Package 'unjoin'

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Version 0.1.0

Description Separate a data frame in two based on key columns. The function unjoin() provides an inside-out version of a nested data frame. This is used to identify duplication and normalize it (in the database sense) by linking

Title Separate a Data Frame by Normalization

Contents

two tables with the redundancy removed. This is a basic requirement for detecting topology within spatial structures that has motivated the need for this package as a building block for workflows within more applied projects.

Depends R (>= 3.3.2)
License GPL-3
Encoding UTF-8
LazyData true
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Imports dplyr (>= 0.5.0), rlang, tibble
Suggests gapminder, tidyr, testthat, covr, spelling
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Language en-US
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Description

Split a table in two and remove repeated values.

Usage

```
unjoin(data, ..., key_col = "idx0")
## S3 method for class 'data.frame'
unjoin(data, ..., key_col = ".idx0")
## S3 method for class 'unjoin'
unjoin(data, ..., key_col = ".idx0")
```

Arguments

data	A data frame.
	Specification of columns to unjoin by. For full details, see the 'dplyr::select" documentation.
key_col	The name of the new column to key the two output data frames.

Details

The data frame on input is treated as "data", the new data frame is treated as the normalized key. This means that the split-off and de-duplicated table has the name given via the 'key_col' argument (defaults to ".idx0") and shares this name with the common key.

It's not yet clear if this flexibility around naming is a good idea, but it enables a simple scheme for chaining unjoins, though you'd better not use the same 'key_col' again.

This is a subset of the tasks done by nest.

See Also

'dplyr::inner_join' for the inverse operation.

'tidyr::nest' for the complementary operation resulting in one nested data frame

Examples

```
library(dplyr)
data("Seatbelts", package= "datasets")
x <- unjoin(as.data.frame(Seatbelts), front, law)
y <- inner_join(x$.idx0, x$data) %>% select(-.idx0)
all.equal(y[colnames(Seatbelts)], as.data.frame(Seatbelts))
```

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```
iris %>% unjoin(-Species)
chickwts %>% unjoin(weight)

if (require("gapminder")) {
   gapminder %>%
     group_by(country, continent) %>%
     unjoin()

   gapminder %>%
     unjoin(-country, -continent)
   unjoin(gapminder)
}
unjoin(iris, Petal.Width) %>% unjoin(Species, key_col = ".idx1")
```

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