

# Package ‘eatGADS’

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**Title** Data Management of Large Hierarchical Data

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**Description** Import 'SPSS' data, handle and change 'SPSS' meta data, store and access large hierarchical data in 'SQLite' data bases.

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applyChangeMeta	<i>Apply Meta Data Changes.</i>
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---

**Description**

Function to apply meta data changes to a GADSdat object specified by a change table extracted by [getChangeMeta](#).

**Usage**

```

applyChangeMeta(changeTable, GADSdat, ...)

## S3 method for class 'varChanges'
applyChangeMeta(changeTable, GADSdat, ...)

## S3 method for class 'valChanges'
applyChangeMeta(
  changeTable,
  GADSdat,
  existingMeta = c("stop", "value", "value_new", "drop"),
  ...
)

```

**Arguments**

changeTable	Change table as provided by <a href="#">getChangeMeta</a> .
GADSdat	GADSdat object imported via eatGADS.
...	further arguments passed to or from other methods.
existingMeta	If values are recoded, which meta data should be used (see details)?

**Details**

Values for which the change columns contain NA remain unchanged. If changes are performed on value levels, recoding into existing values can occur. In these cases, `existingMeta` determines how the resulting meta data conflicts are handled, either raising an error if any occur ("stop"), keeping the original meta data for the value ("value") or using the meta data in the `changeTable` or, if incomplete, from the recoded value ("value\_new").

Furthermore, one might recode multiple old values in the same new value. This is currently only possible with `existingMeta = "drop"`, which drops all related meta data on value level.

**Value**

Returns the modified GADSdat object.

**Examples**

```
# Change a variable name and label
varChangeTable <- getChangeMeta(pisa, level = "variable")
varChangeTable[1, c("varName_new", "varLabel_new")] <- c("IDstud", "Person ID")

pisa2 <- applyChangeMeta(varChangeTable, GADSdat = pisa)
```

---

applyLookup	<i>Recode via lookup table.</i>
-------------	---------------------------------

---

**Description**

Recode one or multiple variables based on a lookup table created via [createLookup](#) (and potentially formatted by [collapseColumns](#)).

**Usage**

```
applyLookup(GADSdat, lookup, suffix = NULL)
```

**Arguments**

GADSdat	A GADSdat object.
lookup	Lookup table created by <a href="#">createLookup</a> and - if necessary - collapsed by <a href="#">collapseColumns</a> . Column names must be <code>c("variable", "value", "value_new")</code> .
suffix	Suffix to add to the existing variable names. If NULL, the old variables will be overwritten.

## Details

If there are missing values in the column `value_new`, NAs are inserted as new values and a warning is issued.

The complete work flow when using a lookup table to recode multiple variables in a GADSdat could be: (0) optional: Recode empty strings to NA (necessary, if the look up table is written to excel). (1) create a lookup table with `createLookup`. (2) Save the lookup table to `.xlsx` with `write_xlsx` from `eatAnalysis`. (3) fill out the lookup table via Excel. (4) Import the lookup table back to R via `read_excel` from `readxl`. (5) Apply the final lookup table with `applyLookup`.

See `applyLookup_expandVar` for recoding a single variable into multiple variables.

## Value

Returns a recoded GADSdat.

## Examples

```
## create an example GADSdat
iris2 <- iris
iris2$Species <- as.character(iris2$Species)
gads <- import_DF(iris2)

## create Lookup
lu <- createLookup(gads, recodeVars = "Species")
lu$value_new <- c("plant 1", "plant 2", "plant 3")

## apply lookup table
gads2 <- applyLookup(gads, lookup = lu, suffix = "_r")

## only recode some values
lu2 <- createLookup(gads, recodeVars = "Species")
lu2$value_new <- c("plant 1", "plant 2", NA)
gads3 <- applyLookup(gads, lookup = lu2, suffix = "_r")
```

---

`applyLookup_expandVar` *Recode via lookup table into multiple variables.*

---

## Description

Recode one or multiple variables based on a lookup table created via `createLookup`. In contrast to `applyLookup`, this function allows the creation of multiple resulting variables from a single input variable. All variables in lookup except `variable` and `value` are treated as recode columns.

## Usage

```
applyLookup_expandVar(GADSdat, lookup)
```

**Arguments**

GADSdat	A GADSdat object.
lookup	Lookup table created by <a href="#">createLookup</a> .

**Details**

If a variable contains information that should be split into multiple variables via manual recoding, `applyLookup_expandVar` can be used. If there are missing values in any recode column, NAs are inserted as new values. A warning is issued only for the first column.

The complete work flow when using a lookup table to expand variables in a GADSdat based on manual recoding could be: (1) create a lookup table with [createLookup](#). (2) Save the lookup table to `.xlsx` with `write_xlsx` from `eatAnalysis`. (3) fill out the lookup table via Excel. (4) Import the lookup table back to R via `read_excel` from `readxl`. (5) Apply the final lookup table with `applyLookup_expandVar`.

See [applyLookup](#) for simply recoding variables in a GADSdat.

**Value**

Returns a recoded GADSdat.

**Examples**

```
## create an example GADSdat
example_df <- data.frame(ID = 1:6,
                        citizenship = c("germ", "engl", "germ usa", "china",
                                       "austral morocco", "nothin"),
                        stringsAsFactors = FALSE)
gads <- import_DF(example_df)

## create Lookup
lu <- createLookup(gads, recodeVars = "citizenship", addCol = c("cit_1", "cit_2"))
lu$cit_1 <- c("German", "English", "German", "Chinese", "Australian", NA)
lu$cit_2 <- c(NA, NA, "USA", NA, "Morocco", NA)

## apply lookup table
gads2 <- applyLookup_expandVar(gads, lookup = lu)
```

---

applyNumCheck

*Apply recodes according to a numerical check data.frame.*

---

**Description**

Applies recodes as specified by a `numCheck` data.frame, as created by [createNumCheck](#).

**Usage**

```
applyNumCheck(GADSdat, numCheck)
```

**Arguments**

GADSdat	A GADSdat object.
numCheck	A data.frame as created by <a href="#">createNumCheck</a> .

**Details**

This function is currently under development.

**Value**

A recoded GADSdat.

**Examples**

```
# tbd
```

---

assimilateValLabels *Assimilate value labels.*

---

**Description**

Assimilate all value labels of multiple variables as part of a GADSdat or all\_GADSdat object.

**Usage**

```
assimilateValLabels(GADSdat, varNames, lookup = NULL)
```

**Arguments**

GADSdat	GADSdat object imported via eatGADS.
varNames	Character string of a variable name.
lookup	Look up data.frame.

**Details**

Assimilation can be performed using all existing value labels or a look up table containing at least all existing value labels. Missing codes are reused based on the meta data of the first variable in varNames.

**Value**

Returns the GADSdat object with changed meta data and recoded values.

**Examples**

```
# Example data set
fac1_df <- data.frame(id = 1:3, fac1 = c("Eng", "Aus", "Ger"),
                     fac2 = c("Ger", "Franz", "Ita"),
                     fac3 = c("Kor", "Chi", "Alg"),
                     stringsAsFactors = TRUE)
fac1_gads <- import_DF(fac1_df)

assimilateValLabels(fac1_gads, varNames = paste0("fac", 1:3))
```

---

calculateScale	<i>Calculate a scale.</i>
----------------	---------------------------

---

**Description**

Calculate a scale variable based on multiple items.

**Usage**

```
calculateScale(
  GADSdat,
  items,
  scale,
  maxNA = length(items),
  reportDescr = FALSE
)
```

**Arguments**

GADSdat	A data.frame or GADSdat object.
items	A character vector with all item variable names.
scale	A character vector with the scale name.
maxNA	Maximum number of allowed NA values on the items.
reportDescr	Should descriptive statistics be reported for the calculated scale.

**Details**

Descriptive statistics (including Cronbach's alpha, credit to the psy package) are calculated and printed to the console. The new scale variable is automatically inserted right after the last item in the original GADSdat.

**Value**

Returns a GADSdat containing the newly computed variable.



**Examples**

```
##
items <- paste0("norms_", letters[1:6])
pisa_new <- calculateScale(pisa, items = items, scale = "norms")
```

---

cbind.GADSdat	<i>Bind two GADSdat objects into a single GADSdat object by columns.</i>
---------------	--

---

**Description**

Is a secure way to cbind the data and the meta data of two GADSdat objects. Currently, only limited merging options are supported.

**Usage**

```
## S3 method for class 'GADSdat'
cbind(..., deparse.level = 1)
```

**Arguments**

... Multiple GADSdat objects imported via eatGADS.  
 deparse.level Argument is ignored in this method.

**Details**

If there are duplicate variables (except the variables specified in the by argument), these variables are removed from y. The meta data is joined for the remaining variables via rbind.

**Value**

Returns a GADSdat object.

---

changeMissings	<i>Change missing code.</i>
----------------	-----------------------------

---

**Description**

Change or add missing codes of a variable as part of a GADSdat or all\_GADSdat object.

**Usage**

```
changeMissings(GADSdat, varName, value, missings)
```

**Arguments**

GADSdat	GADSdat object imported via eatGADS.
varName	Character string of a variable name.
value	Numeric values.
missings	Character string of the new missing codes, either "miss" or "valid".

**Details**

Applied to a GADSdat or all\_GADSdat object, this function is a wrapper of [getChangeMeta](#) and [applyChangeMeta](#).

**Value**

Returns the GADSdat object with changed meta data.

**Examples**

```
# Set a specific value to missing
pisa2 <- changeMissings(pisa, varName = "computer_age",
                        value = 5, missings = "miss")

# Set multiple values to missing
pisa3 <- changeMissings(pisa, varName = "computer_age",
                        value = 1:4,
                        missings = c("miss", "miss", "miss", "miss"))

# Set a specific value to not missing
pisa4 <- changeMissings(pisa2, varName = "computer_age",
                        value = 5, missings = "valid")
```

---

changeSPSSformat      *Change SPSS format.*

---

**Description**

Change the SPSS format of a variable as part of a GADSdat or all\_GADSdat object.

**Usage**

```
changeSPSSformat(GADSdat, varName, format)
```

**Arguments**

GADSdat	GADSdat object imported via eatGADS.
varName	Character string of variable names.
format	A single string containing the new SPSS format, for example 'A25' or 'F10'.

**Details**

Applied to a GADSdat or all\_GADSdat object, this function is a wrapper of [getChangeMeta](#) and [applyChangeMeta](#).

**Value**

Returns the GADSdat object with changed meta data..

**Examples**

```
pisa2 <- changeSPSSformat(pisa, varName = "idstud",  
                          format = "F10.0")
```

---

changeValLabels	<i>Change value labels.</i>
-----------------	-----------------------------

---

**Description**

Change or add value labels of a variable as part of a GADSdat or all\_GADSdat object.

**Usage**

```
changeValLabels(GADSdat, varName, value, valLabel)
```

**Arguments**

GADSdat	GADSdat object imported via eatGADS.
varName	Character string of a variable name.
value	Numeric values.
valLabel	Character string of the new value labels.

**Details**

Applied to a GADSdat or all\_GADSdat object, this function is a wrapper of [getChangeMeta](#) and [applyChangeMeta](#).

**Value**

Returns the GADSdat object with changed meta data.

**Examples**

```
# Change existing value labels
pisa2 <- changeValLabels(pisa, varName = "repeated",
                        value = c(1, 2),
                        valLabel = c("no grade repetition", "grade repetition"))

# Add value label to unlabeled value
mtcars_g <- import_DF(mtcars)
mtcars_g2 <- changeValLabels(mtcars_g, varName = "cyl",
                            value = c(4, 6, 8),
                            valLabel = c("four", "six", "eight"))
```

---

changeVarLabels	<i>Change the variable label.</i>
-----------------	-----------------------------------

---

**Description**

Change the variable label of a variable as part of a GADSdat or all\_GADSdat object.

**Usage**

```
changeVarLabels(GADSdat, varName, varLabel)
```

**Arguments**

GADSdat	GADSdat object imported via eatGADS.
varName	Character string of variable names.
varLabel	Character string of the new variable labels.

**Details**

Applied to a GADSdat or all\_GADSdat object, this function is a wrapper of [getChangeMeta](#) and [applyChangeMeta](#).

**Value**

Returns the GADSdat object with changed meta data.

**Examples**

```
# Change one variable label
pisa2 <- changeVarLabels(pisa, varName = "repeated",
                        varLabel = c("Has a grade been repeated?"))
```

---

changeVarNames	<i>Change Variable Names.</i>
----------------	-------------------------------

---

**Description**

Change variable names of a GADSdat or all\_GADSdat object.

**Usage**

```
changeVarNames(GADSdat, oldNames, newNames)
```

**Arguments**

GADSdat	GADSdat object imported via eatGADS.
oldNames	Vector containing the old variable names.
newNames	Vector containing the new variable names, in identical order as oldNames.

**Details**

Applied to a GADSdat or all\_GADSdat object, this function is a wrapper of [getChangeMeta](#) and [applyChangeMeta](#)

**Value**

Returns the GADSdat object with changed variable names.

**Examples**

```
# Change multiple variable name
pisa2 <- changeVarNames(pisa, oldNames = c("idstud", "idschool"),
                        newNames = c("IDstud", "IDSchool"))
```

---

check4SPSS	<i>Check SPSS Compliance of Meta Data</i>
------------	---

---

**Description**

Function to check if variable names and labels, value labels and missing codes comply with SPSS requirements for meta data.

**Usage**

```
check4SPSS(GADSdat)
```

**Arguments**

GADSdat            GADSdat object imported via eatGADS.

**Details**

The function measures the length of variable names ("varNames\_length", maximum of 64 characters) variable labels ("varLabels", maximum of 256 characters), value labels ("valLabels", maximum of 120 characters). Furthermore, missing codes are counted ("missings", maximum of three missing codes for character variables) and special characters are flagged in variable names ("varNames\_special"). Check results are reported back on variable level, with the exception of "valLabels", which is a list with entries per violating variable.

**Value**

Returns a list with the entries "varNames\_special", "varNames\_length", "varLabels", "valLabels" and "missings".

**Examples**

```
# Change example data set (create a violating label)
pisa2 <- changeVarLabels(pisa, varName = "computer_age",
                        varLabel = paste(rep("3", 125), collapse = ""))

check4SPSS(pisa2)
```

---

checkEmptyValLabels    *Check Value Labels*

---

**Description**

Check value labels for (a) value labels with no occurrence in the data (checkEmptyValLabels) and (b) values with no value labels (checkMissingValLabels).

**Usage**

```
checkEmptyValLabels(
  GADSdat,
  vars = namesGADS(GADSdat),
  valueRange = NULL,
  output = c("list", "data.frame")
)

checkMissingValLabels(GADSdat, vars = namesGADS(GADSdat), valueRange = NULL)
```

**Arguments**

GADSdat	A GADSdat object.
vars	Character vector with the variable names to which checkValLabels() should be applied.
valueRange	[optional] Numeric vector of length 2: In which range should numeric values be checked? If specified, only numeric values are returned and strings are omitted.
output	Should the output be structured as a "list" or a "data.frame"?

**Details**

NAs are excluded from this check. Designated missing codes are reported normally.

**Value**

Returns a list of length vars or a data.frame.

**Functions**

- checkEmptyValLabels: check for superfluous value labels
- checkMissingValLabels: check for missing value labels

**Examples**

```
# Check a categorical and a metric variable
checkMissingValLabels(pisa, vars = c("g8g9", "age"))
checkEmptyValLabels(pisa, vars = c("g8g9", "age"))

# Check while defining a specific value range
checkMissingValLabels(pisa, vars = c("g8g9", "age", "idschool"),
  valueRange = c(0, 5))
checkEmptyValLabels(pisa, vars = c("g8g9", "age", "idschool"),
  valueRange = c(0, 5))
```

---

 checkFormat

---

*Check and Adjust SPSS Format*


---

**Description**

Function to check if SPSS format statements are specified correctly in a GADSdat object.

**Usage**

```
checkFormat(GADSdat, type = "SPSS", changeFormat = TRUE)
```

**Arguments**

GADSDat	GADSDat object imported via eatGADS.
type	If type='other', the function nchar will be used to determine character lengths and decimals are not rounded to 16 decimal places. With type='SPSS' additional width for character variables will be added in order to let SPSS read in lengthy characters correctly and .
changeFormat	If changeFormat=TRUE the GADSDat meta data will be updated otherwise only information will be reported.

**Details**

The function compares SPSS format statements "format" and actual character length and decimal places of all variables in a GADSDat object and its meta data information. Mismatches are reported and can be automatically adjusted.

**Value**

Returns a GADSDat object.

**Examples**

```
# Change example meta information (create a value label with incorrect missing code)
pisa2 <- checkFormat(pisa)
```

---

checkMissings

*Check and Adjust Missing Coding*

---

**Description**

Function to check if missings are coded and labeled correctly in a GADSDat object.

**Usage**

```
checkMissings(
  GADSDat,
  missingLabel = "missing",
  addMissingCode = TRUE,
  addMissingLabel = FALSE
)
```



**Arguments**

GADSDat	GADSDat object imported via eatGADS.
missingLabel	Single string indicating how missing labels are commonly named in the value labels.
addMissingCode	If TRUE, missing codes are added according to occurrence of "missingLabel" in "valLabel".
addMissingLabel	If TRUE, "generic missing" is added according to occurrence of "miss" in "missings". As often various value labels for missings are used, this argument should be used with great care.

**Details**

The function compares value labels "valLabels" and missing codes "missings" of a GADSDat object and its meta data information. Mismatches are reported and can be automatically adjusted.

**Value**

Returns a GADSDat object.

**Examples**

```
# Change example data set (create a value label with incorrect missing code)
pisa2 <- changeValLabels(pisa, varName = "computer_age",
                        value = 5, valLabel = "missing: No computer use")

pisa3 <- checkMissings(pisa2)
```

---

checkTrendStructure    *Checks compatibility of two eatGADS data bases.*

---

**Description**

This function checks if both data bases perform identical joins via foreign keys, if they contain the same variable names and if these variables have the same value labels. Results of this comparison are reported on data table level as messages and as an output list.

**Usage**

```
checkTrendStructure(filePath1, filePath2)
```

**Arguments**

filePath1	Path of the first eatGADS .db file.
filePath2	Path of the second eatGADS .db file.

**Details**

An error is thrown if the key structure or the data table structure differs between the two data bases. Differences regarding meta data for missing value labels and for variables labels (and formatting) are ignored.

**Value**

Returns a report list.

---

checkUniqueness	<i>Check uniqueness of a variable.</i>
-----------------	--

---

**Description**

Function to check if a variable is unique for all cases of an identifier variable.

**Usage**

```
checkUniqueness(GADSdat, varName, idVar)
```

**Arguments**

GADSdat	GADSdat object imported via eatGADS.
varName	Single string containing the variable name for which the check should be performed.
idVar	Single string containing the identifier variable name.

**Details**

For example if missing values are multiple imputed and data is stored in a long format, checking the uniqueness of a variable within an identifier can be tricky. This function automates this task.

**Value**

Returns either TRUE if the variable is unique within each value for idVar or a GADSdat object including the not unique cases.

**Examples**

```
## create an example GADSdat
iris2 <- iris
iris2$Species <- as.character(iris2$Species)
gads <- import_DF(iris2, checkVarNames = FALSE)

## check uniqueness
checkUniqueness(gads, varName = "Sepal.Length", idVar = "Species")
```

---

checkUniqueness2	<i>Check uniqueness of a variable.</i>
------------------	--

---

### Description

Function to check if a variable is unique for all cases of an identifier variable. This is a fast and more efficient version of [checkUniqueness](#) which always returns a logical of length one.

### Usage

```
checkUniqueness2(GADSdat, varName, idVar, impVar)
```

### Arguments

GADSdat	GADSdat object imported via eatGADS.
varName	Single string containing the variable name for which the check should be performed.
idVar	Single string containing the name of the identifier variable.
impVar	Single string containing the name of the imputation number.

### Details

For example if missing values are multiple imputed and data is stored in a long format, checking the uniqueness of a variable within an identifier can be tricky. This function automates this task via reshaping the data into wide format and testing equality among the reshaped variables. . Similar functionality (via matrices) is covered by `lme4::isNested`, which is more general and performs similarly.

### Value

Returns a logical of length one.

### Examples

```
## create an example GADSdat
l <- 1000
long_df <- data.table::data.table(id = sort(rep(1:l, 15)),
                                  v1 = sort(rep(1:l, 15)),
                                  imp = rep(1:15, l))

gads <- import_DF(long_df)
## check uniqueness
checkUniqueness2(gads, varName = "v1", idVar = "id", impVar = "imp")
```

---

checkValue	<i>Check for a specific value</i>
------------	-----------------------------------

---

### Description

Function to look for occurrences of a specific value in a GADSdat.

### Usage

```
checkValue(GADSdat, value, vars = namesGADS(GADSdat))
```

### Arguments

GADSdat	GADSdat object imported via eatGADS.
value	Single string indicating how missing labels are commonly named in the value labels.
vars	Character vector with the variable names to which checkValue should be applied.

### Details

The function checks occurrences of a specific value in a set of variables (default: all variables) in the GADSdat and outputs a vector containing the count of occurrences for all variables in which the value occurs. It explicitly supports checking for NA.

### Value

A named integer.

### Examples

```
# for all variables in the data
checkValue(pisa, value = 99)

# only for specific variables in the data
checkValue(pisa, vars = c("idschool", "g8g9"), value = 99)
```

---

checkVarNames	<i>Check names for SQLite conventions.</i>
---------------	--

---

**Description**

Applies variable names changes to GADSdat or all\_GADSdat objects.

**Usage**

```
checkVarNames(GADSdat)
```

**Arguments**

GADSdat            GADSdat or all\_GADSdat object imported via eatGADS.

**Details**

Illegal names in a SQLite data base include SQLite keywords (see [sqlite\\_keywords](#)) and names with a "." in it.

**Value**

Returns the original object with updated variable names.

**Examples**

```
# Change example data set (create an invalid variable name)
pisa2 <- changeVarNames(pisa, oldNames = "computer_age",
                        newNames = "computer.age")

pisa3 <- checkVarNames(pisa2)
```

---

clean_cache	<i>Clean temporary cache.</i>
-------------	-------------------------------

---

**Description**

Deprecated. The cached data base is now cleaned when the R sessions ends automatically.

**Usage**

```
clean_cache(tempPath = tempdir())
```

**Arguments**

tempPath            Local directory in which the data base was temporarily be stored.

**Details**

Cleans the temporary cache, specified by `tempdir()`. This function had to be executed at the end of an R session if `getGADS_fast` or `getTrendGADS` with `fast = TRUE` had been used.

**Value**

Returns nothing.

---

collapseColumns	<i>Collapse two columns of a lookup table.</i>
-----------------	--

---

**Description**

Collapse two columns or format a single column of a lookup table created by `createLookup`.

**Usage**

```
collapseColumns(lookup, recodeVars, prioritize)
```

**Arguments**

lookup	For example a lookup table <code>data.frame</code> as created via <code>createLookup</code> .
recodeVars	Character vector of column names which should be collapsed (currently only up to two variables are supported).
prioritize	Character vector of length 1. Which of the columns in <code>recodeVars</code> should be prioritized, if multiple values are available? If <code>recodeVars</code> is of length 1, this argument can be omitted.

**Details**

If a lookup table is created by `createLookup`, different recoding columns can be specified by the `addCols` argument. This might be the case if two raters suggest recodes or one rater corrects recodes by another rater in a separate column. After the recoding columns have been filled out, `collapseColumns` can be used to either:

(a) Collapse two recoding columns into one recoding column. This might be desirable, if the two columns contain missing values. `prioritize` can be used to specify, which of the two columns should be prioritized if both columns contain valid values.

(b) Format the lookup table for `applyLookup`, if `recodeVars` is a single variable. This simply renames the single variable specified under `recodeVars`.

**Value**

Returns a `data.frame` that can be used for `applyLookup`, with the columns:

variable	Variable names
value	Old values
value_new	New values. Renamed and/or collapsed column.

**Examples**

```
## (a) Collapse two columns
# create example recode data.frame
lookup_raw <- data.frame(variable = c("var1"), value = c("germa", "German", "dscherman"),
  recode1 = c(NA, "English", "German"),
  recode2 = c("German", "German", NA), stringsAsFactors = FALSE)

# collapse columns
lookup <- collapseColumns(lookup_raw, recodeVars = c("recode1", "recode2"), prioritize = "recode2")

## (b) Format one column
# create example recode data.frame
lookup_raw2 <- data.frame(variable = c("var1"), value = c("germa", "German", "dscherman"),
  recode1 = c("German", "German", "German"), stringsAsFactors = FALSE)

# collapse columns
lookup2 <- collapseColumns(lookup_raw2, recodeVars = c("recode1"))
```

collapseMC\_Text

*Recode a multiple choice variable according to a character variable.***Description**

Recode an labeled integer variable (based on an multiple choice item), according to a character variable (e.g. an open answer item).

**Usage**

```
collapseMC_Text(
  GADSdat,
  mc_var,
  text_var,
  mc_code4text,
  var_suffix = "_r",
  label_suffix = "(recoded)"
)
```

**Arguments**

GADSdat	A GADSdat object.
mc_var	The variable name of the multiple choice variable.
text_var	The variable name of the text variable.
mc_code4text	The value label in mc_var that indicates that information from the text variable should be used.
var_suffix	Variable name suffix for the newly created variables. If NULL, variables are overwritten.

`label_suffix` Variable label suffix for the newly created variable (only added in the meta data). If NULL no suffix is added.

### Details

Multiple choice variables can be represented as labeled integer variables in a GADSDat. Multiple choice items with a forced choice frequently contain an open answer category. However, sometimes open answers overlap with the existing categories in the multiple choice item. `collapseMC_Text` allows recoding the multiple choice variable based on the open answer variable.

`mc_code4text` indicates when entries in the `text_var` should be used. Additionally, entries in the `text_var` are also used when there are missings on the `mc_var`. New values for the `mc_var` are added in the meta data, while preserving the initial ordering of the value labels. Newly added value labels are sorted alphabetically.

For more details see the help vignette: `vignette("recoding_forcedChoice", package = "eatGADS")`.

### Value

Returns a GADSDat containing the newly computed variable.

### Examples

```
# Example gads
example_df <- data.frame(ID = 1:5, mc = c("blue", "blue", "green", "other", "other"),
                        open = c(NA, NA, NA, "yellow", "blue"),
                        stringsAsFactors = FALSE)
example_df$mc <- as.factor(example_df$mc)
gads <- import_DF(example_df)

# recode
gads2 <- collapseMC_Text(gads, mc_var = "mc", text_var = "open",
                        mc_code4text = "other")
```

---

`collapseMultiMC_Text` *Recode multiple choice variable with multiple variables.*

---

### Description

Recode multiple variables (representing a single multiple choice item) based on multiple character variables (representing a text field).

### Usage

```
collapseMultiMC_Text(
  GADSDat,
  mc_vars,
  text_vars,
  mc_var_4text,
```



```

var_suffix = "_r",
label_suffix = "(recoded)",
invalid_miss_code = -98,
invalid_miss_label = "Missing: Invalid response",
notext_miss_code = -99,
notext_miss_label = "Missing: By intention"
)

```

## Arguments

GADSdat	A GADSdat object.
mc_vars	A character vector with the variable names of the multiple choice variable. Names of the character vector are the corresponding values that are represented by the individual variables. Creation by <a href="#">matchValues_varLabels</a> is recommended.
text_vars	A character vector with the names of the text variables which should be collapsed.
mc_var_4text	The name of the multiple choice variable that signals that information from the text variable should be used. This variable is recoded according to the final status of the text variables.
var_suffix	Variable suffix for the newly created GADSdat. If an empty character, the existing variables are overwritten.
label_suffix	Suffix added to variable label for the newly created or modified variables in the GADSdat.
invalid_miss_code	Missing code which is given to new character variables if all text entries were recoded into the dichotomous variables.
invalid_miss_label	Value label for invalid_miss_code.
notext_miss_code	Missing code which is given to empty character variables.
notext_miss_label	Value label for notext_miss_code.

## Details

If a multiple choice item can be answered with ticking multiple boxes, multiple variables in the data set are necessary to represent this item. In this case, an additional text field for further answers can also contain multiple values at once. However, some of the answers in the text field might be redundant to the dummy variables. `collapseMultiMC_Text` allows to recode multiple MC items of this kind based on multiple text variables. The recoding can be prepared by expanding the single text variable ([createLookup](#) and [applyLookup\\_expandVar](#)) and by matching the dummy variables to its underlying values stored in variable labels ([matchValues\\_varLabels](#)).

The function recodes the dummy variables according to the character variables. Additionally, the `mc_var_4text` variable is recoded according to the final status of the `text_vars` (exception: if the text variables were originally NA, `mc_var_4text` is left as it was).

Missing values in the character variables can be represented either by NAs or by empty characters. The multiple choice variables specified with `mc_vars` can only contain the values 0, 1 and missing codes. The value 1 must always represent "this category applies". If necessary, use `recodeGADS` for recoding.

For cases for which the `text_vars` contain only values that can be recoded into the `mc_vars`, all new `text_vars` are given specific missing codes (see `invalid_miss_code` and `invalid_miss_label`). All remaining NAs on the character variables are given a specific missing code (`notext_miss_code`).

### Value

Returns a GADSdat containing the newly computed variables.

### Examples

```
# Prepare example data
mt2 <- data.frame(ID = 1:4, mc1 = c(1, 0, 0, 0), mc2 = c(0, 0, 0, 0), mc3 = c(0, 1, 1, 0),
  text1 = c(NA, "Eng", "Aus", "Aus2"), text2 = c(NA, "Franz", NA, "Ger"),
  stringsAsFactors = FALSE)
mt2_gads <- import_DF(mt2)
mt3_gads <- changeVarLabels(mt2_gads, varName = c("mc1", "mc2", "mc3"),
  varLabel = c("Lang: Eng", "Aus spoken", "other"))

## All operations (see also respective help pages of functions for further explanations)
mc_vars <- matchValues_varLabels(mt3_gads, mc_vars = c("mc1", "mc2", "mc3"),
  values = c("Aus", "Eng", "Eng"), label_by_hand = c("other" = "mc3"))

out_gads <- collapseMultiMC_Text(mt3_gads, mc_vars = mc_vars,
  text_vars = c("text1", "text2"), mc_var_4text = "mc3")

out_gads2 <- multiChar2fac(out_gads, vars = c("text1_r", "text2_r"))

final_gads <- remove2NAchar(out_gads2, vars = c("text1_r_r", "text2_r_r"),
  max_num = 1, na_value = -99, na_label = "missing: excessive answers")
```

---

compareGADS

*Compare two GADS.*

---

### Description

Compare multiple variables of two GADSdat or all\_GADSdat objects.

### Usage

```
compareGADS(
  GADSdat_old,
  GADSdat_new,
  varNames,
  output = c("list", "data.frame", "aggregated")
)
```

**Arguments**

GADSdat_old	GADSdat object imported via eatGADS.
GADSdat_new	GADSdat object imported via eatGADS.
varNames	Character string of variable names to be compared.
output	How should the output be structured?

**Details**

Returns "all equal" if the variable is identical across the objects or a data.frame containing a frequency table with the values which have been changed. Especially useful for checks after recoding.

**Value**

Returns either a list with "all equal" and data.frames or a single data.frame.

**Examples**

```
# Recode a GADS
pisa2 <- recodeGADS(pisa, varName = "schtype",
                   oldValues = 3, newValues = 9)
pisa2 <- recodeGADS(pisa2, varName = "language",
                   oldValues = 1, newValues = 15)

# Compare
compareGADS(pisa, pisa2,
            varNames = c("ganztag", "schtype", "language"), output = "list")
compareGADS(pisa, pisa2,
            varNames = c("ganztag", "schtype", "language"), output = "data.frame")
compareGADS(pisa, pisa2,
            varNames = c("ganztag", "schtype", "language"), output = "aggregated")
```

---

composeVar

*Create a composite variable.*

---

**Description**

Create a composite variable out of two variables.

**Usage**

```
composeVar(GADSdat, sourceVars, primarySourceVar, newVar)
```

**Arguments**

GADSdat	GADSdat or all_GADSdat object imported via eatGADS.
sourceVars	Character vector of length two containing the variable names which represent the sources of information.
primarySourceVar	Character vector containing a single variable name. Which of the sourceVars should be preferred?
newVar	Character vector containing the name of the new composite variable.

**Details**

A common use case for creating a composite variable is if there are multiple sources for the same information. For example, a child and the parents are asked about the child's native language. In such cases a composite variable contains information from both variables, meaning that one source is preferred and the other source is used to substitute missing values.

**Value**

The modified GADSdat.

**Examples**

```
# example data
dat <- data.frame(ID = 1:4,
  nat_lang_child = c("Engl", "Ger", "missing", "missing"),
  nat_lang_father = c("Engl", "Engl", "Ger", "missing"),
  stringsAsFactors = TRUE)
gads <- import_DF(dat)
changeMissings(gads, "nat_lang_child", value = 3, missings = "miss")
changeMissings(gads, "nat_lang_father", value = 3, missings = "miss")

# compose variable
composeVar(gads, sourceVars = c("nat_lang_child", "nat_lang_father"),
  primarySourceVar = "nat_lang_child", newVar = "nat_lang_comp")
```

---

createGADS

*Create an eatGADS data base.*

---

**Description**

Creates a relational data base containing hierarchically stored data with meta information (e.g. value and variable labels).

**Usage**

```
createGADS(allList, pkList, fkList, filePath)
```

**Arguments**

allList	An object created via <a href="#">mergeLabels</a> .
pkList	List of primary keys.
fkList	List of foreign keys.
filePath	Path to the db file to write (including name); has to end on '.db'.

**Details**

Uses [createDB](#) from the eatDB package to create a relational data base. For details on how to define keys see the documentation of [createDB](#).

**Value**

Creates a data base in the given path, returns NULL.

**Examples**

```
# see createDB vignette
```

---

createLookup	<i>Extract values for recoding.</i>
--------------	-------------------------------------

---

**Description**

Extract unique values from one or multiple variables of a GADSdat object for recoding (e.g. via an Excel spreadsheet).

**Usage**

```
createLookup(GADSdat, recodeVars, sort_by = NULL, addCols = c("value_new"))
```

**Arguments**

GADSdat	A GADSdat object.
recodeVars	Character vector of variable names which should be recoded.
sort_by	By which column (variable and/or value) should the long format data.frame be sorted? If NULL, no sorting is performed.
addCols	Character vector of additional column names for recoding purposes.

**Details**

If recoding of one or multiple variables is more complex, a lookup table can be created for later application via [applyLookup](#) or [applyLookup\\_expandVar](#). The function allows the extraction of the values of multiple variables and sorting of these unique values via `variable` and/or `values`. If `addCols` are specified the lookup table has to be formatted via [collapseColumns](#), before it can be applied to recode data.

**Value**

Returns a data frame in long format with the following variables:

variable	Variables as specified in recodeVars
value	Unique values of the variables specified in recodeVars
value_new	This is the default for addCols. If different additional column names are supplied, this column is missing.

**Examples**

```
# create example GADS
dat <- data.frame(ID = 1:4, var1 = c(NA, "Eng", "Aus", "Aus2"),
                 var2 = c(NA, "French", "Ger", "Ita"),
                 stringsAsFactors = FALSE)
gads <- import_DF(dat)

# create Lookup table for recoding
lookup <- createLookup(gads, recodeVars = c("var1", "var2"), sort_by = c("value", "variable"))

# create Lookup table for recoding by multiple recoders
lookup2 <- createLookup(gads, recodeVars = c("var1", "var2"), sort_by = c("value", "variable"),
                      addCols = c("value_recoder1", "value_recoder2"))
```

---

createNumCheck                      *Create data.frame for specification of numerical plausibility checks.*

---

**Description**

All numerical variables without value labels in a GADSdat are selected and a data.frame is created, which allows the specification of minima and maxima.

**Usage**

```
createNumCheck(GADSdat)
```

**Arguments**

GADSdat                      A GADSdat object.

**Details**

This function is currently under development.

**Value**

A data.frame with the following variables:

variable	All numerical variables in the GADSdat
varLabel	Corresponding variable labels
min	Minimum value for the specific variable.
max	Maximum value for the specific variable.
value_new	Which value should be inserted if values exceed the specified range?

**Examples**

```
# tbd
```

---

dummies2char	<i>Transform dummy variables to character variables.</i>
--------------	--

---

**Description**

Convert a set of dummy variables into a set of character variables.

**Usage**

```
dummies2char(GADSdat, dummies, dummyValues, charNames)
```

**Arguments**

GADSdat	A GADSdat object.
dummies	A character vector with the names of the dummy variables.
dummyValues	A vector with the values which the dummy variables represent.
charNames	A character vector containing the new variable names.

**Details**

A set of dummy variables is transformed to an equal number of character variables. The character variables are aligned to the left and the remaining character variables are set to NA. For each new variable the missing codes of the respective dummy variable are reused.

**Value**

Returns a GADSdat.

## Examples

```
## create an example GADSdat
dummy_df <- data.frame(d1 = c("eng", "no eng", "eng"),
                      d2 = c("french", "french", "no french"),
                      d3 = c("no ger", "ger", "no ger"),
                      stringsAsFactors = TRUE)
dummy_g <- import_DF(dummy_df)

## transform dummy variables
dummy_g2 <- dummies2char(dummy_g, dummies = c("d1", "d2", "d3"),
                        dummyValues = c("english", "french", "german"),
                        charNames = c("char1", "char2", "char3"))
```

---

eatGADS

*eatGADS: Data management of hierarchical SPSS files via R and SQLite*

---

## Description

The eatGADS package provides various groups of functions: importing data (mainly sav-files), handling and modifying meta data on variable level, creating a fixed form SQLite data base and using the SQLite data base.

## Importing data

SPSS data can be imported via [import\\_spss](#), R data.frames via [import\\_DF](#).

## Creating the GADS

Hierarchical data sets are combined via [mergeLabels](#) and the data base is created via [createGADS](#). For this, the package eatDB is utilized. See also [createDB](#).

## Using the GADS

The content of a data base can be obtained via [namesGADS](#). Data is extracted from the data base via [getGADS](#) for a single GADS and via [getTrendGADS](#) for trend analysis. The resulting object is a GADSdat object. Meta data can be extracted via [extractMeta](#), either from the GADSdat object or directly from the data base. Data can be extracted from the GADSdat object via [extractData](#).



---

equalGADS	<i>Test if Two GADSdat Objects are (Nearly) Equal</i>
-----------	---

---

**Description**

Run tests to check whether two GADSdat objects are (nearly) equal. Variable names, number of rows in the data, meta data and data differences are checked and reported as a list output.

**Usage**

```
equalGADS(
  target,
  current,
  metaExceptions = c("display_width", "labeled"),
  tolerance = sqrt(.Machine$double.eps)
)
```

**Arguments**

target	A GADSdat object.
current	A GADSdat object.
metaExceptions	Should certain meta data columns be excluded from the comparison?
tolerance	A numeric value greater than or equal to 0. Differences smaller than tolerance are not reported. The default value is close to 1.5e-8.

**Value**

Returns a list.

---

export_tibble	<i>Transform a GADSdat to a tibble</i>
---------------	--

---

**Description**

haven's [read\\_spss](#) stores data together with meta data (e.g. value and variable labels) in a tibble with attributes on variable level. This function transforms a GADSdat object to such a tibble.

**Usage**

```
export_tibble(GADSdat)
```

**Arguments**

GADSdat	GADSdat object imported via eatGADS.
---------	--------------------------------------

**Details**

This function is mainly intended for internal use.

**Value**

Returns a tibble.

**Examples**

```
pisa_tbl <- export_tibble(pisa)
```

---

extractData

*Extract Data*

---

**Description**

Extract data.frame from a GADSdat object for analyses in R. Value labels can be selectively applied via defining convertLabels and convertVariables. For extracting meta data see [extractMeta](#).

**Usage**

```
extractData(
  GADSdat,
  convertMiss = TRUE,
  convertLabels = "character",
  convertVariables = NULL,
  dropPartialLabels = TRUE
)
```

**Arguments**

GADSdat	A GADSdat object.
convertMiss	Should values tagged as missing values be recoded to NA?
convertLabels	If "numeric", values remain as numerics. If "factor" or "character", values are recoded to their labels. Corresponding variable type is applied.
convertVariables	Character vector of variables names, which labels should be applied to. All other variables remain as numeric variables in the data. If not specified [default], value labels are applied to all variables for which labels are available. Variable names not in the actual GADS are silently dropped.
dropPartialLabels	Should value labels for partially labeled variables be dropped? If TRUE, the partial labels will be dropped. If FALSE, the variable will be converted to the class specified in convertLabels.

**Details**

A GADSdat object includes actual data (GADSdat\$dat) and the corresponding meta data information (GADSdat\$labels). extractData extracts the data and applies relevant meta data on value level (missing conversion, value labels), so the data can be used for analyses in R. Variable labels are retained as label attributes on column level.

If factor are extracted via convertLabels == "factor", an attempt is made to preserve the underlying integers. If this is not possible, a warning is issued. As SPSS has almost no limitations regarding the underlying values of labeled integers and R's factor format is very strict (no 0, only integers increasing by + 1), this procedure can lead to frequent problems.

**Value**

Returns a data frame.

**Examples**

```
# Extract Data for Analysis
dat <- extractData(pisa)

# convert labeled variables to factors
dat <- extractData(pisa, convertLabels = "factor")

# convert only some variables to factor, all others remain numeric
dat <- extractData(pisa, convertLabels = "factor", convertVariables = c("schtype", "ganztag"))

# convert only some variables to character, all others remain numeric
dat <- extractData(pisa, convertLabels = "factor", convertVariables = c("schtype", "ganztag"))
# schtype is now character
table(dat$schtype)
# schtype remains numeric
table(dat$gender)
```

---

extractDataOld

*Extract Data while merging linking errors.*

---

**Description**

Support for linking error data bases has been removed from eatGADS. extractDataOld provides (for the time being) backwards compatibility, so linking errors can still be merged automatically.

**Usage**

```
extractDataOld(
  GADSdat,
  convertMiss = TRUE,
  convertLabels = "character",
  dropPartialLabels = TRUE,
```

```

    convertVariables = NULL
  )

```

### Arguments

**GADSdat** A GADSdat object.

**convertMiss** Should values coded as missing values be recoded to NA?

**convertLabels** If "numeric", values remain as numerics. If "factor" or "character", values are recoded to their labels. Corresponding variable type is applied.

**dropPartialLabels** Should value labels for partially labeled variables be dropped? If TRUE, the partial labels will be dropped. If FALSE, the variable will be converted to the class specified in `convertLabels`.

**convertVariables** Character vector of variables names, which labels should be applied to. If not specified (default), value labels are applied to all variables for which labels are available. Variable names not in the actual GADS are silently dropped.

### Details

See [extractData](#) for the current functionality.

### Value

Returns a data frame.

---

extractGADSdat	<i>Extract single GADSdat from all_GADSdat</i>
----------------	--

---

### Description

Function to extract a single GADSdat from an all\_GADSdat object.

### Usage

```
extractGADSdat(all_GADSdat, name)
```

### Arguments

**all\_GADSdat** all\_GADSdat object

**name** A character vector with length 1 with the name of the GADSdat

### Details

GADSdat objects can be merged into a single all\_GADSdat object via [mergeLabels](#). This function, performs the reverse action, extracting a single GADSdat object.

**Value**

Returns an GADSdat object.

**Examples**

```
# see createGADS vignette
```

---

extractMeta	<i>Get Meta Data</i>
-------------	----------------------

---

**Description**

Extract meta data (e.g. variable and values labels) from an eatGADS object. This can be a GADSdat, an all\_GADSdat, a labels data.frame, or the path to an existing data base.

**Usage**

```
extractMeta(GADSobject, vars = NULL)
```

**Arguments**

GADSobject	Either a GADSdat object or a path to an existing eatGADS data base.
vars	A character vector containing variable names. If NULL (default), all available meta information is returned.

**Details**

Meta data is stored tidily in all GADSdat objects as a separate long format data frame. This information can be extracted for a single or multiple variables.

**Value**

Returns a long format data frame with meta information.

**Examples**

```
# Extract Meta data from data base
db_path <- system.file("extdata", "pisa.db", package = "eatGADS")
extractMeta(db_path, vars = c("schtype", "sameteach"))

# Extract Meta data from loaded/imported GADS
extractMeta(pisa, vars = c("schtype", "sameteach"))
```

---

extractVars	<i>Extract or remove variables from a GADSdat.</i>
-------------	--

---

### Description

Extract or remove variables and their meta data from a GADSdat object.

### Usage

```
extractVars(GADSdat, vars)
```

```
removeVars(GADSdat, vars)
```

### Arguments

GADSdat            GADSdat object.

vars                A character vector containing the variables names in the GADSdat.

### Details

Both functions simply perform the variable removal or extraction from the underlying `data.frame` in the GADSdat object followed by calling [updateMeta](#).

### Value

Returns a GADSdat object.

### Examples

```
## create an example GADSdat
example_df <- data.frame(ID = 1:4,
  age = c(12, 14, 16, 13),
  citizenship1 = c("German", "English", "Polish", "Chinese"),
  citizenship2 = c(NA, "German", "Chinese", "Polish"),
  stringsAsFactors = TRUE)
gads <- import_DF(example_df)

## remove variables from GADSdat
gads2 <- removeVars(gads, vars = c("citizenship2", "age"))

## extract GADSdat with specific variables
gads3 <- extractVars(gads, vars = c("ID", "citizenship1"))
```

---

fac2dummies	<i>Transform a factor variable to dummy variables.</i>
-------------	--

---

**Description**

Convert a factor variable with n levels to n dummy variables.

**Usage**

```
fac2dummies(GADSdat, var)
```

**Arguments**

GADSdat	A data.frame or GADSdat object.
var	A character vector with the name of the factor variable.

**Details**

Newly created variables are named as the original variable with the suffix "\_a", "\_b" and so on. Variable labels are created by using the original variable label (if available) and adding the value label of the corresponding level. All missing codes are forwarded to all dummy variables.

**Value**

Returns a GADSdat containing the newly computed variables.

**Examples**

```
## create an example GADSdat
suppressMessages(gads <- import_DF(iris))

## transform factor variable
gads2 <- fac2dummies(gads, var = "Species")
```

---

fac2dummies_complex	<i>Transform a complex factor variable to dummy variables.</i>
---------------------	--

---

**Description**

Convert a factor variable with complex factor levels (factor levels contain combinations of other factor levels) to dummy variables. Dummy variables are coded 1 ("yes") and 0 ("no").

**Usage**

```
fac2dummies_complex(GADSdat, var)
```

**Arguments**

GADSdat            A data.frame or GADSdat object.  
var                 A character vector with the name of the factor variable.

**Details**

The basic functionality of this function is analogous to [fac2dummies](#). However, the function expects factor levels to only go to 9. Higher numbers are treated as combinations of factor levels, for example "13" as "1" and "3".

**Value**

Returns a GADSdat containing the newly computed variables.

**Examples**

```
## create an example GADSdat
df_fac <- data.frame(id = 1:6, fac = c("Opt a", "Opt c, Opt b", "Opt c",
"Opt b", "Opt a, Opt b", "Opt a, Opt b, Opt c"), stringsAsFactors = TRUE)
g_fac <- import_DF(df_fac)
g_fac <- recodeGADS(g_fac, varName = "fac", oldValues = c(1, 2, 3, 4, 5, 6),
                    newValues = c(1, 12, 123, 2, 3, 23))

## transform factor variable
fac2dummies_complex(g_fac, "fac")
```

---

fillImputations            *Fill imputed values.*

---

**Description**

Fill imputed values in a imputed GADSdat\_imp object with original, not imputed values from a GADSdat.

**Usage**

```
fillImputations(GADSdat, GADSdat_imp, varName, varName_imp = varName, id, imp)
```

**Arguments**

GADSdat            A GADSdat object.  
GADSdat\_imp        A GADSdat object.  
varName            A character vector of length 1 containing the variable name in GADSdat.  
varName\_imp        A character vector of length 1 containing the variable name in GADSdat\_imp.  
id                  A character vector of length 1 containing the unique identifier column of both GADSdat.  
imp                 A character vector of length 1 containing the imputation number in GADSdat\_imp.



**Details**

This function only fills in missing values in the imputed variable from the not imputed variable. It provides parts of the functionality of `subImputations` but does not check whether values have been mistakenly imputed. However, performance is increased substantially.

**Value**

The modified `GADSdat_imp..`

**Examples**

```
# tbd
```

---

fixEncoding	<i>Remove special characters.</i>
-------------	-----------------------------------

---

**Description**

Remove special characters from a character vector or a `GADSdat` object. Also suitable to fix encoding problems of a character vector or a `GADSdat` object, which was encoded presumably using UTF-8 and imported using ASCII encoding.

**Usage**

```
fixEncoding(x, input = c("other", "ASCII", "BRISE"))
```

**Arguments**

x	A character vector or <code>GADSdat</code> object.
input	Which encoding was used in <code>import_spss</code> .

**Details**

If entries are all upper case, special characters are also transformed to all upper case (e.g., "AE" instead of "Ae").

**Value**

The modified character vector or `GADSdat` object.

**Examples**

```
fixEncoding(c("\U00C4pfel", "\U00C4PFEL", paste0("\U00DC", "ben"), paste0("\U00DC", "BEN")))
```

---

getChangeMeta	<i>Extract table for Meta Data Changes.</i>
---------------	---

---

**Description**

Function to obtain a data frame from a GADSdat object for for changes to meta data on variable or on value level.

**Usage**

```
getChangeMeta(GADSdat, level = "variable")
```

**Arguments**

GADSdat	GADSdat object imported via eatGADS.
level	'variable' or 'value'.

**Details**

Changes on variable level include variable names (varName), variable labels (varLabel), SPSS format ((format)) and display width (display\_width). Changes on value level include values (value), value labels (valLabel) and missing codes (missings).

**Value**

Returns the meta data sheet for all variables including the corresponding change columns.

**Examples**

```
# For changes on variable level
varChangeTable <- getChangeMeta(pisa, level = "variable")

# For changes on value level
valChangeTable <- getChangeMeta(pisa, level = "value")
```

---

getGADS	<i>Get data from GADS data base.</i>
---------	--------------------------------------

---

**Description**

Extracts variables from a GADS data base. Only the specified variables are extracted. Note that this selection determines the format of the data. frame that is extracted.

**Usage**

```
getGADS(vSelect = NULL, filePath)
```

**Arguments**

vSelect            Character vector of variable names.  
 filePath         Path of the existing eatGADS data base file.

**Details**

See [createDB](#) and [dbPull](#) for further explanation of the query and merging processes.

**Value**

Returns a GADSdat object.

**Examples**

```
# Use data base within package
db_path <- system.file("extdata", "pisa.db", package = "eatGADS")
pisa_gads <- getGADS(db_path, vSelect = c("schtype", "sameteach"))
```

---

<code>getGADS_fast</code>	<i>Get data from GADS data base fast from server directory.</i>
---------------------------	---

---

**Description**

Extracts variables from a eatGADS data base. Only the specified variables are extracted. Note that this selection determines the format of the data frame that is extracted. CAREFUL: This function uses a local temporary directory to speed up loading the data base from a server and caches the data base locally for a running R session. The temporary data base is removed automatically when the running R session is terminated.

**Usage**

```
getGADS_fast(vSelect = NULL, filePath, tempPath = tempdir())
```

**Arguments**

vSelect            Character vector of variable names.  
 filePath         Path of the existing eatGADS data base file.  
 tempPath         Local directory in which the data base can temporarily be stored. Using the default is recommended.

**Details**

A random temporary directory is used for caching the data base and is removed, when the R sessions terminates. See [createDB](#) and [dbPull](#) for further explanation of the query and merging processes.

**Value**

Returns a GADSdat object.

---

getTrendGADS	<i>Get data for trend reports.</i>
--------------	------------------------------------

---

### Description

Extracts variables from multiple eatGADS data bases. Data can then be extracted from the GADSdat object via [extractData](#). For extracting meta data from a data base or a GADSdat object see [extractMeta](#). To speed up the data loading, [getGADS\\_fast](#) is used per default.

### Usage

```
getTrendGADS(  
  filePaths,  
  vSelect = NULL,  
  years,  
  fast = TRUE,  
  tempPath = tempdir(),  
  verbose = TRUE  
)
```

### Arguments

filePaths	Character vectors with paths to the eatGADS db files.
vSelect	Variables from all GADS to be selected (as character vector).
years	A numeric vector with identical length as filePaths.
fast	Should <a href="#">getGADS_fast</a> be used for data loading instead of <a href="#">getGADS</a> ? Using the default is heavily recommended.
tempPath	The directory, in which both GADS will be temporarily stored. Using the default is heavily recommended.
verbose	Should the loading process be reported?

### Details

This function extracts data from multiple GADS data bases. All data bases have to be created via [createGADS](#). The data bases are joined via `rbind()` and a variable year is added, corresponding to the argument years. The GADSdat object can then further be used via [extractData](#). See [createDB](#) and [dbPull](#) for further explanation of the querying and merging processes.

### Value

Returns a GADSdat object.

### Examples

```
# See getGADS vignette
```

---

getTrendGADSOld	<i>Get data for trend reports.</i>
-----------------	------------------------------------

---

### Description

Support for linking error data bases has been removed from eatGADS. `getGADSOld` provides (for the time being) backwards compatibility, so linking errors can still be extracted automatically.

### Usage

```
getTrendGADSOld(  
  filePath1,  
  filePath2,  
  lePath = NULL,  
  vSelect = NULL,  
  years,  
  fast = TRUE,  
  tempPath = tempdir()  
)
```

### Arguments

<code>filePath1</code>	Path of the first eatGADS db file.
<code>filePath2</code>	Path of the second eatGADS db file.
<code>lePath</code>	Path of the linking error db file. If NULL, no linking errors are added to the data.
<code>vSelect</code>	Variables from both GADS to be selected (as character vector).
<code>years</code>	A numeric vector of length 2. The first elements corresponds to <code>filePath1</code> , the second element to <code>filePath2</code> .
<code>fast</code>	Should <code>getGADS_fast</code> be used for data loading instead of <code>getGADS</code> ? Using the default is heavily recommended.
<code>tempPath</code>	The directory, in which both GADS will be temporarily stored. Using the default is heavily recommended.

### Details

See `getGADS` for the current functionality.

### Value

Returns a `GADSDat` object.

### Examples

```
# See getGADS vignette
```

---

import_convertLabel	<i>Import an object imported via convertLabel</i>
---------------------	---

---

### Description

Function to import a data.frame object created by convertLabel for use in eatGADS. If possible, importing data via [import\\_spss](#) should always be preferred.

### Usage

```
import_convertLabel(df, checkVarNames = TRUE)
```

### Arguments

df	A data.frame.
checkVarNames	Should variable names be checked for violations of SQLite and R naming rules?

### Details

convertLabel from R package eatAnalysis converts an object imported via read.spss (from the foreign package) to a data.frame with factors and variable labels stored in variable attributes.

### Value

Returns a list with the actual data dat and a data frame with all meta information in long format labels.

---

import_DF	<i>Import R data.frame</i>
-----------	----------------------------

---

### Description

Function to import a data.frame object for use in eatGADS while extracting value labels from factors.

### Usage

```
import_DF(df, checkVarNames = TRUE)
```

### Arguments

df	A data.frame.
checkVarNames	Should variable names be checked for violations of SQLite and R naming rules?

**Details**

Factors are integers with labeled variable levels. `import_DF` extracts these labels and stores them in a separate meta data `data.frame`. See [import\\_spss](#) for detailed information.

**Value**

Returns a list with the actual data `dat` and a data frame with all meta information in long format labels.

**Examples**

```
dat <- import_DF(iris, checkVarNames = FALSE)

# Inspect Meta data
extractMeta(dat)

# Extract Data
dat <- extractData(dat, convertLabels = "character")
```

---

import\_raw

---

*Import R data frame with explicit meta data sheets*


---

**Description**

Function to import a `data.frame` object for use in eatGADS while adding explicit variable and value meta information through separate `data.frames`.

**Usage**

```
import_raw(df, varLabels, valLabels = NULL, checkVarNames = TRUE)
```

**Arguments**

<code>df</code>	A <code>data.frame</code> .
<code>varLabels</code>	A <code>data.frame</code> containing the variable labels. All variables in the data have to have exactly one column in this <code>data.frame</code> .
<code>valLabels</code>	A <code>data.frame</code> containing the value labels. All referenced variables have to appear in the data, but not all variables in the data have to receive value labels. Can be omitted.
<code>checkVarNames</code>	Should variable names be checked for violations of SQLite and R naming rules?

**Details**

The argument `varLabels` has to contain exactly two variables, namely `varName` and `varLabel`. `valLabels` has to contain exactly four variables, namely `varName`, `value`, `valLabel` and `missings`. The column `value` can only contain numerical values. The column `missings` can only contain the values "valid" and "miss". Variables of type factor are not supported in any of the `data.frames`.

**Value**

Returns a list with the actual data `dat` and with all meta information in long format labels.

**Examples**

```
dat <- data.frame(ID = 1:5, grade = c(1, 1, 2, 3, 1))
varLabels <- data.frame(varName = c("ID", "grade"),
                        varLabel = c("Person Identifier", "School grade Math"),
                        stringsAsFactors = FALSE)
valLabels <- data.frame(varName = c("grade", "grade", "grade"),
                        value = c(1, 2, 3),
                        valLabel = c("very good", "good", "sufficient"),
                        missings = c("valid", "valid", "valid"),
                        stringsAsFactors = FALSE)

gads <- import_raw(df = dat, varLabels = varLabels, valLabels = valLabels, checkVarNames = FALSE)

# Inspect Meta data
extractMeta(gads)

# Extract Data
dat <- extractData(gads, convertLabels = "character")
```

---

import\_raw2

---

*Import R data frame with a explicit meta data sheet*


---

**Description**

Function to create a GADSdat object based on a `dat` data.frame and a `labels` data.frame.

**Usage**

```
import_raw2(dat, labels)
```

**Arguments**

`dat`                    A `dat` data.frame containing all actual data.  
`labels`                A `labels` data.frame containing all meta data.

**Details**

A GADSdat is basically a list with two elements: a `dat` and a `labels` data.frame. If these elements are separated, they can be cleanly tied together again by `import_raw2`. The function performs extensive checks on the integrity of the resulting GADSdat object. See [import\\_spss](#) and [import\\_raw](#) for further details.



**Value**

Returns a GADSdat object.

**Examples**

```
dat <- data.frame(ID = 1:5, grade = c(1, 1, 2, 3, 1))
varLabels <- data.frame(varName = c("ID", "grade"),
                        varLabel = c("Person Identifier", "School grade Math"),
                        stringsAsFactors = FALSE)
valLabels <- data.frame(varName = c("grade", "grade", "grade"),
                        value = c(1, 2, 3),
                        valLabel = c("very good", "good", "sufficient"),
                        missings = c("valid", "valid", "valid"),
                        stringsAsFactors = FALSE)

gads <- import_raw(df = dat, varLabels = varLabels, valLabels = valLabels, checkVarNames = FALSE)

# separate the GADSdat object
dat <- gads$dat
labels <- gads$labels

# rejoin it
dat <- import_raw2(dat, labels)
```

---

import\_RDS

*Import RDS file*


---

**Description**

Function to import a data.frame stored as a .RDS file while extracting value labels from factors.

**Usage**

```
import_RDS(filePath, checkVarNames = TRUE)
```

**Arguments**

`filePath` Source file location, ending on .RDS.  
`checkVarNames` Should variable names be checked for violations of SQLite and R naming rules?

**Details**

Factors are integers with labeled variable levels. `import_RDS` extracts these labels and stores them in a separate meta data data.frame. See [import\\_DF](#) for detailed information. This function is a wrapper around [import\\_DF](#).

**Value**

Returns a list with the actual data `dat` and a data frame with all meta information in long format labels.

---

import\_spss

*Import SPSS data*

---

**Description**

Function to import `.sav` files while extracting meta information, e.g. variable and value labels.

**Usage**

```
import_spss(
  filePath,
  checkVarNames = TRUE,
  labeledStrings = c("drop", "keep", "transform"),
  encoding = NULL
)
```

**Arguments**

<code>filePath</code>	Source file location, ending on <code>.sav</code> .
<code>checkVarNames</code>	Should variable names be checked for violations of SQLite and R naming rules?
<code>labeledStrings</code>	Should strings as labeled values be allowed? If <code>"drop"</code> (default), all labeled strings are dropped and NAs occur in the meta data. If <code>"transform"</code> , all underlying values are transformed to numeric. If <code>"keep"</code> , value labels stay untouched. However, the latter possibly corrupts all labeled values.
<code>encoding</code>	The character encoding used for the file. The default, <code>NULL</code> , use the encoding specified in the file, but sometimes this value is incorrect and it is useful to be able to override it.

**Details**

SPSS files (`.sav`) store variable and value labels and assign specific formatting to variables. `import_spss` imports data from SPSS, while storing this meta-information separately in a long format data frame. Value labels and missing labels are used to identify missing values (see [checkMissings](#)). Time and date variables are converted to character.

In some special cases, `.sav` files seem to consist of a mix of different encoding types. In such cases, haven might throw an error if the encoding argument is not specified or UTF-8 is selected as encoding. To circumvent this problem we recommend using `encoding = "ASCII"` and fixing the resulting issues manually. For example, [fixEncoding](#) provides some fixes for encoding issues specific to the German language.

**Value**

Returns a list with the actual data `dat` and a data frame with all meta information in long format labels.

**Examples**

```
# Use spss data from within package
spss_path <- system.file("extdata", "pisa.zsav", package = "eatGADS")
pisa_gads <- import_spss(spss_path)
```

---

`import_stata`*Import Stata data*

---

**Description**

Function to import `.dta` files while extracting meta information, e.g. variable and value labels.

**Usage**

```
import_stata(filePath, checkVarNames = TRUE, labeledStrings = FALSE)
```

**Arguments**

<code>filePath</code>	Source file location, ending on <code>.dta</code> .
<code>checkVarNames</code>	Should variable names be checked for violations of SQLite and R naming rules?
<code>labeledStrings</code>	Should strings as labeled values be allowed? This possibly corrupts all labeled values.

**Details**

Stata files (`.dta`) store variable and value labels and assign specific formatting to variables. `import_stata` imports data from Stata, while storing this meta-information separately in a long format data frame. Time and date variables are converted to character.

**Value**

Returns a list with the actual data `dat` and a data frame with all meta information in long format labels.

---

inspectDifferences     *Inspect differences in a variable.*

---

## Description

Inspect differences between two GADSdat objects in a specific variable.

## Usage

```
inspectDifferences(varName, GADSdat1, GADSdat2, id)
```

## Arguments

varName	A character vector of length 1 containing the variable name.
GADSdat1	A GADSdat object.
GADSdat2	A GADSdat object.
id	A character vector of length 1 containing the unique identifier column of both GADSdat.

## Details

Two GADSdat objects can be compared using [equalGADS](#). If differences in the data are indicated for specific variables, these variables can be further inspected using `inspectDifferences`.

## Value

A list.

## Examples

```
# create a second GADS with different data
pisa2 <- pisa
pisa2$dat$age[400:nrow(pisa$dat)] <- sample(pisa2$dat$age[400:nrow(pisa$dat)])

# inspect via equalGADS()
equalGADS(pisa, pisa2)

# inspect via inspectDifferences()
inspectDifferences("age", GADSdat1 = pisa, GADSdat2 = pisa2, id = "idstud")
```

---

`inspectMetaDifferences`*Inspect differences in a variable.*

---

## Description

Inspect differences between two GADSdat objects in a specific variable.

## Usage

```
inspectMetaDifferences(varName, GADSdat1, GADSdat2)
```

## Arguments

<code>varName</code>	A character vector of length 1 containing the variable name.
<code>GADSdat1</code>	A GADSdat object.
<code>GADSdat2</code>	A GADSdat object.

## Details

Two GADSdat objects can be compared using [equalGADS](#). If differences in the meta data are indicated for specific variables, these variables can be further inspected using `inspectMetaDifferences`.

## Value

A list.

## Examples

```
# create a second GADS with different meta data
pisa2 <- pisa
pisa2 <- changeVarLabels(pisa2, varName = "sameteach", varLabel = "Same math teacher")
pisa2 <- recodeGADS(pisa2, varName = "sameteach", oldValues = c(1, 2), newValues = c(0, 1))

# inspect via equalGADS()
equalGADS(pisa, pisa2)

# inspect via inspectMetaDifferences()
inspectMetaDifferences("sameteach", GADSdat1 = pisa, GADSdat2 = pisa2)
```

---

labelsGADS	<i>Labels from relational eatGADS data base.</i>
------------	--

---

**Description**

Returns the variable and value labels of all variables in the eatGADS data base.

**Usage**

```
labelsGADS(filePath)
```

**Arguments**

filePath            Path of the existing eatGADS data base.

**Details**

Variable, value and missing labels as stored in the original SPSS-files and factors from R files are converted to long format for storage in the data base. labelsGADS returns them as a long format data frame.

**Value**

Returns a long format data frame including variable names, labels, values, value labels and missing labels.

**Examples**

```
# Extract Meta data from data base
db_path <- system.file("extdata", "pisa.db", package = "eatGADS")
metaData <- labelsGADS(db_path)
```

---

matchValues_varLabels	<i>Match regular expressions and variable names.</i>
-----------------------	--

---

**Description**

Using variable labels, matchValues\_varLabels matches a vector of regular expressions to a set of variable names.

**Usage**

```
matchValues_varLabels(GADSdat, mc_vars, values, label_by_hand = character(0))
```

**Arguments**

GADSdat	A GADSdat object.
mc_vars	A vector containing the names of the variables, which should be matched according to their variable labels.
values	A character vector containing the regular expressions for which the varLabel column should be searched.
label_by_hand	Additional value - mc_var pairs. Necessary, if for some mc_vars no value exists.

**Details**

Multiple choice items can be stored as multiple dichotomous variables with the information about the variable stored in the variable labels. The function `collapseMultiMC_Text` can be used to collapse such dichotomous variables and a character variable, but requires a character vector with variables names of the multiple choice variables. `matchValues_varLabels` creates such a vector based on matching regular expressions (`values`) to variable labels.

Note that all variables in `mc_vars` have to be assigned exactly one value (and vice versa). If a variable name is missing in the output, an error will be thrown. In this case, the `label_by_hand` argument should be used to specify the regular expression variable name pair manually.

**Value**

Returns a named character vector. Values of the vector are the variable names in the GADSdat, names of the vector are the regular expressions.

**Examples**

```
# Prepare example data
mt2 <- data.frame(ID = 1:4, mc1 = c(1, 0, 0, 0), mc2 = c(0, 0, 0, 0), mc3 = c(0, 1, 1, 0),
  text1 = c(NA, "Eng", "Aus", "Aus2"), text2 = c(NA, "Franz", NA, NA),
  stringsAsFactors = FALSE)

mt2_gads <- import_DF(mt2)

mt3_gads <- changeVarLabels(mt2_gads, varName = c("mc1", "mc2", "mc3"),
  varLabel = c("Lang: Eng", "Aus spoken", "other"))

out <- matchValues_varLabels(mt3_gads, mc_vars = c("mc1", "mc2", "mc3"),
  values = c("Aus", "Eng", "Eng"),
  label_by_hand = c("other" = "mc3"))
```

---

merge.GADSdat

---

*Merge two GADSdat objects into a single GADSdat object.*


---

**Description**

Is a secure way to merge the data and the meta data of two GADSdat objects. Currently, only limited merging options are supported.

**Usage**

```
## S3 method for class 'GADSdat'
merge(x, y, by, all = TRUE, all.x = all, all.y = all, ...)
```

**Arguments**

x	GADSdat object imported via eatGADS.
y	GADSdat object imported via eatGADS.
by	A character vector.
all	A character vector (either a full join or an inner join).
all.x	See merge.
all.y	See merge.
...	Further arguments are currently not supported but have to be included for R CMD checks.

**Details**

If there are duplicate variables (except the variables specified in the `by` argument), these variables are removed from `y`. The meta data is joined for the remaining variables via `rbind`.

**Value**

Returns a GADSdat object.

---

mergeLabels

*Prepare data and metadata*

---

**Description**

Transform multiple GADSdat objects into a list ready for data base creation.

**Usage**

```
mergeLabels(...)
```

**Arguments**

...	GADSdat objects, as named arguments in the correct merge order.
-----	---

**Details**

The function `createGADS` takes multiple GADSdat objects as input. The function preserves the ordering in which the objects are supplied, which is then used for the merging order in `createGADS`. Additionally, the separate lists of meta information for each GADSdat are merged and a data frame unique identifier is added.



**Value**

Returns an `all_GADSdat` object, which consists of list with a list of all data frames "datList" and a single data frame containing all meta data information "allLabels".

**Examples**

```
# see createGADS vignette
```

---

miss2NA	<i>Recode Missings to NA</i>
---------	------------------------------

---

**Description**

Recode Missings to NA according to missing labels in label data.frame.

**Usage**

```
miss2NA(GADSdat)
```

**Arguments**

GADSdat          A GADSdat object.

**Details**

Missings are imported as their values via `import_spss`. Using the value labels in the labels data.frame, miss2NA recodes these missings codes to NA. This function is mainly intended for internal use.

**Value**

Returns a data.frame with NA instead of missing codes.

---

multiChar2fac	<i>Transform multiple character variables to factors with identical levels.</i>
---------------	---

---

**Description**

Convert multiple character variables to factors, while creating a common set of value labels, which is identical across variables.

**Usage**

```
multiChar2fac(GADSdat, vars, var_suffix = "_r", label_suffix = "(recoded)")
```

**Arguments**

GADSdat	A data.frame or GADSdat object.
vars	A character vector with all variables that should be transformed to factor.
var_suffix	Variable suffix for the newly created GADSdat. If an empty character, the existing variables are overwritten.
label_suffix	Suffix added to variable label for the newly created variable in the GADSdat.

**Details**

If a set of variables has the same possible values, it is desirable that these variables share the same value labels, even if some of the values do not occur on the individual variables. This function allows the transformation of multiple character variables to factors while assimilating the value labels. The SPSS format of the newly created variables is set to F10.0.

If necessary, missing codes can be set after transformation via [checkMissings](#) for setting missing codes depending on value labels for all variables or [changeMissings](#) for setting missing codes for specific values in a specific variable.

**Value**

Returns a GADSdat containing the newly computed variable.

**Examples**

```
## create an example GADSdat
example_df <- data.frame(ID = 1:4,
  citizenship1 = c("German", "English", "missing by design", "Chinese"),
  citizenship2 = c("missing", "German", "missing by design", "Polish"),
  stringsAsFactors = FALSE)
gads <- import_DF(example_df)

## transform multiple strings
gads2 <- multiChar2fac(gads, vars = c("citizenship1", "citizenship2"))

## set values to missings
gads3 <- checkMissings(gads2, missingLabel = "missing")
```

---

namesGADS

*Variables names of a GADS.*


---

**Description**

Variables names of a GADSdat object, a all\_GADSdat object or a eatGADS data base.

**Usage**

```
namesGADS(GADS)
```

**Arguments**

GADS                    A GADSdat object, a all\_GADSdat or the path to an existing eatGADS data base.

**Details**

If the function is applied to a GADSdat object, a character vector with all variable names is returned. If the function is applied to a all\_GADSdat object or to the path of a eatGADS data base, a named list is returned. Each list entry represents a data table in the object.

**Value**

Returns a character vector or a named list of character vectors.

**Examples**

```
# Extract variable names from data base
db_path <- system.file("extdata", "pisa.db", package = "eatGADS")
namesGADS(db_path)

# Extract variable names from loaded/imported GADS
namesGADS(pisa)
```

---

orderLike	<i>Order the variables in a GADSdat.</i>
-----------	--

---

**Description**

Order the variables in a GADSdat according to a character vector. If there are discrepancies between the two sets, a warning is issued.

**Usage**

```
orderLike(GADSdat, newOrder)
```

**Arguments**

GADSdat                A GADSdat object.  
newOrder                A character vector containing the order of variables.

**Details**

The variables in the dat and in the labels section are ordered. Variables not contained in the character vector are moved to the end of the data.

**Value**

Returns a GADSdat object.

---

pisa	<i>PISA Plus Example Data</i>
------	-------------------------------

---

### Description

A small example data set from the German PISA Plus campus files as distributed by the Forschungsdatenzentrum, IQB.

### Usage

```
pisa
```

### Format

A data.frame with 500 rows and 133 variables, including:

**idstud** Person ID variable  
**idschool** School ID variable  
**sctype** School type  
 ...

### Source

Research Data Center at the Institute for Educational Quality Improvement (2020). Programme for International Student Assessment - Plus 2012, 2013 (PISA Plus 2012-2013) - Campus File (Version 1) [Data set]. Berlin: Institute for Educational Quality Improvement. doi: [10.5159/IQB\\_PISA\\_Plus\\_201213\\_CF\\_v1](https://doi.org/10.5159/IQB_PISA_Plus_201213_CF_v1)

---

recode2NA	<i>Recode a value to NA.</i>
-----------	------------------------------

---

### Description

Recode a value in multiple variables in a GADSdat to NA.

### Usage

```
recode2NA(GADSdat, recodeVars = namesGADS(GADSdat), value = "")
```

### Arguments

GADSdat	A GADSdat object.
recodeVars	Character vector of variable names which should be recoded.
value	Which value should be recoded to NA?

## Details

If there are value labels given to the specified value, these are removed. Number of recodes per variable are reported.

If a data set is imported from .sav character variables frequently contain empty strings. Especially if parts of the data are written to .xlsx this can cause problems (e.g. as look up tables from [createLookup](#)), as most function which write to .xlsx convert empty strings to NAs. `recodeString2NA` can be used to recode all empty strings to NA beforehand.

## Value

Returns the recoded GADSdat.

## Examples

```
# create example GADS
dat <- data.frame(ID = 1:4, var1 = c("", "Eng", "Aus", "Aus2"),
                 var2 = c("", "French", "Ger", "Ita"),
                 stringsAsFactors = FALSE)
gads <- import_DF(dat)

# recode empty strings
gads2 <- recode2NA(gads)

# recode numeric value
gads3 <- recode2NA(gads, recodeVars = "ID", value = 1)
```

---

recodeGADS

*Recode a variable.*

---

## Description

Recode a variable as part of a GADSdat or all\_GADSdat object.

## Usage

```
recodeGADS(
  GADSdat,
  varName,
  oldValues,
  newValues,
  existingMeta = c("stop", "value", "value_new", "drop")
)
```

## Arguments

GADSdat	GADSdat object imported via eatGADS.
varName	Name of the variable to be recoded.
oldValues	Vector containing the old values.
newValues	Vector containing the new values (in the respective order as oldValues).
existingMeta	If values are recoded, which meta data should be used (see details)?

## Details

Applied to a GADSdat or all\_GADSdat object, this function is a wrapper of [getChangeMeta](#) and [applyChangeMeta](#). Beyond that, unlabeled variables and values are recoded as well. `oldValues` and `newValues` are matched by ordering in the function call.

If changes are performed on value levels, recoding into existing values can occur. In these cases, `existingMeta` determines how the resulting meta data conflicts are handled, either raising an error if any occur ("stop"), keeping the original meta data for the value ("value") or using the meta data in the `changeTable` or, if incomplete, from the recoded value ("value\_new").

Furthermore, one might recode multiple old values in the same new value. This is currently only possible with `existingMeta = "drop"`, which drops all related meta data on value level.

Missing values (NA) are supported in `oldValues` but not in `newValues`. For recoding values to NA see [recode2NA](#) instead. For recoding character variables, using lookup tables via [createLookup](#) is recommended. For changing value labels see [changeValLabels](#).

## Value

Returns a GADSdat.

## Examples

```
# Example gads
example_df <- data.frame(ID = 1:5, color = c("blue", "blue", "green", "other", "other"),
                        animal = c("dog", "Dog", "cat", "hors", "horse"),
                        age = c(NA, 16, 15, 23, 50),
                        stringsAsFactors = FALSE)
example_df$animal <- as.factor(example_df$animal)
gads <- import_DF(example_df)

# simple recode
gads2 <- recodeGADS(gads, varName = "animal",
                   oldValues = c(3, 4), newValues = c(7, 8))
```

---

recodeString2NA	<i>Recode a string to NA.</i>
-----------------	-------------------------------

---

**Description**

Deprecated, use [recode2NA](#) instead..

**Usage**

```
recodeString2NA(GADSdat, recodeVars = namesGADS(GADSdat), string = "")
```

**Arguments**

GADSdat	A GADSdat object.
recodeVars	Character vector of variable names which should be recoded.
string	Which string should be recoded to NA?

**Value**

Returns the recoded GADSdat.

---

remove2NAchar	<i>Shorten multiple text variables while giving NA codes.</i>
---------------	---

---

**Description**

Shorten text variables from a certain number on while coding overflowing answers as complete missings.

**Usage**

```
remove2NAchar(GADSdat, vars, max_num = 2, na_value, na_label)
```

**Arguments**

GADSdat	A GADSdat object.
vars	A character vector with the names of the text variables.
max_num	Maximum number of text variables. Additional text variables will be removed and NA codes given accordingly.
na_value	Which NA value should be given in cases of too many values on text variables.
na_label	Which value label should be given to the na_value.

**Details**

In some cases, multiple text variables contain the information of one variable (e.g. multiple answers to an open item). If this is a case, sometimes the number text variables displaying this variable should be limited. `remove2NAchar` allows shortening multiple character variables, this means character variables after `max_num` are removed from the `GADSdat`. Cases, which had valid responses on these removed variables are coded as missings (using `na_value` and `na_label`).

**Value**

Returns the modified `GADSdat`.

**Examples**

```
## create an example GADSdat
example_df <- data.frame(ID = 1:4,
  citizenship1 = c("German", "English", "missing by design", "Chinese"),
  citizenship2 = c(NA, "German", "missing by design", "Polish"),
  citizenship3 = c(NA, NA, NA, "German"),
  stringsAsFactors = FALSE)
gads <- import_DF(example_df)

## shorten character variables
gads2 <- remove2NAchar(gads, vars = c("citizenship1", "citizenship2", "citizenship3"),
  na_value = -99, na_label = "missing: too many answers")
```

---

<code>removeValLabels</code>	<i>Remove value labels.</i>
------------------------------	-----------------------------

---

**Description**

Remove value labels of a variable as part of a `GADSdat` or `all_GADSdat` object.

**Usage**

```
removeValLabels(GADSdat, varName, value, valLabel = NULL)
```

**Arguments**

<code>GADSdat</code>	GADSdat object imported via <code>eatGADS</code> .
<code>varName</code>	Character string of a variable name.
<code>value</code>	Numeric values.
<code>valLabel</code>	[optional] Regular expressions in the value labels corresponding to <code>value</code> .

**Details**

If the argument `valLabel` is provided the function checks for `value` and `valLabel` pairs in the meta data that match both arguments.



**Value**

Returns the GADSdat object with changed meta data.

**Examples**

```
# Remove a label based on value
extractMeta(pisa, "schtype")
pisa2 <- removeValLabels(pisa, varName = "schtype", value = 1)
extractMeta(pisa2, "schtype")

# Remove multiple labels based on value
extractMeta(pisa, "schtype")
pisa3 <- removeValLabels(pisa, varName = "schtype", value = 1:3)
extractMeta(pisa3, "schtype")

# Remove multiple labels based on value - valLabel combination
extractMeta(pisa, "schtype")
pisa4 <- removeValLabels(pisa, varName = "schtype",
  value = 1:3, valLabel = c("Gymnasium", "other", "several courses"))
extractMeta(pisa4, "schtype")
```

---

reuseMeta

*Use meta data for a variable from another GADSdat.*


---

**Description**

Transfer meta information from one GADSdat to another.

**Usage**

```
reuseMeta(
  GADSdat,
  varName,
  other_GADSdat,
  other_varName = NULL,
  missingLabels = NULL,
  addValueLabels = FALSE
)
```

**Arguments**

GADSdat	GADSdat object imported via eatGADS.
varName	Name of the variable that should get the new meta data.
other_GADSdat	GADSdat object imported via eatGADS including the desired meta information. Can also be a GADS db or an all_GADSdat object.
other_varName	Name of the variable that should get the new meta data in the other_GADSdat.

- `missingLabels` How should meta data for missing values be treated? If `NULL`, missing values are transferred as all other labels. If `"drop"`, missing labels are dropped (useful for imputed data). If `"leave"`, missing labels remain untouched. If `"only"`, all valid value labels are dropped.
- `addValueLabels` Should only value labels be added and all other meta information retained?

### Details

Transfer of meta information can mean substituting the complete meta information, only adding value labels, adding only `"valid"` or adding only `"miss"` missing labels. See the arguments `missingLabels` and `addValueLabels` for further information.

### Value

Returns the original object with updated meta data.

### Examples

```
# see createGADS vignette
```

---

<code>splitGADS</code>	<i>Split GADSdat into hierarchy levels.</i>
------------------------	---

---

### Description

Split a `GADSdat` into multiple, specified hierarchical levels.

### Usage

```
splitGADS(GADSdat, nameList)
```

### Arguments

- `GADSdat` A `GADSdat` object.
- `nameList` A list of character vectors. The names in the list correspond to the hierarchy levels.

### Details

The function takes a `GADSdat` object and splits it into its desired hierarchical levels (a `all_GADSdat` object). Hierarchy level of a variable is also accessible in the meta data via the column `data_table`. If not all variable names are included in the `nameList`, the missing variables will be dropped.

### Value

Returns an `all_GADSdat` object, which consists of list with a list of all data frames `"datList"` and a single data frame containing all meta data information `"allLabels"`. For more details see also [mergeLabels](#).

**Examples**

```
# see createGADS vignette
```

---

stringAsNumeric	<i>Transform string to numeric.</i>
-----------------	-------------------------------------

---

**Description**

Transform a string variable within a GADSdat or all\_GADSdat object to a numeric variable.

**Usage**

```
stringAsNumeric(GADSdat, varName)
```

**Arguments**

GADSdat	GADSdat object imported via eatGADS.
varName	Character string of a variable name.

**Details**

Applied to a GADSdat or all\_GADSdat object, this function uses [asNumericIfPossible](#) to change the variable class and changes the format column in the meta data.

**Value**

Returns the GADSdat object with with the changed variable.

---

subImputations	<i>Substitute imputed values.</i>
----------------	-----------------------------------

---

**Description**

Substitute imputed values in a imputed GADSdat\_imp object with original, not imputed values from a GADSdat.

**Usage**

```
subImputations(GADSdat, GADSdat_imp, varName, varName_imp = varName, id, imp)
```

**Arguments**

GADSdat	A GADSdat object.
GADSdat_imp	A GADSdat object.
varName	A character vector of length 1 containing the variable name in GADSdat.
varName_imp	A character vector of length 1 containing the variable name in GADSdat_imp.
id	A character vector of length 1 containing the unique identifier column of both GADSdat.
imp	A character vector of length 1 containing the imputation number in GADSdat_imp.

**Details**

There are two cases in which values are substituted: (a) there are missings in varName\_imp, (b) values have been imputed even though there is valid information in varName.

**Value**

The modified GADSdat\_imp..

**Examples**

```
# tbd
```

---

updateMeta	<i>Update meta data.</i>
------------	--------------------------

---

**Description**

Update the meta data of a GADSdat or all\_GADSdat object according to the variables in a new data object.

**Usage**

```
updateMeta(GADSdat, newDat)
```

**Arguments**

GADSdat	GADSdat or all_GADSdat object.
newDat	data.frame or list of data.frames with the modified data. tibbles and data.tables are currently not supported and need to be transformed to data.frames before-hand.

**Details**

If the data of a GADSdat or a all\_GADSdat has changed (supplied via newDat), updateMeta assimilates the corresponding meta data set. If variables have been removed, the corresponding meta data is also removed. If variables have been added, empty meta data is added for these variables. Factors are transformed to numerical and their levels added to the meta data set.

**Value**

Returns the original object with updated meta data (and removes factors from the data).

**Examples**

```
# see createGADS vignette
```

---

write_spss	<i>Write a GADSdat object to a file</i>
------------	---

---

**Description**

Write a GADSdat object, which contains meta information as value and variable labels to an SPSS file (sav) or Stata file (dta). See 'details' for some important limitations.

**Usage**

```
write_spss(GADSdat, filePath)
```

```
write_stata(GADSdat, filePath)
```

**Arguments**

GADSdat	A GADSdat object.
filePath	Path of sav file to write.

**Details**

The provided functionality relies on havens [write\\_sav](#) and [write\\_dta](#) functions.

Currently known limitations for write\_spss are: (a) value labels for long character variables (> A10) are dropped, (b) under specific conditions very long character variables (> A254) are incorrectly displayed as multiple character variables in SPSS. Furthermore, write\_spss currently does not support exporting date or time variables.

Currently known limitations for write\_stata are: (a) Variable format is dropped, (b) missing codes are dropped.

**Value**

Writes file to disc, returns NULL.

## Examples

```
# write to spss
tmp <- tempfile(fileext = ".sav")
write_spss(pisa, tmp)

# write to stata
tmp <- tempfile(fileext = ".dta")
write_stata(pisa, tmp)
```

---

write_spss2	<i>Write a GADSDat object to txt and SPSS syntax</i>
-------------	--

---

## Description

Write a GADSDat object to a text file (txt) and an accompanying SPSS syntax file containing all meta information (e.g. value and variable labels).

## Usage

```
write_spss2(
  GADSDat,
  txtPath,
  spsPath = NULL,
  savPath = NULL,
  dec = ".",
  fileEncoding = "UTF-8",
  chkFormat = TRUE,
  ...
)
```

## Arguments

GADSDat	A GADSDat object.
txtPath	Path of .txt file to write, including file name and ending .txt. No default.
spsPath	Path of .sps file to write, including file name and ending .sps. Default Path is txtPath.
savPath	Path of .sav file to write, including file name and ending .sav. Default Path is spsPath.
dec	Decimal delimiter for your SPSS version. Other values for dec than ", " or "." are not implemented yet.
fileEncoding	Data file encoding for SPSS. Default is "UTF-8".
chkFormat	Whether format checks via checkFormat should be performed.
...	Arguments to pass to checkFormat in particular changeFormat=FALSE if needed.

**Details**

This function is based on eatPreps `writeSpss` function and is currently under development.

**Value**

Writes a `txt` and an `sav` file to disc, returns nothing.

**Examples**

```
# write to spss
tmp_txt <- tempfile(fileext = ".txt")
write_spss2(pisa, txtPath = tmp_txt)
```

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