

Package ‘ttservice’

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Type Package

Title A Service for Tidy Transcriptomics Software Suite

Version 0.1.2

Description It provides generic methods that are used by more than one package, avoiding conflicts. This package will be imported by 'tidySingleCellExperiment' and 'tidyseurat'. The implemented method is `join_features()`.

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Depends R (>= 4.0.0)

Imports methods

Encoding UTF-8

RoxygenNote 7.1.1

NeedsCompilation no

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<code>join_features</code>	<i>join_features</i>
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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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