

Package ‘dataCompareR’

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Title Compare Two Data Frames and Summarise the Difference

Version 0.1.4

Description Easy comparison of two tabular data objects in R. Specifically designed to show differences between two sets of data in a useful way that should make it easier to understand the differences, and if necessary, help you work out how to remedy them. Aims to offer a more useful output than `all.equal()` when your two data sets do not match, but isn't intended to replace `all.equal()` as a way to test for equality.

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BugReports <https://github.com/capitalone/dataCompareR/issues>

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allVarMatchMessage	<i>allVarMatchMessage</i>
--------------------	---------------------------

Description

Returns data about matching

Usage

```
allVarMatchMessage(x)
```

Arguments

x An dataCompareR object

Value

A string containing the required message

checkEmpty

checkEmpty

Description

Checks if a df is actually a single NA, or has no columns

Usage

```
checkEmpty(df)
```

Arguments

df a data frame

Value

None. Stops if empty.

Examples

```
## Not run: checkEmpty(iris)
```

checkForRCompareCol

checkForRcompareCol

Description

checkForRcompareCol

Usage

```
checkForRCompareCol(df1)
```

Arguments

df1 a data frame

Value

None. Stops if error.

Examples

```
## Not run: checkForRcompareCol(iris)
```

checkKeysExist	<i>checkKeysExist</i>
----------------	-----------------------

Description

checkKeysExist

Usage

```
checkKeysExist(df, keys)
```

Arguments

df	a data frame
keys	a list of expected columns

Value

None. Stops if keys are not present as column names in df.

Examples

```
## Not run: checkKeysExist(iris, 'columnName')
```

checkNA	<i>CheckNA</i>
---------	----------------

Description

Checks a data frame is NA - if so, stops

Usage

```
checkNA(df)
```

Arguments

df	A (probable) dataframe
----	------------------------

Value

Nothing. Errors is df is NA

checkUniqueness *Checks that a list of indexes are unique*

Description

Checks that a list of indexes are unique

Usage

```
checkUniqueness(df_indices)
```

Arguments

df_indices A vector of values

Value

Boolean - true if all values in vector are unique, false if not

Examples

```
## Not run: checkUniqueness(c('car', 'van', 'van'))  
## Not run: checkUniqueness(c('car', 'van', 'bus'))
```

cleanColNames *cleanColNames : get colnames, remove leading and trailing whitespace and push to upper case*

Description

cleanColNames : get colnames, remove leading and trailing whitespace and push to upper case

Usage

```
cleanColNames(DF)
```

Arguments

DF Input dataframe

Value

colInfo dataframe containing original and treated column names of DF

coerceData	<i>coerceData</i>
------------	-------------------

Description

coerceData

Usage

```
coerceData(doa, dob)
```

Arguments

doa	Data object A (any object that can be coerced to a data frame)
dob	Data object B (any object that can be coerced to a data frame)

Value

A list of 2 data frames, which is DOA and DOB coerced as data.frames

Examples

```
## Not run: irisMatrix <- as.matrix(iris)
## Not run: coerceData(irisMatrix,iris)
```

coerceFactorsToChar	<i>coerceFactorsToChar: convert all factor type fields to characters</i>
---------------------	--

Description

coerceFactorsToChar: convert all factor type fields to characters

Usage

```
coerceFactorsToChar(DF)
```

Arguments

DF	Input dataframe
----	-----------------

Value

DF with factor fields converted to character type

Examples

```
## Not run: coerceFactorsToChar(iris)
```

collapseClasses *collapseClasses. Collapse the classes of an object to a single string*

Description

collapseClasses. Collapse the classes of an object to a single string

Usage

```
collapseClasses(x)
```

Arguments

x any object

Value

a string listing the classes of x, separated by commas

Examples

```
## Not run: collapseClasses(iris)
## Not run: collapseClasses("hello")
```

colsWithUnequalValues *colsWithUnequalValues: a dataframe summarising a column with unequal values*

Description

colsWithUnequalValues: a dataframe summarising a column with unequal values

Usage

```
colsWithUnequalValues(x, mismatches)
```

Arguments

x the column to be considered
mismatches - a mismatches object from an dataCompareR object

Value

data frame with a summary of the mismatching column

compareData	<i>Compare data. Wrapper for comparison functionality.</i>
-------------	--

Description

Compare data. Wrapper for comparison functionality.

Usage

```
compareData(DFA, DFB, keys = NULL, maxMismatches)
```

Arguments

DFA	dataframe as returned from prepareData
DFB	dataframe as returned from prepareData
keys	vector of chars - names of index variables
maxMismatches	Integer. The max number of mismatches to assess, after which dataCompareR will stop (without producing a dataCompareR object). Designed to improve performance for large datasets.

Value

mismatchObject containing mismatch data for each of the variables in the dataframes

Examples

```
## Not run: compareData(iris, iris)

## Not run: iris2 <- iris
## Not run: iris2[1,1] <- 5.2
## Not run: iris2[2,1] <- 5.2
## Not run: compareData(iris, iris2)

## Not run: compareData(pressure, pressure, keys = 'temperature')
```

compareNames	<i>compareNames : compare the intersect of colInfoA and colInfoB and return boolean of matched columns for each data frame</i>
--------------	--

Description

compareNames : compare the intersect of colInfoA and colInfoB and return boolean of matched columns for each data frame

Usage

```
compareNames(colInfoA, colInfoB)
```

Arguments

colInfoA input data frames with original and treated column names
colInfoB input data frames with original and treated column names

```
createAntiSubset        Create a dataframe of the rows that don't match
```

Description

Create a dataframe of the rows that don't match

Usage

```
createAntiSubset(index_antisubset, original_keys, index_key, df)
```

Arguments

index_antisubset Vector of mismatching indices
original_keys A character array
index_key A character array
df A data frame

Value

A dataframe containing the dropped rows

```
createCleaningInfo        Converts cleaning info into a format consumable by updateCompare-Object.
```

Description

Converts cleaning info into a format consumable by updateCompareObject.

Usage

```
createCleaningInfo(compObj, cleaningInfo)
```

Arguments

compObj dataCompareRobject to be updated
 cleaningInfo list of cleaning information

Value

compObj updated dataCompareRobject

createColMatching *Converts the output of the column matching logic to something consumable by updateCompareObject.*

Description

Converts the output of the column matching logic to something consumable by updateCompareObject.

Usage

```
createColMatching(compObj, colMatchInfo)
```

Arguments

compObj dataCompareRobject instance to be updated
 colMatchInfo List output from the column matching logic

Value

compObj updated with colMatching block

createCompareObject *Generates an empty list of the correct class to store results*

Description

Generates an empty list of the correct class to store results

Usage

```
createCompareObject()
```

Value

A list of class dataCompareRObject

createMeta	<i>Takes the raw info for the meta block of the output and puts it in a format usable by the updateCompareObject function</i>
------------	---

Description

Takes the raw info for the meta block of the output and puts it in a format usable by the updateCompareObject function

Usage

```
createMeta(dataCompareRobject, DFA, DFB, arguments, timestamp, roundDigits)
```

Arguments

dataCompareRobject	Object of class dataCompareRobject
DFA	First data set passed in to the dataCompareR function
DFB	Second data set passed in to the dataCompareR function
arguments	Collection of arguments passed to compare object with labels that match the dataCompareR arg definitions
timestamp	Timestamp
roundDigits	The number of digits to round to, using round

Value

dataCompareRobject

createMismatches	<i>Create mismatch object</i>
------------------	-------------------------------

Description

Create mismatch object

Usage

```
createMismatches(compObj, misObj, keys)
```

Arguments

compObj	RCompareObject, output from processFlow
misObj	MismatchObject, output from compareData (processFlow)
keys	Character vector, the keys matched on, to allow removal of any extra columns introduced by the compare process

Value

The mismatch object

createMismatchObject *Create mismatch object*

Description

Create mismatch object

Usage

```
createMismatchObject(dat_a, dat_b, dat_eq, str_index)
```

Arguments

dat_a	dataframe, output from prepareData
dat_b	dataframe, output from prepareDate
dat_eq	dataframe, output from locateMismatches
str_index,	vector of index variables (could have length 1)

Value

An dataCompareR mismatch object

Examples

```
## Not run: createMismatchObject(dataA, dataB, mism, idx)
```

createReportText	<i>createReportText: prepares text which is used in the summary report Saves R markdown and HTML reports in the area specified by the user. Reports are called RcompareReport.Rmd (.html) Uses knitr package to create tables in the markdown (createReportText function) and HTML report.</i>
------------------	--

Description

createReportText: prepares text which is used in the summary report Saves R markdown and HTML reports in the area specified by the user. Reports are called RcompareReport.Rmd (.html) Uses knitr package to create tables in the markdown (createReportText function) and HTML report.

Usage

```
createReportText(x)
```

Arguments

x input object which summary comparison information

Value

text in R markdown format

Examples

```
## Not run: createReportText(x=MysummaryCompareObject)
```

createRowMatching	<i>function for updating a compare object with information passed to it from the match rows function</i>
-------------------	--

Description

function for updating a compare object with information passed to it from the match rows function

Usage

```
createRowMatching(compObj, x, matchKey)
```

Arguments

compObj dataCompareRobject to be updated

x Object of information with classes related to the relevant section of the data-CompareRobject

matchKey the list of keys based on which the row matching was performed

Value

compObj Updated dataCompareRobject

createTextSummary *createTextSummary: create a text based summary of an dataCompareR object*

Description

createTextSummary: create a text based summary of an dataCompareR object

Usage

```
createTextSummary(x, ...)
```

Arguments

x an dataCompareR object
... Arguments passed on to other functions

Value

cat's lines to the screen (or to be captured) cat(newLine)

currentObjVersion *Place to store and access the current object version.*

Description

Place to store and access the current object version.

Usage

```
currentObjVersion()
```

Value

currentVersion int of the version number

executeCoercions *executeCoercions:*

Description

executeCoercions:

Usage

```
executeCoercions(DFA, DFB, WhitespaceTrim = TRUE)
```

Arguments

DFA	Input dataframe A
DFB	Input dataframe B
WhitespaceTrim	User defined boolean for whether leading/trailing white space is trimmed in strings (TRUE / FALSE)

Value

out list containing 3 data frames DFA, DFB and DataTypes

DFA Dataframe with factor fields converted to character type and white space trimming (if option is selected by the user)

DFB Dataframe with factor fields converted to character type and white space trimming (if option is selected by the user)

DataTypes Dataframe with field types before and after cleaning for both DFA and DFB

Examples

```
## Not run: executeCoercions(DFA=iris,DFB=iris,WhitespaceTrim= TRUE)
```

generateMismatchData *Extract data from a dataCompareR comparison*

Description

Produces a list of two data frames, containing the mismatched rows from the two input tables

Note that this function requires the user to pass in the two data frames used in the initial comparison. If this data does not match that used for the generation of the dataCompareR object the results produced will not be accurate.

Usage

```
generateMismatchData(x, dfA, dfB, ...)
```


Arguments

x	A dataCompareRobject.
dfA	Data frame (or object coercable to a data frame). One of the two data frames used in the initial rCompare call.
dfB	Data frame (or object coercable to a data frame). One of the two data frames used in the initial rCompare call.
...	Unused currently, may be used in future

Value

mismatchData A list containing two objects: mismatched rows in first data object and mismatched rows in second data object

See Also

Other dataCompareR.functions: [print.dataCompareRobject\(\)](#), [rCompare\(\)](#), [saveReport\(\)](#), [summary.dataCompareRobject\(\)](#)

getCoercions	<i>Subsets on the variables that have a coercion.</i>
--------------	---

Description

Subsets on the variables that have a coercion.

Usage

```
getCoercions(typesDf)
```

Arguments

typesDf	Dataframe of type information from the executeCoercion function
---------	---

Value

coercedT Subset version of typesDf where a coercion occurred

getMismatchColNames *Extracts the column names only in one data frame from a table of match information*

Description

Extracts the column names only in one data frame from a table of match information

Usage

```
getMismatchColNames(colMatchInfo, colNameCol, matchFlagCol)
```

Arguments

colMatchInfo Dataframe with column names, match flag
colNameCol Name of the column with the column names
matchFlagCol Name of the column with the match flag

Value

Vector of column names that do not match

is.dataCompareObject *Check object is of class dataCompareObject*

Description

Check object is of class dataCompareObject

Usage

```
is.dataCompareObject(x)
```

Arguments

x An object

Value

A boolean: TRUE if object is class dataCompareObject and FALSE if not

isNotNull	<i>isNotNull: is object not null</i>
-----------	--------------------------------------

Description

isNotNull: is object not null

Usage

```
isNotNull(x)
```

Arguments

x an object

Value

boolean is object null T/F

Examples

```
## Not run: isNotNull(NULL)
## Not run: isNotNull(5)
```

isSingleNA	<i>isSingleNA</i>
------------	-------------------

Description

Boolean function - T if x is a single NA. False otherwise.

Usage

```
isSingleNA(x)
```

Arguments

x literally anything

Value

boolean

listObsNotVerbose *listObsNotVerbose*

Description

Return a summary of mismatching data

Usage

```
listObsNotVerbose(i, x, uniquevarlist, nObs)
```

Arguments

i	The position of the element we want to compare
x	An dataCompareR object
uniquevarlist	A list of the variables in the compare
nObs	How many observations to return

Value

A list of mismatching observations from start/end of mismatches

listObsVerbose *listObsVerbose*

Description

Return all mismatching data

Usage

```
listObsVerbose(i, x)
```

Arguments

i	The position of the element we want to compare
x	An dataCompareR object

Value

A list of mismatching observations

locateMismatches	<i>Checks whether elements in two input data frames are equal.</i>
------------------	--

Description

Checks whether elements in two input data frames are equal.

Usage

```
locateMismatches(DFA, DFB, keys = NULL, maxMismatches = NA)
```

Arguments

DFA	input data frame
DFB	input data frame
keys	character vector of index variables
maxMismatches	Integer. The max number of mismatches to assess, after which dataCompareR will stop (without producing a dataCompareR object). Designed to improve performance for large datasets.

Value

data frame containing keys and boolean logic of match/no match for each element If data types are not equal returns FALSE. Treats NA and NaN as unequal.

makeValidKeys	<i>makeValidKeys</i>
---------------	----------------------

Description

Correct syntactically invalid Keys

Usage

```
makeValidKeys(keys)
```

Arguments

keys	A character vector
------	--------------------

Value

A character vector with syntactically valid names

Examples

```
## Not run: makeValidKeys(c(" hello", "__BAD NAME__"))
```

makeValidNames	<i>makeValidNames</i>
----------------	-----------------------

Description

Correct syntactically invalid names in a data frame

Usage

```
makeValidNames(df)
```

Arguments

df	A data frame
----	--------------

Value

A data frame with syntactically valid names

Examples

```
## Not run: makeValidNames(iris)
```

matchColumns	<i>matchColumns : create subset of DFA and DFB to contain matching column names for both data frames</i>
--------------	--

Description

matchColumns : create subset of DFA and DFB to contain matching column names for both data frames

Usage

```
matchColumns(DFA, DFB)
```

Arguments

DFA	input data frame
DFB	input data frame

Value

matchColOut named list of data frames. subsetA,subsetB contain only columns common to both data frames. colInfoA,colInfoB contain mapping of column names from original to treated and boolean indicator of common columns.

matchMultiIndex	<i>Generate two dataframes that contain the same rows based on a two-column index</i>
-----------------	---

Description

Generate two dataframes that contain the same rows based on a two-column index

Usage

```
matchMultiIndex(df_a, df_b, indices)
```

Arguments

df_a	A dataframe
df_b	A dataframe
indices	A char vector

Value

A list containing the two dataframes, subsetting by shared indices, and a list which itself contains the vectors for the dropped rows

matchNoIndex	<i>Generate two dataframes that contain the same rows based on a two-column index</i>
--------------	---

Description

Generate two dataframes that contain the same rows based on a two-column index

Usage

```
matchNoIndex(df_a, df_b)
```

Arguments

df_a	A dataframe
df_b	A dataframe

Value

A list containing the two dataframes, subsetting to the size of the smaller one, and a list containing vectors of the rows dropped.

matchRows	<i>Generate two dataframes and returns subsets of these dataframes that have shared rows.</i>
-----------	---

Description

Generate two dataframes and returns subsets of these dataframes that have shared rows.

Usage

```
matchRows(df_a, df_b, indices = NA)
```

Arguments

df_a	A dataframe
df_b	A dataframe
indices	The indices to match rows between df_a and df_b. Can be NA, single character, or a vector of characters

Value

A list containing the two dataframes, subsetting by shared indices, and a list which itself contains dataframes for the dropped rows

matchSingleIndex	<i>Generate two dataframes that contain the same rows based on a single index</i>
------------------	---

Description

Generate two dataframes that contain the same rows based on a single index

Usage

```
matchSingleIndex(df_a, df_b, index_key, original_keys)
```

Arguments

df_a	A dataframe
df_b	A dataframe
index_key	A character vector
original_keys	A character vector

Value

A list containing the two dataframes, subsetting by shared indices, and a list which itself contains the vectors for the dropped rows

metaDataInfo	<i>Creates a list of info about the dataframe.</i>
--------------	--

Description

Creates a list of info about the dataframe.

Usage

```
metaDataInfo(name, df)
```

Arguments

name	The variable name of the df from the dataCompareR function call
df	A data frame

Value

dfInfo A list of info about the data frame

mismatchHighStop	<i>mismatchHighStop Checks if we've exceeded threshold of mismatches</i>
------------------	--

Description

mismatchHighStop Checks if we've exceeded threshold of mismatches

Usage

```
mismatchHighStop(trueFalseMatrix, maxMismatches)
```

Arguments

trueFalseMatrix	a matrix of true/false
maxMismatches	number of mismatches at which the routine stops

Value

Nothing. Stops if threshold exceeded

orderColumns	<i>orderColumns: order columns by treated column names</i>
--------------	--

Description

orderColumns: order columns by treated column names

Usage

```
orderColumns(colInfo)
```

Arguments

colInfo	dataframe containing original and treated column names of DF
---------	--

Value

ordered colInfo dataframe containing original and treated column names of DF

outputSectionHeader	<i>outputSectionHeader: creates an outputSectionHeader</i>
---------------------	--

Description

outputSectionHeader: creates an outputSectionHeader

Usage

```
outputSectionHeader(headerName)
```

Arguments

headerName	a header name
------------	---------------

Value

character a character based section headers

prepareData	<i>prepareData Prepares data for comparison in 3 stages. 1. Match columns - filter dataframes to those columns that match and summarise differences 2. Match rows - filter dataframes to those rows that match and summarise differences 3. Coerce data</i>
-------------	---

Description

prepareData Prepares data for comparison in 3 stages. 1. Match columns - filter dataframes to those columns that match and summarise differences 2. Match rows - filter dataframes to those rows that match and summarise differences 3. Coerce data

Usage

```
prepareData(dfA, dfB, keys = NA, trimChars = TRUE)
```

Arguments

dfA	data frame. The first data object. dataCompareR will attempt to coerce all data objects to data frames.
dfB	data frame. The second data object. dataCompareR will attempt to coerce all data objects to data frames.
keys	String. Name of identifier column(s) used to compare dfA and dfB. NA if no identifier (row order will be used instead), a character for a single column name, or a vector of column names to match of multiple columns
trimChars	Boolean. If true, strings and factors have whitespace trimmed before comparison.

Value

dataCompareRObject containing details of the comparison

Examples

```
## Not run: dfA <- iris
## Not run: dfB <- iris
## Not run: keys <- NA
## Not run: prepareData(dfA,dfB,keys, trimChars = TRUE)
```

```
print.dataCompareRobject
```

Printing RCompare Output

Description

Prints a brief report of an dataCompareR object to the screen.

Usage

```
## S3 method for class 'dataCompareRobject'  
print(x, nVars = 5, nObs = 5, verbose = FALSE, ...)
```

Arguments

x	an object of class "dataCompareR", usually a result of a call to rCompare .
nVars	the number of mismatched columns to print and extract rows for
nObs	the number of rows to print from the top and bottom of the mismatched list for each selected column
verbose	logical; if TRUE will print out the full list of columns and rows that do not match
...	Passes additional arguments to print

See Also

Other dataCompareR.functions: [generateMismatchData\(\)](#), [rCompare\(\)](#), [saveReport\(\)](#), [summary.dataCompareRobject](#)

Examples

```
rc1 <- rCompare(iris,iris)  
print(rc1)
```

```
print.summary.dataCompareRobject
```

Printing summaryRCompare Output

Description

Printing summaryRCompare Output

Usage

```
## S3 method for class 'summary.dataCompareRobject'  
print(x, ...)
```

Arguments

- x an object of class "summary.dataCompareRobject", usually a result of a call to [summary.dataCompareRobject](#).
- ... Additional arguments passed on to [createTextSummary](#)

Examples

```
rc1 <- rCompare(iris,iris)
summary(rc1)
```

 processFlow

processFlow Handles the process flow for the whole package

Description

processFlow Handles the process flow for the whole package

Usage

```
processFlow(dfa, dfb, roundDigits, keys, mismatches, trimChars, argsIn)
```

Arguments

- dfa Dataframe. One of the two data frames to be compared
- dfb Dataframe. One of the two data frames to be compared
- roundDigits Integer. If NA, numerics are not rounded before comparison. If /coderoundDigits is specified, numerics are rounded to /coderoundDigits decimal places using [round](#).
- keys The keys used to match rows between dfa and dfb
- mismatches Integer. The max number of mismatches to assess, after which dataCompareR will stop (without producing a dataCompareR object). Designed to improve performance for large datasets.
- trimChars Boolean. Do we trim characters before comparing?
- argsIn The arguments that were passed to the main dataCompareR function

Value

dataCompareRobject containing details of the comparison

rCompare	<i>Compare two data frames</i>
----------	--------------------------------

Description

Compare two data frames (or objects coercible to data frames) and produce a `dataCompareR` object containing details of the matching and mismatching elements of the data. See `vignette("dataCompareR")` for more details.

Usage

```
rCompare(
  dfA,
  dfB,
  keys = NA,
  roundDigits = NA,
  mismatches = NA,
  trimChars = FALSE
)
```

Arguments

<code>dfA</code>	data frame. The first data object. <code>dataCompareR</code> will attempt to coerce all data objects to data frames.
<code>dfB</code>	data frame. The second data object. <code>dataCompareR</code> will attempt to coerce all data objects to data frames.
<code>keys</code>	String. Name of identifier column(s) used to compare <code>dfA</code> and <code>dfB</code> . <code>NA</code> if no identifier (row order will be used instead), a character for a single column name, or a vector of column names to match of multiple columns
<code>roundDigits</code>	Integer. If <code>NA</code> , numerics are not rounded before comparison. If specified, numerics are rounded to the specified number of decimal places using <code>round</code> .
<code>mismatches</code>	Integer. The max number of mismatches to assess, after which <code>dataCompareR</code> will stop (without producing an <code>dataCompareR</code> object). Designed to improve performance for large data sets.
<code>trimChars</code>	Boolean. If true, strings and factors have whitespace trimmed before comparison.

Value

An `dataCompareR` object. An S3 object containing details of the comparison between the two data objects. Can be used with `summary`, `print`, `saveReport` and `generateMismatchData`

See Also

Other `dataCompareR`.functions: `generateMismatchData()`, `print.dataCompareRobject()`, `saveReport()`, `summary.dataCompareRobject()`

Examples

```

iris2 <- iris
iris2 <- iris2[1:130,]
iris2[1,1] <- 5.2
iris2[2,1] <- 5.2
rCompare(iris,iris2,key=NA)
compDetails <- rCompare(iris,iris2,key=NA, trimChars = TRUE)
print(compDetails)
summary(compDetails)

pressure2 <- pressure
pressure2[2,2] <- pressure2[2,2] + 0.01
rCompare(pressure2,pressure2,key='temperature')
rCompare(pressure2,pressure2,key='temperature', mismatches = 10)

```

rcompObjItemLength	<i>rcompObjItemLength: return length of an item, returning 0 if null, and handling the fact that we might have a data frames or a vector</i>
--------------------	--

Description

rcompObjItemLength: return length of an item, returning 0 if null, and handling the fact that we might have a data frames or a vector

Usage

```
rcompObjItemLength(x)
```

Arguments

x an object

Value

length, numeric

rounddf	<i>Round all numeric fields in a data frame</i>
---------	---

Description

Round all numeric fields in a data frame

Usage

```
rounddf(df, roundDigits)
```

Arguments

df	A data frame to round
roundDigits	Number of digits to round to

Value

A rounded data frame

saveReport	<i>Save a report based on a dataCompareR object</i>
------------	---

Description

Saves R markdown and HTML reports in the area specified by the user.

Uses knitr and markdown to create reports. Reports have the extensions .Rmd or .html. By default the table.css style sheet is used for format the html output.

Usage

```
saveReport(
  compareObject,
  reportName,
  reportLocation = ".",
  HTMLReport = TRUE,
  showInViewer = TRUE,
  stylesheet = NA,
  printAll = FALSE,
  ...
)
```

Arguments

compareObject	a dataCompareR object.
reportName	String. The name of the report. Reports will be saved as reportName.Rmd and (optionally) reportName.html in reportLocation
reportLocation	String. Location to save reports specified by the user. The R markdown and (optionally) HTML reports will be saved in this area
HTMLReport	Boolean. Option to output html report.
showInViewer	Boolean. Does the html report open automatically in the viewer?
stylesheet	String. Optional link to customised css stylesheet
printAll	Boolean. If TRUE, all mis-matches in the data are printed to the file. This acts as a shortcut to get all mismatches in the report, compared to passing the number in mismatchCount. When TRUE, overrides the mismatchCount field passed via ellipses
...	Optional arguments which will be passed to summary, for example mismatchCount

See Also

Other dataCompareR.functions: [generateMismatchData\(\)](#), [print.dataCompareRobject\(\)](#), [rCompare\(\)](#), [summary.dataCompareRobject\(\)](#)

Examples

```
## Not run: saveReport(rcObj, reportName = 'testReport')
```

subsetDataColumns	<i>subsetDataColumns : create subset of DFA and DFB to contain matching column names for both data frames</i>
-------------------	---

Description

subsetDataColumns : create subset of DFA and DFB to contain matching column names for both data frames

Usage

```
subsetDataColumns(DFA, DFB, colInfoList)
```

Arguments

DFA	input data frame
DFB	input data frame
colInfoList	named list containing the column mapping data frames and the list of common column names

Value

matchColOut named list of data frames. subsetA,subsetB contain only columns common to both data frames. colInfoA,colInfoB contain mapping of column names from original to treated and boolean indicator of common columns.

```
summary.dataCompareObject
```

Summarizing RCompare Output

Description

Summarizing RCompare Output

Usage

```
## S3 method for class 'dataCompareObject'
summary(object, mismatchCount = 5, ...)
```

Arguments

object	an dataCompareR object, usually a result of a call to rCompare .
mismatchCount	Integer. How many mismatches to include in tables
...	Passes any additional arguments (not used in current version)

Value

The function `summary.dataCompareR` computes and returns a list of summary details from the `dataCompareR` output given in `object` containing

datanameA	name of the first dataframe in the compare call
datanameB	name of the second dataframe in the compare call
nrowA	the number of rows in datanameA
nrowB	the number of rows in datanameB
version	the version of rCompare used to generate the dataCompareR object object
runtime	the date and time the dataCompareR object object was created
rversion	the version of R used
datasetSummary	a data frame containing the meta data information on datanameA and datanameB
ncolCommon	the number of columns of the same name contained in both datanameA and datanameB
ncolInAOnly	the number of columns only in datanameA
ncolInBOnly	the number of columns only in datanameB
ncolID	the number of columns used to match rows in datanameA and datanameB
typeMismatch	a data frame detailing which columns in both datanameA and datanameB have different class types
typeMismatchN	the number of columns with different variable types
nrowCommon	the number of rows with matching ID columns in both datanameA and datanameB
nrowInAOnly	the number of rows with non matching ID columns in datanameA

nrowInBOnly	the number of rows with non matching ID columns in datanameB
nrowSomeUnequal	the number of matched rows where at least one value is unequal
nrowAllEqual	the number of matched rows where all values are equal
ncolsAllEqual	the number of matched columns where all values are equal
ncolsSomeUnequal	the number of matched columns where at least one value is unequal
colsWithUnequalValues	a data frame detailing the mismatches for each matched column
nrowNAmisMatch	the number of matched numeric rows that contain a NA
maxDifference	the maximum difference between numeric columns from all matched columns

See Also

Other dataCompareR.functions: [generateMismatchData\(\)](#), [print.dataCompareObject\(\)](#), [rCompare\(\)](#), [saveReport\(\)](#)

Examples

```
rc1 <- rCompare(iris,iris)
summary(rc1)
```

trimCharVars	<i>trimCharVars: trim white spaces in character variables from an input dataframe</i>
--------------	---

Description

trimCharVars: trim white spaces in character variables from an input dataframe

Usage

```
trimCharVars(DF)
```

Arguments

DF Input dataframe

Value

DF with preceding and trailing white spaces removed from character fields

Examples

```
## Not run: trimCharVars(iris)
```

updateCompareObject *Generic function for updating a compare object with information passed to it, that has methods based on the class of the info argument.*

Description

Generic function for updating a compare object with information passed to it, that has methods based on the class of the info argument.

Usage

```
updateCompareObject(x, compObj)
```

Arguments

x	Object of information with classes related to the relevant section of the data-CompareRobject
compObj	dataCompareRobject to be updated

Value

compObj Updated dataCompareRobject

updateCompareObject.cleaninginfo
Updates cleaning info in the compare object

Description

Updates cleaning info in the compare object

Usage

```
## S3 method for class 'cleaninginfo'
updateCompareObject(x, compObj)
```

Arguments

x	list of type cleaninginfo with data types
compObj	dataCompareRobject to be updated

Value

compObj updated dataCompareRobject

updateCompareObject.colmatching
Adds a colMatching block to the output

Description

Adds a colMatching block to the output

Usage

```
## S3 method for class 'colmatching'  
updateCompareObject(x, compObj)
```

Arguments

x	List of class colmatching with column matching info
compObj	dataCompareRobject instance to be updated

Value

compObj Updated dataCompareRobject

updateCompareObject.matches
Adds a colMatching block to the output

Description

Adds a colMatching block to the output

Usage

```
## S3 method for class 'matches'  
updateCompareObject(x, compObj)
```

Arguments

x	List of class 'matches' with column matching info
compObj	dataCompareRobject instance to be updated

Value

compObj Updated dataCompareRobject

`updateCompareObject.meta`*Takes raw info for meta and adds it to the compare object*

Description

Takes raw info for meta and adds it to the compare object

Usage

```
## S3 method for class 'meta'  
updateCompareObject(x, compObj)
```

Arguments

<code>x</code>	List of class 'meta' with data related to meta
<code>compObj</code>	dataCompareRobject to be appended

Value

`compObj` dataCompareRobject updated with meta block

`updateCompareObject.mismatches`*Adds a colMatching block to the output*

Description

Adds a colMatching block to the output

Usage

```
## S3 method for class 'mismatches'  
updateCompareObject(x, compObj)
```

Arguments

<code>x</code>	List of class 'mismatches' with column matching info
<code>compObj</code>	dataCompareRobject instance to be updated

Value

`compObj` Updated dataCompareRobject

```
updateCompareObject.rowmatching
      Adds a rowMatching block to the output
```

Description

Adds a rowMatching block to the output

Usage

```
## S3 method for class 'rowmatching'
updateCompareObject(x, compObj)
```

Arguments

x	List of class rowMatching with row matching info
compObj	dataCompareRobject instance to be updated

Value

compObj Updated dataCompareRobject

```
validateArguments      validateArguments
```

Description

validateArguments

Usage

```
validateArguments(
  matchKey = NA,
  roundDigits = NA,
  coerceCols = TRUE,
  maxMismatch = NA
)
```

Arguments

matchKey	A character or character vector of column names to match on
roundDigits	Integer. If NA, numerics are not rounded before comparison. If specified, numerics are rounded to the specified number of decimal places using round .
coerceCols	Boolean - do we coerce columns names?
maxMismatch	Cap for number of mismatches

Value

Nothing. Errors if any parameters are invalid.

Examples

```
## Not run: validateArguments('plantName',1E-8,T,1000)
## Not run: validateArguments('colorName',1E-9,F,10)
```

validateData	<i>validateData : routine to validate the input data</i>
--------------	--

Description

validateData : routine to validate the input data

Usage

```
validateData(df1, df2, keys = NA)
```

Arguments

df1	a data frame
df2	a data frame
keys	Keys used

Value

None. Stops if error.

Examples

```
## Not run: validateData(iris,iris)
```

variableDetails	<i>Create variable mismatch details</i>
-----------------	---

Description

Create variable mismatch details

Usage

```
variableDetails(dat)
```


Arguments

dat The mismatch data

Value

mismatch details

variableMismatches *Create variable mismatch table*

Description

Create variable mismatch table

Usage

```
variableMismatches(varname, vals_a, vals_b, vector_eq)
```

Arguments

varname, variable to create mismatch table for
 vals_a, variables from dfA
 vals_b, variables from dfB
 vector_eq, a list of columns which are equal

Value

Mismatch table

warnLargeData *Warn users if the calculation is likely to be slow*

Description

Checks if there are more than 20E6 elements for comparison. If there are, spits out a warning message that the calculation may run slowly

Usage

```
warnLargeData(nrow_dfa, ncol_dfa, nrow_dfb, ncol_dfb)
```

Arguments

nrow_dfa	number of rows in first data frame
ncol_dfa	number of columns in first data frame
nrow_dfb	number of rows in second data frame
ncol_dfb	number of columns in second data frame

Value

Nothing

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