Package ‘tidyomics’

May 4, 2024

Title  Easily install and load the tidyomics ecosystem

Version  1.0.0

Description  The tidyomics ecosystem is a set of packages for ‘omic data analysis that work together in harmony; they share common data representations and API design, consistent with the tidyverse ecosystem. The tidyomics package is designed to make it easy to install and load core packages from the tidyomics ecosystem with a single command.

License  MIT + file LICENSE

URL  https://github.com/tidyomics/tidyomics

BugReports  https://github.com/tidyomics/tidyomics/issues

Depends  R (>= 4.2)

Imports  tidySummarizedExperiment, tidySingleCellExperiment, tidyseurat, tidybulk, plyranges, nullranges, purrr, rlang, stringr, cli, utils

Suggests  tidyr, dplyr, tibble, ggplot2, mockr (>= 0.2.0), knitr (>= 1.41), rmarkdown (>= 2.20), testthat (>= 3.1.6)

VignetteBuilder  knitr

Biarch  true

biocViews  AssayDomain, Infrastructure, RNASeq, DifferentialExpression, GeneExpression, Normalization, Clustering, QualityControl, Sequencing, Transcription, Transcriptomics

Config/testthat/edition  3

Encoding  UTF-8

RoxygenNote  7.3.1

git_url  https://git.bioconductor.org/packages/tidyomics

git_branch  RELEASE_3_19

git_last_commit  647e4ef

git_last_commit_date  2024-04-30

Repository  Bioconductor 3.19

Date/Publication  2024-05-03
Description

This function lists all the conflicts between packages in the tidyomics and other packages that you have loaded.

Usage

tidyomics_conflicts(only = NULL)

Arguments

only Set this to a character vector to restrict to conflicts only with these packages.

Details

There are four conflicts that are deliberately ignored: intersect, union, setequal, and setdiff from dplyr. These functions make the base equivalents generic, so shouldn’t negatively affect any existing code.

Value

All conflicts between tidyomics packages and other packages that you have loaded.

Examples

tidyomics_conflicts()
tidyomics_packages

List all packages loaded by the tidyomics metapackage

Description
List all packages loaded by the tidyomics metapackage

Usage
tidyomics_packages(include_self = TRUE)

Arguments
include_self Include tidyomics in the list?

Value
All packages loaded by the tidyomics metapackage.

Examples
tidyomics_packages()
Index

tidyomics_conflicts, 2
 tidyomics_packages, 3