdlb/wiki/MissingHandling>

**See Also**

[sunk](#)

---

checkDesign	<i>Check Datasets for test design deviations</i>
-------------	--

---

**Description**

Check data frames according to test design for valid codes instead of expected sysMis and for sysMis instead of valid codes.

**Usage**

```
checkDesign (dat, booklets, blocks, rotation, sysMis="NA", id="idstud")
```

**Arguments**

dat	A data frame
booklets	A data frame with booklet information. See 'Details'.
blocks	A data frame with block information. See 'Details'.
rotation	A data frame with rotation information. See 'Details'.
sysMis	sysMis identifier as character. Default is "NA".
id	Case-id identifier as character. Default is "idstud".

**Details**

tbd

**Author(s)**

Karoline Sachse

---

checkInput	<i>Check Input Data Frames</i>
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---

**Description**

Check input data frames for consistency and replace missing information with default values (if necessary).

**Usage**

```
checkInput(values, subunits, units, checkValues = TRUE, checkUnits = TRUE)
```

**Arguments**

values	A data frame with code information. See 'Details'
subunits	A data frame with subunit information. See 'Details'
units	A data frame with unit information. See 'Details'.
checkValues	Logical: Should data frame values be checked?
checkUnits	Logical: Should data frame units be checked?

**Details**

This function is largely for internal use and is called by `makeInputLists` before lists are generated. Examples of data frames `values`, `subunits` and `units` can be found via `data(inputList)`.

**Value**

A list containing the checked and (if necessary) defaulted input data frames:

<code>values</code>	Checked data frame with code information. Will be returned if <code>checkValues = TRUE</code> .
<code>subunits</code>	A data frame with subunit information.
<code>units</code>	A data frame with unit information. Will be returned if <code>checkUnits = TRUE</code> .

**Warning**

Function will not check input data frames if `checkValues` and `checkUnits` are both `FALSE`.

**Author(s)**

Nicole Haag

**See Also**

[makeInputLists](#)

---

<code>checkLink</code>	<i>checkLink</i>
------------------------	------------------

---

**Description**

checks whether items in a dataset are linked via design

**Usage**

```
checkLink ( dat, na = NA, verbose = TRUE)
```

**Arguments**

<code>dat</code>	A data.frame where all columns denote test items
<code>na</code>	character string specifying values to be treat as missing by design
<code>verbose</code>	logical: Should output printed to console?

**Value**

A logical value, i.e. `TRUE` or `FALSE`, indicating whether items in dataset are linked to each other.

**Author(s)**

Sebastian Weirich

---

collapseMissings	<i>Collapse Missings</i>
------------------	--------------------------

---

## Description

converts character missings of different types to 0 or NA

## Usage

```
collapseMissings(dat, missing.rule = NULL, items)
```

## Arguments

<code>dat</code>	data frame containing character missings (e.g. type 'mbd' - missing by design)
<code>missing.rule</code>	list, definition how to recode distinct missings in dataset. See details for default.
<code>items</code>	character vector containing column names of the data frames whose character missings are to be collapsed

## Details

Default `missing.rule` in `collapseMissings` is: text volume insufficient = 0 , missing not reached = 0 , missing coding impossible = NA , missing by design = NA , missing invalid response = 0 , missing by intention = 0

The results of `collapseMissings` will be written to a protocol file with sunk.

## Value

A data frame with recoded missings.

## Author(s)

Karoline Sachse, Martin Hecht

## References

For missing types see <http://code.google.com/p/zkdlb/wiki/MissingHandling>

## Examples

```
data(inputDat)
dat1 <- inputDat[[1]] # get first dataset from inputDat
datColMis <- collapseMissings(dat = dat1,
missing.rule = list(mvi = 0 ,mnr = 0 ,mci = 0 ,mbd = NA ,mir = 0 ,mbi = 0),
items=colnames(dat1)[- c(1:2)])
```

---

commonItems	<i>identify common items of groups</i>
-------------	--

---

## Description

This function identifies items that groups of persons have in common.

## Usage

```
commonItems ( dat , group.var , na = NA , uncommon = FALSE , simplify = TRUE )
```

## Arguments

dat	data.frame
group.var	group variable in data.frame , either numeric indicator of column or column name
na	missing specification
uncommon	if TRUE a vector of uncommon items is additionally returned
simplify	if TRUE a character vector is returned (only in case of 2 groups and uncommon=FALSE)

## Details

dat must only contain the group variable and the items, if further variables are in dat they are treated as items

## Value

returns a list of all group.var combinations with character vectors of common item names if uncommon=TRUE a vector of uncommon (unique) items of each group is additionally returned  
names of list are both group names concatenated by "|"

## Author(s)

Martin Hecht

## Examples

```
data(science1)
d <- science1[,c("version",science1.items)]

# common items are listed for each combination of groups
str ( commonItems ( dat = d , group.var = "version" , na = "mbd" ) )

# uncommon items are returned as well
str ( commonItems ( dat = d , group.var = "version" , na = "mbd" , uncommon = TRUE ) )
```

---

commonItems.percent	<i>calculate the percentage of common items of groups</i>
---------------------	---

---

### Description

This function calculates the percentage of items that groups of persons have in common.

### Usage

```
commonItems.percent ( dat , group.var , na = NA , xlsx = NULL )
```

### Arguments

dat	data.frame
group.var	group variable in data.frame , eihter numeric indicator of column or column name
na	missing specification
xlsx	full path (directory + file name) to Excel to be written (don't forget ".xlsx" suffix)

### Details

dat must only contain the group variable and the items, if further variables are in dat they are treated as items

### Value

returns a data.frame with common item percentage(s)

### Author(s)

Martin Hecht

### Examples

```
data(science1)
d <- science1[,c("version",science1.items)]
( commonItems.percent ( dat = d , group.var = "version" , na = "mbd" ) )
```

---

compareModels	<i>compare ConQuest models</i>
---------------	--------------------------------

---

### Description

retrieves model information ( sample size, deviance, number of parameters ) and calculates AIC and BIC; if more than 1 model is specified models are compared ( AIC difference, BIC difference, Chi square prob. )

### Usage

```
compareModels ( path , xlsx = NULL )
```

**Arguments**

path	either 1 of 4 inputs: [1] full path (directory + file name) of a ConQuest shw file [2] a list of ConQuest shw files (full paths) [3] a character vector of ConQuest shw files (full paths) [4] a folder in which it will be searched for ConQuest shw files
xlsx	full path (directory + file name) to Excel to be written (don't forget ".xlsx" suffix)

**Value**

returns a list of 2 data.frames: the first called 'models' contains model information; the second called 'model.comparison' contains information of model comparison

**Author(s)**

Martin Hecht

**Examples**

```
## Not run:
# just run any example of \link{automateModels}
# then:
#   compareModels ( <folder> )
# e.g. compareModels ( "C:/temp/automateModels/Example3" )

## End(Not run)
```

---

ConQuest.Log.Example1.log.bz2

*Example Log File from ConQuest*

---

**Description**

This is a text file with the log from a ConQuest analysis It can be accessed via bzfile ( file.path( .Library , "eat/extdata/ConQuest.Log.Example1.log.bz2" ) )

**Format**

txt

---

crop

*crop*

---

**Description**

remove trailing and leading characters from character strings

**Usage**

```
crop ( x , char = " " )
```



**Arguments**

x	character string
char	character to be removed from beginning and end of x

**Author(s)**

Martin Hecht, Sebastian Weirich

---

detect.suppression	<i>detect suppression effects in regression models</i>
--------------------	--

---

**Description**

This function detects suppression effects in regression models.

**Usage**

```
detect.suppression ( dat , dependent , independent , full.return = FALSE , xlsx.path = NULL )
```

**Arguments**

dat	data.frame with data to be used
dependent	dependent variable in regression model
independent	character vector of independent variables in regression model
full.return	if FALSE a data.frame as a quadratic matrix with suppression effects (TRUE/FALSE) of independent variables is returned if TRUE a data.frame with all calculated terms ist returned
xlsx.path	full path of Excel file that results should be written to

**Details**

formulae (13.39a) and (13.39b) decribed in Bortz (1999) page 446 are used  
if full.return=TRUE a data.frame is returned.

Columns are:

rownames: <dependent variable> ~ <independent variables> | <independent variable that is tested for suppression>

multiple.reg: logical, indicates wether there are 2 (FALSE) or more than 2 (TRUE) independent variables in the regression model

dep: dependent variabel in regression model

pred: independent variable that is investigated on suppression effect

preds: independent variables in regression model besides pred

cor\_pred\_c: correlation of pred and dependent variable

cor\_pred\_fitted\_c: correlation of predicted pred by indepenent variables and dependent variable

r.sq\_pred: R squared from model predicting pred by independent variables

rterm.minus: right term in formula (13.39a)

`rterm.plus`: right termn in formula (13.39b)  
`rterm.minus.diff`: difference of `rterm.minus` and `cor_pred_c`  
`rterm.plus.diff`: difference of `cor_pred_c` and `rterm.plus`  
 (positive difference of `rterm.minus.diff` or `rterm.plus.diff` indicates suppression effect)  
`rterm.minus.log`: logical value of formula (13.39a)  
`rterm.plus.log`: logical value of formula (13.39b)  
`suppression`: logical, `rterm.minus.log` | `rterm.plus.log`  
 if `full.return=FALSE` a data.frame as quadratic matrix is returned:  
 rows and columns are independent variables  
 diagonal includes suppression for suppression effect of variable in multiple regression  
 triangles include suppression for bivariate independent variables, "row" suppresses "column"

### Value

depends on options `full.return`

### Author(s)

Martin Hecht

### References

for formulae used by `detect.suppression` see  
 Bortz, J. (1999). Statistik fuer Sozialwissenschaftler. 5. Auflage. Berlin: Springer. p. 446

---

dichotomize	<i>dichotomize a numeric vector</i>
-------------	-------------------------------------

---

### Description

dichotomize a numeric vector by median or mean split

### Usage

```
dichotomize ( numvec , method = c("median","mean") , randomize = TRUE , ... )
```

### Arguments

<code>numvec</code>	numeric vector
<code>method</code>	either median or mean split
<code>randomize</code>	logical, if TRUE elements that equal the split threshold are randomly assigned to one of the two groups if FALSE default behavior of <code>cut</code> is used
<code>...</code>	arguments are passed to <a href="#">set.seed</a> and <a href="#">cut</a>

### Value

returns vector with dichotomization indicators

**Author(s)**

Martin Hecht

**Examples**

```

numvec <- c(1,2,3,4,5)
dichotomize ( numvec )

# set seed for random assignment of elements that match split threshold by passing argument 'seed' to function
# ( '3' in numvec is on threshold if median is used )
dichotomize ( numvec , seed = 12345 )

# set level names by passing argument 'labels' to cut function
dichotomize ( numvec , labels = c ( "low" , "high" ) )

```

equating.rasch

*Align Item Parameters from Separate Analyses***Description**

This function can be used to align two sets of item parameters from two different Rasch analyses (e.g., two populations of examinees of differing abilities) so that they are on the same scale. The item parameters of one group are transformed to the scale of the other group by adding a constant.

**Usage**

```
equating.rasch(x, y, theta = seq( -4, 4, len=100), method = c("Mean-Mean", "Haebara", "Stocking-Lord"))
```

**Arguments**

x	A data.frame with item names and parameters for group 1. This is the group which will be linked to the scale of group 2. The data.frame has to follow the structure: First column contains item names for the focal group, second column contains item parameters, and, if <code>compute.dif = TRUE</code> , third column contains the standard errors of the item parameters.
y	A data.frame with item names and parameters for group 2. This is the group for which the scale is defined. The data.frame has to follow the structure: First column contains item names for the focal group, second column contains item parameters, and, if <code>compute.dif = TRUE</code> , third column contains the standard errors of the item parameters.
theta	theta values where the test characteristic curves are evaluated
method	Method for determining the linking constant, either Mean-Mean, Haebara or Stocking-Lord
compute.dif	Logical: Whether differential item functioning in the two groups should be examined.

## Details

equating.rasch provides three methods to determine this constant: Mean-Mean the difference of the item parameter means of both samples are obtained. Haebara additionally takes the difference between item characteristic curves into account. Stocking-Lord additionally takes the test characteristic functions in account, thus minimizing differences in expected scores rather than observed scores or parameters. In most practical applications, the three linking constants should be fairly similar.

When `compute.dif = TRUE`, differential item functioning (DIF) in anchor items is examined. This can be useful to examine items with large shifts, which can be subsequently excluded from the linking procedure. DIF is computed according to the formula in Lord (1980). Additionally, the magnitude of DIF is categorized as small, moderate or large according to criteria established by the Educational Testing Service (ETS): category A (small DIF) if  $|DIF| < 0.43$  or not significantly  $> 0$ , category B (moderate DIF) if  $0.43 < |DIF| < 0.64$  and  $|DIF|$  significantly  $> 0$ , and category C (large DIF) if  $|DIF| > 0.64$  and significantly  $> 0.43$ .

## Value

A list with the following components:

<code>B.est</code>	Linking constants determined by all three methods
<code>descriptives</code>	A list with the number of items used for linking, linking variance and standard deviation, and the linking error
<code>anchor</code>	A data.frame with all item parameters used for linking from both samples and the transformed parameters for group 1. If <code>compute.dif = TRUE</code> , additional statistics for DIF are also included.
<code>transf.par</code>	A data.frame with all item parameters from both samples and the transformed parameters for group 1.

## Author(s)

Alexander Robitzsch

## References

Kolen, M. J. & Brennan, R. L. (2004). *Test equating, scaling, and linking: Methods and practices*. New York: Springer. Yen, W. M., & Fitzpatrick, A. R. (2006). *Item response theory*. In R. L. Brennan (Ed.), *Educational Measurement* (4th ed., pp. 111-153). Westport, CT: American Council on Education.

## See Also

[bi.linking](#)

---

ex5	<i>Example 5 results</i>
-----	--------------------------

---

**Description**

R object created by running Example 5 of [automateModels](#)

**Usage**

```
data(ex5)
```

**Format**

complex list structure

---

exploreDesign	<i>explore data design</i>
---------------	----------------------------

---

**Description**

explore data structure with respect to specific missing code (e.g. "missing by design")

**Usage**

```
exploreDesign ( dat , na = NA , id = NULL , itemsPerPerson = TRUE , personsPerItem = TRUE )
```

**Arguments**

dat	data.frame
na	missing specification
id	id variable in dat if exists
itemsPerPerson	logical , if TRUE items per person list is returned
personsPerItem	logical , if TRUE persons per item list is returned

**Value**

depends on itemsPerPerson and personsPerItem , if both are TRUE a list with both elements is returned

**Author(s)**

Martin Hecht

**Examples**

```
data(science1)
d <- science1[,!colnames(science1) %in% science1.context.vars]
design <- exploreDesign ( dat = d , na = "mbd" , id = "id" )
str(design)
```

---

fill.na	<i>fill NAs in a vector</i>
---------	-----------------------------

---

**Description**

fill NAs with non-NA values depending on left (forward) or right (backward) non-NA value

**Usage**

```
fill.na ( vec , backwards = FALSE , na.rm = FALSE )
```

**Arguments**

vec	a vector
backwards	if FALSE NAs are filled forward, if TRUE NAs are filled backwards
na.rm	if TRUE NAs at start and end of vector are removed

**Value**

a vector with filled NAs

**Author(s)**

Martin Hecht

**Examples**

```
( vec <- c ( NA , 1 , NA , NA , 2 , NA , 3 , NA ) )
fill.na ( vec )
fill.na ( vec , backwards = TRUE )
```

---

get.dsc	<i>Read ConQuest 'descriptives' Output Files.</i>
---------	---

---

**Description**

Reads ConQuest files with descriptive statistics for the estimated latent variables generated by the 'descriptives' statement.

**Usage**

```
get.dsc(file)
```

**Arguments**

file	Character string with the name of the ConQuest descriptives file.
------	---

**Value**

A named list of  $n$  elements with  $n$  being the number of groups for which descriptive statistics were computed. The names of the list are the group names. Each list contains the following elements:

- |               |   |
|---------------|---|
| single.values | A data frame containing the group name, dimension names, the number of observations, mean, standard deviation and variance for each of the latent dimensions. If the file contains descriptive statistics for plausible values, the number of rows in the data frame corresponds to the number of plausible values. |
| aggregates    | A data frame containing the group name, dimension names and aggregated statistics for the mean, standard deviation and variance for each of the latent dimensions as well as (in a separate row) their standard errors.   |

**Author(s)**

Sebastian Weirich

**References**

See pp.162 of Wu, M.L., Adams, R.J., Wilson, M.R., & Haldane, S.A. (2007). *ACER ConQuest Version 2.0. Generalised Item Response Modeling Software*. Camberwell, Victoria: ACER Press.

---

get.equ	<i>Reads equivalence table created in Conquest analysis.</i>
---------	--

---

**Description**

Reads Conquest files comprising equivalence tables for MLE or WLE parameters.

**Usage**

```
get.equ(file)
```

**Arguments**

file	Character string of the Conquest equ-file.
------	--

**Value**

A list of  $n+1$  elements, with  $n$  the number of dimensions in the analysis. Each element is a data.frame, whose name corresponds to the name of the dimension the values belongs to. All data.frames except the last one give the transformation of each possible raw score to the WLE or MLE score including it's standard error. First column in each data.frame contains the raw score, second column the transformed WLE or MLE score, third columns it's standard error.

The last element of the list give some sparse information about the model specifications.

**References**

See Conquest manual, pp.162.

---

get.history	<i>Reads Conquest history files.</i>
-------------	--------------------------------------

---

**Description**

Reads Conquest history file comprising parameter estimates of each iteration.

**Usage**

```
get.history(file, shw.object)
```

**Arguments**

file	Character string of the Conquest history file.
shw.object	Optional: R-Object created by get.shw(). Necessary to label the columns of the history file.

**Value**

A data.frame according to the corresponding Conquest history file. First column comprises the iteration number, second column the deviance of the corresponding iteration. Estimates of model parameters are listed in further columns.

**Author(s)**

Sebastian Weirich

---

get.item.par	<i>get item parameters</i>
--------------	----------------------------

---

**Description**

obtain item parameters from [automateModels](#) results

**Usage**

```
get.item.par ( results )
```

**Arguments**

results	return object from automateModels
---------	-----------------------------------

**Value**

returns a data.frame with item parameters from automateModels run:

**Author(s)**

Martin Hecht



## Examples

```
## Not run:
# example results structure from \code{automateModels}
data ( ex5 )
#
( item.par <- get.item.par ( ex5 ) )

## End(Not run)
```

get.itn

*Read ConQuest 'itanal' Output Files*

## Description

Reads ConQuest files comprising item analyses generated by the 'itanal' statement.

## Usage

```
get.itn(file)
```

## Arguments

file                      Character string with the name of the ConQuest item analysis file.

## Value

A data frame with one row per item response category containing the following columns:

item.nr	Number of the item in the analysis
item.name	Name of the item
Label	Response category label
Score	Score of this response category
n.valid	Total number of students who responded to this item
Abs.Freq	Number of students who gave this response
Rel.Freq	Number of students who gave this response as a percentage of the total number of respondents to the item
p	Percentage of students who answered this item correctly
pt.bis	Point-biserial for this response
t.value	T-Value of the significance test whether the point-biserial correlation is different from 0
p.value	p-Value of the significance test whether the point-biserial correlation is different from 0
PV1.Avg.1	Mean ability of students who gave this response (based on plausible values)
PV1.SD.1	Standard deviation of ability of students who gave this response (based on plausible values)
pbic	Item discrimination
threshold	Item threshold
delta	Item delta

If the model is multidimensional, the mean and standard deviation of the ability of students who gave the respective response will be shown for each dimension.

**Author(s)**

Sebastian Weirich

**References**

See pp.193 of Wu, M.L., Adams, R.J., Wilson, M.R., & Haldane, S.A. (2007). *ACER ConQuest Version 2.0. Generalised Item Response Modeling Software*. Camberwell, Victoria: ACER Press.

---

get.latent.corr

get latent correlations, covariance and variances

---

**Description**

retrieve latent correlations, covariance and variances from ConQuest shw files

**Usage**

```
get.latent.corr ( path , xlsx = NULL , covariance = TRUE , variance = TRUE , sort = TRUE )
```

**Arguments**

path	either 1 of 4 inputs: [1] full path (directory + file name) of a ConQuest shw file [2] a list of ConQuest shw files (full paths) [3] a character vector of ConQuest shw files (full paths) [4] a folder in which it will be searched for ConQuest shw files
xlsx	full path (directory + file name) to Excel to be written (don't forget ".xlsx" suffix)
covariance	logical: should covariance(s) be extracted (default: TRUE)
variance	logical: should variance(s) be extracted (default: TRUE)
sort	logical: if TRUE (default) the latent correlation matrix ist sorted as in the analysis with most dimensions; if FALSE the latent correlation matrix ist not sorted, instead the order is determined by the order of dimensions in the analyses (first to last)

**Value**

returns a data.frame with correlations, covariance and variances of ConQuest analysis/analyses

**Author(s)**

Martin Hecht

**Examples**

```
## Not run:
# just run any example of \link{automateModels}
# then:
#   get.latent.corr ( <folder> )
# e.g. get.latent.corr ( "C:/temp/automateModels/Example1" )

## End(Not run)
```

---

get.person.par	<i>get person parameters</i>
----------------	------------------------------

---

**Description**

obtain person parameters from [automateModels](#) results

**Usage**

```
get.person.par ( results )
```

**Arguments**

results            return object from automateModels

**Value**

returns a data.frame with person parameters from automateModels run:

**Author(s)**

Martin Hecht

**Examples**

```
## Not run:  
# example results structure from \code{automateModels}  
data ( ex5 )  
#  
( person.par <- get.person.par ( ex5 ) )  
  
## End(Not run)
```

---

get.plausible	<i>Read ConQuest Plausible Values Output Files</i>
---------------	--

---

**Description**

This function reads ConQuest plausible value files and automatically identifies the number of cases, the number of plausible values and the number of dimensions.

**Usage**

```
get.plausible(file)
```

**Arguments**

file                Character string with the name of the ConQuest plausible values file.

Value

A data frame with one row per person containing the following columns:

case	Case number
ID	Identifier for this case
pv	Plausible value. Columns are named pv.[name of dimension]_[number of plausible value]. For example, pv.reading_6 refers to the 6th plausible value of reading dimension.
eap	Expected <i>a posteriori</i> ability estimate for this person. Columns are named eap.[name of dimension]
eap.se	Standard error of the EAP estimate. Columns are named eap.se.[name of dimension]

Author(s)

Sebastian Weirich

References

See pp.230 of Wu, M.L., Adams, R.J., Wilson, M.R., & Haldane, S.A. (2007). *ACER ConQuest Version 2.0. Generalised Item Response Modeling Software*. Camberwell, Victoria: ACER Press.

---

get.q3	get.q3
--------	--------

---

Description

get Q3 statistics

Usage

get.q3 ( results )

Arguments

results                      results (structured list) from automateModels run

Value

list (analyses) of data.frames in matrix format containing Q3 statistics

Author(s)

Martin Hecht

get.shw

*Read ConQuest showfiles***Description**

Function reads Conquest showfiles and transforms them into a R list of data frames.

**Usage**

```
get.shw(file, dif.term = NULL, split.dif = TRUE,
        abs.dif.bound = 0.64, sig.dif.bound = 0.43)
```

**Arguments**

file	Character string of the Conquest showfile to be read in.
dif.term	Optional: Character string. Name of the term considered to be DIF-term. Must match corresponding term in showfile.
split.dif	Logical: When TRUE, DIF-Parameter are only given for Reference group.
abs.dif.bound	When DIF-Parameter are evaluated, this specifies the critical value for absolute DIF.
sig.dif.bound	When DIF-Parameter are evaluated, this specifies the critical value for confidence interval DIF.

**Details**

Function searches for 'TERM'-statements in Conquest showfile and reads the tables associated with. If one statement is specified to contain DIF analyses, absolute DIF value is computed  $2 \times [\text{group-specific parameter}]$ . Confidence intervals for 90, 95 and 99 percent are computed via the standard error of specific parameters. If both criteria - absolute DIF exceeds `abs.dif.bound` and the confidence interval does not include `sig.dif.bound`, item is considered to have DIF.

**Value**

A list of data frames, named by the 'TERM'-statements in Conquest showfile, plus an additional data frame named `regression` with regression coefficients when latent linear regression model was specified in Conquest analysis, plus an additional data frame named `cov.structure` with covariance and correlation matrix of latent dimensions. If uni-dimensional model is specified, the variance of the latent dimension is given instead. If one term was specified as DIF-statement, the corresponding data frame is augmented with additional columns for confidence intervals and indicators specifying significant DIF.

Each data frame corresponding to a 'TERM' statement contains following columns:

item.nr	Item number
item	Name of item
ESTIMATE	Estimated difficulty of item
ERROR	Standard error of estimated item difficulty
outfit	Item's 'Outfit'
outfit.ci.lb	Lower bound of the outfit confidence interval

outfit.ci.ub	Upper bound of the outfit confidence interval
outfit.t	T-value for outfit
infit	Items's 'Infit'
infit.ci.lb	Lower bound of the infit confidence interval
infit.ci.ub	Upper bound of the infit confidence interval
infit.t	T-value for infit
abs.dif	Only for DIF analysis. Absolute DIF, computed as $2 \times [\text{group-specific parameter}]$ .
ci.lb	Lower bound confidence interval for specific significance level of 90, 95 or 99 percent.
ci.ub	Upper bound confidence interval for specific significance level of 90, 95 or 99 percent.
sig	Indicates whether the corresponding item matches both DIF criteria. See details.

When latent regression was specified, the last element of the returned list is a data frame with regression coefficients, corresponding to the number of dimensions and the number of regressors. Regressor names, regression coefficients and its standard errors are given for each dimension.

Rows represent the regressors, columns represent the latent dimension to which the regression is fitted.

### Author(s)

Sebastian Weirich

---

get.wle

*Read ConQuest WLE or MLE Output Files.*

---

### Description

Read Conquest files comprising maximum likelihood estimates (MLE) or weighted likelihood estimates (WLE).

### Usage

```
get.wle(file)
```

### Arguments

**file** Character string with the name of the ConQuest MLE or WLE file.

### Value

A data frame with one row per person containing the following columns.

case	Case number
ID	Identifier for this case
n.solved	Number of items this person answered correctly
n.total	Number of total items presented to this person

wle	WLE or MLE estimate. The last number of the columns name indicates the dimension the WLE or MLE estimate belongs to.
wle.se	Standard error of WLE or MLE estimate. The last number of the columns name indicates the dimension the WLE or MLE estimate belongs to.

**Author(s)**

Sebastian Weirich

**References**

See pp.230 of Wu, M.L., Adams, R.J., Wilson, M.R., & Haldane, S.A. (2007). *ACER ConQuest Version 2.0. Generalised Item Response Modeling Software*. Camberwell, Victoria: ACER Press.

---

getConquestVersion	<i>get version (build) of ConQuest</i>
--------------------	--

---

**Description**

get version (build) of ConQuest

**Usage**

```
getConquestVersion ( path.conquest , asDate = TRUE )
```

**Arguments**

path.conquest	full path to ConQuest executable console
asDate	if TRUE an object of class 'date' is returned if FALSE a character string is returned

**Value**

depends on option 'asDate'

**Author(s)**

Martin Hecht

**Examples**

```
getConquestVersion ( "c:/ConQuest/console_Feb2007.exe" )
```

---

inputDat

*List of Three Datasets from Educational Assessment*


---

### Description

Simulated data for three booklets for an educational assessment study.

### Usage

```
data(inputDat)
```

### Format

This list contains 3 data frames, each with the following columns:

**ID** Person-ID

**Hisei** A continuous covariate.

**Ixx** Item responses to a selection of 30 test items.

### Details

code, subunit and unit descriptions are stored in dataset [inputList](#).

### Examples

```
data(inputDat)
str(inputDat)
```

---

inputList

*Data Frames with Code, Subunit and Unit Information for Datasets in  
[inputDat](#)*


---

### Description

These data frames contain information about codes, subunits and units for the datasets in [inputDat](#) and are necessary inputs for functions [automateDataPreparation](#), [checkData](#), [recodeData](#) and [aggregateData](#).

### Usage

```
data(inputList)
```



**Format**

A list with three data frames:

1. **units**: Unit information, contains the following columns:
  - unit** Unit name.
  - unitType** Subunit types: ID = ID variable; TI = test item; CV = context variable.
  - unitLabel** Unit label, to be used by [writeSpss](#).
  - unitDescription** Unit description.
  - unitAggregateRule** Aggregate rule for unit: SUM; MEAN.
  - unitScoreRule** Scoring rule for unit (not sure how this will be used in the future.)
2. **subunits**: Subunit information, contains the following columns:
  - unit** Unit name, for which subunits are given.
  - subunit** Subunit name.
  - subunitType** Subunit types: ' ? '.
  - subunitLabel** Subunit label, to be used by [writeSpss](#).
  - subunitDescription** Subunit descriptions.
  - subunitPosition** Subunit position in test booklet (e.g., line 1).
  - subunitTransniveau** Subunit transformation level.
  - subunitRecoded** Name of recoded subunit.
  - subunitLabelRecoded** Label for recoded subunit, to be used when [writeSpss](#) is applied to a dataset produced by [recodeData](#).
3. **values**: Value information, contains the following columns:
  - subunit** Subunit name, for which values are given.
  - value** Valid values for the respective subunit.
  - valueRecode** Recode values for the respective value.
  - valueType** Value types: vc = valid code; mbd = missing – by design; mvi = missing – volume insufficient; mnrr = missing – not reached; mci = missing – coding impossible; mbi = missing – by intention.
  - valueLabel** Value labels, to be used by [writeSpss](#).
  - valueDescription** Value descriptions.
  - valueLabelRecoded** Labels for recoded values, to be used when [writeSpss](#) is applied to a dataset produced by [recodeData](#).
  - valueDescriptionRecoded** Descriptions for recoded values.
4. **unitRecodings**: Unit recoding information, contains the following columns:
  - unit** Unit name
  - value** Valid values for the respective unit.
  - valueRecode** Recode values for the respective value.
  - valueType** Value types: vc = valid code; mbd = missing – by design; mvi = missing – volume insufficient; mnrr = missing – not reached; mci = missing – coding impossible; mbi = missing – by intention.
  - valueLabel** Value labels, to be used by [writeSpss](#).
  - valueDescription** Value descriptions.
  - valueLabelRecoded** Labels for recoded values, to be used when [writeSpss](#) is applied to a dataset produced by [recodeData](#).
5. **savFiles**: information for [loadSav](#), contains the following columns:

**filename** SPSS filenames

**case.id** ID variable in the respective dataset, used by [mergeData](#)

6. newID: information for [mergeData](#), contains the following columns:

**key** one of the entries should be master-id

**value** the corresponding value; how the ID variable in the final dataset shall be named

7. aggrMiss: missing aggregation pattern for [aggregateData](#)

## Examples

```
data(inputList)
str(inputList)
```

---

isConverged	<i>check convergence of ConQuest models</i>
-------------	---

---

## Description

checks if ConQuest models in a directory have converged or not

## Usage

```
isConverged ( path , txt = FALSE )
```

## Arguments

path	main path of ConQuest models, or a path to a ConQuest shw-file
txt	if TRUE a convergence summary is written to convergence_summary.txt in path, and a file (either "_CONVERGED_" or "_N_O_T_CONVERGED_") is written to each model directory if FALSE a data.frame of convergence information is returned

## Details

if path is a directory, isConverged checks recursively in path for shw files; alternatively path can be a full path to a single shw-file. models that converged, but the solution is not the best solution ( ConQuest: "At termination the solution was not the best attained solution" ), are treated as not converged

## Value

depends on txt if no shw-files are found NULL is returned

## Author(s)

Martin Hecht

---

loadSav	<i>loadSav</i>
---------	----------------

---

## Description

read SPSS data files and change id names, if necessary

## Usage

```
loadSav(path = getwd(), savFiles = NULL, oldIDS, newID, correctDigits = FALSE, truncateSpaceChar
```

## Arguments

```
path
savFiles
oldIDS
newID
correctDigits
truncateSpaceChar
```

## Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random,
##--or do help(data=index) for the standard data sets.

## The function is currently defined as
function ( path=getwd(), savFiles=NULL, oldIDS, newID, correctDigits=FALSE, truncateSpaceChar = TRUE ) {
  funVersion <- "loadSAV_0.0.2"
  if(missing(oldIDS)) {stop(paste("Error in ",funVersion,": 'oldIDS' is missing.\n",sep="")) }
  if(missing(newID)) {stop(paste("Error in ",funVersion,": 'newID' is missing.\n",sep="")) }
  if(length(newID)!=1) {stop(paste("Error in ",funVersion,": 'newID' has to be of length 1.\n",sep="")) }
  # if(!exists("read.spss")) {library(foreign)}
  if(!is.null(savFiles)) {
    fileExists <- file.exists(file.path(path,savFiles))
    if(all(!fileExists)) {
      stop(paste("Error in ",funVersion,": None of the files specified in 'savFiles' were found in ",path, ".\n",sep=""))
    }
    if(!all(fileExists)) {
      cat(paste(funVersion,": Following files specified in 'savFiles' were not found in ",path, ".\n",sep=""))
      notFoundFiles <- savFiles[!fileExists]
      FoundFiles <- savFiles[fileExists]
      cat(paste(notFoundFiles,collapse=", "))
      cat("\nOnly found files will be read in.\n")
      savFiles <- savFiles[fileExists]
    }
  }
  if(is.null(savFiles)) {
    savFiles <- list.files(path=path,pattern=".sav|.SAV",recursive=FALSE)
    if(length(savFiles)==0) {
      stop(paste("No '.sav'-files found in ",path, ".\n",sep=""))
    }
  }
}
```

```

    }
    cat(paste(funVersion,": Found ", length(savFiles), " 'savFiles' in ",path,"\n",sep=""))
  }
  ### hier beginnt das eigentliche Einlesen
  allDataFrames <- NULL
  for (i in seq(along=savFiles)) {
    file.i <- data.frame(read.spss(file.path(path,savFiles[i]),to.data.frame=FALSE, use.value.1
    idCol <- unique(unlist(lapply(oldIDS, FUN=function(ii) {grep(ii,colnames(file.i))})))
    if(length(idCol)<1) {
      stop(paste("Error in ",funVersion,": None of the specified 'oldIDS' were found in dataset"))
    }
    if(length(idCol)>1) {
      stop(paste("Error in ",funVersion,": More than one of the specified 'oldIDS' were found in dataset"))
    }
    colnames(file.i)[idCol] <- newID
    ### Leerzeichen abschnipseln
    if(truncateSpaceChar == TRUE) {
      for (ii in 1:ncol(file.i)) {
        file.i[,ii] <- crop(file.i[,ii])
      }
    }
    ### Stelligkeitskorrektur
    if(correctDigits == TRUE) {
      colsToCorrect <- lapply(1:ncol(file.i), FUN=function(ii) { sort(unique(nchar(file.i[,ii]))
      options(warn = -1)
      colsToCorrect <- which( unlist( lapply(colsToCorrect, FUN=function(ii) { all(ii == c(1
      options(warn = 0)
      if(length(colsToCorrect)>0) {
        cat(paste(funVersion,": ",length(colsToCorrect)," columns are corrected for column width"))
        for (ii in colsToCorrect) {
          file.i[,ii] <- gsub(" ", "0", formatC(as.character(file.i[,ii]),width=2))
        }
      }
    }
    allDataFrames[[i]] <- file.i
  }
  return(allDataFrames)
}

```

log2init

*Convert ConQuest Log to ConQuest Init***Description**

Convert a ConQuest logfile to ConQuest covariance, regression and item init files

**Usage**

```
log2init ( log.path , out.path = NULL , iteration = c("highestLikelihood","last","first") , out.path )
```

**Arguments**

log.path	full path to or connection of ConQuest logfile
out.path	path of output files , if NULL folder of log.path is defaulted

iteration            either "highestLikelihood" (default), "last" or "first", or a number  
 out.files.suffix        suffix to be added to output file names

### Details

ConQuest tends to not completely write out log if running and option 'update = yes' is used. To avoid warnings and malfunction manually delete the last potentially incomplete iteration from log-file.

### Value

writes files to out.path

### Author(s)

Martin Hecht

### Examples

```
## Not run:
log2init ( bzfile ( file.path( .Library , "eat/extdata/ConQuest.Log.Example1.log.bz2" ) ) , "c:/temp" )

## End(Not run)
```

---

long2matrix	<i>long2matrix</i>
-------------	--------------------

---

### Description

transforms long format data.frame into a matrix format data.frame

### Usage

```
long2matrix ( dat , sort = TRUE , triangle = NULL ,
force.diagonal = FALSE , exclude.diagonal = FALSE ,
long2matrix = TRUE )
```

### Arguments

dat	data.frame with columns "row" , "col" , "val"
sort	sort rows and columns of matrix
triangle	if not NULL a symmetric matrix will be constructed available options are "upper" , "lower" , "both"
force.diagonal	a diagonal is forced into matrix even if no diagonal elements are in dat
exclude.diagonal	the diagonal is excluded if possible
long2matrix	if FALSE dat is not transformed

**Details**

WARNING: This function seems to be buggy. Do not use it or use it with care.

**Value**

```
long2matrix = TRUE
      data.frame in matrix format
long2matrix = FALSE
      data.frame in long format
```

**Author(s)**

Martin Hecht

**Examples**

```
d1 <- data.frame (
  "row" = c ( "v1" , "v2" , "v2" , "v3" , "v1" , "v3" ) ,
  "col" = c ( "v1" , "v3" , "v2" , "v1" , "v2" , "v3" ) ,
  "val" = c ( 1 , 5 , 4 , 3 , 2 , 6 ) , stringsAsFactors = FALSE )

# unsorted matrix
long2matrix ( dat = d1 , sort = FALSE )
# sorted by default
long2matrix ( dat = d1 )
# extract upper triangle of symmetric matrix
long2matrix ( dat = d1 , triangle = "upper" )
# exclude diagonal elements
long2matrix ( dat = d1 , triangle = "upper" , exclude.diagonal = TRUE )
# if full matrix ("both" triangles) is requested, the diagonal cannot be excluded, option is ignored
long2matrix ( dat = d1 , triangle = "both" , exclude.diagonal = TRUE )

# no diagonal elements are specified
d2 <- data.frame (
  "row" = c ( "v2" , "v1" , "v1" ) ,
  "col" = c ( "v3" , "v3" , "v2" ) ,
  "val" = c ( 5 , 3 , 2 ) , stringsAsFactors = FALSE )

long2matrix ( dat = d2 )
# diagonal is set (with NAs)
long2matrix ( dat = d2 , triangle = "upper" , force.diagonal = TRUE )
```

---

long2symmatrix

*long2symmatrix*


---

**Description**

transforms long format data.frame into a symmetric matrix format data.frame

**Usage**

```
long2symmatrix ( dat , sort = FALSE , triangle = c ("both","lower","upper") ,
  include.diagonal = TRUE , full.symmetric = FALSE )
```

**Arguments**

<code>dat</code>	data.frame with columns "row" , "col" , "val"
<code>sort</code>	sort rows and columns of matrix, can be either logical (if TRUE variables are alphabetically sorted) or a character vector that indicates order
<code>triangle</code>	if "lower" or "upper" only this triangle is extracted (the other is set to NA), if "both" both triangles are extracted
<code>include.diagonal</code>	logical, should diagonal elements be included or not
<code>full.symmetric</code>	if TRUE

**Details**

WARNING: This function has not been thoroughly tested. if `sort = FALSE` and `triangle = "lower"` matrix is sorted by occurrence on `dat$row` if `sort = FALSE` and `triangle = "upper"` matrix is sorted by occurrence on `dat$col` `triangle = "both"` implies `sort = TRUE`

**Value**

data.frame in "matrix format"

**Author(s)**

Martin Hecht

**Examples**

```
long <- data.frame (
  "row" = c ( "v1" , "v2" , "v2" , "v3" , "v1" , "v3" ) ,
  "col" = c ( "v1" , "v3" , "v2" , "v1" , "v2" , "v3" ) ,
  "val" = c ( 1 , 5 , 4 , 3 , 2 , 6 ) , stringsAsFactors = FALSE )

long2symmatrix ( long )

long2symmatrix ( long , triangle = "lower" )
long2symmatrix ( long , triangle = "upper" )
long2symmatrix ( long , triangle = "both" )

long2symmatrix ( long , triangle = "lower" , include.diagonal = FALSE)
long2symmatrix ( long , triangle = "upper" , include.diagonal = FALSE)
long2symmatrix ( long , triangle = "both" , include.diagonal = FALSE)

long2symmatrix ( long , sort = c("v2","v3") )
long2symmatrix ( long , sort = c("v2","v3") , triangle = "lower" , include.diagonal = FALSE )

long2symmatrix ( long , full.symmetric = TRUE )
long2symmatrix ( long , full.symmetric = TRUE , triangle = "lower" )
long2symmatrix ( long , full.symmetric = TRUE , triangle = "lower" , include.diagonal = FALSE )
```

---

make.dummies	<i>dummy coded variables</i>
--------------	------------------------------

---

## Description

creates dummy coded variables using [dummy.code](#) names of dummy coded variables can be customized and added to the input data.frame

## Usage

```
make.dummies ( dat , cols , colname.as.prefix = TRUE , delimiter = "." , capitalize = FALSE , no
```

## Arguments

dat	data.frame
cols	colnames of variables to be dummy coded
colname.as.prefix	logical, if TRUE the original variable name is added as prefix
delimiter	logical, if TRUE (and colname.as.prefix = TRUE) variable name and "level" name are delimited by delimiter
capitalize	logical, if TRUE "levels" are capitalized
nchar	numeric, if TRUE "levels" are truncated to length nchar
add	logical, if TRUE dummy coded variables are added to dat
sort.into.dat	logical, if TRUE (and add = TRUE) dummy coded variables are added and sorted into dat

## Value

returns data.frame with dummy coded variables, depending on add either the original data.frame (dat) is appended with new dummy code variables or they are purely returned

## Author(s)

Martin Hecht

## Examples

```
## Not run:
data(science1)

science1.dum <- make.dummies ( science1 , c("sex","booklet") )
str ( science1.dum[,3:10] )

science1.dum <- make.dummies ( science1 , c("sex","booklet") , nchar = 1 )
str ( science1.dum[,3:10] )

science1.dum <- make.dummies ( science1 , c("sex","booklet") , delimiter = "_" )
str ( science1.dum[,3:10] )

science1.dum <- make.dummies ( science1 , c("sex","booklet") , delimiter = "" , capitalize = TRUE )
str ( science1.dum[,3:10] )
```



```

science1.dum <- make.dummies ( science1 , c("sex","booklet") , colname.as.prefix = FALSE )
str ( science1.dum[,3:10] )

science1.dum <- make.dummies ( science1 , c("sex","booklet") , sort.into.dat = FALSE )
str ( science1.dum[, (ncol(science1.dum)-5):ncol(science1.dum)] )

science1.dum <- make.dummies ( science1 , c("sex","booklet") , add = FALSE )
str ( science1.dum )

## End(Not run)

```

---

make.link.dummy	<i>make.link.dummy</i>
-----------------	------------------------

---

## Description

create a structure as input for [bi.linking](#)

## Usage

```
make.link.dummy ( dfr , analysis.name = "dummy.analysis" , scale.name = "dummy.scale", group.name
```

## Arguments

dfr	data.frame with items, item difficulty ("b") and standard error of b ("b.se"); col-names must be "item", "b", "b.se"
analysis.name	name of analysis
scale.name	name of scale (dimension)
group.name	name of (person) group

## Value

returns a structure as if created by [automateModels](#) with data contained in dfr; this object can be used as input for [bi.linking](#)

## Author(s)

Martin Hecht

## Examples

```

## Not run:
dfr <- data.frame (
  "item" = c ( "BioKno01" , "CheKno02" , "PhyKno03" ) ,
  "b"     = c ( -3.14      , -2.24      , -3.42      ) ,
  "b.se"  = c ( 0.612     , 0.453     , 0.783     )
)
link.dummy <- make.link.dummy ( dfr )

## End(Not run)

```

---

makeCodebookInput	<i>Make Input Data Frames From IQB-Codebooks</i>
-------------------	--

---

**Description**

Make Input Data Frames From IQB-Codebooks

**Usage**

```
makeCodebookInput(codebook)
```

**Arguments**

codebook              dataframe IQB-Codebook

**Details**

xxx

**Value**

xxx

---

makeInputLists	<i>Generate Input Lists for Functions checkData, recodeData and aggregateData</i>
----------------	---

---

**Description**

Transforms information given in values, subunits and units in a format that is used by checkData, recodeData and aggregateData.

**Usage**

```
makeInputLists(values, subunits, units, recodedData = TRUE)
makeInputCheckData(values, subunits, units)
makeInputRecodeData(values, subunits)
makeInputAggregateData(subunits, units, recodedData = TRUE)
```

**Arguments**

values	A data frame with code information. See Details.
subunits	A data frame with subunit information. See Details.
units	A data frame with unit information. See Details.
recodedData	Logical indicating whether colnames in dataset to aggregate are the subunit names (as in subunits\$subunit) or recoded subunit names (as in subunits\$subunitRecoded). Default is TRUE, meaning that colnames are recoded subitem names. This parameter is only relevant when input for aggregateData is generated.

**Details**

This function generates specific inputs for the data preparation functions `checkData`, `recodeData` and `aggregateData`. It is largely for internal use of these functions, who call their respective version.

Examples of data frames values, subunits and units can be found via `data(inputLists)`.

**Value**

A list with several of the following entries (depending on which version of the function is called):

<code>varinfoRaw</code>	A list with information about variables and their values expected in raw data.
<code>varinfoRecoded</code>	A list with information about variables and their values expected in recoded data.
<code>varinfoAggregated</code>	A list with information about variables and their values expected in aggregated data.
<code>recodeinfo</code>	A list with information needed for recoding of data.
<code>aggregateinfo</code>	A list with information needed for aggregation of data.

**Author(s)**

Nicole Haag

**Examples**

```
data(inputList)
lists <- makeInputLists(inputList$values, inputList$subunits, inputList$units, recodedData = TRUE)
str(lists)
```

---

makeNumeric

---

*Change Character Variables to numeric*


---

**Description**

Converts character variables, which contain only values, to `numeric`. Character variables containing letters are not converted. This avoids warnings, if conversion to `numeric` is attempted for variables, which contain characters.

**Usage**

```
makeNumeric(variable)
```

**Arguments**

<code>variable</code>	Variable to be changed to <code>numeric</code> .
-----------------------	--

**Value**

Variable converted to `numeric`, if possible.

**Author(s)**

Nicole Haag

**Examples**

```
a <- c("1", "2", "3", "4")
b <- c("1", "2", "x", "4")
makeNumeric(a)
makeNumeric(b)
```

mergeData

*Merge Data Frames using one Key Variable***Description**

Merges several data frames and matches them using one key variable

**Usage**

```
mergeData(newID = "ID", datList, oldIDs=NULL, addMbd = FALSE, writeLog=FALSE)
```

**Arguments**

newID	character string containing the key variable's name in the merged dataset
datList	list of data frames to be merged
oldIDs	character vector OR numeric vector containing either names of the key variables in datList or their column number in each dataframe in datList default is a vector containing replicates of the value of newID.
addMbd	logical; string "mbd" (missing by design) will be added instead of NA
writeLog	logical; if Logfile shall be written via <a href="#">sunk</a> .

**Value**

A data frame containing unique cases and unique variables. All cases and all variables that could be identified the original data frames will be kept and matched.

**Author(s)**

Karoline Sachse, Nicole Haag

**Examples**

```
data(inputDat)
str(inputDat)

mergedDataset <- mergeData("person-id", inputDat, c("idstud", "idstud", "idstud"), addMbd=TRUE)
str(mergedDataset)

mergedDataset <- mergeData("idstud", inputDat, writeLog=FALSE)
str(mergedDataset)
```

---

modus	<i>modus</i>
-------	--------------

---

**Description**

calculates modus (most frequent value)

**Usage**

```
modus ( x , randTies = FALSE )
```

**Arguments**

x	a vector
randTies	if ties occur draw a randomized value out of tied values

**Value**

returns the modus (most frequent element)

**Author(s)**

Martin Hecht

**Examples**

```
## Not run:
x <- c ( 1 , 1 , 2 , 2 )
( modus ( x ) )
( modus ( x , randTies = TRUE ) )

x <- c ( 1 , NA , NA )
( modus ( x ) )

x <- c ( "x" , "x" , "y" )
( modus ( x ) )

## End(Not run)
```

---

multiseq	<i>multiple sequences</i>
----------	---------------------------

---

**Description**

creates a sequence for every unique value in a vector

**Usage**

```
multiseq ( v )
```

**Arguments**

`v`                      a vector

**Value**

a vector with multiple sequences

**Author(s)**

Martin Hecht

**Examples**

```
v <- c("a", "a", "a", "c", "b", "b", "a")
( multiseq ( v ) )
```

---

plotDevianceChange	<i>plot deviance change</i>
--------------------	-----------------------------

---

**Description**

extract or plot (on console or to pdf) deviance change from ConQuest logfile

**Usage**

```
plotDevianceChange ( path , plot = TRUE , pdf = FALSE , out.path = NULL , extreme.crit = 0.75 )
```

**Arguments**

<code>path</code>	full path to or connection of ConQuest logfile, or just a path (in which ConQuest logfiles are to be (recursively) searched for)
<code>plot</code>	if TRUE deviance change plot is created
<code>pdf</code>	if TRUE plot ist written to pdf
<code>out.path</code>	path for pdf output file
<code>extreme.crit</code>	numeric, threshold criterion to remove outliers, is multiplied with standard deviation of deviance change

**Details**

ConQuest tends to not completely write out log if running and option 'update = yes' is used. To avoid warnings and malfunction manually delete the last potentially incomplete iteration from logfile. Points below 0 are red; if model converged ( see `link{isConverged}` for details ), the last point is larger and green

**Value**

depends on `plot` and `pdf`; if both are FALSE the deviance change data is returned, this is a named vector with `names = iteration number` and `values = deviance change from previous iteration`; if more than one ConQuest logfile is processed a list of named vectors is returned

**Author(s)**

Martin Hecht

**Examples**

```
## Not run:
plotDevianceChange ( path = file.path( .Library , "eat/extdata/ConQuest.Log.Example1.log.bz2" ) )
plotDevianceChange ( path = file.path( .Library , "eat/extdata/ConQuest.Log.Example1.log.bz2" ) , plot = F )

## End(Not run)
```

---

plotDistributions	<i>plot latent distribution</i>
-------------------	---------------------------------

---

**Description**

creates latent distribution plots of two distributions on the same metric (e.g. persons and items)

**Usage**

```
plotDistributions ( distr1 , distr2 , distr1.name = "Persons" , distr2.name = "Items" , pdf = NU
```

**Arguments**

distr1	numeric vector of person estimates
distr2	numeric vector of item estimates
distr1.name	name of distribution 1 (e.g. "Persons")
distr2.name	name of distribution 2 (e.g. "Items")
pdf	pdf output file
title	title for graph
scale.unit	name of units
distr1.color	color of distribution 1
distr2.color	color of distribution 2
alpha	controls transparency of graph, see <a href="#">geom_density</a>

**Author(s)**

Martin Hecht

**Examples**

```
## Not run:
persons <- rnorm ( 5000 )
items <- rnorm ( 200 ) + 1

plotDistributions ( persons , items )

## End(Not run)
```

---

read.txt	<i>read text files</i>
----------	------------------------

---

## Description

reads (compressed) text files with specific method

## Usage

```
read.txt ( path , read.function = c ( "readLines" , "read.table" , "read.csv" , "read.csv2" , "r
```

## Arguments

path	either directory, file, list of directories, list of files, vector of directories or vector of files
read.function	function to read in txt files, <a href="#">bzfile</a> , <a href="#">read.table</a> , <a href="#">read.csv</a> , <a href="#">read.csv2</a> , <a href="#">read.delim</a> , or <a href="#">read.delim2</a>
file.ext	character, extension of files that are to be read, extensions of compressed files are ignored, that means that file.ext refers to extension of uncompressed file and extension of compressed file without compression extension
simplify	logical, if TRUE list is unlisted if of length 1, if FALSE always a list is returned
...	arguments passed to function used as read.function; if path is (list/vector of) directory/ies, arguments 'all.files', 'recursive', 'pattern' and 'ignore.case' can be passed to <a href="#">list.files</a> that is used to get all compressed files from directory

## Details

reads text files with specific read function (read.function); compressed files are automatically uncompressed depending on their extension, see [zip2con](#) for supported compression types; if path is a single file that does not exists, it is searched for a compressed file with this name, if found this is used

## Value

returns list of read in files (also see simplify); names of list are file names (full path) without compression extension; if path is not processable NULL is returned, or (when multiple files are processed) it is not appended to return list

## Author(s)

Martin Hecht

## Examples

```
## Not run:
fl <- file.path( .Library , "eat/extdata/ConQuest.Log.Example1.log.bz2" )
lns <- read.txt ( fl )
lns <- read.txt ( bzfile ( fl ) )
lns <- read.txt ( list ( fl , fl ) )
lns <- read.txt ( c ( fl , fl ) )
str ( lns )
```



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

---

readDaemonXlsx	<i>read xlsx-Files produced by ZKDaemon</i>
----------------	---

---

### Description

read xlsx-Files produced by ZKDaemon

### Usage

```
readDaemonXlsx(filename)
```

### Arguments

filename	A character string containing path, name and extension of .xlsx produced by ZKDaemon. Caution! Sheet order is important (see Details).
----------	--

### Details

Compulsory: 1st sheet: units. 2nd sheet: subunits. 3rd sheet: values. Optional: 4th sheet: unitRe-codings. 5th sheet: savFiles. 6th sheet: newID. 7th sheet: aggregateMissings. 8th sheet: unitProperties. 9th sheet: property labels. 10th sheet: booklets.

### Value

A list of data frames containing information that is required by [automateDataPreparation](#)

### Author(s)

Karoline Sachse

### Examples

```
str(inputList)
```

---

readSpss	<i>Read SPSS Data Files and Truncate Space in String Variables and Change Column Width</i>
----------	--

---

### Description

Read SPSS Data Files and Truncate Space in String Variables and Change Column Width

### Usage

```
readSpss(file, correctDigits = FALSE, truncateSpaceChar = TRUE)
```

**Arguments**

file	Name of the SPSS data file to be read in
correctDigits	Logical: whether codes should be transformed to have uniform width in each column, see Details.
truncateSpaceChar	Logical: whether string variables should be trimmed to remove leading and trailing spaces.

**Details**

coming soon

**Value**

A data frame with trimmed character variables and corrected codes (if specified). All columns are of mode character.

**Author(s)**

Nicole Haag, Sebastian Weirich

---

recodeData

*Recode Datasets with Missing Values*


---

**Description**

Recode datasets with special consideration of missing values.

**Usage**

```
recodeData(dat, values, subunits)
```

**Arguments**

dat	A data frame
values	A data frame with code information. See 'Details'.
subunits	A data frame with subunit information. See 'Details'.

**Details**

recodeData recodes data frames with special consideration of missing values. The results of recodeData will be written to a protocol file with sunk. recodeData will give warnings, if missing or incomplete recode informations are found. Values without recode information will NOT be recoded!

Examples of data frames values and subunits can be found via data(inputList)

**Value**

A data frame with recoded variables according to the specifications in values and subunits. Column names will be the names specified in subunits\$subunitRecoded.

**Author(s)**

Martin Hecht, Christiane Penk, Nicole Haag

**References**

<http://code.google.com/p/zkdlb/wiki/MissingHandling>

**See Also**

[aggregateData](#), [checkData](#)

**Examples**

```
data(inputDat)
data(inputList)
# library(car)

dat1 <- inputDat[[1]] # get first dataset from inputDat
datRec <- recodeData(dat1, inputList$values, inputList$subunits)
str(datRec)
```

---

recodeMbiToMnr

*Recode Missing by Intention to Missing not Reached*


---

**Description**

recodeMbiToMnr converts codes for missing by intention to missing not reached

**Usage**

```
recodeMbiToMnr (dat, id, booklets, blocks, rotation, nMbi = 2)
```

**Arguments**

dat	A dataset. Missing by intention needs to be coded mbi.
id	Name or column number of identifier (ID) variable in dataset.
booklets	specification of booklets
blocks	block specification
rotation	booklet information
nMbi	Number of mbi-Codes required at the end of a block to code mnr. Needs to be $\geq 1$ .

**Details**

In order to code mnr, a certain number of subitems at the end of a block need to be coded mbi. This number can be specified with the argument nMbi. The default is 2, i.e. if the last and second to last subitem in a block are coded mbi, both subitems will be recoded to mnr. If nMbi is larger than the number of subitems in a given block, no subitem in this block will be recoded.

If all subitems in a block are coded mbi, none of them will be recoded to mnr.

**Value**

A data frame with missing not reached coded as `mnr`. For each person with at least one `mnr` in the returned dataset the names of recoded variables are given as an attribute to `dat`.

**Author(s)**

Nicole Haag

**Examples**

```
data(inputDat)
data(inputList)
```

---

`reinsort.col`*reinsort.col*

---

**Description**

insert columns of dataframe in specific position

**Usage**

```
reinsort.col ( dat , toreinsort , after )
```

**Arguments**

<code>dat</code>	data.frame on which operation should be performed
<code>toreinsort</code>	column name(s) or numeric indicator(s) that should be relocated
<code>after</code>	column name or numeric indicator after that <code>toreinsort</code> should be located

**Value**

data.frame

**Author(s)**

Martin Hecht





---

rmNArows	<i>remove NA rows from data</i>
----------	---------------------------------

---

## Description

remove rows that are completely or partially NA from data.frame or matrix

## Usage

```
rmNArows ( dat , cols = NULL , tolerance = 0 , cumulate = TRUE , remove = TRUE , verbose = FALSE )
```

## Arguments

dat	data.frame or matrix
cols	columns to include, can be a list of vectors to specify column subsets
tolerance	number of non-NA cells that are "tolerated", can be a list corresponding to cols
cumulate	if TRUE, tolerance is cumulated; if FALSE, exact tolerance is used
remove	if TRUE, columns and rows are removed; if FALSE, identified rows are returned
verbose	if TRUE removed columns and rows are printed on output window

## Value

depends on option remove

## Author(s)

Martin Hecht

## See Also

calls [rmNA](#) and [rmNAcols](#)

## Examples

```
# example matrix
( mat <- matrix( c( 1,1,1,1,1, 1,1,1,1,NA, 1,1,1,NA,NA, 1,1,NA,NA,NA, 1,NA,NA,NA,NA, NA,NA,NA,NA,NA ) , ncol=15 ) )

# remove row with entirely NA (row 6)
rmNArows( mat , verbose = TRUE )

# remove row with NA on column 3, 4, 5 (rows 4, 5, 6)
rmNArows( mat , c(3,4,5) , verbose = TRUE )
rmNArows( mat , c(-1,-2) , verbose = TRUE )

# tolerance=1 , 1 non-NA is permitted (rows 5 and 6)
rmNArows( mat , tolerance=1 , verbose = TRUE )

# tolerance=5 , 5 non-NA are permitted (all rows are removed)
rmNArows( mat , tolerance=5 , verbose = TRUE )

# do not cumulate / exact tolerance (row 1 is removed)
rmNArows( mat , tolerance=5 , cumulate=FALSE , verbose = TRUE )
```

```
rmNArows( mat , tolerance=5 , cumulate=FALSE , remove = FALSE )

# two subsets of columns
rmNArows( mat , cols = list( c(1, 2), c(4, 5) ) , verbose = TRUE )

# two subsets of columns with different tolerance
rmNArows( mat , cols = list( c(1), c(2, 3, 4, 5) ) , tolerance = list( 0 , 1 ) , verbose = TRUE )

# identify rows, no deletion
rmNArows( mat , cols = list( c(1), c(2, 3, 4, 5) ) , tolerance = list( 0 , 1 ) , remove = FALSE )
```

---

science1

*Science achievement test data*


---

### Description

This data set contains responses of 420 students on 185 science items. Additional variables are included: id, grade, sex, booklet, track, version, and four dummy coded variables that indicate Track x Version groups. An incomplete block design was used with 4 booklets. Codes on items are: "0" - wrong "1" - right "mbd" - missing by design "mbi" - missing by intention "mir" - missing due to irregular response

### Usage

```
data(science1)
```

### Format

'data.frame': 420 obs. of 195 variables

### Source

Simulated data

---

science1.context.vars *Science achievement test data - Context variable names*


---

### Description

This vector contains the names of context variables in data set [science1](#)

### Format

chr [1:9]



---

```
science1.item.characteristics
```

*Science achievement test data - Item characteristics*

---

### Description

This data frame contains item characteristics for usage with [automateModels](#) and data set [science1](#)

### Format

'data.frame': 185 obs. of 3 variables

---

```
science1.items
```

*Science achievement test data - Item names*

---

### Description

This vector contains the names items in data set [science1](#)

### Format

chr [1:185]

---

```
science1.scales
```

*Science achievement test data - Scale definition*

---

### Description

This data frame contains scale definitions for usage with [automateModels](#) and data set [science1](#)

### Format

'data.frame': 185 obs. of 7 variables

---

```
science1.testlets
```

*Science achievement test data - Testlet definition as dummy codes*

---

### Description

This data frame contains testlet definitions as dummy codes for usage with [automateModels](#) and data set [science1](#)

### Format

'data.frame': 185 obs. of 54 variables

---

set.col.type	<i>set type of variable in data.frame</i>
--------------	---

---

**Description**

converts type of column(s) to "character" , "numeric" , "logical" , "integer" or "factor"

**Usage**

```
set.col.type ( dat , col.type = list ( "character" = NULL ) , verbose = FALSE , ... )
```

**Arguments**

dat	data.frame
col.type	named list of variable names that are to be converted. names of list is conversion type ( "character" , "numeric" , "numeric.if.possible" , "logical" , "integer" or "factor" )
verbose	if TRUE variables that have been converted are printed
...	arguments to be passed to <a href="#">asNumericIfPossible</a>

**Details**

use col.type="numeric.if.possible" if conversion to numeric should be tested upfront, see [asNumericIfPossible](#) for details

**Author(s)**

Martin Hecht

**Examples**

```
str ( d <- data.frame ( "var1" = 1 , "var2" = TRUE , "var3" = FALSE , "var4" = as.factor ( 1 ) , "var5" = a
str ( set.col.type ( d ) )
str ( set.col.type ( d , list ( "numeric" = NULL ) ) )
str ( set.col.type ( d , list ( "character" = c ( "var1" , "var2" ) , "numeric" = "var3" , "logical" = "var
str ( set.col.type ( d , list ( "numeric.if.possible" = NULL ) ) )
str ( set.col.type ( d , list ( "numeric.if.possible" = NULL ) , transform.factors = TRUE ) )
str ( set.col.type ( d , list ( "numeric.if.possible" = NULL ) , transform.factors = TRUE , maintain.factor
```

---

sortDatByNames	<i>sort data.frame by colnames and/or rownames</i>
----------------	--

---

**Description**

specify new colnames and/or rownames order, data.frame is sorted in accordance

**Usage**

```
sortDatByNames ( dat , col.order = NULL , row.order = NULL , warn = TRUE )
```

**Arguments**

<code>dat</code>	data.frame
<code>col.order</code>	character vector of colnames in new order
<code>row.order</code>	character vector of rownames in new order
<code>warn</code>	logical, if TRUE warnings are printed on output window if <code>col.order/row.order</code> do not correspond to colnames/rownames resp.

**Value**

data.frame

**Author(s)**

Martin Hecht

**Examples**

```
dat <- data.frame ( matrix ( rnorm ( 100 ) , ncol = 10 ) )
colnames ( dat ) <- paste ( "X" , 10:1 , sep = "" )
rownames ( dat ) <- paste ( "X" , 11:2 , sep = "" )
dat

# sort data.frame by 'col.order' and 'row.order'
sortDatByNames ( dat , paste ( "X" , 1:10 , sep = "" ) , paste ( "X" , 2:11 , sep = "" ) )
```

---

source.it.all

*source.it.all*


---

**Description**

sources \*.R files of folder

**Usage**

```
source.it.all ( folder="p:/ZKD/development" , use.zkd.conv = TRUE , development = TRUE , develop
```

**Arguments**

<code>folder</code>	folder with *.R files
<code>development</code>	if TRUE development versions are sourced (if non-existent the latest stable is sourced or nothing is sourced, see option <code>development.only</code> ) if FALSE stable versions are sourced
<code>use.zkd.conv</code>	if TRUE R files in folder are checked to be consistent with specific ("zkd") versioning convention \ if FALSE all R files in folder are sourced
<code>development.only</code>	if TRUE only development versions are sourced \ if FALSE stable versions are included
<code>exclude</code>	character vector of R files that should not be sourced

**Value**

sources R files

**Author(s)**

Martin Hecht, Christiane Penk

---

sunk	<i>sunk</i>
------	-------------

---

**Description**

writes output to file

**Usage**

```
sunk ( cmd = NULL , path = NULL , write = TRUE , console.output = TRUE , new.file = FALSE , text
```

**Arguments**

cmd	character string of element to write, may be either text (e.g. "write me to file") or a function call (e.g. "summary(lm)")
path	path (folder and name) to output file if NULL path is defaulted to getwd()+"sunk.txt" all environments are searched for sunk.path, if sunk.path is found (exists), it is used
write	logical, if TRUE (default) output is written to file
console.output	logical, if TRUE (default) output is displayed on console
new.file	logical, if TRUE the output file is created if FALSE (default) output is appended to existing file
text.on.error	logical, sunk checks if the character string 'cmd' is an evaluable expression if TRUE (default), 'cmd' is treated as text if an error occurs when trying to evaluate string if FALSE, sunk stops on errors/not evaluable expressions
text.out.method	choose "cat" (default) or "print" as the output method for text

**Value**

writes to disk

**Author(s)**

Martin Hecht

---

userSpecifiedList	<i>userSpecifiedList</i>
-------------------	--------------------------

---

## Description

When a function requires several arguments as a list, `userSpecifiedList` is designed to 'match' users arguments to default argument structure.

## Usage

```
userSpecifiedList(l, l.default, el.default = NULL)
```

## Arguments

<code>l</code>	A named or unnamed list or vector of elements.
<code>l.default</code>	The default list of arguments needed by a function.
<code>el.default</code>	if length of <code>l</code> is longer than 1, <code>el.default</code> can be set to an numeric value to select one default element

## Value

A list of arguments where the user specified arguments are matched into default arguments. If `el.default` is set, one element is returned.

## Author(s)

Sebastian Weirich

## Examples

```
default.arguments <- list(logfile = TRUE, systemfile = TRUE, history = TRUE, covariance = TRUE, reg_coefficient = TRUE)
users.arguments   <- c(FALSE, FALSE)
userSpecifiedList ( l = users.arguments, l.default = default.arguments)

users.arguments   <- list(history = FALSE)
userSpecifiedList ( l = users.arguments, l.default = default.arguments)

users.arguments   <- FALSE
names(users.arguments) <- "covariance"
userSpecifiedList ( l = users.arguments, l.default = default.arguments)
```

writeSpss

*Export Datasets to SPSS***Description**

Writes data and SPSS syntax files.

**Usage**

```
writeSpss(dat, values, subunits, units,
  filedat = "zkddata.txt", filesps = "readZkdData.sps",
  missing.rule = list(mvi = 0, mnr = 0, mci = NA, mbd = NA, mir = 0, mbi = 0),
  path = getwd(), sep = "\t", dec = ",", silent = FALSE)
```

**Arguments**

dat	A data frame
values	A data frame with code information. See 'Details'.
subunits	A data frame with subunit information. See 'Details'.
units	A data frame with unit information. See 'Details'.
filedat	A character string with the name of the output data file.
filesps	A character string with the name of the output syntax file.
missing.rule	A list containing recode information for character missings. See 'References' for description of default values.
path	A character string containing the path of the output file. The value in path is appended to filedat and filesps. By default, files are written to the current R working directory. If path=NULL then no file path appending is done.
sep	The separator between the data fields.
dec	The decimal separator for numerical data.
silent	A logical flag stating whether the names of the files should be printed.

**Details**

This function automates most of the work needed to export a dataset to SPSS. It uses a modified version of writeForeignSPSS() from the foreign package and of mids2spss() from the mice package. The modified version allows for a choice of the field and decimal separators, makes some improvements to the formatting and provides variable labels and value labels according to the information in the data frames values, subunits and units.

Examples of data frames values, subunits and units can be found on data(inputList)

The SPSS syntax file has the proper file names and separators set, so in principle it should run and read the data without alteration. SPSS is more strict than R with respect to the paths. Always use the full path, otherwise SPSS may not be able to find the data file.

**Value**

Used for its side effects. The return value is NULL.

**Author(s)**

Nicole Haag

**References**<http://code.google.com/p/zkdlb/wiki/MissingHandling>


---

yen.q3	<i>yen.q3</i>
--------	---------------

---

**Description**

Q3 statistics

**Usage**

yen.q3 ( dat , theta , b , progress = T )

**Arguments**

dat	bla
theta	bla
b	bla
progress	bla

---

zip2con	<i>convert compressed file(s) to connection(s)</i>
---------	--

---

**Description**

convert compressed file(s) to a list of connection(s)

**Usage**

zip2con ( path , ... )

**Arguments**

path	either directory, file, list of directories, list of files, vector of directories or vector of files
...	arguments passed to file handling function <a href="#">bzfile</a> ; if path is (list/vector of) directory/ies, arguments 'all.files', 'recursive', and 'ignore.case' can be passed to <a href="#">list.files</a> that is used to get all compressed files from directory

**Details**

function converts file(s) to connections by calling the appropriate uncompress function depending on file extension; currently supported are files with extensions "bz2" that are processed by [bzfile](#)

**Value**

returns list of connection(s); names of list are file names (full path) without compression extension; if path is already a connection it is returned as named list if path is not processable NULL is returned, or (when multiple files are processed) it is not appended to return list

**Author(s)**

Martin Hecht

**Examples**

```
## Not run:
fl <- file.path( .Library , "eat/extdata/ConQuest.Log.Example1.log.bz2" )
zip2con ( fl )
zip2con ( bzfile ( fl ) )
zip2con ( list ( fl , fl ) )
zip2con ( c ( fl , fl ) )

## End(Not run)
```



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