# Package: tidyomics (via r-universe)

June 30, 2024

**Title** Easily install and load the tidyomics ecosystem

**Version** 1.1.0

**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

**Repository** https://bioc.r-universe.dev

**RemoteUrl** https://github.com/bioc/tidyomics

**RemoteRef** HEAD

**RemoteSha** 37001b55f2912cf09bf5a8d6f3c91d3be498bca0

# Contents

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tidyomics_conflicts        *Conflicts between the tidyomics and other packages*

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### 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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