Package 'validate'

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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. Supports checks implied by an SDMX DSD file as well. See also Van der Loo and De Jonge (2018) <doi:10.1002/9781118897126>, Chapter 6 and the JSS paper (2021) <doi:10.18637/jss.v097.i10>.

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VignetteBuilder knitr

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`+,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)
```

add_indicators *Add indicator values as columns to a data frame*

Description

Compute and add externally defined indicators to data frame. If necessary, values are recycled over records.

Usage

```
add_indicators(dat, x)
```

Arguments

dat	[data.frame]
x	[indicator] or [indication] object. See examples.

Value

dat with extra columns defined by x attached.

Examples

```
ii <- indicator(
 hihi = 2*sqrt(height)
 , haha = log10(weight)
 , lulz = mean(height)
 , wo0t = median(weight)
)

# note: mean and median are repeated
add_indicators(women, ii)

# compute indicators first, then add
out <- confront(women, ii)
add_indicators(women, out)
```

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.

keys	If confront was called with key=
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(), event(), names<-,rule,character-method, 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(), event(), names<-,rule,character-method, 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(), event(), names<-,rule,character-method, 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 confrontation. 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(), event(), keyset(), 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(), event(), names<-,rule,character-method, 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

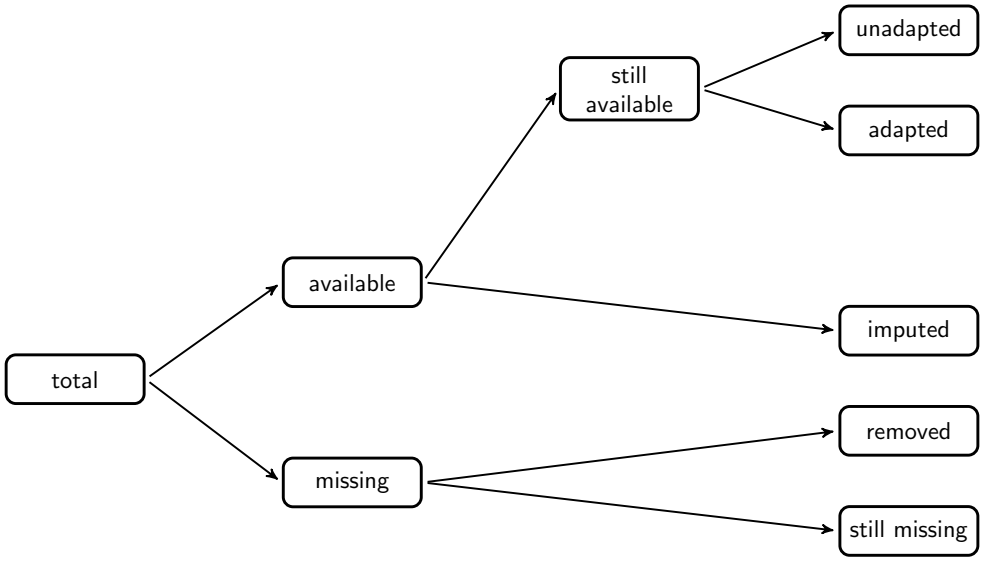
`...`	For `cells`: data frames, comma separated. Names will become column names in the output. For `plot` or `barplot`: graphical parameters (see `par`).
`.list`	A `list` of data frames; will be concatenated with objects in `...`
`compare`	How to compare the datasets.

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(), event(), names<-,rule,character-method, 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:

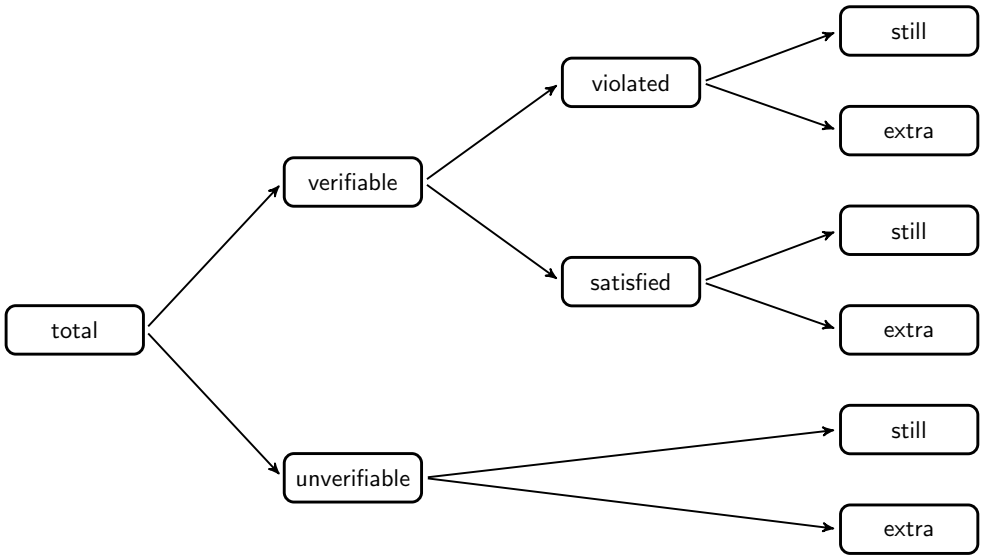
- Number of validations performed
- Number of validations that evaluate to NA (unverifiable)
- Number of validations that evaluate to a logical (verifiable)
- Number of validations that evaluate to TRUE
- Number of validations that evaluate to FALSE
- Number of extra validations that evaluate to NA (new 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 confronting 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()`, `event()`, `names<-,rule,character-method`, `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 = NULL, ...)

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

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

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

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

## S4 method for signature 'data.frame,validator,environment'
```

```
confront(dat, x, ref, key = NULL, ...)

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

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

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.

Reference data

Reference data is typically a `list` with a items such as a code list, or a data frame of which rows match the rows of the data under scrutiny.

See Also

voptions

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

Other validation-methods: aggregate,validation-method, all,validation-method, any,validation-method, barplot,validation-method, check_that(), compare(), event(), names<-,rule,character-method, plot,validation-method, sort,validation-method, summary(), validation-class, values()

Other indication-methods: event(), 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'))
```

`contains_exactly` *Check records using a predifined table of (im)possible values*

Description

Given a set of keys or key combinations, check whether all thos combinations occur, or check that they do not occur. Supports globbing and regular expressions.

Usage

```
contains_exactly(keys, by = NULL, allow_duplicates = FALSE)

contains_at_least(keys, by = NULL)

contains_at_most(keys, by = NULL)

does_not_contain(keys)
```

Arguments

`keys`	A data frame or bare (unquoted) name of a data frame passed as a reference to `confront` (see examples). The column names of `keys` must also occurr in the columns of the data under scrutiny.

by A bare (unquoted) variable or list of variable names that occur in the data under scrutiny. The data will be split into groups according to these variables and the check is performed on each group.

allow_duplicates [logical] toggle whether key combinations can occur more than once.

Details

contains_exactly	dataset contains exactly the key set, no more, no less.
contains_at_least	dataset contains at least the given keys.
contains_at_most	all keys in the data set are contained the given keys.
does_not_contain	The keys are interpreted as forbidden key combinations.

Value

For contains_exactly, contains_at_least, and contains_at_most a logical vector with one entry for each record in the dataset. Any group not conforming to the test keys will have FALSE assigned to each record in the group (see examples).

For contains_at_least: a logical vector equal to the number of records under scrutiny. It is FALSE where key combinations do not match any value in keys.

For does_not_contain: a logical vector with size equal to the number of records under scrutiny. It is FALSE where key combinations do not match any value in keys.

Globbing

Globbing is a simple method of defining string patterns where the asterisks (*) is used a wildcard. For example, the globbing pattern "abc*" stands for any string starting with "abc".

See Also

Other cross-record-helpers: do_by(), exists_any(), hb(), hierarchy(), is_complete(), is_linear_sequence(), is_unique()

Examples

```
## Check that data is present for all quarters in 2018-2019
dat <- data.frame(
    year    = rep(c("2018","2019"),each=4)
  , quarter = rep(sprintf("Q%d",1:4), 2)
  , value   = sample(20:50,8)
)

# Method 1: creating a data frame in-place (only for simple cases)
rule <- validator(contains_exactly(
           expand.grid(year=c("2018","2019"), quarter=c("Q1","Q2","Q3","Q4"))
```

```
          )
        )
out <- confront(dat, rule)
values(out)

# Method 2: pass the keyset to 'confront', and reference it in the rule.
# this scales to larger key sets but it needs a 'contract' between the
# rule definition and how 'confront' is called.

keyset <- expand.grid(year=c("2018","2019"), quarter=c("Q1","Q2","Q3","Q4"))
rule <- validator(contains_exactly(all_keys))
out <- confront(dat, rule, ref=list(all_keys = keyset))
values(out)

## Globbing (use * as a wildcard)

# transaction data
transactions <- data.frame(
    sender   = c("S21", "X34", "S45","Z22")
  , receiver = c("FG0", "FG2", "DF1","KK2")
  , value    = sample(70:100,4)
)

# forbidden combinations: if the sender starts with "S",
# the receiver can not start "FG"
forbidden <- data.frame(sender="S*",receiver = "FG*")

rule <- validator(does_not_contain(glob(forbidden_keys)))
out <- confront(transactions, rule, ref=list(forbidden_keys=forbidden))
values(out)


## Quick interactive testing
# use 'with':
with(transactions, does_not_contain(forbidden))



## Grouping

# data in 'long' format
dat <- expand.grid(
  year = c("2018","2019")
  , quarter = c("Q1","Q2","Q3","Q4")
  , variable = c("import","export")
)
dat$value <- sample(50:100,nrow(dat))


periods <- expand.grid(
  year = c("2018","2019")
  , quarter = c("Q1","Q2","Q3","Q4")
)
```

```
rule <- validator(contains_exactly(all_periods, by=variable))

out <- confront(dat, rule, ref=list(all_periods=periods))
values(out)

# remove one  export record

dat1 <- dat[-15,]
out1 <- confront(dat1, rule, ref=list(all_periods=periods))
values(out1)
values(out1)
```

`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]]
```

---

do_by *split-apply-combine for vectors, with equal-length outptu*

Description

Group x by one or more categorical variables, compute an aggregate, repeat that aggregate to match the size of the group, and combine results. The functions sum_by and so on are convenience wrappers that call do_by internally.

Usage

```
do_by(x, by, fun, ...)

sum_by(x, by, na.rm = FALSE)

mean_by(x, by, na.rm = FALSE)

min_by(x, by, na.rm = FALSE)

max_by(x, by, na.rm = FALSE)
```

Arguments

x	A bare variable name
by	a bare variable name, or a list of bare variable names, used to split x into groups.
fun	[function] A function that aggregates x to a single value.
...	passed as extra arguments to fun (e.g. na.rm=TRUE
na.rm	Toggle ignoring NA

See Also

Other cross-record-helpers: contains_exactly(), exists_any(), hb(), hierarchy(), is_complete(), is_linear_sequence(), is_unique()

Examples

```
x <- 1:10
y <- rep(letters[1:2], 5)
do_by(x, by=y, fun=max)
do_by(x, by=y, fun=sum)
```

---

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(), event(), keyset(), 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)
```

event *Get or set event information metadata from a 'confrontation' object.*

Description

The purpose of event information is to store information that allows for identification of the confronting event.

Usage

```
event(x)

event(x) <- value

## S4 method for signature 'confrontation'
event(x)

## S4 replacement method for signature 'confrontation'
event(x) <- value
```

Arguments

x	an object of class confrontation
value	[character] vector of length 4 with event identifiers.

Value

A a character vector with elements "agent", which defaults to the R version and platform returned by R.version, a timestamp ("time") in ISO 8601 format and a "actor" which is the user name returned by Sys.info(). The last element is called "trigger" (default NA_character_), which can be used to administrate the event that triggered the confrontation.

References

Mark van der Loo and Olav ten Bosch (2017) Design of a generic machine-readable validation report structure, version 1.0.0.

See Also

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

Other validation-methods: aggregate,validation-method, all,validation-method, any,validation-method, barplot,validation-method, check_that(), compare(), confront(), names<-,rule,character-method, plot,validation-method, sort,validation-method, summary(), validation-class, values()

Other indication-methods: confront(), indication-class, summary()

Examples

```
data(retailers)
rules <- validator(turnover >= 0, staff >=0)
cf <- confront(retailers, rules)
event(cf)

# adapt event information
u <- event(cf)
u["trigger"] <- "spontaneous validation"
event(cf) <- u
event(cf)
```

`exists_any` *Test for (unique) existence*

Description

Group records according to (zero or more) classifying variables. Test for each group whether at least one (`exists`) or precisely one (`exists_one`) record satisfies a condition.

Usage

```
exists_any(rule, by = NULL, na.rm = FALSE)

exists_one(rule, by = NULL, na.rm = FALSE)
```

Arguments

`rule`	`[expression]` A validation rule
by	A bare (unquoted) variable name or a list of bare variable names, that will be used to group the data.
`na.rm`	`[logical]` Toggle to ignore results that yield `NA`.

Value

A `logical` vector, with the same number of entries as there are rows in the entire data under scrutiny. If a test fails, all records in the group are labeled with `FALSE`.

See Also

Other cross-record-helpers: `contains_exactly()`, `do_by()`, `hb()`, `hierarchy()`, `is_complete()`, `is_linear_sequence()`, `is_unique()`

Examples

```
# Test whether each household has exactly one 'head of household'

dd <- data.frame(
   hhid   = c(1,  1,  2,  1,  2,  2,  3 )
 , person = c(1,  2,  3,  4,  5,  6,  7 )
 , hhrole = c("h","h","m","m","h","m","m")
)
v <- validator(exists_one(hhrole=="h", hhid))
values(confront(dd, v))

# same, but now with missing value in the data
dd <- data.frame(
    hhid   = c(1,  1,  2,  1,  2,  2,  3 )
  , person = c(1,  2,  3,  4,  5,  6,  7 )
  , hhrole = c("h",NA,"m","m","h","m","h")
)
values(confront(dd, v))

# same, but now we ignore the missing values
v <- validator(exists_one(hhrole=="h", hhid, na.rm=TRUE))
values(confront(dd, v))
```

`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)
```

---

field_format *Check whether a field conforms to a regular expression*

Description

A convenience wrapper around grepl to make rule sets more readable.

Usage

```
field_format(x, pattern, type = c("glob", "regex"), ...)
```

Arguments

x	Bare (unquoted) name of a variable. Otherwise a vector of class character. Coerced to character as necessary.
pattern	[character] a regular expression
type	[character] How to interpret pattern. In globbing, the asterisk ('*') is used as a wildcard that stands for 'zero or more characters'.
...	passed to grepl

See Also

Other format-checkers: field_length(), number_format()

field_length *Check number of code points*

Description

A convenience function testing for field length.

Usage

```
field_length(x, n = NULL, min = NULL, max = NULL, ...)
```

Arguments

x	Bare (unquoted) name of a variable. Otherwise a vector of class character. Coerced to character as necessary.
n	Number of code points required.
min	Mimimum number of code points
max	Maximum number of code points
...	passed to nchar (for example type="width")

Value

A [logical] of size length(x).

Details

The number of code points (string length) may depend on current locale settings or encoding issues, including those caused by inconsistent choices of UTF normalization.

See Also

Other format-checkers: field_format(), number_format()

Examples

```
df <- data.frame(id = 11001:11003, year = c("2018","2019","2020"), value = 1:3)
rule <- validator(field_length(year, 4), field_length(id, 5))
out <- confront(df, rule)
as.data.frame(out)
```

hb *Hiridoglu-Berthelot function*

Description

A function to measure 'outlierness' for skew distributed data with long right tails. The method works by measuring deviation from a reference value, by default the median. Deviation from above is measured as the ratio between observed and refence values. Deviation from below is measured as the inverse: the ratio between reference value and observed values.

Usage

```
hb(x, ref = stats::median, ...)
```

Arguments

`x`	`[numeric]`
`ref`	`[function]` or `[numeric]`
`...`	arguments passed to `ref` after `x`

Value

$\max\{x/ref(x), ref(x)/x\} - 1$ if `ref` is a function, otherwise $\max\{x/ref, ref/x\} - 1$

References

Hidiroglou, M. A., & Berthelot, J. M. (1986). Statistical editing and imputation for periodic business surveys. Survey methodology, 12(1), 73-83.

See Also

Other cross-record-helpers: `contains_exactly()`, `do_by()`, `exists_any()`, `hierarchy()`, `is_complete()`, `is_linear_sequence()`, `is_unique()`

Examples

```
x <- seq(1,20,by=0.1)
plot(x,hb(x), 'l')
```

`hierarchy` *Check aggregates defined by a hierarchical code list*

Description

Check all aggregates defined by a code hierarchy.

Usage

```
hierarchy(
  values,
  labels,
  hierarchy,
  by = NULL,
  tol = 1e-08,
  na_value = TRUE,
  aggregator = sum,
  ...
)
```

Arguments

`values`	bare (unquoted) name of a variable that holds values that must aggregate according to the `hierarchy`.
`labels`	bare (unquoted) name of variable holding a grouping variable (a code from a hierarchical code list)
`hierarchy`	`[data.frame]` defining a hierarchical code list. The first column must contain (child) codes, and the second column contains their corresponding parents.
`by`	A bare (unquoted) variable or list of variable names that occur in the data under scrutiny. The data will be split into groups according to these variables and the check is performed on each group.
`tol`	`[numeric]` tolerance for equality checking
`na_value`	`[logical]` or `NA`. Value assigned to values that do not occurr in checks.
`aggregator`	`[function]` that aggregates children to their parents.
`...`	arguments passed to `aggregator` (e.g. `na.rm=TRUE`).

Value

A `logical` vector with the size of `length(values)`. Every element involved in an aggregation error is labeled `FALSE` (aggregate plus aggregated elements). Elements that are involved in correct aggregations are set to `TRUE`, elements that are not involved in any check get the value `na_value` (by default: `TRUE`).

See Also

Other cross-record-helpers: contains_exactly(), do_by(), exists_any(), hb(), is_complete(), is_linear_sequence(), is_unique()

Examples

```
# We check some data against the built-in NACE revision 2 classification.
data(nace_rev2)
head(nace_rev2[1:4]) # columns 3 and 4 contain the child-parent relations.

d <- data.frame(
     nace   = c("01","01.1","01.11","01.12", "01.2")
   , volume = c(100 ,70    , 30    ,40     , 25    )
)
# It is possible to perform checks interactively
d$nacecheck <- hierarchy(d$volume, labels = d$nace, hierarchy=nace_rev2[3:4])
# we have that "01.1" == "01.11" + "01.12", but not "01" == "01.1" +  "01.2"
print(d)

# Usage as a valiation rule is as follows
rules <- validator(hierarchy(volume, labels = nace, hierarchy=validate::nace_rev_2[3:4]))
confront(d, rules)

# you can also pass a hierarchy as a reference, for example.

rules <- validator(hierarchy(volume, labels = nace, hierarchy=ref$nacecodes))
out <- confront(d, rules, ref=list(nacecodes=nace_rev2[3:4]))
summary(out)

# set a output to NA when a code does not occur in the code list.
d <- data.frame(
     nace   = c("01","01.1","01.11","01.12", "01.2", "foo")
   , volume = c(100 ,70    , 30    ,40     , 25     , 60)
)

d$nacecheck <- hierarchy(d$volume, labels = d$nace, hierarchy=nace_rev2[3:4]
                         , na_value = NA)
# we have that "01.1" == "01.11" + "01.12", but not "01" == "01.1" +  "01.2"
print(d)
```

---

in_range *Check variable range*

Description

Test wether a variable falls within a range.

Usage

```
in_range(x, min, max, ...)

## Default S3 method:
in_range(x, min, max, strict = FALSE, ...)

## S3 method for class 'character'
in_range(x, min, max, strict = FALSE, format = "auto", ...)
```

Arguments

x	A bare (unquoted) variable name.
min	lower bound
max	upper bound
...	arguments passed to other methods
strict	[logical] Toggle between including the range boundaries (default) or not including them (when strict=TRUE).
format	[character] of NULL. If format=NULL the character vector is interpreted as is. And the whether a character lies within a character range is determined by the collation order set by the current locale. See the details of "<". If format is not NULL, it specifies how to interpret the character vector as a time period. It can take the value "auto" for automatic detection or a specification passed to strptime. Automatically detected periods are of the form year: "2020", year-Mmonth: "2020M01", yearQquarter: "2020Q3", or year-Qquarter: "2020-Q3".

Examples

```
d <- data.frame(
   number = c(3,-2,6)
 , time   = as.Date(c("2018-02-01", "2018-03-01", "2018-04-01"))
 , period = c("2020Q1", "2021Q2", "2020Q3")
)

rules <- validator(
   in_range(number, min=-2, max=7, strict=TRUE)
 , in_range(time,   min=as.Date("2017-01-01"), max=as.Date("2018-12-31"))
 , in_range(period, min="2020Q1", max="2020Q4")
)

result <- confront(d, rules)
values(result)
```

is_complete *Test for completeness of records*

Description

Utility function to make common tests easier.

Usage

```
is_complete(...)

all_complete(...)
```

Arguments

...	When used in a validation rule: a bare (unquoted) list of variable names. When used directly, a comma-separated list of vectors of equal length.

Value

For `is_complete` A logical vector that is `FALSE` for each record that has at least one missing value.

For `all_unique` a single `TRUE` or `FALSE`.

See Also

Other cross-record-helpers: `contains_exactly()`, `do_by()`, `exists_any()`, `hb()`, `hierarchy()`, `is_linear_sequence()`, `is_unique()`

Examples

```
d <- data.frame(X = c('a','b',NA,'b'), Y = c(NA,'apple','banana','apple'), Z=1:4)
v <- validator(is_complete(X, Y))
values(confront(d, v))
```

is_linear_sequence *Check whether a variable represents a linear sequence*

Description

A variable $X = (x_1, x_2, \ldots, x_n)$ $(n \geq 0)$ represents a *linear sequence* when $x_{j+1} - x_j$ is constant for all $j \geq 1$. That is, elements in the series are equidistant and without gaps.

Usage

```
is_linear_sequence(x, by = NULL, ...)

## S3 method for class 'numeric'
is_linear_sequence(
  x,
  by = NULL,
  begin = NULL,
  end = NULL,
  sort = TRUE,
  tol = 1e-08,
  ...
)

## S3 method for class 'Date'
is_linear_sequence(x, by = NULL, begin = NULL, end = NULL, sort = TRUE, ...)

## S3 method for class 'POSIXct'
is_linear_sequence(
  x,
  by = NULL,
  begin = NULL,
  end = NULL,
  sort = TRUE,
  tol = 1e-06,
  ...
)

## S3 method for class 'character'
is_linear_sequence(
  x,
  by = NULL,
  begin = NULL,
  end = NULL,
  sort = TRUE,
  format = "auto",
  ...
)

in_linear_sequence(x, ...)

## S3 method for class 'character'
in_linear_sequence(
  x,
  by = NULL,
  begin = NULL,
  end = NULL,
  sort = TRUE,
```

```
  format = "auto",
  ...
)

## S3 method for class 'numeric'
in_linear_sequence(
  x,
  by = NULL,
  begin = NULL,
  end = NULL,
  sort = TRUE,
  tol = 1e-08,
  ...
)

## S3 method for class 'Date'
in_linear_sequence(x, by = NULL, begin = NULL, end = NULL, sort = TRUE, ...)

## S3 method for class 'POSIXct'
in_linear_sequence(
  x,
  by = NULL,
  begin = NULL,
  end = NULL,
  sort = TRUE,
  tol = 1e-06,
  ...
)
```

Arguments

x	An R vector.
by	bare (unquoted) variable name or a list of unquoted variable names, used to split x into groups. The check is executed for each group.
...	Arguments passed to other methods.
begin	Optionally, a value that should equal `min(x)`
end	Optionally, a value that should equal `max(x)`
sort	`[logical]`. When set to `TRUE`, x is sorted within each group before testing.
tol	numerical tolerance for gaps.
format	`[character]`. How to interpret x as a time period. Either `"auto"` for automatic detection or a specification passed to strptime. Automatically detected periods are of the form year: `"2020"`, yearMmonth: `"2020M01"`, yearQquarter: `"2020Q3"`, or year-Qquarter: `"2020-Q3"`.

Details

Presence of a missing value (NA) in x will result in NA, except when `length(x) <= 2` and `start` and `end` are `NULL`. Any sequence of length ≤ 2 is a linear sequence.

Value

For `is_linear_sequence`: a single `TRUE` or `FALSE`, equal to `all(in_linear_sequence)`.

For `in_linear_sequence`: a `logical` vector with the same length as `x`.

See Also

Other cross-record-helpers: `contains_exactly()`, `do_by()`, `exists_any()`, `hb()`, `hierarchy()`, `is_complete()`, `is_unique()`

Examples

```
is_linear_sequence(1:5) # TRUE
is_linear_sequence(c(1,3,5,4,2)) # FALSE
is_linear_sequence(c(1,3,5,4,2), sort=TRUE) # TRUE
is_linear_sequence(NA_integer_) # TRUE
is_linear_sequence(NA_integer_, begin=4) # FALSE
is_linear_sequence(c(1, NA, 3)) # FALSE


d <- data.frame(
    number = c(pi, exp(1), 7)
  , date = as.Date(c("2015-12-17","2015-12-19","2015-12-21"))
  , time = as.POSIXct(c("2015-12-17","2015-12-19","2015-12-20"))
)

rules <- validator(
    is_linear_sequence(number)  # fails
  , is_linear_sequence(date)    # passes
  , is_linear_sequence(time)    # fails
)
summary(confront(d,rules))

## check groupwise data
dat <- data.frame(
   time = c(2012, 2013, 2012, 2013, 2015)
 , type = c("hi", "hi", "ha", "ha", "ha")
)
rule <- validator(in_linear_sequence(time, by=type))
values(confront(dat, rule)) ## 2xT, 3xF


rule <- validator(in_linear_sequence(time, type))
values( confront(dat, rule) )
```

is_unique *Test for uniquenes of records*

Description

Test for uniqueness of columns or combinations of columns.

Usage

```
is_unique(...)

all_unique(...)

n_unique(...)
```

Arguments

...	When used in a validation rule: a bare (unquoted) list of variable names. When used directly, a comma-separated list of vectors of equal length.

Value

For is_unique A logical vector that is FALSE for each record that has a duplicate.

For all_unique a single TRUE or FALSE.

For number_unique a single number representing the number of unique values or value combinations in the arguments.

See Also

Other cross-record-helpers: contains_exactly(), do_by(), exists_any(), hb(), hierarchy(), is_complete(), is_linear_sequence()

Examples

```
d <- data.frame(X = c('a','b','c','b'), Y = c('banana','apple','banana','apple'), Z=1:4)
v <- validator(is_unique(X, Y))
values(confront(d, v))

# example with groupwise test
df <- data.frame(x=c(rep("a",3), rep("b",3)),y=c(1,1,2,1:3))
v <- validator(is_unique(y, by=x))
values(confront(d,v))
```

keyset *Get key set stored with a confrontation*

Description

Get key set stored with a confrontation

Usage

```
keyset(x)

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

Arguments

x	an object of class confrontation

Value

If a confrontation is created with the key= option set, this function returns the key set, otherwise NULL

See Also

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

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 = NULL, verbose = TRUE, ...)` Dump logging info to csv file. All arguments in '...' except row.names are passed to 'write.csv'

`initialize(..., verbose = TRUE, label = "")` 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 = NULL, ...)` Dump logging info to csv file. All arguments in '...' except row.names are passed to 'write.csv'

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

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

`plot()` plot rule comparisons

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(), event(), keyset(), 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)
```

---

nace_rev2 *NACE classification code table*

Description

Statistical Classification of Economic Activities.

- Order [integer]
- Level [integer] NACE level
- Code [character] NACE code
- Parent [character] parent code of "Code"
- Description [character]
- This_item_includes [character]
- This_item_also_includes [character]
- Rulings [character]
- This_item_excludes [character]
- Reference_to_ISIC_Rev._4 [character]

Format

A csv file, one NACE code per row.

References

This codelist was downloaded on 2020-10-21 from Eurostat

See Also

hierarchy

Other datasets: retailers, samplonomy

`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`

Get names from `confrontation` object

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

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

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()`

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

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]]
```

`number_format` *Check the layouts of numbers.*

Description

Convenience function to check layout of numbers stored as a character vector.

Usage

```
number_format(x, format = NULL, min_dig = NULL, max_dig = NULL, dec = ".")
```

Arguments

`x`	`[character]` vector. If `x` is not of type `character` it will be converted.
`format`	`[character]` denoting the number format (see below).
`min_dig`	`[numeric]` minimal number of digits after decimal separator.
`max_dig`	`[numeric]` maximum number of digits after decimal separator.
`dec`	`[character]` decimal seperator.

Details

If `format` is specified, then `min_dig`, `max_dig` and `dec` are ignored.

Numerical formats can be specified as a sequence of characters. There are a few special characters:

- `d` Stands for digit.
- `*` (digit globbing) zero or more digits

Here are some examples.

`"d.dd"`	One digit, a decimal point followed by two digits.
`"d.ddddddddEdd"`	Scientific notation with eight digits behind the decimal point.
`"0.ddddddddEdd"`	Same, but starting with a zero.
`"d,dd*"`	one digit before the comma and at least two behind it.

See Also

Other format-checkers: `field_format()`, `field_length()`

Examples

```
df <- data.frame(number = c("12.34","0.23E55","0.98765E12"))
rules <- validator(
   number_format(number, format="dd.dd")
   , number_format(number, "0.ddEdd")
   , number_format(number, "0.*Edd")
)

out <- confront(df, rules)
values(out)

# a few examples, without 'validator'
number_format("12.345", min_dig=2) # TRUE
number_format("12.345", min_dig=4) # FALSE
number_format("12.345", max_dig=2) # FALSE
number_format("12.345", max_dig=5) # TRUE
number_format("12,345", min_dig=2, max_dig=3, dec=",") # TRUE
```

---

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]]
```

---

part_whole_relation *Test whether details combine to a chosen aggregate*

Description

Data in 'long' format often contain records representing totals (or other aggregates) as well as records that contain details that add up to the total. This function facilitates checking the part-whole relation in such cases.

Usage

```
part_whole_relation(
  values,
  labels,
  whole,
  part = NULL,
  aggregator = sum,
  tol = 1e-08,
  by = NULL,
  ...
)
```

Arguments

values	A bare (unquoted) variable name holding the values to aggregate
labels	A bare (unquoted) variable name holding the labels indicating whether a value is an aggregate or a detail.
whole	[character] literal label or pattern recognizing a whole in labels. Use glob or rx to label as a globbing or regular expression pattern (see examples).
part	[character] vector of label values or pattern recognizing a part in labels. Use glob or rx to label as a globbing or regular expression pattern. When labeled with glob or rx, it must be a single string. If 'part' is left unspecified, all values not recognized as an aggregate are interpreted as details that must be aggregated to the whole.
aggregator	[function] used to aggregate subsets of x. It should accept a numeric vector and return a single number.
tol	[numeric] tolerance for equality checking
by	Name of variable, or list of bare variable names, used to split the values and labels before computing the aggregates.
...	Extra arguments passed to aggregator (for example na.rm=TRUE).

Value

A logical vector of size length(value).

Examples

```
df <- data.frame(
   id = 10011:10020
 , period   = rep(c("2018Q1", "2018Q2", "2018Q3", "2018Q4","2018"),2)
 , direction = c(rep("import",5), rep("export", 5))
 , value     = c(1,2,3,4,10, 3,3,3,3,13)
)
## use 'rx' to interpret 'whole' as a regular expression.
rules <- validator(
  part_whole_relation(value, period, whole=rx("^\\d{4}$")
  , by=direction)
)

out <- confront(df, rules, key="id")
as.data.frame(out)
```

---

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 validation results

Description

Creates a barplot of validation result. For each validation rule, a stacked bar is plotted with percentages of failing, passing, and missing results.

Usage

```
## S4 method for signature 'validation'
plot(
  x,
  y,
  fill = c("#FE2712", "#66B032", "#dddddd"),
  col = fill,
```

```
  rulenames = names(x),
  labels = c("Fails", "Passing", "Missing", "Total"),
  title = NULL,
  xlab = NULL,
  ...
)
```

Arguments

x	a confrontation object.
y	not used
fill	[character] vector of length 3. Colors representing fails, passes, and missings
col	Edge colors for the bars.
rulenames	[character] vector of size length(x). If not specified, names are taken from x.
labels	[character] vector of length 4. Replace legend annotation.
title	[character] Change the default title.
xlab	[character] Change the title
...	not used

Details

The plot function tries to be smart about placing labels on the y axis. When the number of bars becomes too large, no y axis annotation will be shown and the bars will become space-filling.

See Also

Other validation-methods: aggregate,validation-method, all,validation-method, any,validation-method, barplot,validation-method, check_that(), compare(), confront(), event(), names<-,rule,character-method, 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. There are two data sets. The `SBS2000` dataset is equal to the `retailers` data set except that it has a record identifier (called `id`) column.

- id: A unique identifier (only in SBS2000)
- 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: Costs assiciated to staff
- total.costs: Total costs made
- profit: Amount of profit
- vat: Turnover reported for Value Added Tax

Format

A csv file, one retailer per row.

See Also

Other datasets: `nace_rev2`, `samplonomy`

run_validation_file *Run a file with confrontations. Capture results*

Description

A validation script is a regular R script, intersperced with `confront` or `check_that` statements. This function will run the script file and capture all output from calls to these functions.

Usage

```
run_validation_file(file, verbose = TRUE)

run_validation_dir(dir = "./", pattern = "^validate.+[rR]", verbose = TRUE)

## S3 method for class 'validations'
print(x, ...)

## S3 method for class 'validations'
summary(object, ...)
```

Arguments

file	[character] location of an R file.
verbose	[logical] toggle verbose output.
dir	[character] path to directory.
pattern	[characer] regular expression that selects validation files to run.
x	An R object
...	Unused
object	An R object

Value

run_validation_file: An object of class validations. This is a list of objects of class validation.

run_validation_dir: An object of class validations. This is a list of objects of class validation.

print: NULL, invisibly.

summary: A data frame similar to the data frame returned when summarizing a validation object. There are extra columns listing each call, file and first and last line where the code occurred.

---

rx *Label objects for interpretation as pattern*

Description

Label objects (typically strings or data frames containing keys combinations) to be interpreted as regular expression or globbing pattern.

Usage

```
rx(x)

glob(x)
```

Arguments

x	Object to label as regular expression (rx(x)) or globbing (glob(x)) pattern.

---

samplonomy *Economic data on Samplonia*

Description

Simulated economic time series representing GDP, Import, Export and Balance of Trade (BOT) of Samplonia. Samplonia is a fictional Island invented by Jelke Bethelehem (2009). The country has 10 000 inhabitants. It consists of two provinces: Agria and Induston. Agria is a rural province consisting of the mostly fruit and vegetable producing district of Wheaton and the mostly cattle producing Greenham. Induston has four districts. Two districts with heavy industry named Smokeley and Mudwater. Newbay is a young, developing district while Crowdon is where the rich Samplonians retire. The current data set contains several time series from Samplonia's national accounts system in long format.

There are annual and quarterly time series on GDP, Import, Export and Balance of Trade, for Samplonia as a whole, for each province and each district. BOT is defined as Export-Import for each region and period; quarterly figures are expected to add up to annual figures for each region and measure, and subregions are expected to add up to their super-regions.

- region: Region (Samplonia, one if its 2 provinces, or one of its 6 districts)
- freq: Frequency of the time series
- period: Period (year or quarter)
- measure: The economic variable (gdp, import, export, balance)
- value: The value

The data set has been endowed with the following errors.

- For Agria, the 2015 GDP record is not present.
- For Induston, the 2018Q3 export value is missing (NA)
- For Induston, there are two different values for the 2018Q2 Export
- For Crowdon, the 2015Q1 balance value is missing (NA).
- For Wheaton, the 2019Q2 import is missing (NA).

Format

An RData file.

References

J. Bethlehem (2009), Applied Survey Methods: A Statistical Perspective. John Wiley & Sons, Hoboken, NJ.

See Also

Other datasets: nace_rev2, retailers

`satisfying` *Select records (not) satisfying rules*

Description

Apply validation rules or validation results to a data set and select only those that satisfy all or violate at least one rule.

Usage

```
satisfying(x, y, include_missing = FALSE, ...)

violating(x, y, include_missing = FALSE, ...)

lacking(x, y, ...)
```

Arguments

`x`	A `data.frame`
`y`	a `validator` object or a `validation` object.
`include_missing`	Toggle: also select records that have `NA` output for a rule?
`...`	options passed to `confront`

Value

For `satisfying`, the records in `x` satisfying all rules or validation outcomes in `y`. For `violating` the records in `x` violating at least one of the rules or validation outcomes in `y`

Note

An error is thrown if the rules or validation results in `y` can not be interpreted record-by record (e.g. when one of the rules is of the form `mean(foo)>0`).

Examples

```
rules <- validator(speed >= 12, dist < 100)
satisfying(cars, rules)
violating(cars, rules)

out <- confront(cars, rules)
summary(out)
satisfying(cars, out)
violating(cars, out)
```

sdmx_codelist *Get code list from an SDMX REST API endpoint.*

Description

`sdmx_codelist` constructs an URL for `rsdmx::readSDMX` and extracts the code IDs. Code lists are downloaded once and cached for the duration of the R session.

`estat_codelist` gets a code list from the REST API provided at `ec.europa.eu/tools/cspa_services_global/sdmxregi` It is a convenience wrapper that calls `sdmx_codelist`.

`global_codelist` gets a code list from the REST API provided at `https://registry.sdmx.org/webservice/data.html`. It is a convenience wrapper that calls `sdmx_codelist`.

Usage

```
sdmx_codelist(
  endpoint,
  agency_id,
  resource_id,
  version = "latest",
  what = c("id", "all")
)

estat_codelist(resource_id, agency_id = "ESTAT", version = "latest")

global_codelist(resource_id, agency_id = "SDMX", version = "latest")
```

Arguments

`endpoint`	`[character]` REST API endpoint of the SDMX registry
`agency_id`	`[character]` Agency ID (e.g. `"ESTAT"`)
`resource_id`	`[character]` Resource ID (e.g. `"CL_ACTIVITY"`)
`version`	`[character]` Version of the code list.
`what`	`[character]` Return a `character` with code id's, or a data frame with all information.

See Also

Other sdmx: `sdmx_endpoint()`, `validator_from_dsd()`

Other sdmx: `sdmx_endpoint()`, `validator_from_dsd()`

Examples

```
# here we download the CL_ACTIVITY codelist from the  ESTAT registry.
```

```
## Not run:
 codelist <- sdmx_codelist(
   endpoint = "https://registry.sdmx.org/ws/public/sdmxapi/rest/"
   , agency_id = "ESTAT"
   , resource_id = "CL_ACTIVITY"

## End(Not run)

## Not run:
  estat_codelist("CL_ACTIVITY")

## End(Not run)
## Not run:
  global_codelist("CL_AGE") )
  global_codelist("CL_CONF_STATUS")
  global_codelist("CL_SEX")

## End(Not run)
# An example of using SDMX information, downloaded from the SDMX global
# registry
## Not run:
 # economic data from the country of Samplonia
 data(samplonomy)
 head(samplonomy)

 rules <- validator(
   , freq %in% global_codelist("CL_FREQ")
   , value >= 0
 )
 cf <- confront(samplonomy, rules)
 summary(cf)


## End(Not run)
```

---

sdmx_endpoint *Get URL for known SDMX registry endpoints*

Description

Convenience function storing URLs for SDMX endpoints.

Usage

```
sdmx_endpoint(registry = NULL)
```

Arguments

registry	[character] name of the endpoint (case insensitve). If registry is NULL (the default), the list of supported endpoints is returned.

See Also

Other sdmx: sdmx_codelist(), validator_from_dsd()

Examples

```
sdmx_endpoint()
sdmx_endpoint("ESTAT")
sdmx_endpoint("global")
```

---

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.

keys	If confront was called with key=
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()`, `event()`, `names<-,rule,character-method`, `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(), event(), indication-class

Other validation-methods: aggregate,validation-method, all,validation-method, any,validation-method, barplot,validation-method, check_that(), compare(), confront(), event(), names<-,rule,character-method, 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.

Uniqueness, completeness

These can be tested in principle with the 'dot' syntax. However, there are some convenience functions: `is_complete`, `all_complete` `is_unique`, `all_unique`.

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 `confront`ation 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 cookbook on how to read rules from and write rules to file:

```
vignette("cookbook",package="validate")
```

---

validate *Data Validation Infrastructure*

Description

Data often suffer from errors and missing values. 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 cookbook for a comprehensive introduction.

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.

Please use `citation("validate")` to get a citation for (scientific) publications.

`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()`, `event()`, `names<-,rule,character-method`, `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 syntax help file).
.data	(optional) A data.frame with columns "rule", "name", and "description"

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)
```

validator_from_dsd *Extract a rule set from an SDMX DSD file*

Description

Data Structure Definitions contain references to code lists. This function extracts those references and generates rules that check data against code lists in an SDMX registry.

Usage

```
validator_from_dsd(endpoint, agency_id, resource_id, version = "latest")
```

Arguments

endpoint	[character] REST API endpoint of the SDMX registry
agency_id	[character] Agency ID (e.g. "ESTAT")
resource_id	[character] Resource ID (e.g. "CL_ACTIVITY")
version	[character] Version of the code list.

Value

An object of class validator.

See Also

Other sdmx: sdmx_codelist(), sdmx_endpoint()

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(), event(), keyset(), length,expressionset-method

Other validation-methods: aggregate,validation-method, all,validation-method, any,validation-method, barplot,validation-method, check_that(), compare(), confront(), event(), names<-,rule,character-method, 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)

- `variables(rule)`: Retrieve unique variable names
- `variables(list)`: Alias to `names.list`
- `variables(data.frame)`: Alias to `names.data.frame`
- `variables(environment)`: Alias to `ls`
- `variables(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)
```

---

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

```
# 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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