Package ‘ttservice’

June 20, 2023

Type Package

Title A Service for Tidy Transcriptomics Software Suite

Version 0.3.6

Description It provides generic methods that are used by more than one package, avoiding conflicts. This package will be imported by 'tidySingleCellExperiment' and 'tidyseurat'.

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Depends R (>= 4.0.0)

Imports dplyr, Matrix

Suggests methods

Encoding UTF-8

RoxygenNote 7.2.3

NeedsCompilation no

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Repository CRAN

Date/Publication 2023-06-20 12:50:02 UTC

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aggregate_cells  Aggregate cells

Description

Combine cells into groups based on shared variables and aggregate feature counts.

Usage

aggregate_cells(
  .data,
  .sample = NULL,
  slot = "data",
  assays = NULL,
  aggregation_function = Matrix::rowSums
)

Arguments

.data 
A tidySingleCellExperiment object

.sample 
A vector of variables by which cells are aggregated

slot 
The slot to which the function is applied

assays 
The assay to which the function is applied

aggregation_function 
The method of cell-feature value aggregation

Value

A tibble object

Examples

print("pbmc_small |> aggregate_cells(c(groups, ident), assays = \"counts\")")

bind_rows

#’ Efficiently bind multiple data frames by row and column

Description

This is an efficient implementation of the common pattern of ‘do.call(rbind, dfs)’ or ‘do.call(cbind, dfs)’ for binding many data frames into one.

This is an efficient implementation of the common pattern of ‘do.call(rbind, dfs)’ or ‘do.call(cbind, dfs)’ for binding many data frames into one.
bind_rows

Usage

bind_rows(..., .id = NULL, add.cell.ids = NULL)
bind_cols(..., .id = NULL)

Arguments

... Data frames to combine.
   Each argument can either be a data frame, a list that could be a data frame, or a
   list of data frames.
   When row-binding, columns are matched by name, and any missing columns
   will be filled with NA.
   When column-binding, rows are matched by position, so all data frames must
   have the same number of rows. To match by value, not position, see mutate-
   joins.

.id Data frame identifier.
   When ‘.id’ is supplied, a new column of identifiers is created to link each row
   to its original data frame. The labels are taken from the named arguments to
   ‘bind_rows()’. When a list of data frames is supplied, the labels are taken from
   the names of the list. If no names are found a numeric sequence is used instead.

add.cell.ids from Seurat 3.0 A character vector of length(x = c(x, y)). Appends the corre-
   sponding values to the start of each objects’ cell names.

Details

The output of ‘bind_rows()’ will contain a column if that column appears in any of the inputs.

The output of ‘bind_rows()’ will contain a column if that column appears in any of the inputs.

Value

‘bind_rows()’ and ‘bind_cols()’ return the same type as the first input, either a data frame, ‘tbl_df’,
   or ‘grouped_df’.
   ‘bind_rows()' and 'bind_cols()' return the same type as the first input, either a data frame, ‘tbl_df’,
   or ‘grouped_df’.

Examples

print("small_pbmc |> bind_rows(small_pbmc")

print("small_pbmc |> bind_cols((annotation_column)")
join_features

Description
join_features() extracts and joins information for specific features

Usage
join_features(
  .data,
  features = NULL,
  all = FALSE,
  exclude_zeros = FALSE,
  shape = "long",
  ...
)

Arguments
.data A tidy SingleCellExperiment object
features A vector of feature identifiers to join
all If TRUE return all
exclude_zeros If TRUE exclude zero values
shape Format of the returned table "long" or "wide"
... Parameters to pass to join wide, i.e. assay name to extract feature abundance from and gene prefix, for shape="wide"

Details
This function extracts information for specified features and returns the information in either long or wide format.

Value
A ‘tbl’ containing the information for the specified features

Examples

print("this is a method definition. Example is not applicable")
# <SCE_object> |> join_features(features=c("HLA-DRA", "LYZ"))
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