

Package: rsample (via r-universe)

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Title General Resampling Infrastructure

Version 1.2.1.9000

Description Classes and functions to create and summarize different types of resampling objects (e.g. bootstrap, cross-validation).

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URL <https://rsample.tidymodels.org>,
<https://github.com/tidymodels/rsample>

BugReports <https://github.com/tidymodels/rsample/issues>

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<code>.get_fingerprint</code>	<i>Obtain a identifier for the resamples</i>
-------------------------------	--

Description

This function returns a hash (or NA) for an attribute that is created when the `rset` was initially constructed. This can be used to compare with other resampling objects to see if they are the same.

Usage

```
.get_fingerprint(x, ...)  
  
## Default S3 method:  
.get_fingerprint(x, ...)  
  
## S3 method for class 'rset'  
.get_fingerprint(x, ...)
```

Arguments

<code>x</code>	An <code>rset</code> or <code>tune_results</code> object.
<code>...</code>	Not currently used.

Value

A character value or `NA_character_` if the object was created prior to `rsample` version 0.1.0.

Examples

```
set.seed(1)  
.get_fingerprint(vfold_cv(mtcars))  
  
set.seed(1)  
.get_fingerprint(vfold_cv(mtcars))  
  
set.seed(2)  
.get_fingerprint(vfold_cv(mtcars))  
  
set.seed(1)  
.get_fingerprint(vfold_cv(mtcars, repeats = 2))
```

`add_resample_id`*Augment a data set with resampling identifiers*

Description

For a data set, `add_resample_id()` will add at least one new column that identifies which resample that the data came from. In most cases, a single column is added but for some resampling methods, two or more are added.

Usage

```
add_resample_id(.data, split, dots = FALSE)
```

Arguments

<code>.data</code>	A data frame.
<code>split</code>	A single <code>rset</code> object.
<code>dots</code>	A single logical: should the id columns be prefixed with a "." to avoid name conflicts with <code>.data</code> ?

Value

An updated data frame.

See Also

`labels.rsplit`

Examples

```
library(dplyr)

set.seed(363)
car_folds <- vfold_cv(mtcars, repeats = 3)

analysis(car_folds$plits[[1]]) %>%
  add_resample_id(car_folds$plits[[1]]) %>%
  head()

car_bt <- bootstraps(mtcars)

analysis(car_bt$plits[[1]]) %>%
  add_resample_id(car_bt$plits[[1]]) %>%
  head()
```

apparent

Sampling for the Apparent Error Rate

Description

When building a model on a data set and re-predicting the same data, the performance estimate from those predictions is often called the "apparent" performance of the model. This estimate can be wildly optimistic. "Apparent sampling" here means that the analysis and assessment samples are the same. These resamples are sometimes used in the analysis of bootstrap samples and should otherwise be avoided like old sushi.

Usage

```
apparent(data, ...)
```

Arguments

data	A data frame.
...	These dots are for future extensions and must be empty.

Value

A tibble with a single row and classes `apparent`, `rset`, `tbl_df`, `tbl`, and `data.frame`. The results include a column for the data split objects and one column called `id` that has a character string with the resample identifier.

Examples

```
apparent(mtcars)
```

`as.data.frame.rsplit`
Convert an rsplit object to a data frame

Description

The analysis or assessment code can be returned as a data frame (as dictated by the `data` argument) using `as.data.frame.rsplit()`. `analysis()` and `assessment()` are shortcuts.

Usage

```
## S3 method for class 'rsplit'
as.data.frame(x, row.names = NULL, optional = FALSE, data = "analysis", ...)

analysis(x, ...)

## Default S3 method:
analysis(x, ...)

## S3 method for class 'rsplit'
analysis(x, ...)

assessment(x, ...)

## Default S3 method:
assessment(x, ...)

## S3 method for class 'rsplit'
assessment(x, ...)
```

Arguments

<code>x</code>	An <code>rsplit</code> object.
<code>row.names</code>	NULL or a character vector giving the row names for the data frame. Missing values are not allowed.
<code>optional</code>	A logical: should the column names of the data be checked for legality?
<code>data</code>	Either "analysis" or "assessment" to specify which data are returned.
<code>...</code>	Not currently used.

Examples

```
library(dplyr)
set.seed(104)
folds <- vfold_cv(mtcars)

model_data_1 <- folds$splits[[1]] %>% analysis()
holdout_data_1 <- folds$splits[[1]] %>% assessment()
```

Description

A bootstrap sample is a sample that is the same size as the original data set that is made using replacement. This results in analysis samples that have multiple replicates of some of the original rows of the data. The assessment set is defined as the rows of the original data that were not included in the bootstrap sample. This is often referred to as the "out-of-bag" (OOB) sample.

Usage

```
bootstraps(  
  data,  
  times = 25,  
  strata = NULL,  
  breaks = 4,  
  pool = 0.1,  
  apparent = FALSE,  
  ...  
)
```

Arguments

<code>data</code>	A data frame.
<code>times</code>	The number of bootstrap samples.
<code>strata</code>	A variable in <code>data</code> (single character or name) used to conduct stratified sampling. When not <code>NULL</code> , each resample is created within the stratification variable. Numeric <code>strata</code> are binned into quartiles.
<code>breaks</code>	A single number giving the number of bins desired to stratify a numeric stratification variable.
<code>pool</code>	A proportion of data used to determine if a particular group is too small and should be pooled into another group. We do not recommend decreasing this argument below its default of 0.1 because of the dangers of stratifying groups that are too small.
<code>apparent</code>	A logical. Should an extra resample be added where the analysis and holdout subset are the entire data set. This is required for some estimators used by the summary() function that require the apparent error rate.
<code>...</code>	These dots are for future extensions and must be empty.

Details

The argument `apparent` enables the option of an additional "resample" where the analysis and assessment data sets are the same as the original data set. This can be required for some types of analysis of the bootstrap results.

With a `strata` argument, the random sampling is conducted *within the stratification variable*. This can help ensure that the resamples have equivalent proportions as the original data set. For a categorical variable, sampling is conducted separately within each class. For a numeric stratification variable, `strata` is binned into quartiles, which are then used to stratify. Strata below 10% of the total are pooled together; see [make_strata\(\)](#) for more details.

Value

A tibble with classes `bootstraps`, `rset`, `tbl_df`, `tbl`, and `data.frame`. The results include a column for the data split objects and a column called `id` that has a character string with the resample identifier.

Examples

```

bootstraps(mtcars, times = 2)
bootstraps(mtcars, times = 2, apparent = TRUE)

library(purrr)
library(modeldata)
data(wa_churn)

set.seed(13)
resample1 <- bootstraps(wa_churn, times = 3)
map_dbl(
  resample1$splits,
  function(x) {
    dat <- as.data.frame(x)$churn
    mean(dat == "Yes")
  }
)

set.seed(13)
resample2 <- bootstraps(wa_churn, strata = churn, times = 3)
map_dbl(
  resample2$splits,
  function(x) {
    dat <- as.data.frame(x)$churn
    mean(dat == "Yes")
  }
)

set.seed(13)
resample3 <- bootstraps(wa_churn, strata = tenure, breaks = 6, times = 3)
map_dbl(
  resample3$splits,
  function(x) {
    dat <- as.data.frame(x)$churn
    mean(dat == "Yes")
  }
)

```

Description

Cluster cross-validation splits the data into V groups of disjointed sets using k-means clustering of some variables. A resample of the analysis data consists of $V-1$ of the folds/clusters while the assessment set contains the final fold/cluster. In basic cross-validation (i.e. no repeats), the number of resamples is equal to V .

Usage

```
clustering_cv(
  data,
  vars,
  v = 10,
  repeats = 1,
  distance_function = "dist",
  cluster_function = c("kmeans", "hclust"),
  ...
)
```

Arguments

<code>data</code>	A data frame.
<code>vars</code>	A vector of bare variable names to use to cluster the data.
<code>v</code>	The number of partitions of the data set.
<code>repeats</code>	The number of times to repeat the clustered partitioning.
<code>distance_function</code>	Which function should be used for distance calculations? Defaults to <code>stats::dist()</code> . You can also provide your own function; see Details.
<code>cluster_function</code>	Which function should be used for clustering? Options are either "kmeans" (to use <code>stats::kmeans()</code>) or "hclust" (to use <code>stats::hclust()</code>). You can also provide your own function; see Details.
<code>...</code>	Extra arguments passed on to <code>cluster_function</code> .

Details

The variables in the `vars` argument are used for k-means clustering of the data into disjointed sets or for hierarchical clustering of the data. These clusters are used as the folds for cross-validation. Depending on how the data are distributed, there may not be an equal number of points in each fold. You can optionally provide a custom function to `distance_function`. The function should take a data frame (as created via `data[vars]`) and return a `stats::dist()` object with distances between data points.

You can optionally provide a custom function to `cluster_function`. The function must take three arguments:

- `dists`, a `stats::dist()` object with distances between data points
- `v`, a length-1 numeric for the number of folds to create
- `...`, to pass any additional named arguments to your function

The function should return a vector of cluster assignments of length `nrow(data)`, with each element of the vector corresponding to the matching row of the data frame.

Value

A tibble with classes `rset`, `tbl_df`, `tbl`, and `data.frame`. The results include a column for the data split objects and an identification variable `id`.

Examples

```
data(ames, package = "modeldata")
clustering_cv(ames, vars = c(Sale_Price, First_Flr_SF, Second_Flr_SF), v = 2)
```

complement

Determine the Assessment Samples

Description

This method and function help find which data belong in the analysis and assessment sets.

Usage

```
complement(x, ...)

## S3 method for class 'rsplit'
complement(x, ...)

## S3 method for class 'rof_split'
complement(x, ...)

## S3 method for class 'sliding_window_split'
complement(x, ...)

## S3 method for class 'sliding_index_split'
complement(x, ...)

## S3 method for class 'sliding_period_split'
complement(x, ...)

## S3 method for class 'apparent_split'
complement(x, ...)
```

Arguments

x	An rsplit object.
...	Not currently used.

Details

Given an rsplit object, complement() will determine which of the data rows are contained in the assessment set. To save space, many of the rsplit objects will not contain indices for the assessment split.

Value

A integer vector.

See Also[populate\(\)](#)**Examples**

```
set.seed(28432)
fold_rs <- vfold_cv(mtcars)
head(fold_rs$splits[[1]]$in_id)
fold_rs$splits[[1]]$out_id
complement(fold_rs$splits[[1]])
```

form_pred

*Extract Predictor Names from Formula or Terms***Description**

While [all.vars\(\)](#) returns all variables used in a formula, this function only returns the variables explicitly used on the right-hand side (i.e., it will not resolve dots unless the object is terms with a data set specified).

Usage

```
form_pred(object, ...)
```

Arguments

object	A model formula or stats::terms() object.
...	Arguments to pass to all.vars()

Value

A character vector of names

Examples

```
form_pred(y ~ x + z)
form_pred(terms(y ~ x + z))

form_pred(y ~ x + log(z))
form_pred(log(y) ~ x + z)

form_pred(y1 + y2 ~ x + z)
form_pred(log(y1) + y2 ~ x + z)

# will fail:
# form_pred(y ~ .)

form_pred(terms(mpg ~ (.)^2, data = mtcars))
form_pred(terms(~ (.)^2, data = mtcars))
```

get_rsplrit	<i>Retrieve individual rsplits objects from an rset</i>
-------------	---

Description

Retrieve individual rsplits objects from an rset

Usage

```
get_rsplrit(x, index, ...)

## S3 method for class 'rset'
get_rsplrit(x, index, ...)

## Default S3 method:
get_rsplrit(x, index, ...)
```

Arguments

x	The rset object to retrieve an rsplit from.
index	An integer indicating which rsplit to retrieve: 1 for the rsplit in the first row of the rset, 2 for the second, and so on.
...	Not currently used.

Value

The rsplit object in row index of rset

Examples

```
set.seed(123)
(starting_splits <- group_vfold_cv(mtcars, cyl, v = 3))
get_rsplrit(starting_splits, 1)
```

group_bootstraps	<i>Group Bootstraps</i>
------------------	-------------------------

Description

Group bootstrapping creates splits of the data based on some grouping variable (which may have more than a single row associated with it). A common use of this kind of resampling is when you have repeated measures of the same subject. A bootstrap sample is a sample that is the same size as the original data set that is made using replacement. This results in analysis samples that have multiple replicates of some of the original rows of the data. The assessment set is defined as the rows of the original data that were not included in the bootstrap sample. This is often referred to as the "out-of-bag" (OOB) sample.

Usage

```
group_bootstraps(
  data,
  group,
  times = 25,
  apparent = FALSE,
  ...,
  strata = NULL,
  pool = 0.1
)
```

Arguments

<code>data</code>	A data frame.
<code>group</code>	A variable in <code>data</code> (single character or name) used for grouping observations with the same value to either the analysis or assessment set within a fold.
<code>times</code>	The number of bootstrap samples.
<code>apparent</code>	A logical. Should an extra resample be added where the analysis and holdout subset are the entire data set. This is required for some estimators used by the summary() function that require the apparent error rate.
<code>...</code>	These dots are for future extensions and must be empty.
<code>strata</code>	A variable in <code>data</code> (single character or name) used to conduct stratified sampling. When not <code>NULL</code> , each resample is created within the stratification variable. Numeric strata are binned into quartiles.
<code>pool</code>	A proportion of data used to determine if a particular group is too small and should be pooled into another group. We do not recommend decreasing this argument below its default of 0.1 because of the dangers of stratifying groups that are too small.

Details

The argument `apparent` enables the option of an additional "resample" where the analysis and assessment data sets are the same as the original data set. This can be required for some types of analysis of the bootstrap results.

Value

An tibble with classes `group_bootstraps` `bootstraps`, `rset`, `tbl_df`, `tbl`, and `data.frame`. The results include a column for the data split objects and a column called `id` that has a character string with the resample identifier.

Examples

```
data(ames, package = "modeldata")

set.seed(13)
group_bootstraps(ames, Neighborhood, times = 3)
```

```
group_bootstraps(ames, Neighborhood, times = 3, apparent = TRUE)
```

group_mc_cv

Group Monte Carlo Cross-Validation

Description

Group Monte Carlo cross-validation creates splits of the data based on some grouping variable (which may have more than a single row associated with it). One resample of Monte Carlo cross-validation takes a random sample (without replacement) of groups in the original data set to be used for analysis. All other data points are added to the assessment set. A common use of this kind of resampling is when you have repeated measures of the same subject.

Usage

```
group_mc_cv(
  data,
  group,
  prop = 3/4,
  times = 25,
  ...,
  strata = NULL,
  pool = 0.1
)
```

Arguments

data	A data frame.
group	A variable in data (single character or name) used for grouping observations with the same value to either the analysis or assessment set within a fold.
prop	The proportion of data to be retained for modeling/analysis.
times	The number of times to repeat the sampling.
...	These dots are for future extensions and must be empty.
strata	A variable in data (single character or name) used to conduct stratified sampling. When not NULL, each resample is created within the stratification variable. Numeric strata are binned into quartiles.
pool	A proportion of data used to determine if a particular group is too small and should be pooled into another group. We do not recommend decreasing this argument below its default of 0.1 because of the dangers of stratifying groups that are too small.

Value

A tibble with classes group_mc_cv, rset, tbl_df, tbl, and data.frame. The results include a column for the data split objects and an identification variable.

Examples

```
data(ames, package = "modeldata")

set.seed(123)
group_mc_cv(ames, group = Neighborhood, times = 5)
```

group_vfold_cv

*Group V-Fold Cross-Validation***Description**

Group V-fold cross-validation creates splits of the data based on some grouping variable (which may have more than a single row associated with it). The function can create as many splits as there are unique values of the grouping variable or it can create a smaller set of splits where more than one group is left out at a time. A common use of this kind of resampling is when you have repeated measures of the same subject.

Usage

```
group_vfold_cv(
  data,
  group = NULL,
  v = NULL,
  repeats = 1,
  balance = c("groups", "observations"),
  ...,
  strata = NULL,
  pool = 0.1
)
```

Arguments

data	A data frame.
group	A variable in data (single character or name) used for grouping observations with the same value to either the analysis or assessment set within a fold.
v	The number of partitions of the data set. If left as NULL (the default), v will be set to the number of unique values in the grouping variable, creating "leave-one-group-out" splits.
repeats	The number of times to repeat the V-fold partitioning.
balance	If v is less than the number of unique groups, how should groups be combined into folds? Should be one of "groups", which will assign roughly the same number of groups to each fold, or "observations", which will assign roughly the same number of observations to each fold.
...	These dots are for future extensions and must be empty.

strata	A variable in data (single character or name) used to conduct stratified sampling. When not NULL, each resample is created within the stratification variable. Numeric strata are binned into quartiles.
pool	A proportion of data used to determine if a particular group is too small and should be pooled into another group. We do not recommend decreasing this argument below its default of 0.1 because of the dangers of stratifying groups that are too small.

Value

A tibble with classes `group_vfold_cv`, `rset`, `tbl_df`, `tbl`, and `data.frame`. The results include a column for the data split objects and an identification variable.

Examples

```
data(ames, package = "modeldata")

set.seed(123)
group_vfold_cv(ames, group = Neighborhood, v = 5)
group_vfold_cv(
  ames,
  group = Neighborhood,
  v = 5,
  balance = "observations"
)
group_vfold_cv(ames, group = Neighborhood, v = 5, repeats = 2)

# Leave-one-group-out CV
group_vfold_cv(ames, group = Neighborhood)

library(dplyr)
data(Sacramento, package = "modeldata")

city_strata <- Sacramento %>%
  group_by(city) %>%
  summarize(strata = mean(price)) %>%
  summarize(city = city,
            strata = cut(strata, quantile(strata), include.lowest = TRUE))

sacramento_data <- Sacramento %>%
  full_join(city_strata, by = "city")

group_vfold_cv(sacramento_data, city, strata = strata)
```


Description

`initial_split()` creates a single binary split of the data into a training set and testing set. `initial_time_split()` does the same, but takes the *first* `prop` samples for training, instead of a random selection. `group_initial_split()` creates splits of the data based on some grouping variable, so that all data in a "group" is assigned to the same split.

Usage

```
initial_split(data, prop = 3/4, strata = NULL, breaks = 4, pool = 0.1, ...)

initial_time_split(data, prop = 3/4, lag = 0, ...)

training(x, ...)

## Default S3 method:
training(x, ...)

## S3 method for class 'rsplit'
training(x, ...)

testing(x, ...)

## Default S3 method:
testing(x, ...)

## S3 method for class 'rsplit'
testing(x, ...)

group_initial_split(data, group, prop = 3/4, ..., strata = NULL, pool = 0.1)
```

Arguments

<code>data</code>	A data frame.
<code>prop</code>	The proportion of data to be retained for modeling/analysis.
<code>strata</code>	A variable in <code>data</code> (single character or name) used to conduct stratified sampling. When not <code>NULL</code> , each resample is created within the stratification variable. Numeric <code>strata</code> are binned into quartiles.
<code>breaks</code>	A single number giving the number of bins desired to stratify a numeric stratification variable.
<code>pool</code>	A proportion of data used to determine if a particular group is too small and should be pooled into another group. We do not recommend decreasing this argument below its default of 0.1 because of the dangers of stratifying groups that are too small.
<code>...</code>	These dots are for future extensions and must be empty.
<code>lag</code>	A value to include a lag between the assessment and analysis set. This is useful if lagged predictors will be used during training and testing.

x	An rsplit object produced by <code>initial_split()</code> or <code>initial_time_split()</code> .
group	A variable in data (single character or name) used for grouping observations with the same value to either the analysis or assessment set within a fold.

Details

`training()` and `testing()` are used to extract the resulting data.

With a `strata` argument, the random sampling is conducted *within the stratification variable*. This can help ensure that the resamples have equivalent proportions as the original data set. For a categorical variable, sampling is conducted separately within each class. For a numeric stratification variable, `strata` is binned into quartiles, which are then used to stratify. Strata below 10% of the total are pooled together; see `make_strata()` for more details.

Value

An rsplit object that can be used with the `training()` and `testing()` functions to extract the data in each split.

Examples

```
set.seed(1353)
car_split <- initial_split(mtcars)
train_data <- training(car_split)
test_data <- testing(car_split)

data(drinks, package = "modeldata")
drinks_split <- initial_time_split(drinks)
train_data <- training(drinks_split)
test_data <- testing(drinks_split)
c(max(train_data$date), min(test_data$date)) # no lag

# With 12 period lag
drinks_lag_split <- initial_time_split(drinks, lag = 12)
train_data <- training(drinks_lag_split)
test_data <- testing(drinks_lag_split)
c(max(train_data$date), min(test_data$date)) # 12 period lag

set.seed(1353)
car_split <- group_initial_split(mtcars, cyl)
train_data <- training(car_split)
test_data <- testing(car_split)
```

initial_validation_split

Create an Initial Train/Validation/Test Split

Description

`initial_validation_split()` creates a random three-way split of the data into a training set, a validation set, and a testing set. `initial_validation_time_split()` does the same, but instead of a random selection the training, validation, and testing set are in order of the full data set, with the first observations being put into the training set. `group_initial_validation_split()` creates similar random splits of the data based on some grouping variable, so that all data in a "group" are assigned to the same partition.

Usage

```
initial_validation_split(
  data,
  prop = c(0.6, 0.2),
  strata = NULL,
  breaks = 4,
  pool = 0.1,
  ...
)

initial_validation_time_split(data, prop = c(0.6, 0.2), ...)

group_initial_validation_split(
  data,
  group,
  prop = c(0.6, 0.2),
  ...,
  strata = NULL,
  pool = 0.1
)

## S3 method for class 'initial_validation_split'
training(x, ...)

## S3 method for class 'initial_validation_split'
testing(x, ...)

validation(x, ...)

## Default S3 method:
validation(x, ...)

## S3 method for class 'initial_validation_split'
validation(x, ...)
```

Arguments

`data` A data frame.

prop	A length-2 vector of proportions of data to be retained for training and validation data, respectively.
strata	A variable in data (single character or name) used to conduct stratified sampling. When not NULL, each resample is created within the stratification variable. Numeric strata are binned into quartiles.
breaks	A single number giving the number of bins desired to stratify a numeric stratification variable.
pool	A proportion of data used to determine if a particular group is too small and should be pooled into another group. We do not recommend decreasing this argument below its default of 0.1 because of the dangers of stratifying groups that are too small.
...	These dots are for future extensions and must be empty.
group	A variable in data (single character or name) used for grouping observations with the same value to either the analysis or assessment set within a fold.
x	An object of class <code>initial_validation_split</code> .

Details

`training()`, `validation()`, and `testing()` can be used to extract the resulting data sets. Use `validation_set()` to create an `rset` object for use with functions from the `tune` package such as `tune::tune_grid()`.

With a `strata` argument, the random sampling is conducted *within the stratification variable*. This can help ensure that the resamples have equivalent proportions as the original data set. For a categorical variable, sampling is conducted separately within each class. For a numeric stratification variable, `strata` is binned into quartiles, which are then used to stratify. Strata below 10% of the total are pooled together; see `make_strata()` for more details.

Value

An `initial_validation_split` object that can be used with the `training()`, `validation()`, and `testing()` functions to extract the data in each split.

See Also

`validation_set()`

Examples

```
set.seed(1353)
car_split <- initial_validation_split(mtcars)
train_data <- training(car_split)
validation_data <- validation(car_split)
test_data <- testing(car_split)

data(drinks, package = "modeldata")
drinks_split <- initial_validation_time_split(drinks)
train_data <- training(drinks_split)
validation_data <- validation(drinks_split)
```

```

c(max(train_data$date), min(validation_data$date))

data(ames, package = "modeldata")
set.seed(1353)
ames_split <- group_initial_validation_split(ames, group = Neighborhood)
train_data <- training(ames_split)
validation_data <- validation(ames_split)
test_data <- testing(ames_split)

```

int_pctl	<i>Bootstrap confidence intervals</i>
----------	---------------------------------------

Description

Calculate bootstrap confidence intervals using various methods.

Usage

```

int_pctl(.data, ...)

## S3 method for class 'bootstraps'
int_pctl(.data, statistics, alpha = 0.05, ...)

int_t(.data, ...)

## S3 method for class 'bootstraps'
int_t(.data, statistics, alpha = 0.05, ...)

int_bca(.data, ...)

## S3 method for class 'bootstraps'
int_bca(.data, statistics, alpha = 0.05, .fn, ...)

```

Arguments

<code>.data</code>	A data frame containing the bootstrap resamples created using <code>bootstraps()</code> . For t- and BCa-intervals, the <code>apparent</code> argument should be set to <code>TRUE</code> . Even if the <code>apparent</code> argument is set to <code>TRUE</code> for the percentile method, the <code>apparent</code> data is never used in calculating the percentile confidence interval.
<code>...</code>	Arguments to pass to <code>.fn</code> (<code>int_bca()</code> only).
<code>statistics</code>	An unquoted column name or dplyr selector that identifies a single column in the data set containing the individual bootstrap estimates. This must be a list column of tidy tibbles (with columns <code>term</code> and <code>estimate</code>). Optionally, users can include columns whose names begin with a period and the intervals will be created for each combination of these variables and the <code>term</code> column. For t-intervals, a standard tidy column (usually called <code>std.error</code>) is required. See the examples below.

alpha	Level of significance.
.fn	A function to calculate statistic of interest. The function should take an <code>rsplit</code> as the first argument and the ... are required.

Details

Percentile intervals are the standard method of obtaining confidence intervals but require thousands of resamples to be accurate. T-intervals may need fewer resamples but require a corresponding variance estimate. Bias-corrected and accelerated intervals require the original function that was used to create the statistics of interest and are computationally taxing.

Value

Each function returns a tibble with columns `.lower`, `.estimate`, `.upper`, `.alpha`, `.method`, and `term`. `.method` is the type of interval (eg. "percentile", "student-t", or "BCa"). `term` is the name of the estimate. Note the `.estimate` returned from `int_pctl()` is the mean of the estimates from the bootstrap resamples and not the estimate from the apparent model.

References

<https://rsample.tidymodels.org/articles/Applications/Intervals.html>

Davison, A., & Hinkley, D. (1997). *Bootstrap Methods and their Application*. Cambridge: Cambridge University Press. doi:10.1017/CBO9780511802843

See Also

[reg_intervals\(\)](#)

Examples

```
library(broom)
library(dplyr)
library(purrr)
library(tibble)
library(tidyr)

# -----

lm_est <- function(split, ...) {
  lm(mpg ~ disp + hp, data = analysis(split)) %>%
    tidy()
}

set.seed(52156)
car_rs <-
  bootstraps(mtcars, 500, apparent = TRUE) %>%
  mutate(results = map(splits, lm_est))

int_pctl(car_rs, results)
int_t(car_rs, results)
```

```

int_bca(car_rs, results, .fn = lm_est)

# -----

# putting results into a tidy format
rank_corr <- function(split) {
  dat <- analysis(split)
  tibble(
    term = "corr",
    estimate = cor(dat$sqft, dat$price, method = "spearman"),
    # don't know the analytical std.error so no t-intervals
    std.error = NA_real_
  )
}

set.seed(69325)
data(Sacramento, package = "modeldata")
bootstraps(Sacramento, 1000, apparent = TRUE) %>%
  mutate(correlations = map(splits, rank_corr)) %>%
  int_pctl(correlations)

# -----

# An example of computing the interval for each value of a custom grouping
# factor (type of house in this example)

# Get regression estimates for each house type
lm_est <- function(split, ...) {
  analysis(split) %>%
    tidyr::nest(.by = c(type)) %>%
    # Compute regression estimates for each house type
    mutate(
      betas = purrr::map(data, ~ lm(log10(price) ~ sqft, data = .x) %>% tidy())
    ) %>%
    # Convert the column name to begin with a period
    rename(.type = type) %>%
    select(.type, betas) %>%
    unnest(cols = betas)
}

set.seed(52156)
house_rs <-
  bootstraps(Sacramento, 1000, apparent = TRUE) %>%
  mutate(results = map(splits, lm_est))

int_pctl(house_rs, results)

```

Description

Produce a vector of resampling labels (e.g. "Fold1") from an rset object. Currently, `nested_cv()` is not supported.

Usage

```
## S3 method for class 'rset'
labels(object, make_factor = FALSE, ...)

## S3 method for class 'vfold_cv'
labels(object, make_factor = FALSE, ...)
```

Arguments

object	An rset object.
make_factor	A logical for whether the results should be a character or a factor.
...	Not currently used.

Value

A single character or factor vector.

Examples

```
labels(vfold_cv(mtcars))
```

labels.rsplitt	<i>Find Labels from rsplitt Object</i>
----------------	--

Description

Produce a tibble of identification variables so that single splits can be linked to a particular resample.

Usage

```
## S3 method for class 'rsplitt'
labels(object, ...)
```

Arguments

object	An rsplitt object
...	Not currently used.

Value

A tibble.

See Also

`add_resample_id`

Examples

```
cv_splits <- vfold_cv(mtcars)
labels(cv_splits$splits[[1]])
```

loo_cv

Leave-One-Out Cross-Validation

Description

Leave-one-out (LOO) cross-validation uses one data point in the original set as the assessment data and all other data points as the analysis set. A LOO resampling set has as many resamples as rows in the original data set.

Usage

```
loo_cv(data, ...)
```

Arguments

<code>data</code>	A data frame.
<code>...</code>	These dots are for future extensions and must be empty.

Value

An tibble with classes `loo_cv`, `rset`, `tbl_df`, `tbl`, and `data.frame`. The results include a column for the data split objects and one column called `id` that has a character string with the resample identifier.

Examples

```
loo_cv(mtcars)
```

make_splits

Constructors for split objects

Description

Constructors for split objects

Usage

```

make_splits(x, ...)

## Default S3 method:
make_splits(x, ...)

## S3 method for class 'list'
make_splits(x, data, class = NULL, ...)

## S3 method for class 'data.frame'
make_splits(x, assessment, ...)

```

Arguments

x	A list of integers with names "analysis" and "assessment", or a data frame of analysis or training data.
...	Not currently used.
data	A data frame.
class	An optional class to give the object.
assessment	A data frame of assessment or testing data, which can be empty.

Examples

```

df <- data.frame(
  year = 1900:1999,
  value = 10 + 8*1900:1999 + runif(100L, 0, 100)
)
split_from_indices <- make_splits(
  x = list(analysis = which(df$year <= 1980),
          assessment = which(df$year > 1980)),
  data = df
)
split_from_data_frame <- make_splits(
  x = df[df$year <= 1980,],
  assessment = df[df$year > 1980,]
)
identical(split_from_indices, split_from_data_frame)

```

make_strata*Create or Modify Stratification Variables*

Description

This function can create strata from numeric data and make non-numeric data more conducive for stratification.

Usage

```
make_strata(x, breaks = 4, nunique = 5, pool = 0.1, depth = 20)
```

Arguments

x	An input vector.
breaks	A single number giving the number of bins desired to stratify a numeric stratification variable.
nunique	An integer for the number of unique value threshold in the algorithm.
pool	A proportion of data used to determine if a particular group is too small and should be pooled into another group. We do not recommend decreasing this argument below its default of 0.1 because of the dangers of stratifying groups that are too small.
depth	An integer that is used to determine the best number of percentiles that should be used. The number of bins are based on $\min(5, \text{floor}(n / \text{depth}))$ where $n = \text{length}(x)$. If x is numeric, there must be at least 40 rows in the data set (when depth = 20) to conduct stratified sampling.

Details

For numeric data, if the number of unique levels is less than nunique, the data are treated as categorical data.

For categorical inputs, the function will find levels of x that occur in the data with percentage less than pool. The values from these groups will be randomly assigned to the remaining strata (as will data points that have missing values in x).

For numeric data with more unique values than nunique, the data will be converted to being categorical based on percentiles of the data. The percentile groups will have no more than 20 percent of the data in each group. Again, missing values in x are randomly assigned to groups.

Value

A factor vector.

Examples

```

set.seed(61)
x1 <- rpois(100, lambda = 5)
table(x1)
table(make_strata(x1))

set.seed(554)
x2 <- rpois(100, lambda = 1)
table(x2)
table(make_strata(x2))

# small groups are randomly assigned
x3 <- factor(x2)
table(x3)
table(make_strata(x3))

x4 <- rep(LETTERS[1:7], c(37, 26, 3, 7, 11, 10, 2))
table(x4)
table(make_strata(x4))
table(make_strata(x4, pool = 0.1))
table(make_strata(x4, pool = 0.0))

# not enough data to stratify
x5 <- rnorm(20)
table(make_strata(x5))

set.seed(483)
x6 <- rnorm(200)
quantile(x6, probs = (0:10) / 10)
table(make_strata(x6, breaks = 10))

```

manual_rset

Manual resampling

Description

`manual_rset()` is used for constructing the most minimal rset possible. It can be useful when you have custom `rsplit` objects built from `make_splits()`, or when you want to create a new rset from splits contained within an existing rset.

Usage

```
manual_rset(splits, ids)
```

Arguments

<code>splits</code>	A list of "rsplit" objects. It is easiest to create these using <code>make_splits()</code> .
<code>ids</code>	A character vector of ids. The length of <code>ids</code> must be the same as the length of <code>splits</code> .

Examples

```
df <- data.frame(x = c(1, 2, 3, 4, 5, 6))

# Create an rset from custom indices
indices <- list(
  list(analysis = c(1L, 2L), assessment = 3L),
  list(analysis = c(4L, 5L), assessment = 6L)
)

splits <- lapply(indices, make_splits, data = df)

manual_rset(splits, c("Split 1", "Split 2"))

# You can also use this to create an rset from a subset of an
# existing rset
resamples <- vfold_cv(mtcars)
best_split <- resamples[5, ]
manual_rset(best_split$splits, best_split$id)
```

mc_cv

Monte Carlo Cross-Validation

Description

One resample of Monte Carlo cross-validation takes a random sample (without replacement) of the original data set to be used for analysis. All other data points are added to the assessment set.

Usage

```
mc_cv(data, prop = 3/4, times = 25, strata = NULL, breaks = 4, pool = 0.1, ...)
```

Arguments

<code>data</code>	A data frame.
<code>prop</code>	The proportion of data to be retained for modeling/analysis.
<code>times</code>	The number of times to repeat the sampling.
<code>strata</code>	A variable in <code>data</code> (single character or name) used to conduct stratified sampling. When not <code>NULL</code> , each resample is created within the stratification variable. Numeric strata are binned into quartiles.
<code>breaks</code>	A single number giving the number of bins desired to stratify a numeric stratification variable.
<code>pool</code>	A proportion of data used to determine if a particular group is too small and should be pooled into another group. We do not recommend decreasing this argument below its default of 0.1 because of the dangers of stratifying groups that are too small.
<code>...</code>	These dots are for future extensions and must be empty.

Details

With a `strata` argument, the random sampling is conducted *within the stratification variable*. This can help ensure that the resamples have equivalent proportions as the original data set. For a categorical variable, sampling is conducted separately within each class. For a numeric stratification variable, `strata` is binned into quartiles, which are then used to stratify. Strata below 10% of the total are pooled together; see [make_strata\(\)](#) for more details.

Value

An tibble with classes `mc_cv`, `rset`, `tbl_df`, `tbl`, and `data.frame`. The results include a column for the data split objects and a column called `id` that has a character string with the resample identifier.

Examples

```
mc_cv(mtcars, times = 2)
mc_cv(mtcars, prop = .5, times = 2)

library(purrr)
data(wa_churn, package = "modeldata")

set.seed(13)
resample1 <- mc_cv(wa_churn, times = 3, prop = .5)
map_dbl(
  resample1$splits,
  function(x) {
    dat <- as.data.frame(x)$churn
    mean(dat == "Yes")
  }
)

set.seed(13)
resample2 <- mc_cv(wa_churn, strata = churn, times = 3, prop = .5)
map_dbl(
  resample2$splits,
  function(x) {
    dat <- as.data.frame(x)$churn
    mean(dat == "Yes")
  }
)

set.seed(13)
resample3 <- mc_cv(wa_churn, strata = tenure, breaks = 6, times = 3, prop = .5)
map_dbl(
  resample3$splits,
  function(x) {
    dat <- as.data.frame(x)$churn
    mean(dat == "Yes")
  }
)
```

nested_cv	<i>Nested or Double Resampling</i>
-----------	------------------------------------

Description

nested_cv() can be used to take the results of one resampling procedure and conduct further resamples within each split. Any type of resampling used in rsample can be used.

Usage

```
nested_cv(data, outside, inside)
```

Arguments

data	A data frame.
outside	The initial resampling specification. This can be an already created object or an expression of a new object (see the examples below). If the latter is used, the data argument does not need to be specified and, if it is given, will be ignored.
inside	An expression for the type of resampling to be conducted within the initial procedure.

Details

It is a bad idea to use bootstrapping as the outer resampling procedure (see the example below)

Value

An tibble with nested_cv class and any other classes that outer resampling process normally contains. The results include a column for the outer data split objects, one or more id columns, and a column of nested tibbles called inner_resamples with the additional resamples.

Examples

```
## Using expressions for the resampling procedures:
nested_cv(mtcars, outside = vfold_cv(v = 3), inside = bootstraps(times = 5))

## Using an existing object:
folds <- vfold_cv(mtcars)
nested_cv(mtcars, folds, inside = bootstraps(times = 5))

## The dangers of outer bootstraps:
set.seed(2222)
bad_idea <- nested_cv(mtcars,
  outside = bootstraps(times = 5),
  inside = vfold_cv(v = 3)
)

first_outer_split <- get_rsplitted(bad_idea, 1)
```

```

outer_analysis <- analysis(first_outer_split)
sum(grepl("Camaro Z28", rownames(outer_analysis)))

## For the 3-fold CV used inside of each bootstrap, how are the replicated
## `Camaro Z28` data partitioned?
first_inner_split <- get_rsplitted(bad_idea$inner_resamples[[1]], 1)
inner_analysis <- analysis(first_inner_split)
inner_assess <- assessment(first_inner_split)

sum(grepl("Camaro Z28", rownames(inner_analysis)))
sum(grepl("Camaro Z28", rownames(inner_assess)))

```

permutations

Permutation sampling

Description

A permutation sample is the same size as the original data set and is made by permuting/shuffling one or more columns. This results in analysis samples where some columns are in their original order and some columns are permuted to a random order. Unlike other sampling functions in `rsample`, there is no assessment set and calling `assessment()` on a permutation split will throw an error.

Usage

```
permutations(data, permute = NULL, times = 25, apparent = FALSE, ...)
```

Arguments

<code>data</code>	A data frame.
<code>permute</code>	One or more columns to shuffle. This argument supports tidyselect selectors. Multiple expressions can be combined with <code>c()</code> . Variable names can be used as if they were positions in the data frame, so expressions like <code>x:y</code> can be used to select a range of variables. See language for more details.
<code>times</code>	The number of permutation samples.
<code>apparent</code>	A logical. Should an extra resample be added where the analysis is the standard data set.
<code>...</code>	These dots are for future extensions and must be empty.

Details

The argument `apparent` enables the option of an additional "resample" where the analysis data set is the same as the original data set. Permutation-based resampling can be especially helpful for computing a statistic under the null hypothesis (e.g. `t`-statistic). This forms the basis of a permutation test, which computes a test statistic under all possible permutations of the data.

Value

A tibble with classes `permutations`, `rset`, `tbl_df`, `tbl`, and `data.frame`. The results include a column for the data split objects and a column called `id` that has a character string with the resample identifier.

Examples

```
permutations(mtcars, mpg, times = 2)
permutations(mtcars, mpg, times = 2, apparent = TRUE)

library(purrr)
resample1 <- permutations(mtcars, starts_with("c"), times = 1)
resample1$splits[[1]] %>% analysis()

resample2 <- permutations(mtcars, hp, times = 10, apparent = TRUE)
map_dbl(resample2$splits, function(x) {
  t.test(hp ~ vs, data = analysis(x))$statistic
})
```

populate

Add Assessment Indices

Description

Many `rsplit` and `rset` objects do not contain indicators for the assessment samples. `populate()` can be used to fill the slot for the appropriate indices.

Usage

```
populate(x, ...)
```

Arguments

<code>x</code>	A <code>rsplit</code> and <code>rset</code> object.
<code>...</code>	Not currently used.

Value

An object of the same kind with the integer indices.

Examples

```
set.seed(28432)
fold_rs <- vfold_cv(mtcars)

fold_rs$splits[[1]]$out_id
complement(fold_rs$splits[[1]])
```

```

populate(fold_rs$splits[[1]])$out_id

fold_rs_all <- populate(fold_rs)
fold_rs_all$splits[[1]]$out_id

```

reg_intervals	<i>A convenience function for confidence intervals with linear-ish parametric models</i>
---------------	--

Description

A convenience function for confidence intervals with linear-ish parametric models

Usage

```

reg_intervals(
  formula,
  data,
  model_fn = "lm",
  type = "student-t",
  times = NULL,
  alpha = 0.05,
  filter = term != "(Intercept)",
  keep_reps = FALSE,
  ...
)

```

Arguments

formula	An R model formula with one outcome and at least one predictor.
data	A data frame.
model_fn	The model to fit. Allowable values are "lm", "glm", "survreg", and "coxph". The latter two require that the survival package be installed.
type	The type of bootstrap confidence interval. Values of "student-t" and "percentile" are allowed.
times	A single integer for the number of bootstrap samples. If left NULL, 1,001 are used for t-intervals and 2,001 for percentile intervals.
alpha	Level of significance.
filter	A logical expression used to remove rows from the final result, or NULL to keep all rows.
keep_reps	Should the individual parameter estimates for each bootstrap sample be retained?
...	Options to pass to the model function (such as family for <code>stats::glm()</code>).

Value

A tibble with columns "term", ".lower", ".estimate", ".upper", ".alpha", and ".method". If keep_reps = TRUE, an additional list column called ".replicates" is also returned.

References

Davison, A., & Hinkley, D. (1997). *Bootstrap Methods and their Application*. Cambridge: Cambridge University Press. doi:10.1017/CBO9780511802843

Bootstrap Confidence Intervals, <https://rsample.tidymodels.org/articles/Applications/Intervals.html>

See Also

`int_pctl()`, `int_t()`

Examples

```
set.seed(1)
reg_intervals(mpg ~ I(1 / sqrt(displacement)), data = mtcars)

set.seed(1)
reg_intervals(mpg ~ I(1 / sqrt(displacement)), data = mtcars, keep_reps = TRUE)
```

reshuffle_rset	<i>"Reshuffle" an rset to re-generate a new rset with the same parameters</i>
----------------	---

Description

This function re-generates an rset object, using the same arguments used to generate the original.

Usage

```
reshuffle_rset(rset)
```

Arguments

rset The rset object to be reshuffled

Value

An rset of the same class as rset.

Examples

```
set.seed(123)
(starting_splits <- group_vfold_cv(mtcars, cyl, v = 3))
reshuffle_rset(starting_splits)
```

reverse_splits

Reverse the analysis and assessment sets

Description

This functions "swaps" the analysis and assessment sets of either a single `rsplit` or all `rsplits` in the `splits` column of an `rset` object.

Usage

```
reverse_splits(x, ...)

## Default S3 method:
reverse_splits(x, ...)

## S3 method for class 'permutations'
reverse_splits(x, ...)

## S3 method for class 'perm_split'
reverse_splits(x, ...)

## S3 method for class 'rsplit'
reverse_splits(x, ...)

## S3 method for class 'rset'
reverse_splits(x, ...)
```

Arguments

<code>x</code>	An <code>rset</code> or <code>rsplit</code> object.
<code>...</code>	Not currently used.

Value

An object of the same class as `x`

Examples

```
set.seed(123)
starting_splits <- vfold_cv(mtcars, v = 3)
reverse_splits(starting_splits)
reverse_splits(starting_splits$splits[[1]])
```

rolling_origin	<i>Rolling Origin Forecast Resampling</i>
----------------	---

Description**[Superseded]**

This resampling method is useful when the data set has a strong time component. The resamples are not random and contain data points that are consecutive values. The function assumes that the original data set are sorted in time order.

This function is superseded by [sliding_window\(\)](#), [sliding_index\(\)](#), and [sliding_period\(\)](#) which provide more flexibility and control. Superseded functions will not go away, but active development will be focused on the new functions.

Usage

```
rolling_origin(
  data,
  initial = 5,
  assess = 1,
  cumulative = TRUE,
  skip = 0,
  lag = 0,
  ...
)
```

Arguments

data	A data frame.
initial	The number of samples used for analysis/modeling in the initial resample.
assess	The number of samples used for each assessment resample.
cumulative	A logical. Should the analysis resample grow beyond the size specified by initial at each resample?.
skip	A integer indicating how many (if any) <i>additional</i> resamples to skip to thin the total amount of data points in the analysis resample. See the example below.
lag	A value to include a lag between the assessment and analysis set. This is useful if lagged predictors will be used during training and testing.
...	These dots are for future extensions and must be empty.

Details

The main options, `initial` and `assess`, control the number of data points from the original data that are in the analysis and assessment set, respectively. When `cumulative = TRUE`, the analysis set will grow as resampling continues while the assessment set size will always remain static. `skip` enables the function to not use every data point in the resamples. When `skip = 0`, the resampling data sets will increment by one position. Suppose that the rows of a data set are consecutive days.

Using `skip = 6` will make the analysis data set to operate on *weeks* instead of days. The assessment set size is not affected by this option.

Value

An tibble with classes `rolling_origin`, `rset`, `tbl_df`, `tbl`, and `data.frame`. The results include a column for the data split objects and a column called `id` that has a character string with the resample identifier.

See Also

[sliding_window\(\)](#), [sliding_index\(\)](#), and [sliding_period\(\)](#) for additional time based resampling functions.

Examples

```
set.seed(1131)
ex_data <- data.frame(row = 1:20, some_var = rnorm(20))
dim(rolling_origin(ex_data))
dim(rolling_origin(ex_data, skip = 2))
dim(rolling_origin(ex_data, skip = 2, cumulative = FALSE))

# You can also roll over calendar periods by first nesting by that period,
# which is especially useful for irregular series where a fixed window
# is not useful. This example slides over 5 years at a time.
library(dplyr)
library(tidyr)
data(drinks, package = "modeldata")

drinks_annual <- drinks %>%
  mutate(year = as.POSIXlt(date)$year + 1900) %>%
  nest(data = c(-year))

multi_year_roll <- rolling_origin(drinks_annual, cumulative = FALSE)

analysis(multi_year_roll$splits[[1]])
assessment(multi_year_roll$splits[[1]])
```

Description

This page lays out the compatibility between `rsample` and `dplyr`. The `rset` objects from `rsample` are a specific subclass of tibbles, hence standard `dplyr` operations like joins as well row or column modifications work. However, whether the operation returns an `rset` or a tibble depends on the details of the operation.

The overarching principle is that any operation which leaves the specific characteristics of an rset intact will return an rset. If an operation modifies any of the following characteristics, the result will be a tibble rather than an rset:

- Rows: The number of rows needs to remain unchanged to retain the rset property. For example, you can't have a 10-fold CV object without 10 rows. The order of the rows can be changed though and the object remains an rset.
- Columns: The splits column and the id column(s) are required for an rset and need to remain untouched. They cannot be dropped, renamed, or modified if the result should remain an rset.

Joins:

The following affect all of the dplyr joins, such as `left_join()`, `right_join()`, `full_join()`, and `inner_join()`.

The resulting object is an rset if the number of rows is unaffected. Rows can be reordered but not added or removed, otherwise the resulting object is a tibble.

operation	same rows, possibly reordered	add or remove rows
<code>join(rset, tbl)</code>	rset	tibble

Row Operations:

The resulting object is an rset if the number of rows is unaffected. Rows can be reordered but not added or removed, otherwise the resulting object is a tibble.

operation	same rows, possibly reordered	add or remove rows
<code>rset[ind,]</code>	rset	tibble
<code>slice(rset)</code>	rset	tibble
<code>filter(rset)</code>	rset	tibble
<code>arrange(rset)</code>	rset	tibble

Column Operations:

The resulting object is an rset if the required splits and id columns remain unaltered. Otherwise the resulting object is a tibble.

operation	required columns unaltered	required columns removed, renamed, or modified
<code>rset[, ind]</code>	rset	tibble
<code>select(rset)</code>	rset	tibble
<code>rename(rset)</code>	rset	tibble
<code>mutate(rset)</code>	rset	tibble

rsmple2caret	<i>Convert Resampling Objects to Other Formats</i>
--------------	--

Description

These functions can convert resampling objects between **rsmple** and **caret**.

Usage

```
rsmple2caret(object, data = c("analysis", "assessment"))
```

```
caret2rsmple(ctrl, data = NULL)
```

Arguments

object	An rset object. Currently, <code>nested_cv()</code> is not supported.
data	The data that was originally used to produce the ctrl object.
ctrl	An object produced by <code>caret::trainControl()</code> that has had the index and indexOut elements populated by integers. One method of getting this is to extract the control objects from an object produced by train.

Value

`rsmple2caret()` returns a list that mimics the index and indexOut elements of a `trainControl` object. `caret2rsmple()` returns an rset object of the appropriate class.

rset_reconstruct	<i>Extending rsmple with new rset subclasses</i>
------------------	--

Description

`rset_reconstruct()` encapsulates the logic for allowing new rset subclasses to work properly with `vctrs` (through `vctrs::vec_restore()`) and `dplyr` (through `dplyr::dplyr_reconstruct()`). It is intended to be a developer tool, and is not required for normal usage of `rsmple`.

Usage

```
rset_reconstruct(x, to)
```

Arguments

x	A data frame to restore to an rset subclass.
to	An rset subclass to restore to.

Details

rset objects are considered "reconstructable" after a vctrs/dplyr operation if:

- x and to both have an identical column named "splits" (column and row order do not matter).
- x and to both have identical columns prefixed with "id" (column and row order do not matter).

Value

x restored to the rset subclass of to.

Examples

```
to <- bootstraps(mtcars, times = 25)

# Imitate a vctrs/dplyr operation,
# where the class might be lost along the way
x <- tibble::as_tibble(to)

# Say we added a new column to `x`. Here we mock a `mutate()`.
x$foo <- "bar"

# This is still reconstructable to `to`
rset_reconstruct(x, to)

# Say we lose the first row
x <- x[-1, ]

# This is no longer reconstructable to `to`, as `x` is no longer an rset
# bootstraps object with 25 bootstraps if one is lost!
rset_reconstruct(x, to)
```

Description

These resampling functions are focused on various forms of *time series* resampling.

- `sliding_window()` uses the row number when computing the resampling indices. It is independent of any time index, but is useful with completely regular series.
- `sliding_index()` computes resampling indices relative to the index column. This is often a Date or POSIXct column, but doesn't have to be. This is useful when resampling irregular series, or for using irregular lookback periods such as `lookback = lubridate::years(1)` with daily data (where the number of days in a year may vary).
- `sliding_period()` first breaks up the index into less granular groups based on period, and then uses that to construct the resampling indices. This is extremely useful for constructing rolling monthly or yearly windows from daily data.

Usage

```
sliding_window(  
  data,  
  ...,  
  lookback = 0L,  
  assess_start = 1L,  
  assess_stop = 1L,  
  complete = TRUE,  
  step = 1L,  
  skip = 0L  
)
```

```
sliding_index(  
  data,  
  index,  
  ...,  
  lookback = 0L,  
  assess_start = 1L,  
  assess_stop = 1L,  
  complete = TRUE,  
  step = 1L,  
  skip = 0L  
)
```

```
sliding_period(  
  data,  
  index,  
  period,  
  ...,  
  lookback = 0L,  
  assess_start = 1L,  
  assess_stop = 1L,  
  complete = TRUE,  
  step = 1L,  
  skip = 0L,  
  every = 1L,  
  origin = NULL  
)
```

Arguments

<code>data</code>	A data frame.
<code>...</code>	These dots are for future extensions and must be empty.
<code>lookback</code>	The number of elements to look back from the current element when computing the resampling indices of the analysis set. The current row is always included in the analysis set. <ul style="list-style-type: none">• For <code>sliding_window()</code>, a single integer defining the number of rows to look back from the current row.

- For `sliding_index()`, a single object that will be subtracted from the index as `index - lookback` to define the boundary of where to start searching for rows to include in the current resample. This is often an integer value corresponding to the number of days to look back, or a lubridate Period object.
- For `sliding_period()`, a single integer defining the number of groups to look back from the current group, where the groups were defined from breaking up the index according to the period.

In all cases, `Inf` is also allowed to force an expanding window.

`assess_start`, `assess_stop`

This combination of arguments determines how far into the future to look when constructing the assessment set. Together they construct a range of `[index + assess_start, index + assess_stop]` to search for rows to include in the assessment set.

Generally, `assess_start` will always be 1 to indicate that the first value to potentially include in the assessment set should start one element after the current row, but it can be increased to a larger value to create "gaps" between the analysis and assessment set if you are worried about high levels of correlation in short term forecasting.

- For `sliding_window()`, these are both single integers defining the number of rows to look forward from the current row.
- For `sliding_index()`, these are single objects that will be added to the index to compute the range to search for rows to include in the assessment set. This is often an integer value corresponding to the number of days to look forward, or a lubridate Period object.
- For `sliding_period()`, these are both single integers defining the number of groups to look forward from the current group, where the groups were defined from breaking up the index according to the period.

`complete`

A single logical. When using `lookback` to compute the analysis sets, should only complete windows be considered? If set to `FALSE`, partial windows will be used until it is possible to create a complete window (based on `lookback`). This is a way to use an expanding window up to a certain point, and then switch to a sliding window.

`step`

A single positive integer. After computing the resampling indices, `step` is used to thin out the results by selecting every `step`-th result by subsetting the indices with `seq(1L, n_indices, by = step)`. `step` is applied after `skip`. Note that `step` is independent of any time index used.

`skip`

A single positive integer, or zero. After computing the resampling indices, the first `skip` results will be dropped by subsetting the indices with `seq(skip + 1L, n_indices)`. This can be especially useful when combined with `lookback = Inf`, which creates an expanding window starting from the first row. By skipping forward, you can drop the first few windows that have very few data points. `skip` is applied before `step`. Note that `skip` is independent of any time index used.

`index`

The index to compute resampling indices relative to, specified as a bare column name. This must be an existing column in data.

- For `sliding_index()`, this is commonly a date vector, but is not required.
- For `sliding_period()`, it is required that this is a Date or POSIXct vector.

	The index must be an <i>increasing</i> vector, but duplicate values are allowed. Additionally, the index cannot contain any missing values.
period	The period to group the index by. This is specified as a single string, such as "year" or "month". See the <code>.period</code> argument of <code>slider::slide_period()</code> for the full list of options and further explanation.
every	A single positive integer. The number of periods to group together. For example, if the period was set to "year" with an every value of 2, then the years 1970 and 1971 would be placed in the same group.
origin	The reference date time value. The default when left as NULL is the epoch time of 1970-01-01 00:00:00, <i>in the time zone of the index</i> . This is generally used to define the anchor time to count from, which is relevant when the every value is > 1.

See Also

`rolling_origin()`

`slider::slide()`, `slider::slide_index()`, and `slider::slide_period()`, which power these resamplers.

Examples

```
library(vctrs)
library(tibble)
library(modeldata)
data("Chicago")

index <- new_date(c(1, 3, 4, 7, 8, 9, 13, 15, 16, 17))
df <- tibble(x = 1:10, index = index)
df

# Look back two rows beyond the current row, for a total of three rows
# in each analysis set. Each assessment set is composed of the two rows after
# the current row.
sliding_window(df, lookback = 2, assess_stop = 2)

# Same as before, but step forward by 3 rows between each resampling slice,
# rather than just by 1.
rset <- sliding_window(df, lookback = 2, assess_stop = 2, step = 3)
rset

analysis(rset$splits[[1]])
analysis(rset$splits[[2]])

# Now slide relative to the `index` column in `df`. This time we look back
# 2 days from the current row's `index` value, and 2 days forward from
# it to construct the assessment set. Note that this series is irregular,
# so it produces different results than `sliding_window()`. Additionally,
# note that it is entirely possible for the assessment set to contain no
# data if you have a highly irregular series and "look forward" into a
# date range where no data points actually exist!
```

```
sliding_index(df, index, lookback = 2, assess_stop = 2)

# With `sliding_period()`, we can break up our date index into less granular
# chunks, and slide over them instead of the index directly. Here we'll use
# the Chicago data, which contains daily data spanning 16 years, and we'll
# break it up into rolling yearly chunks. Three years worth of data will
# be used for the analysis set, and one years worth of data will be held out
# for performance assessment.
sliding_period(
  Chicago,
  date,
  "year",
  lookback = 2,
  assess_stop = 1
)

# Because `lookback = 2`, three years are required to form a "complete"
# window of data. To allow partial windows, set `complete = FALSE`.
# Here that first constructs two expanding windows until a complete three
# year window can be formed, at which point we switch to a sliding window.
sliding_period(
  Chicago,
  date,
  "year",
  lookback = 2,
  assess_stop = 1,
  complete = FALSE
)

# Alternatively, you could break the resamples up by month. Here we'll
# use an expanding monthly window by setting `lookback = Inf`, and each
# assessment set will contain two months of data. To ensure that we have
# enough data to fit our models, we'll `skip` the first 4 expanding windows.
# Finally, to thin out the results, we'll `step` forward by 2 between
# each resample.
sliding_period(
  Chicago,
  date,
  "month",
  lookback = Inf,
  assess_stop = 2,
  skip = 4,
  step = 2
)
```

Description

The `tidy()` function from the **broom** package can be used on `rset` and `rsplit` objects to generate tibbles with which rows are in the analysis and assessment sets.

Usage

```
## S3 method for class 'rsplit'
tidy(x, unique_ind = TRUE, ...)

## S3 method for class 'rset'
tidy(x, unique_ind = TRUE, ...)

## S3 method for class 'vfold_cv'
tidy(x, ...)

## S3 method for class 'nested_cv'
tidy(x, unique_ind = TRUE, ...)
```

Arguments

<code>x</code>	A <code>rset</code> or <code>rsplit</code> object
<code>unique_ind</code>	Should unique row identifiers be returned? For example, if <code>FALSE</code> then bootstrapping results will include multiple rows in the sample for the same row in the original data.
<code>...</code>	These dots are for future extensions and must be empty.

Details

Note that for nested resampling, the rows of the inner resample, named `inner_Row`, are *relative* row indices and do not correspond to the rows in the original data set.

Value

A tibble with columns `Row` and `Data`. The latter has possible values "Analysis" or "Assessment". For `rset` inputs, identification columns are also returned but their names and values depend on the type of resampling. For `vfold_cv()`, contains a column "Fold" and, if repeats are used, another called "Repeats". `bootstraps()` and `mc_cv()` use the column "Resample".

Examples

```
library(ggplot2)
theme_set(theme_bw())

set.seed(4121)
cv <- tidy(vfold_cv(mtcars, v = 5))
ggplot(cv, aes(x = Fold, y = Row, fill = Data)) +
  geom_tile() +
  scale_fill_brewer()
```

```

set.seed(4121)
rcv <- tidy(vfold_cv(mtcars, v = 5, repeats = 2))
ggplot(rcv, aes(x = Fold, y = Row, fill = Data)) +
  geom_tile() +
  facet_wrap(~Repeat) +
  scale_fill_brewer()

set.seed(4121)
mccv <- tidy(mc_cv(mtcars, times = 5))
ggplot(mccv, aes(x = Resample, y = Row, fill = Data)) +
  geom_tile() +
  scale_fill_brewer()

set.seed(4121)
bt <- tidy(bootstraps(mtcars, time = 5))
ggplot(bt, aes(x = Resample, y = Row, fill = Data)) +
  geom_tile() +
  scale_fill_brewer()

dat <- data.frame(day = 1:30)
# Resample by week instead of day
ts_cv <- rolling_origin(dat,
  initial = 7, assess = 7,
  skip = 6, cumulative = FALSE
)
ts_cv <- tidy(ts_cv)
ggplot(ts_cv, aes(x = Resample, y = factor(Row), fill = Data)) +
  geom_tile() +
  scale_fill_brewer()

```

validation_set

*Create a Validation Split for Tuning***Description**

validation_set() creates a the validation split for model tuning.

Usage

```
validation_set(split, ...)
```

```
## S3 method for class 'val_split'
analysis(x, ...)
```

```
## S3 method for class 'val_split'
assessment(x, ...)
```

```
## S3 method for class 'val_split'
```

```

training(x, ...)

## S3 method for class 'val_split'
validation(x, ...)

## S3 method for class 'val_split'
testing(x, ...)

```

Arguments

split	An object of class <code>initial_validation_split</code> , such as resulting from <code>initial_validation_split()</code> or <code>group_initial_validation_split()</code> .
...	These dots are for future extensions and must be empty.
x	An <code>rsplit</code> object produced by <code>validation_set()</code> .

Value

An tibble with classes `validation_set`, `rset`, `tbl_df`, `tbl`, and `data.frame`. The results include a column for the data split object and a column called `id` that has a character string with the resample identifier.

Examples

```

set.seed(1353)
car_split <- initial_validation_split(mtcars)
car_set <- validation_set(car_split)

```

vfold_cv

V-Fold Cross-Validation

Description

V-fold cross-validation (also known as k-fold cross-validation) randomly splits the data into V groups of roughly equal size (called "folds"). A resample of the analysis data consists of V-1 of the folds while the assessment set contains the final fold. In basic V-fold cross-validation (i.e. no repeats), the number of resamples is equal to V.

Usage

```
vfold_cv(data, v = 10, repeats = 1, strata = NULL, breaks = 4, pool = 0.1, ...)
```

Arguments

data	A data frame.
v	The number of partitions of the data set.
repeats	The number of times to repeat the V-fold partitioning.

strata	A variable in data (single character or name) used to conduct stratified sampling. When not NULL, each resample is created within the stratification variable. Numeric strata are binned into quartiles.
breaks	A single number giving the number of bins desired to stratify a numeric stratification variable.
pool	A proportion of data used to determine if a particular group is too small and should be pooled into another group. We do not recommend decreasing this argument below its default of 0.1 because of the dangers of stratifying groups that are too small.
...	These dots are for future extensions and must be empty.

Details

With more than one repeat, the basic V-fold cross-validation is conducted each time. For example, if three repeats are used with $v = 10$, there are a total of 30 splits: three groups of 10 that are generated separately.

With a strata argument, the random sampling is conducted *within the stratification variable*. This can help ensure that the resamples have equivalent proportions as the original data set. For a categorical variable, sampling is conducted separately within each class. For a numeric stratification variable, strata is binned into quartiles, which are then used to stratify. Strata below 10% of the total are pooled together; see [make_strata\(\)](#) for more details.

Value

A tibble with classes vfold_cv, rset, tbl_df, tbl, and data.frame. The results include a column for the data split objects and one or more identification variables. For a single repeat, there will be one column called id that has a character string with the fold identifier. For repeats, id is the repeat number and an additional column called id2 that contains the fold information (within repeat).

Examples

```
vfold_cv(mtcars, v = 10)
vfold_cv(mtcars, v = 10, repeats = 2)

library(purrr)
data(wa_churn, package = "modeldata")

set.seed(13)
folds1 <- vfold_cv(wa_churn, v = 5)
map_dbl(
  folds1$splits,
  function(x) {
    dat <- as.data.frame(x)$churn
    mean(dat == "Yes")
  }
)

set.seed(13)
folds2 <- vfold_cv(wa_churn, strata = churn, v = 5)
```

```
map_dbl(
  folds2$splits,
  function(x) {
    dat <- as.data.frame(x)$churn
    mean(dat == "Yes")
  }
)

set.seed(13)
folds3 <- vfold_cv(wa_churn, strata = tenure, breaks = 6, v = 5)
map_dbl(
  folds3$splits,
  function(x) {
    dat <- as.data.frame(x)$churn
    mean(dat == "Yes")
  }
)
```

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