Package 'validate'

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Maintainer Mark van der Loo <mark.vanderloo@gmail.com>

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Title Data Validation Infrastructure

LazyData no

Type Package

LazyLoad yes

Description Declare data validation rules and data quality indicators; confront data with them and analyze or visualize the results. The package supports rules that are per-field, in-record, cross-record or cross-dataset. Rules can be automatically analyzed for rule type and connectivity.

Version 0.2.6

Depends R (>= 3.1.3), methods

URL https://github.com/data-cleaning/validate

BugReports https://github.com/data-cleaning/validate/issues

Imports graphics, settings, yaml

Suggests testthat, knitr, rmarkdown

Enhances lumberjack

VignetteBuilder knitr

Collate 'rule.R' 'sugar.R' 'validate_pkg.R' 'parse.R' 'expressionset.R' 'indicator.R' 'validator.R' 'confrontation.R' 'barplot.R' 'compare.R' 'factory.R' 'functions.R' 'lumberjack.R' 'retailers.R' 'utils.R' 'yaml.R'

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Author Mark van der Loo [cre, aut],
Edwin de Jonge [aut],
Paul Hsieh [ctb]

Repository CRAN

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R topics documented:

+,indicator,indicator-method

Combine two indicator objects

Description

Combine two `indicator` objects by addition. A new `indicator` object is created with default (global) option values. Previously set options are ignored.

Usage

```
## S4 method for signature 'indicator,indicator'
e1 + e2
```

Arguments

e1	a `validator`
e2	a `validator`

Examples

```
indicator(mean(x)) + indicator(x/median(x))
```

+,validator,validator-method

Combine two validator objects

Description

Combine two `validator` objects by addition. A new `validator` object is created with default (global) option values. Previously set options are ignored.

Usage

```
## S4 method for signature 'validator,validator'
e1 + e2
```

Arguments

e1	a `validator`
e2	a `validator`

Note

The `names` of the resulting object are made unique using `make.names`.

See Also

Other validator-methods: plot,validator-method, validator

Examples

```
validator(x>0) + validator(x<=1)
```

---

aggregate,validation-method

Aggregate validation results

Description

Aggregate results of a validation.

Usage

```
## S4 method for signature 'validation'
aggregate(x, by = c("rule", "record"), drop = TRUE,
  ...)
```

Arguments

x	An object of class validation
by	Report on violations per rule (default) or per record?
drop	drop list attribute if the result is list of length 1
...	Arguments to be passed to or from other methods.

Value

By default, a data.frame with the following columns.

npass	Number of items passed
nfail	Number of items failing
nNA	Number of items resulting in NA
rel.pass	Relative number of items passed
rel.fail	Relative number of items failing
rel.NA	Relative number of items resulting in NA

If by='rule' the relative numbers are computed with respect to the number of records for which the rule was evaluated. If by='record' the relative numbers are computed with respect to the number of rules the record was tested agains.

When by='record' and not all validation results have the same dimension structure, a list of data.frames is returned.

See Also

Other validation-methods: all,validation-method, any,validation-method, barplot,validation-method, check_that, compare, confront, plot,validation-method, sort,validation-method, summary, validation-class, values

Examples

```
data(retailers)
retailers$id <- paste0("ret",1:nrow(retailers))
v <- validator(
    staff.costs/staff < 25
  , turnover + other.rev==total.rev)

cf <- confront(retailers,v,key="id")
a <- aggregate(cf,by='record')
head(a)

# or, get a sorted result:
s <- sort(cf, by='record')
head(s)
```

---

all,validation-method *Test if all validations resulted in TRUE*

Description

Test if all validations resulted in TRUE

Usage

```
## S4 method for signature 'validation'
all(x, ..., na.rm = FALSE)
```

Arguments

x	validation object (see confront).
...	ignored
na.rm	[logical] If TRUE, NA values are removed before the result is computed.

See Also

Other validation-methods: aggregate,validation-method, any,validation-method, barplot,validation-method, check_that, compare, confront, plot,validation-method, sort,validation-method, summary, validation-class, values

Examples

```
val <- check_that(women, height>60, weight>0)
all(val)
```

`any,validation-method` *Test if any validation resulted in TRUE*

Description

Test if any validation resulted in TRUE

Usage

```
## S4 method for signature 'validation'
any(x, ..., na.rm = FALSE)
```

Arguments

`x`	`validation` object (see `confront`).
`...`	ignored
`na.rm`	[`logical`] If `TRUE`, `NA` values are removed before the result is computed.

See Also

Other validation-methods: `aggregate,validation-method`, `all,validation-method`, `barplot,validation-method`, `check_that`, `compare`, `confront`, `plot,validation-method`, `sort,validation-method`, `summary`, `validation-class`, `values`

Examples

```
val <- check_that(women, height>60, weight>0)
any(val)
```

`as.data.frame,cellComparison-method`
Translate cellComparison objects to data frame

Description

Versions of a data set can be cellwise compared using `cells`. The result is a `cellComparison` object, which can usefully be translated into a data frame.

Usage

```
## S4 method for signature 'cellComparison'
as.data.frame(x, row.names = NULL,
  optional = FALSE, ...)
```

Arguments

x	Object to coerce
row.names	ignored
optional	ignored
...	arguments passed to other methods

Value

A data frame with the following columns.

- status: Row names of the cellComparison object.
- version: Column names of the cellComparison object.
- count: Contents of the cellComparison object.

See Also

Other comparing: as.data.frame,validatorComparison-method, barplot,cellComparison-method, barplot,validatorComparison-method, cells, compare, match_cells, plot,cellComparison-method, plot,validatorComparison-method

Examples

```
data(retailers)

# start with raw data
step0 <- retailers

# impute turnovers
step1 <- step0
step1$turnover[is.na(step1$turnover)] <- mean(step1$turnover,na.rm=TRUE)

# flip sign of negative revenues
step2 <- step1
step2$other.rev <- abs(step2$other.rev)


# create an overview of differences, comparing to the previous step
cells(raw = step0, imputed = step1, flipped = step2, compare="sequential")

# create an overview of differences compared to raw data
out <- cells(raw = step0, imputed = step1, flipped = step2)
out
```

```
# Graphical overview of the changes
plot(out)
barplot(out)

# transform data to data.frame (easy for use with ggplot)
as.data.frame(out)
```

`as.data.frame,confrontation-method`

Coerce a confrontation object to data frame

Description

Results of confronting data with validation rules or indicators are created by a `confront`ation. The result is an object (inheriting from) `confrontation`.

Usage

```
## S4 method for signature 'confrontation'
as.data.frame(x, row.names = NULL,
  optional = FALSE, ...)
```

Arguments

`x`	Object to coerce
`row.names`	ignored
`optional`	ignored
`...`	arguments passed to other methods

Value

A `data.frame` with columns

- `key` Where relevant, and only if `key` was specified in the call to `confront`
- `name` Name of the rule
- `value` Value after evaluation
- `expression` evaluated expression

See Also

Other confrontation-methods: `[,expressionset-method`, `confrontation-class`, `confront`, `errors`, `length,expressionset-method`, `values`

Examples

```
cf <- check_that(women, height > 0, sd(weight) > 0)
as.data.frame(cf)

# add id-column
women$id <- letters[1:15]
i <- indicator(mw = mean(weight), ratio = weight/height)
as.data.frame(confront(women, i, key="id"))
```

`as.data.frame,expressionset-method`

Translate an expressionset to data.frame

Description

Expressions are deparsed and combined in a `data.frame` with (some of) their metadata. Observe that some information may be lost (e.g. options local to the object).

Usage

```
## S4 method for signature 'expressionset'
as.data.frame(x, expand_assignments = TRUE, ...)
```

Arguments

`x`	Object to coerce
`expand_assignments`	Toggle substitution of ':=' assignments.
`...`	arguments passed to other methods

Value

A `data.frame` with elements `rule`, `name`, `label`, `origin`, `description`, and `created`.

See Also

Other expressionset-methods: `as.data.frame`, `created`, `description`, `label`, `meta`, `names<-,rule,character-method`, `origin`, `plot,validator-method`, `summary`, `variables`, `voptions`

`as.data.frame,validatorComparison-method` *Translate a validatorComparison object to data frame*

Description

The performance of versions of a data set with regard to rule-based quality requirements can be compared using using `compare`. The result is a `validatorComparison` object, which can usefully be translated into a data frame.

Usage

```
## S4 method for signature 'validatorComparison'
as.data.frame(x, row.names = NULL,
  optional = FALSE, ...)
```

Arguments

`x`	Object to coerce
`row.names`	ignored
`optional`	ignored
`...`	arguments passed to other methods

Value

A data frame with the following columns.

- `status`: Row names of the `validatorComparison` object.
- `version`: Column names of the `validatorComparison` object.
- `count`: Contents of the `validatorComparison` object.

See Also

Other comparing: `as.data.frame,cellComparison-method`, `barplot,cellComparison-method`, `barplot,validatorComparison-method`, `cells`, `compare`, `match_cells`, `plot,cellComparison-method`, `plot,validatorComparison-method`

Examples

```
data(retailers)

rules <- validator(turnover >=0, staff>=0, other.rev>=0)

# start with raw data
step0 <- retailers

# impute turnovers
```

```
step1 <- step0
step1$turnover[is.na(step1$turnover)] <- mean(step1$turnover,na.rm=TRUE)

# flip sign of negative revenues
step2 <- step1
step2$other.rev <- abs(step2$other.rev)

# create an overview of differences, comparing to the previous step
compare(rules, raw = step0, imputed = step1, flipped = step2, how="sequential")

# create an overview of differences compared to raw data
out <- compare(rules, raw = step0, imputed = step1, flipped = step2)
out

# graphical overview
plot(out)
barplot(out)

# transform data to data.frame (easy for use with ggplot)
as.data.frame(out)
```

`barplot,cellComparison-method`

Barplot of cellComparison object

Description

Versions of a data set can be compared cell by cell using `cells`. The result is a `cellComparison` object. This method creates a stacked bar plot of the results. See also `plot,cellComparison-method` for a line chart.

Usage

```
## S4 method for signature 'cellComparison'
barplot(height, las = 1, cex.axis = 0.8,
  cex.legend = cex.axis, wrap = TRUE, ...)
```

Arguments

`height`	object of class `cellComparison`
`las`	[`numeric`] in `{0,1,2,3}` determining axis label rotation
`cex.axis`	[`numeric`] Magnification with respect to the current setting of `cex` for axis annotation.
`cex.legend`	[`numeric`] Magnification with respect to the current setting of `cex` for legend annotation and title.

wrap	[logical] Toggle wrapping of x-axis labels when their width exceeds the width of the column.
...	Graphical parameters passed to barplot.default.

Note

Before plotting, underscores (_) and dots (.) in x-axis labels are replaced with spaces.

See Also

Other comparing: as.data.frame,cellComparison-method, as.data.frame,validatorComparison-method, barplot,validatorComparison-method, cells, compare, match_cells, plot,cellComparison-method, plot,validatorComparison-method

---

barplot,validation-method

Plot number of violations

Description

Plot number of violations

Usage

```
## S4 method for signature 'validation'
barplot(height, ..., order_by = c("fails", "passes",
  "nNA"), stack_by = c("fails", "passes", "nNA"), topn = Inf,
  add_legend = TRUE, add_exprs = TRUE, colors = c(fails = "#FB9A99",
  passes = "#B2DF8A", nNA = "#FDBF6F"))
```

Arguments

height	an R object defining height of bars (here, a validation object)
...	parameters to be passed to barplot but not height, horiz, border,las, and las.
order_by	(single character) order bars decreasingly from top to bottom by the number of fails, passes or NA's.
stack_by	(3-vector of characters) Stacking order for bar chart (left to right)
topn	If specified, plot only the top n most violated calls
add_legend	Display legend?
add_exprs	Display rules?
colors	Bar colors for validations yielding NA or a violation

Value

A list, containing the bar locations as in barplot

Credits

The default colors were generated with the RColorBrewer package of Erich Neuwirth.

See Also

Other validation-methods: aggregate,validation-method, all,validation-method, any,validation-method, check_that, compare, confront, plot,validation-method, sort,validation-method, summary, validation-class, values

Examples

```
data(retailers)
cf <- check_that(retailers
    , staff.costs < total.costs
    , turnover + other.rev == total.rev
    , other.rev > 0
    , total.rev > 0)
barplot(cf)
```

---

barplot,validatorComparison-method

Barplot of validatorComparison object

Description

The performance of versions of a data set with regard to rule-based quality requirements can be compared using using compare. The result is a validatorComparison object. This method creates a stacked bar plot of the results. See also plot,validatorComparison-method for a line chart.

Usage

```
## S4 method for signature 'validatorComparison'
barplot(height, las = 1, cex.axis = 0.8,
  cex.legend = cex.axis, wrap = TRUE, ...)
```

Arguments

height	object of class validatorComparison
las	[numeric] in {0,1,2,3} determining axis label rotation
cex.axis	[numeric] Magnification with respect to the current setting of cex for axis annotation.
cex.legend	[numeric] Magnification with respect to the current setting of cex for legend annotation and title.
wrap	[logical] Toggle wrapping of x-axis labels when their width exceeds the width of the column.
...	Graphical parameters passed to barplot.default.

Note

Before plotting, underscores (_) and dots (.) in x-axis labels are replaced with spaces.

See Also

Other comparing: as.data.frame,cellComparison-method, as.data.frame,validatorComparison-method, barplot,cellComparison-method, cells, compare, match_cells, plot,cellComparison-method, plot,validatorComparison-method

Examples

```
data(retailers)

rules <- validator(turnover >=0, staff>=0, other.rev>=0)

# start with raw data
step0 <- retailers

# impute turnovers
step1 <- step0
step1$turnover[is.na(step1$turnover)] <- mean(step1$turnover,na.rm=TRUE)

# flip sign of negative revenues
step2 <- step1
step2$other.rev <- abs(step2$other.rev)

# create an overview of differences, comparing to the previous step
compare(rules, raw = step0, imputed = step1, flipped = step2, how="sequential")

# create an overview of differences compared to raw data
out <- compare(rules, raw = step0, imputed = step1, flipped = step2)
out

# graphical overview
plot(out)
barplot(out)

# transform data to data.frame (easy for use with ggplot)
as.data.frame(out)
```

---

cells *Cell counts and differences for a series of datasets*

Description

Cell counts and differences for a series of datasets

Usage

```
cells(..., .list = NULL, compare = c("to_first", "sequential"))
```

Arguments

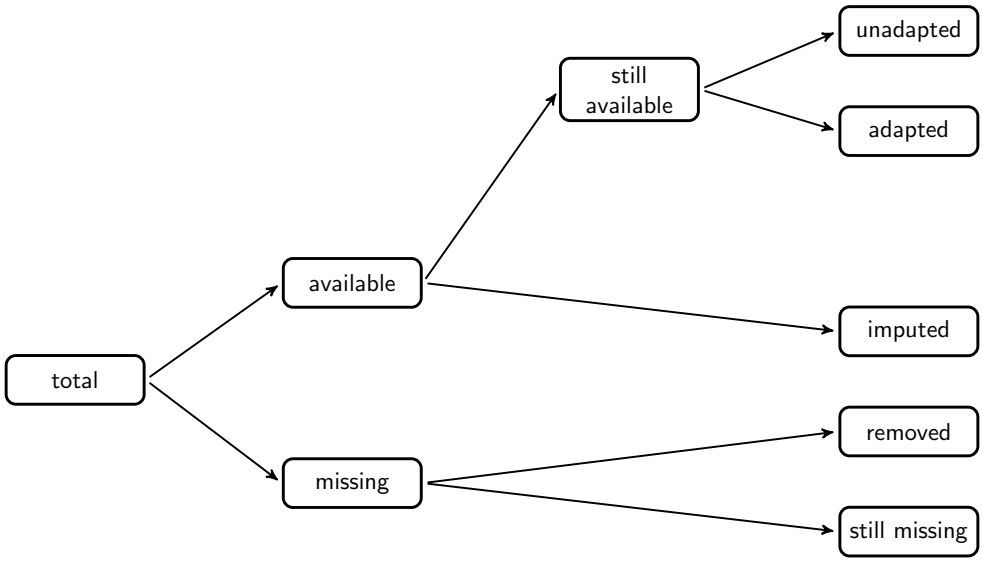
`...`	For `cells`: data frames, comma separated. Names will become column names in the output. For `plot` or `barplot`: graphical parameters (see `par`).
`.list`	A `list` of data frames; will be concatenated with objects in `...`
`compare`	How to compare the datasets.

Value

An object of class `cellComparison`, which is really an array with a few extra attributes. It counts the total number of cells, the number of missings, the number of altered values and changes therein as compared to the reference defined in `how`.

Comparing datasets cell by cell

When comparing the contents of two data sets, the total number of cells in the current data set can be partitioned as in the following figure.



This function computes the partition for two or more datasets, comparing the current set to the first (default) or to the previous (by setting `compare='sequential'`).

Details

This function assumes that the datasets have the same dimensions and that both rows and columns are ordered similarly.

References

The figure is reproduced from MPJ van der Loo and E. De Jonge (2018) *Statistical Data Cleaning with applications in R* (John Wiley & Sons).

See Also

Other comparing: as.data.frame,cellComparison-method, as.data.frame,validatorComparison-method, barplot,cellComparison-method, barplot,validatorComparison-method, compare, match_cells, plot,cellComparison-method, plot,validatorComparison-method

Examples

```
data(retailers)

# start with raw data
step0 <- retailers

# impute turnovers
step1 <- step0
step1$turnover[is.na(step1$turnover)] <- mean(step1$turnover,na.rm=TRUE)

# flip sign of negative revenues
step2 <- step1
step2$other.rev <- abs(step2$other.rev)


# create an overview of differences, comparing to the previous step
cells(raw = step0, imputed = step1, flipped = step2, compare="sequential")

# create an overview of differences compared to raw data
out <- cells(raw = step0, imputed = step1, flipped = step2)
out

# Graphical overview of the changes
plot(out)
barplot(out)

# transform data to data.frame (easy for use with ggplot)
as.data.frame(out)
```

---

check_that *Simple data validation interface*

Description

Simple data validation interface

Usage

```
check_that(dat, ...)
```

Arguments

dat	an R object carrying data
...	a comma-separated set of validating expressions.

Value

An object of class validation

Details

Creates an object of class validator and confronts it with the data. This function is easy to use in combination with the **magrittr** pipe operator.

See Also

Other validation-methods: aggregate,validation-method, all,validation-method, any,validation-method, barplot,validation-method, compare, confront, plot,validation-method, sort,validation-method, summary, validation-class, values

Examples

```
cf <- check_that(women, height>0, height/weight < 0.5)
cf
summary(cf)
barplot(cf)


## Not run:
# this works only after loading the 'magrittr' package
women %>%
  check_that(height>0, height/weight < 0.5) %>%
  summary()

## End(Not run)
```

---

compare *Compare similar data sets*

Description

Compare versions of a data set by comparing their performance against a set of rules or other quality indicators. This function takes two or more data sets and compares the perfomance of data set $2, 3, \ldots$ against that of the first data set (default) or to the previous one (by setting how='sequential').

Usage

```
compare(x, ...)

## S4 method for signature 'validator'
compare(x, ..., .list = list(), how = c("to_first",
  "sequential"))

## S4 method for signature 'indicator'
compare(x, ..., .list = NULL)
```

Arguments

x	An R object
...	data frames, comma separated. Names become column names in the output.
.list	Optional list of data sets, will be concatenated with ....
how	how to compare

Value

For validator: An array where each column represents one dataset. The rows count the following attributes:

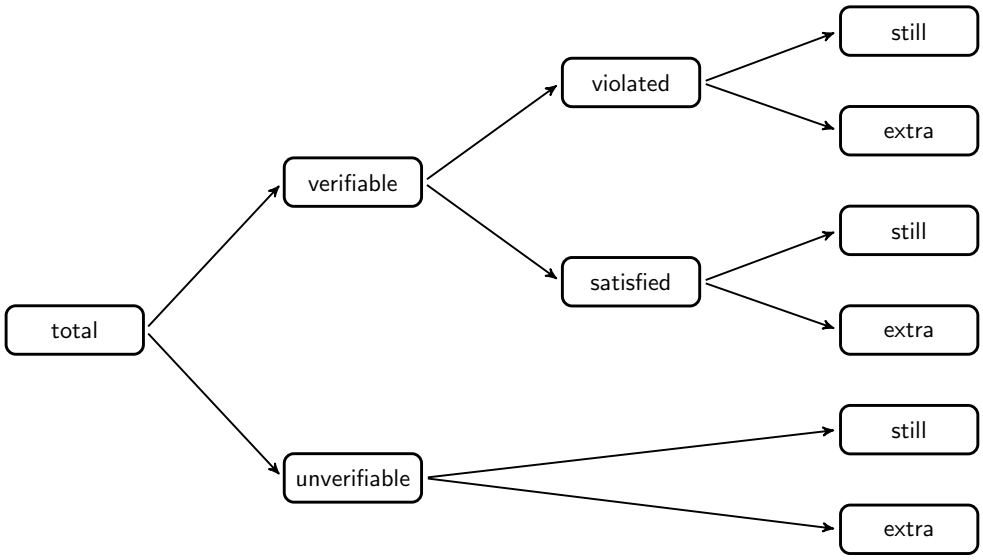
- Number of validations performed
- Number of validations that evaluate to NA (unverifiable)
- Number of validations that evaluate to a logical (verifiable)
- Number of validations that evaluate to TRUE
- Number of validations that evaluate to FALSE
- Number of extra validations that evaluate to NA (new unverifiable)
- Number of validations that still evaluate to NA (still unverifialble)
- Number of validations that still evaluate to TRUE
- Number of extra validations that evaluate to TRUE
- Number of validations that still evaluate to FALSE
- Number of extra validations that evaluate to FALSE

For indicator: A list with the following components:

- numeric: An array collecting results of scalar indicator (e.g. mean(x)).
- nonnumeric: An array collecting results of nonnumeric scalar indicators (e.g. names(which.max(table(x))))
- array: A list of arrays, collecting results of vector-indicators (e.g. x/mean(x))

Comparing datasets by performance against validator objects

Suppose we have a current and a previous version of a data set. Both can be inspected by `confront`ing them with a rule set. The status changes in rule violations can be partitioned as shown in the following figure.



This function computes the partition for two or more datasets, comparing the current set to the first (default) or to the previous (by setting `compare='sequential'`).

References

The figure is reproduced from MPJ van der Loo and E. De Jonge (2018) *Statistical Data Cleaning with applications in R* (John Wiley & Sons).

See Also

Other validation-methods: `aggregate,validation-method`, `all,validation-method`, `any,validation-method`, `barplot,validation-method`, `check_that`, `confront`, `plot,validation-method`, `sort,validation-method`, `summary`, `validation-class`, `values`

Other comparing: `as.data.frame,cellComparison-method`, `as.data.frame,validatorComparison-method`, `barplot,cellComparison-method`, `barplot,validatorComparison-method`, `cells`, `match_cells`, `plot,cellComparison-method`, `plot,validatorComparison-method`

Examples

```
data(retailers)

rules <- validator(turnover >=0, staff>=0, other.rev>=0)

# start with raw data
step0 <- retailers

# impute turnovers
```

```
step1 <- step0
step1$turnover[is.na(step1$turnover)] <- mean(step1$turnover,na.rm=TRUE)

# flip sign of negative revenues
step2 <- step1
step2$other.rev <- abs(step2$other.rev)

# create an overview of differences, comparing to the previous step
compare(rules, raw = step0, imputed = step1, flipped = step2, how="sequential")

# create an overview of differences compared to raw data
out <- compare(rules, raw = step0, imputed = step1, flipped = step2)
out

# graphical overview
plot(out)
barplot(out)

# transform data to data.frame (easy for use with ggplot)
as.data.frame(out)
```

`confront` *Confront data with a (set of) expressionset(s)*

Description

An expressionset is a general class storing rich expressions (basically expressions and some meta data) which we call 'rules'. Examples of expressionset implementations are `validator` objects, storing validation rules and `indicator` objects, storing data quality indicators. The `confront` function evaluates the expressions one by one on a dataset while recording some process meta data. All results are stored in a (subclass of a) `confrontation` object.

Usage

```
confront(dat, x, ref, ...)

## S4 method for signature 'data.frame,indicator,ANY'
confront(dat, x, key = NA_character_,
  ...)

## S4 method for signature 'data.frame,indicator,environment'
confront(dat, x, ref,
  key = NA_character_, ...)

## S4 method for signature 'data.frame,indicator,data.frame'
confront(dat, x, ref,
  key = NA_character_, ...)
```

```
## S4 method for signature 'data.frame,indicator,list'
confront(dat, x, ref,
  key = NA_character_, ...)

## S4 method for signature 'data.frame,validator,ANY'
confront(dat, x, key = NA_character_,
  ...)

## S4 method for signature 'data.frame,validator,environment'
confront(dat, x, ref,
  key = NA_character_, ...)

## S4 method for signature 'data.frame,validator,data.frame'
confront(dat, x, ref,
  key = NA_character_, ...)

## S4 method for signature 'data.frame,validator,list'
confront(dat, x, ref,
  key = NA_character_, ...)
```

Arguments

dat	An R object carrying data
x	An R object carrying rules.
ref	Optionally, an R object carrying reference data. See examples for usage.
...	Options used at execution time (especially 'raise'). See voptions.
key	(optional) name of identifying variable in x.

Using reference data

When reference data sets are given, it is assumed that rows in the reference data are ordered corresponding to the rows of dat, except when a key is specified. In that case, all reference datasets are matched against the rows of dat using key Nonmatching records are removed from datasets in ref. If there are records in dat that are not in ref, then datasets in ref are extended with records containing only NA. In particular, this means that wen reference data is passed in an environment, those reference data sets may altered by the call to confront.

Technically, reference data will be stored in an environment that is the parent of a (created) environment that contains the columns of dat.

See Also

voptions

Other confrontation-methods: [,expressionset-method, as.data.frame,confrontation-method, confrontation-class, errors, length,expressionset-method, values

Other validation-methods: aggregate,validation-method, all,validation-method, any,validation-method, barplot,validation-method, check_that, compare, plot,validation-method, sort,validation-method, summary, validation-class, values

Other indication-methods: indication-class, summary

Examples

```
# a basic validation example
v <- validator(height/weight < 0.5, mean(height) >= 0)
cf <- confront(women, v)
summary(cf)
plot(cf)
as.data.frame(cf)

# an example checking metadata
v <- validator(nrow(.) == 15, ncol(.) > 2)
summary(confront(women, v))

# An example using reference data
v <- validator(weight == ref$weight)
summary(confront(women, v, women))

# Usging custom names for reference data
v <- validator(weight == test$weight)
summary( confront(women,v, list(test=women)) )

# Reference data in an environment
e <- new.env()
e$test <- women
v <- validator(weight == test$weight)
summary( confront(women, v, e) )

# the effect of using a key
w <- women
w$id <- letters[1:nrow(w)]
v <- validator(weight == ref$weight)

# with complete data; already matching
values( confront(w, v, w, key='id'))

# with scrambled rows in reference data (reference gets sorted according to dat)
i <- sample(nrow(w))
values(confront(w, v, w[i,],key='id'))

# with incomplete reference data
values(confront(w, v, w[1:10,],key='id'))
```

`created` *Creation timestamp*

Description

Creation timestamp

Usage

```
created(x, ...)

created(x) <- value

## S4 method for signature 'rule'
created(x, ...)

## S4 replacement method for signature 'rule,POSIXct'
created(x) <- value

## S4 method for signature 'expressionset'
created(x, ...)

## S4 replacement method for signature 'expressionset,POSIXct'
created(x) <- value
```

Arguments

x	and R object
...	Arguments to be passed to other methods
value	Value to set

Value

A POSIXct vector.

See Also

Other expressionset-methods: as.data.frame,expressionset-method, as.data.frame, description, label, meta, names<-,rule,character-method, origin, plot,validator-method, summary, variables, voptions

Examples

```
# retrieve properties
v <- validator(turnover > 0, staff.costs>0)

# number of rules in v:
length(v)

# per-rule
created(v)
origin(v)
```

```
names(v)

# set properties
names(v)[1] <- "p1"

label(v)[1] <- "turnover positive"
description(v)[1] <- "
According to the official definition,
only positive values can be considered
valid turnovers.
"

# short description is also printed:
v

# print all info for first rule
v[[1]]



# retrieve properties
v <- validator(turnover > 0, staff.costs>0)

# number of rules in v:
length(v)

# per-rule
created(v)
origin(v)
names(v)

# set properties
names(v)[1] <- "p1"

label(v)[1] <- "turnover positive"
description(v)[1] <- "
According to the official definition,
only positive values can be considered
valid turnovers.
"

# short description is also printed:
v

# print all info for first rule
v[[1]]
```

`description` *Rule description*

Description

A longer (typically one-paragraph) description of a rule.

Usage

```
description(x, ...)

description(x) <- value

## S4 method for signature 'rule'
description(x, ...)

## S4 replacement method for signature 'rule,character'
description(x) <- value

## S4 method for signature 'expressionset'
description(x, ...)

## S4 replacement method for signature 'expressionset,character'
description(x) <- value
```

Arguments

x	and R object
...	Arguments to be passed to other methods
value	Value to set

Value

A character vector.

See Also

Other expressionset-methods: as.data.frame,expressionset-method, as.data.frame, created, label, meta, names<-,rule,character-method, origin, plot,validator-method, summary, variables, voptions

Examples

```
# retrieve properties
v <- validator(turnover > 0, staff.costs>0)

# number of rules in v:
length(v)

# per-rule
created(v)
origin(v)
```

```
names(v)

# set properties
names(v)[1] <- "p1"

label(v)[1] <- "turnover positive"
description(v)[1] <- "
According to the official definition,
only positive values can be considered
valid turnovers.
"

# short description is also printed:
v

# print all info for first rule
v[[1]]



# retrieve properties
v <- validator(turnover > 0, staff.costs>0)

# number of rules in v:
length(v)

# per-rule
created(v)
origin(v)
names(v)

# set properties
names(v)[1] <- "p1"

label(v)[1] <- "turnover positive"
description(v)[1] <- "
According to the official definition,
only positive values can be considered
valid turnovers.
"

# short description is also printed:
v

# print all info for first rule
v[[1]]
```

---

errors *Get messages from a confrontation object*

Description

Get messages from a confrontation object

Usage

```
errors(x, ...)

## S4 method for signature 'confrontation'
errors(x, ...)

## S4 method for signature 'confrontation'
warnings(x, ...)
```

Arguments

x	An object of class confrontation
...	Arguments to be passed to other methods.

See Also

Other confrontation-methods: [,expressionset-method, as.data.frame,confrontation-method, confrontation-class, confront, length,expressionset-method, values

Examples

```
# create an error, by using a non-existent variable name
cf <- check_that(women, hite > 0, weight > 0)
# retrieve error messages
errors(cf)
```

---

export_yaml *Export to yaml file*

Description

Translate an object to yaml format and write to file.

Usage

```
export_yaml(x, file, ...)

as_yaml(x, ...)

## S4 method for signature 'expressionset'
```

```
export_yaml(x, file, ...)

## S4 method for signature 'expressionset'
as_yaml(x, ...)
```

Arguments

x	An R object
file	A file location or connection (passed to base::write).
...	Options passed to yaml::as.yaml

Details

Both validator and indicator objects can be exported.

Examples

```
v <- validator(x > 0, y > 0, x + y == z)
txt <- as_yaml(v)
cat(txt)


# NOTE: you can safely run the code below. It is enclosed in 'not run'
# statements to prevent the code from being run at test-time on CRAN
## Not run:
export_yaml(v, file="my_rules.txt")

## End(Not run)
```

---

label *Rule label*

Description

A short (typically two or three word) description of a rule.

Usage

```
label(x, ...)

label(x) <- value

## S4 method for signature 'rule'
label(x, ...)

## S4 replacement method for signature 'rule,character'
```

```
label(x) <- value

## S4 method for signature 'expressionset'
label(x, ...)

## S4 replacement method for signature 'expressionset,character'
label(x) <- value
```

Arguments

x	and R object
...	Arguments to be passed to other methods
value	Value to set

Value

A character vector.

See Also

Other expressionset-methods: as.data.frame,expressionset-method, as.data.frame, created, description, meta, names<-,rule,character-method, origin, plot,validator-method, summary, variables, voptions

Examples

```
# retrieve properties
v <- validator(turnover > 0, staff.costs>0)

# number of rules in v:
length(v)

# per-rule
created(v)
origin(v)
names(v)

# set properties
names(v)[1] <- "p1"

label(v)[1] <- "turnover positive"
description(v)[1] <- "
According to the official definition,
only positive values can be considered
valid turnovers.
"

# short description is also printed:
v
```

```
# print all info for first rule
v[[1]]



# retrieve properties
v <- validator(turnover > 0, staff.costs>0)

# number of rules in v:
length(v)

# per-rule
created(v)
origin(v)
names(v)

# set properties
names(v)[1] <- "p1"

label(v)[1] <- "turnover positive"
description(v)[1] <- "
According to the official definition,
only positive values can be considered
valid turnovers.
"

# short description is also printed:
v

# print all info for first rule
v[[1]]
```

`lbj_cells-class` *Logging object to use with the lumberjack package*

Description

Logging object to use with the lumberjack package

Format

A reference class object

Methods

`add(meta, input, output)` Add logging info based on in- and output

`dump(file = "cells.csv", ...)` Dump logging info to csv file. All arguments in '...' except row.names are passed to 'write.csv'

`initialize(..., verbose = TRUE)` Create object. Optionally toggle verbosity.

`log_data()` Return logged data as a data.frame

Details

This obeject can used with the function composition ('pipe') operator of the `lumberjack` package. The logging is based on validate's `cells` function. The output is written to a `csv` file wich contains the following columns.

`step`	`integer`	Step number
`time`	`POSIXct`	Timestamp
`expr`	`character`	Expression used on data
`cells`	`integer`	Total nr of cells in dataset
`available`	`integer`	Nr of non-NA cells
`missing`	`integer`	Nr of empty (NA) cells
`still_available`	`integer`	Nr of cells still available after expr
`unadapted`	`integer`	Nr of cells still available and unaltered
`unadapted`	`integer`	Nr of cells still available and altered
`imputed`	`integer`	Nr of cells not missing anymore

Note

This logger is suited only for operations that do not change the dimensions of the dataset.

See Also

Other loggers: `lbj_rules-class`

---

lbj_rules-class *Logging object to use with the lumberjack package*

Description

Logging object to use with the lumberjack package

Methods

`dump(file = "lbj_rules.csv", ...)` Dump logging info to csv file. All arguments in '...' except row.names are passed to 'write.csv'

`initialize(rules, verbose = TRUE)` Create object. Optionally toggle verbosity.

`log_data()` Return logged data as a data.frame

See Also

Other loggers: `lbj_cells-class`

---

length,expressionset-method *Determine the number of elements in an object.*

Description

Determine the number of elements in an object.

Usage

```
## S4 method for signature 'expressionset'
length(x)

## S4 method for signature 'confrontation'
length(x)
```

Arguments

x	An R object

See Also

Other confrontation-methods: [,expressionset-method, as.data.frame,confrontation-method, confrontation-class, confront, errors, values

---

match_cells *Create matching subsets of a sequence of data*

Description

Create matching subsets of a sequence of data

Usage

```
match_cells(..., .list = NULL, id = NULL)
```

Arguments

...	A sequence of data.frames, possibly in the form of <name>=<value> pairs.
.list	A list of data.frames; will be concatenated with ....
id	Names or indices of columns to use as index.

Value

A list of data.frames, subsetted and sorted so that all cells correspond.

See Also

Other comparing: as.data.frame,cellComparison-method, as.data.frame,validatorComparison-method, barplot,cellComparison-method, barplot,validatorComparison-method, cells, compare, plot,cellComparison-method, plot,validatorComparison-method

---

`meta` *Get or set rule metadata*

Description

Rule metadata are key-value pairs where the value is a simple (atomic) string or number.

Usage

```
meta(x, ...)

meta(x, name) <- value

## S4 method for signature 'rule'
meta(x, ...)

## S4 replacement method for signature 'rule,character'
meta(x, name) <- value

## S4 method for signature 'expressionset'
meta(x, simplify = TRUE, ...)

## S4 replacement method for signature 'expressionset,character'
meta(x, name) <- value
```

Arguments

`x`	an R object
`...`	Arguments to be passed to other methods
`name`	`[character]` metadata key
`value`	Value to set
`simplify`	Gather all metadata into a dataframe?

See Also

Other expressionset-methods: as.data.frame,expressionset-method, as.data.frame, created, description, label, names<-,rule,character-method, origin, plot,validator-method, summary, variables, voptions

Examples

```
v <- validator(x > 0, y > 0)

# metadata is recycled over rules
meta(v,"foo") <- "bar"

# assign metadata to a selection of rules
meta(v[1],"fu") <- 2

# retrieve metadata as data.frame
meta(v)

# retrieve metadata as list
meta(v,simplify=TRUE)
```

---

names<-,rule,character-method

Extract or set names

Description

Extract or set names

When setting names, `values` are recycled and made unique with `make.names`

Usage

```
## S4 replacement method for signature 'rule,character'
names(x) <- value

## S4 method for signature 'expressionset'
names(x)

## S4 replacement method for signature 'expressionset,character'
names(x) <- value
```

Arguments

`x`	An R object
`value`	Value to set

Value

A `character` vector

See Also

Other expressionset-methods: as.data.frame,expressionset-method, as.data.frame, created, description, label, meta, origin, plot,validator-method, summary, variables, voptions

Examples

```
# retrieve properties
v <- validator(turnover > 0, staff.costs>0)

# number of rules in v:
length(v)

# per-rule
created(v)
origin(v)
names(v)

# set properties
names(v)[1] <- "p1"

label(v)[1] <- "turnover positive"
description(v)[1] <- "
According to the official definition,
only positive values can be considered
valid turnovers.
"

# short description is also printed:
v

# print all info for first rule
v[[1]]



# retrieve properties
v <- validator(turnover > 0, staff.costs>0)

# number of rules in v:
length(v)

# per-rule
created(v)
origin(v)
names(v)

# set properties
names(v)[1] <- "p1"

label(v)[1] <- "turnover positive"
description(v)[1] <- "
```

```
According to the official definition,
only positive values can be considered
valid turnovers.
"

# short description is also printed:
v

# print all info for first rule
v[[1]]
```

---

origin *Origin of rules*

Description

A slot to store where the rule originated, e.g. a filename or "command-line" for interactively defined rules.

Usage

```
origin(x, ...)

origin(x) <- value

## S4 method for signature 'rule'
origin(x, ...)

## S4 replacement method for signature 'rule,character'
origin(x) <- value

## S4 method for signature 'expressionset'
origin(x, ...)

## S4 replacement method for signature 'expressionset,character'
origin(x) <- value
```

Arguments

x	and R object
...	Arguments to be passed to other methods
value	Value to set

Value

A character vector.

See Also

Other expressionset-methods: as.data.frame,expressionset-method, as.data.frame, created, description, label, meta, names<-,rule,character-method, plot,validator-method, summary, variables, voptions

Examples

```
# retrieve properties
v <- validator(turnover > 0, staff.costs>0)

# number of rules in v:
length(v)

# per-rule
created(v)
origin(v)
names(v)

# set properties
names(v)[1] <- "p1"

label(v)[1] <- "turnover positive"
description(v)[1] <- "
According to the official definition,
only positive values can be considered
valid turnovers.
"

# short description is also printed:
v

# print all info for first rule
v[[1]]



# retrieve properties
v <- validator(turnover > 0, staff.costs>0)

# number of rules in v:
length(v)

# per-rule
created(v)
origin(v)
names(v)

# set properties
names(v)[1] <- "p1"

label(v)[1] <- "turnover positive"
```

```
description(v)[1] <- "
According to the official definition,
only positive values can be considered
valid turnovers.
"

# short description is also printed:
v

# print all info for first rule
v[[1]]
```

`plot,cellComparison-method`

Line graph of a cellComparison object.

Description

Versions of a data set can be compared cell by cell using `cells`. The result is a `cellComparison` object. This method creates a line-graph, thus suggesting an that an ordered sequence of data sets have been compared. See also `barplot,cellComparison-method` for an unordered version.

Usage

```
## S4 method for signature 'cellComparison'
plot(x, xlab = "", ylab = "", las = 2,
  cex.axis = 0.8, cex.legend = 0.8, ...)
```

Arguments

`x`	a `cellComparison` object.
`xlab`	[`character`] label for x axis (default none)
`ylab`	[`character`] label for y axis (default none)
`las`	[`numeric`] in `{0,1,2,3}` determining axis label rotation
`cex.axis`	[`numeric`] Magnification with respect to the current setting of `cex` for axis annotation.
`cex.legend`	[`numeric`] Magnification with respect to the current setting of `cex` for legend annotation and title.
`...`	Graphical parameters, passed to `plot`. See `par`.

See Also

Other comparing: `as.data.frame,cellComparison-method`, `as.data.frame,validatorComparison-method`, `barplot,cellComparison-method`, `barplot,validatorComparison-method`, `cells`, `compare`, `match_cells`, `plot,validatorComparison-method`

plot,validation-method *Plot a validation object*

Description

The plot function for the confrontation object is identical to the barplot method.

Usage

```
## S4 method for signature 'validation'
plot(x, y, ...)
```

Arguments

x	a confrontation object.
y	not used
...	passed to barplot

See Also

Other validation-methods: aggregate,validation-method, all,validation-method, any,validation-method, barplot,validation-method, check_that, compare, confront, sort,validation-method, summary, validation-class, values

Examples

```
rules <- validator( r1 = staff.costs < total.costs
                  , r2 = turnover + other.rev == total.rev
                  , r3 = other.rev > 0
                  , r4 = total.rev > 0
                  , r5 = nace %in% c("A", "B")
                  )
plot(rules, cex=0.8, show_legend=TRUE)

data(retailers)
cf <- confront(retailers, rules)
plot(cf, main="Retailers check")
```

`plot,validator-method` *Plot a validator object*

Description

The matrix of variables x rules is plotted, in which rules that are recognized as linear (in)equations are differently colored. The augmented matrix is returned, but can also be calculated using `variables(x, as="matrix")`.

Usage

```
## S4 method for signature 'validator'
plot(x, y, use_blocks = TRUE, col = c("#b2df8a",
  "#a6cee3"), cex = 1, show_legend = TRUE, ...)
```

Arguments

`x`	validator object with rules
`y`	not used
`use_blocks`	`logical` if `TRUE` the matrix is sorted according to the connected sub sets of variables (aka blocks).
`col`	`character` with color codes for plotting variables.
`cex`	size of the variables plotted.
`show_legend`	should a legend explaining the colors be drawn?
`...`	passed to image

Value

(invisible) the matrix

See Also

`variables`

Other validator-methods: `+,validator,validator-method`, `validator`

Other expressionset-methods: `as.data.frame,expressionset-method`, `as.data.frame`, `created`, `description`, `label`, `meta`, `names<-,rule,character-method`, `origin`, `summary`, `variables`, `voptions`

Examples

```
rules <- validator( r1 = staff.costs < total.costs
                  , r2 = turnover + other.rev == total.rev
                  , r3 = other.rev > 0
                  , r4 = total.rev > 0
                  , r5 = nace %in% c("A", "B")
                  )
plot(rules, cex=0.8, show_legend=TRUE)
```

```
data(retailers)
cf <- confront(retailers, rules)
plot(cf, main="Retailers check")
```

---

plot,validatorComparison-method

Line graph of validatorComparison object

Description

The performance of versions of a data set with regard to rule-based quality requirements can be compared using using compare. The result is a validatorComparison object. This method creates a line-graph, thus suggesting an that an ordered sequence of data sets have been compared. See also barplot,validatorComparison-method for an unordered version.

Usage

```
## S4 method for signature 'validatorComparison'
plot(x, xlab = "", ylab = "", las = 2,
  cex.axis = 0.8, cex.legend = 0.8, ...)
```

Arguments

x	Object of class validatorComparison.
xlab	[character] label for x axis (default none)
ylab	[character] label for y axis (default none)
las	[numeric] in {0,1,2,3} determining axis label rotation
cex.axis	[numeric] Magnification with respect to the current setting of cex for axis annotation.
cex.legend	[numeric] Magnification with respect to the current setting of cex for legend annotation and title.
...	Graphical parameters, passed to plot. See par.

See Also

Other comparing: as.data.frame,cellComparison-method, as.data.frame,validatorComparison-method, barplot,cellComparison-method, barplot,validatorComparison-method, cells, compare, match_cells, plot,cellComparison-method

retailers *data on Dutch supermarkets*

Description

Anonymized and distorted data on revenue and cost structure for 60 retailers. Currency is in thousands of Euros.

- size: Size class (0=undetermined)
- incl.prob: Probability of inclusion in the sample
- staff: Number of staff
- turnover: Amount of turnover
- other.rev: Amount of other revenue
- total.rev: Total revenue
- staff.costs: Number of staff employed
- total.costs: Total costs made
- profit: Amount of profit
- vat: Turnover reported for Value Added Tax

Format

A csv file, one retailer per row.

sort,validation-method *Aggregate and sort the results of a validation.*

Description

Aggregate and sort the results of a validation.

Usage

```
## S4 method for signature 'validation'
sort(x, decreasing = FALSE, by = c("rule", "record"),
  drop = TRUE, ...)
```

Arguments

x	An object of class validation
decreasing	Sort by decreasing number of passes?
by	Report on violations per rule (default) or per record?
drop	drop list attribute if the result has a single argument.
...	Arguments to be passed to or from other methods.

Value

A `data.frame` with the following columns.

`npass`	Number of items passed
`nfail`	Number of items failing
`nNA`	Number of items resulting in `NA`
`rel.pass`	Relative number of items passed
`rel.fail`	Relative number of items failing
`rel.NA`	Relative number of items resulting in `NA`

If `by='rule'` the relative numbers are computed with respect to the number of records for which the rule was evaluated. If `by='record'` the relative numbers are computed with respect to the number of rules the record was tested agains. By default the most failed validations and records with the most fails are on the top.

When `by='record'` and not all validation results have the same dimension structure, a list of `data.frames` is returned.

See Also

Other validation-methods: `aggregate,validation-method`, `all,validation-method`, `any,validation-method`, `barplot,validation-method`, `check_that`, `compare`, `confront`, `plot,validation-method`, `summary`, `validation-class`, `values`

Examples

```
data(retailers)
retailers$id <- paste0("ret",1:nrow(retailers))
v <- validator(
    staff.costs/staff < 25
  , turnover + other.rev==total.rev)

cf <- confront(retailers,v,key="id")
a <- aggregate(cf,by='record')
head(a)

# or, get a sorted result:
s <- sort(cf, by='record')
head(s)
```

`summary` *Create a summary*

Description

Create a summary

Usage

```
summary(object, ...)

## S4 method for signature 'expressionset'
summary(object, ...)

## S4 method for signature 'indication'
summary(object, ...)

## S4 method for signature 'validation'
summary(object, ...)
```

Arguments

object	An R object
...	Currently unused

Value

A data.frame with the information mentioned below is returned.

Validator and indicator objects

For these objects, the ruleset is split into subsets (blocks) that are disjunct in the sense that they do not share any variables. For each block the number of variables, the number of rules and the number of rules that are linear are reported.

Indication

Some basic information per evaluated indicator is reported: the number of items to which the indicator was applied, the output class, some statistics (min, max, mean , number of NA) and wether an exception occurred (warnings or errors). The evaluated expression is reported as well.

Validation

Some basic information per evaluated validation rule is reported: the number of items to which the rule was applied, the output class, some statistics (passes, fails, number of NA) and wether an exception occurred (warnings or errors). The evaluated expression is reported as well.

See Also

plot,validator-method

Other expressionset-methods: as.data.frame,expressionset-method, as.data.frame, created, description, label, meta, names<-,rule,character-method, origin, plot,validator-method, variables, voptions

Other indication-methods: confront, indication-class

Other validation-methods: aggregate,validation-method, all,validation-method, any,validation-method, barplot,validation-method, check_that, compare, confront, plot,validation-method, sort,validation-method, validation-class, values

Examples

```
data(retailers)
v <- validator(staff > 0, staff.costs/staff < 20, turnover+other.revenue == total.revenue)
summary(v)

cf <- confront(retailers,v)
summary(cf)
```

---

syntax *Syntax to define validation or indicator rules*

Description

A concise overview of the `validate` syntax.

Basic syntax

The basic rule is that an R-statement that evaluates to a `logical` is a validating statement. This is established by static code inspection when `validator` reads a (set of) user-defined validation rule(s).

Comparisons

All basic comparisons, including `>`, `>=`, `==`, `!=`, `<=`, `<`, `%in%` are validating statements. When executing a validating statement, the `%in%` operator is replaced with `%vin%`.

Logical operations

Unary logical operators '`!`', `all()` and `any` define validating statements. Binary logical operations including `&`, `&&`, `|`, `||`, are validating when `P` and `Q` in e.g. `P & Q` are validating. (note that the short-circuits `&&` and `&` onnly return the first logical value, in cases where for `P && Q`, `P` and/or `Q` are vectors. Binary logical implication $P \Rightarrow Q$ (P implies Q) is implemented as `if ( P ) Q`. The latter is interpreted as `!(P) | Q`.

Type checking

Any function starting with `is.` (e.g. `is.numeric`) is a validating expression.

Text search

`grepl` is a validating expression.

Functional dependencies

Armstrong's functional dependencies, of the form $A + B \rightarrow C + D$ are represented using the `~`, e.g. `A + B ~ C + D`. For example `postcode ~ city` means, that when two records have the same value for `postcode`, they must have the same value for `city`.

Reference the dataset as a whole

Metadata such as numer of rows, columns, column names and so on can be tested by referencing the whole data set with the '.'. For example, the rule `nrow(.) == 15` checks whether there are 15 rows in the dataset at hand.

Local, transient assignment

The operator ':=' can be used to set up local variables (during, for example, validation) to save time (the rhs of an assignment is computed only once) or to make your validation code more maintainable. Assignments work more or less like common R assignments: they are only valid for statements coming after the assignment and they may be overwritten. The result of computing the rhs is not part of a confrontation with data.

Groups

Often the same constraints/rules are valid for groups of variables. `validate` allows for compact notation. Variable groups can be used in-statement or by defining them with the `:=` operator.

```
validator( var_group(a,b) > 0 )
```

is equivalent to

```
validator(G := var_group(a,b), G > 0)
```

is equivalent to

```
validator(a>0,b>0).
```

Using two groups results in the cartesian product of checks. So the statement

```
validator( f=var_group(c,d), g=var_group(a,b), g > f)
```

is equivalent to

```
validator(a > c, b > c, a > d, b > d)
```

File parsing

Please see the vignette on how to read rules from and write rules to file:

```
vignette("rule-files",package="validate")
```

`validate` *Data Validation Infrastructure*

Description

Data Validation Infrastructure

Introduction

Data often contain errors and missing data. A necessary step before data analysis is verifying and validating your data. Package `validate` is a toolbox for creating validation rules and checking data against these rules.

Getting started

The easiest way to get started is through the examples given in `check_that`.

The general workflow in `validate` follows the following pattern.

- Define a set of rules or quality indicator using `validator` or `indicator`.
- `confront` data with the rules or indicators,
- Examine the results either graphically or by summary.

There are several convenience functions that allow one to define rules from the commandline, through a (freeform or yaml) file and to investigate and maintain the rules themselves. Please have a look at the introductory vignette for a more thorough introduction on validation rules and the indicators vignette for an introducion on quality indicators. After you're a bit aqcuinted with the package, you will probably be interested in defining your rules separately in a text file. The vignette on rule files will get you started with that.

References

An overview of this package, its underlying ideas and many examples can be found in MPJ van der Loo and E. de Jonge (2018) *Statistical data cleaning with applications in R* John Wiley & Sons.

`validation-class` *Store results of evaluating validating expressions*

Description

Store results of evaluating validating expressions

Details

A object of class `validation` stores a set of results generated by evaluating an `validator` in the context of data along with some metadata.

See Also

Other validation-methods: `aggregate,validation-method`, `all,validation-method`, `any,validation-method`, `barplot,validation-method`, `check_that`, `compare`, `confront`, `plot,validation-method`, `sort,validation-method`, `summary`, `values`

validator *Define validation rules for data*

Description

Define validation rules for data

Usage

```
validator(..., .file, .data)
```

Arguments

`...`	A comma-separated list of validating expressions
`.file`	(optional) A character vector of file locations (see also the section on file parsing in the
`.data`	(optional) A `data.frame` with columns `"rule"`, `"name"`, and `"description"` `syntax` help file).

Value

An object of class `validator` (see `validator-class`).

Validating expressions

Each validating expression should evaluate to a `logical`. Allowed syntax of the expression is described in `syntax`.

See Also

Other validator-methods: `+,validator,validator-method`, `plot,validator-method`

Examples

```
v <- validator(
  height>0
  ,weight>0
  ,height < 1.5*mean(height)
)
cf <- confront(women, v)
summary(cf)
```

values *Get values from object*

Description

Get values from object

Usage

```
values(x, ...)

## S4 method for signature 'confrontation'
values(x, ...)

## S4 method for signature 'validation'
values(x, simplify = TRUE, drop = TRUE, ...)

## S4 method for signature 'indication'
values(x, simplify = TRUE, drop = TRUE, ...)
```

Arguments

x	an R object
...	Arguments to pass to or from other methods
simplify	Combine results with similar dimension structure into arrays?
drop	if a single vector or array results, drop 'list' attribute?

See Also

Other confrontation-methods: [,expressionset-method, as.data.frame,confrontation-method, confrontation-class, confront, errors, length,expressionset-method

Other validation-methods: aggregate,validation-method, all,validation-method, any,validation-method, barplot,validation-method, check_that, compare, confront, plot,validation-method, sort,validation-method, summary, validation-class

variables *Get variable names*

Description

Generic function that extracts names of variables ocurring in R objects.

Usage

```
variables(x, ...)

## S4 method for signature 'rule'
variables(x, ...)

## S4 method for signature 'list'
variables(x, ...)

## S4 method for signature 'data.frame'
variables(x, ...)

## S4 method for signature 'environment'
variables(x, ...)

## S4 method for signature 'expressionset'
variables(x, as = c("vector", "matrix", "list"),
  dummy = FALSE, ...)
```

Arguments

x	An R object
...	Arguments to be passed to other methods.
as	how to return variables: • 'vector' Return the uniqe vector of variables occurring in x. • 'matrix' Return a boolean matrix, each row representing a rule, each column representing a variable. • 'list' Return a named list, each entry containing a character vector with variable names.
dummy	Also retrieve transient variables set with the := operator.

Methods (by class)

- rule: Retrieve unique variable names
- list: Alias to names.list
- data.frame: Alias to names.data.frame
- environment: Alias to ls
- expressionset: Variables occuring in x either as a single list, or per rule.

See Also

Other expressionset-methods: as.data.frame,expressionset-method, as.data.frame, created, description, label, meta, names<-,rule,character-method, origin, plot,validator-method, summary, voptions

Other expressionset-methods: as.data.frame,expressionset-method, as.data.frame, created, description, label, meta, names<-,rule,character-method, origin, plot,validator-method, summary, voptions

Examples

```
v <- validator(
  root = y := sqrt(x)
 , average = mean(x) > 3
 , sum = x + y == z
)
variables(v)
variables(v,dummy=TRUE)
variables(v,matrix=TRUE)
variables(v,matrix=TRUE,dummy=TRUE)
```

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voptions *Set or get options globally or per object.*

Description

There are three ways to specify options for this package.

- Globally. Setting `voptions(option1=value1,option2=value2,...)` sets global options.
- Per object. Setting `voptions(x=<object>, option1=value1,...)`, causes all relevant functions that use that object (e.g. `confront`) to use those local settings.
- At execution time. Relevant functions (e.g. `confront`) take optional arguments allowing one to define options to be used during the current function call

Usage

```
voptions(x = NULL, ...)

## S4 method for signature 'ANY'
voptions(x = NULL, ...)

validate_options(...)

reset(x = NULL)

## S4 method for signature 'ANY'
reset(x = NULL)

## S4 method for signature 'expressionset'
voptions(x = NULL, ...)

## S4 method for signature 'expressionset'
reset(x = NULL)
```

Arguments

x	(optional) an object inheriting from expressionset such as validator or indicator.
...	Name of an option (character) to retrieve options or option = value pairs to set options.

Value

When requesting option settings: a list. When setting options, the whole options list is returned silently.

Options for the validate package

Currently the following options are supported.

- na.value (NA,TRUE,FALSE; NA) Value to return when a validating statement results in NA.
- raise ("none","error","all"; "none") Control if the confront methods catch or raise exceptions. The 'all' setting is useful when debugging validation scripts.
- lin.eq.eps ('numeric'; 1e-8) The precision used when evaluating linear equalities. To be used to control for machine rounding.
- "reset" Reset to factory settings.

See Also

Other expressionset-methods: as.data.frame,expressionset-method, as.data.frame, created, description, label, meta, names<-,rule,character-method, origin, plot,validator-method, summary, variables

Other expressionset-methods: as.data.frame,expressionset-method, as.data.frame, created, description, label, meta, names<-,rule,character-method, origin, plot,validator-method, summary, variables

Examples

```
# the default allowed validation symbols.
voptions('validator_symbols')

# set an option, local to a validator object:
v <- validator(x + y > z)
voptions(v,raise='all')
# check that local option was set:
voptions(v,'raise')
# check that global options have not changed:
voptions('raise')
```

`%vin%` *A consistent set membership operator*

Description

A set membership operator like `%in%` that handles `NA` more consistently with R's other logical comparison operators.

Usage

```
x %vin% table
```

Arguments

`x`	vector or `NULL`: the values to be matched
`table`	vector or `NULL`: the values to be matched against.

Details

R's basic comparison operators (almost) always return `NA` when one of the operands is `NA`. The `%in%` operator is an exception. Compare for example `NA %in% NA` with `NA == NA`: the first results in `TRUE`, while the latter results in `NA` as expected. The `%vin%` operator acts consistent with operators such as `==`. Specifically, `NA` results in the following cases.

- For each position where `x` is `NA`, the result is `NA`.
- When `table` contains an `NA`, each non-matched value in `x` results in `NA`.

Examples

```
# we cannot be sure about the first element:
c(NA, "a") %vin% c("a","b")

# we cannot be sure about the 2nd and 3rd element (but note that they
# cannot both be TRUE):
c("a","b","c") %vin% c("a",NA)

# we can be sure about all elements:
c("a","b") %in% character(0)
```

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