Package 'tidyomics'

November 12, 2026

Title Easily install and load the tidyomics ecosystem

Version 1.8.0

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.

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

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

Depends R (>= 4.2)

Imports tidySummarizedExperiment, tidySingleCellExperiment, tidySpatialExperiment, tidyseurat, plyranges, purrr, rlang, stringr, cli,

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

VignetteBuilder knitr

Biarch true

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

Config/testthat/edition 3

Encoding UTF-8

RoxygenNote 7.3.3

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

git_branch RELEASE_3_23

git_last_commit ad34d08

git_last_commit_date 2026-04-28

Repository Bioconductor 3.23

Date/Publication 2026-11-11

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`tidyomics` *tidyomics*

Description

A helper package to install and attach the core packages of the tidyomics ecosystem.

Usage

```
tidyomics()
```

Value

No value is returned

Examples

```
## Not run:
# Install the core packages of the tidyomics ecosystem
BiocManager::install("tidyomics")

# Attach the core packages of the tidyomics ecosystem
library(tidyomics)

## End(Not run)
```

tidyomics_conflicts *Conflicts between the tidyomics and other packages*

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()
```

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