Package: S4Cartographer (via r-universe)

October 20, 2026

Type Package

Title Visualize S4 class inheritance across R/Bioconductor packages

Version 0.99.3

Description S4 Object-Oriented Programming is fundamental to the Bioconductor ecosystem, enabling modularity and code reuse across hundreds of packages. However, the multi-layered inheritance structures within and between packages can be difficult to navigate. S4Cartographer facilitates the exploration of these relationships by visualizing S4 class hierarchies as directed graphs. By representing classes as nodes and inheritance as edges, it provides a clear overview of complex dependency networks.

URL https://github.com/MalteThodberg/S4Cartographer

BugReports https://github.com/MalteThodberg/S4Cartographer/issues

License GPL (>= 3)

Encoding UTF-8

Depends methods

Imports ggraph, tidygraph, igraph, ggplot2, checkmate, ggthemes, rlang, BiocBaseUtils, utils

RoxygenNote 7.3.3

Suggests BiocSingular, BiocStyle, Biostrings, clusterExperiment, DelayedArray, DESeq2, GenomicAlignments, GenomicFeatures, GenomicFiles, GenomicRanges, HDF5Array, InteractionSet, IRanges, knitr, MultiAssayExperiment, ResidualMatrix, rmarkdown, S4Vectors, ScaledMatrix, SingleCellExperiment, SpatialExperiment, SummarizedExperiment, TileDBArray, VCFArray, XVector

VignetteBuilder knitr

biocViews Software,Visualization,GraphAndNetwork

Config/pak/sysreqs libfontconfig1-dev libfreetype6-dev libglpk-dev libicu-dev libxml2-dev

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

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Contents

getS4Classes 2
getS4Inheritance 3
plotS4ClassGraph 3

Index **5**

`getS4Classes` *Helper: Get S4-classes defined in a set of packages*

Description

This function uses getClasses to get S4-classes from packages and isVirtualClass and isClassUnion to describe them.

Usage

```
getS4Classes(packages)
```

Arguments

`packages`	character: R packages

Value

A data.frame (Superclasses is across packages and Subclasses is within a package)

Examples

```
# Single package
getS4Classes("S4Vectors")

# Multiple packages
getS4Classes(c("IRanges", "GenomicRanges"))
```

getS4Inheritance *Helper: Get S4 inheritance for a set of S4 classes*

Description

This function uses getClassDef to extract inheritance information between S4 classes.

Usage

```
getS4Inheritance(S4Classes, packages)
```

Arguments

S4Classes	character: S4-classes
packages	character: R-package of each S4-class

Value

data.frame

Examples

```
# Single package
one_package <- getS4Classes("GenomicRanges")
getS4Inheritance(S4Classes = one_package$S4Class,
                 packages = one_package$Package)

# Several packages
two_packages <- getS4Classes(c("IRanges", "GenomicRanges"))
getS4Inheritance(S4Classes = two_packages$S4Class,
                 packages = two_packages$Package)
```

plotS4ClassGraph *Plot S4 classes and inheritance as a graph*

Description

This function plots all S4-classes from one or more R-packages as graph, where each node is an S4 class and directed edges represents inheritance. Virtual classes are indicated via node shapes. The graph stops at S4 defined outside the set or R-packages in question.

Usage

```
plotS4ClassGraph(packages, plot = TRUE)
```

Arguments

packages	character: R-packages
plot	logical: Whether to plot (TRUE) or just return the underlying plot data (FALSE)

Value

ggplot if plot=TRUE or list if plot=FALSE

Examples

```
# Single package
plotS4ClassGraph("GenomicRanges")

# Several packages:
plotS4ClassGraph(c("IRanges", "GenomicRanges"))
```

Index

getS4Classes, 2
getS4Inheritance, 3

plotS4ClassGraph, 3