Package: glydraw (via r-universe)

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Title Draw beautiful SNFG cartoons

Version 0.4.1

Description Draw beautiful SNFG cartoons.

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Suggests testthat (>= 3.0.0)

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URL `https://glycoverse.github.io/glydraw/`

Imports glyrepr (>= 0.10.0), rlang, dplyr, ggplot2, igraph, purrr, glyparse, cli, ggview, checkmate, scales, fs, glyexp

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

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Contents

`draw_cartoon` *Draw a Symbol Nomenclature For Glycan (SNFG)*

Description

Draw a Symbol Nomenclature For Glycan (SNFG)

Usage

```
draw_cartoon(
  structure,
  show_linkage = TRUE,
  orient = c("H", "V"),
  highlight = NULL
)
```

Arguments

`structure`	A `glyrepr::glycan_structure()` scalar, or a string of any glycan structure text nomenclatures supported by `glyparse::auto_parse()`.
`show_linkage`	Show linkage annotation or not. Default is TRUE.
`orient`	The orientation of glycan structure. "H" for horizontal, "V" for vertical. Default is "H"
`highlight`	An integer vector specifying the node indices to highlight. This argument is applicable only when `structure` is a `glyrepr::glycan_structure()`. Note that for a `glyrepr::glycan_structure()`, the node indices correspond exactly to the monosaccharides in its printed IUPAC nomenclature. For example, given `glyrepr::as_glycan_structure("Gal(b1-3)[GlcNAc(b1-6)]GalNAc(a1-")`, setting `highlight = c(1, 3)` will highlight the "Gal" and "GalNAc" nodes.

Value

a ggplot2 object

Examples

```
## Not run:
draw_cartoon("Gal(b1-3)GalNAc(a1-")

## End(Not run)
```

`export_cartoons` *Export all glycan structures to figures*

Description

This function calls `draw_cartoon()` on each glycan structure in `x`, then calls `save_cartoon()` to save a figure for each of them. IUPAC-condensed nomenclatures are used as file names. If `x` is a named character vector or named `glyrepr::glycan_structure()` vector, the vector names are used as file names.

Usage

```
export_cartoons(
  x,
  dirname,
  file_ext = "png",
  dpi = 300,
  show_linkage = TRUE,
  orient = c("H", "V")
)
```

Arguments

`x`	A `glyexp::experiment()`, a `glyrepr::glycan_structure()` vector, or a character vector of any glycan structure text nomenclatures supported by `glyparse::auto_parse()`.
`dirname`	Directory name to save the cartoons. If it does not exist, it is created.
`file_ext`	File extension supported by `ggplot2::ggsave()`. Defaults to "png".
`dpi`	Dots per inch. Defaults to 300.
`show_linkage`	Show linkage annotation or not. Default is TRUE.
`orient`	The orientation of glycan structure. "H" for horizontal, "V" for vertical. Default is "H"

Value

The function returns the list of cartoons implicitly.

Examples

```
## Not run:
library(glyexp)
export_cartoons(real_experiment, "path/to/save")

## End(Not run)
```

`save_cartoon` *Save fixed-size glycan cartoon image to local device.*

Description

In theory, you can just use `ggplot2::ggsave()` to save the cartoons plotted by `draw_cartoon()`. However, you can have trouble finding the best sizes for each cartoon to make them look alike. This function is designed to save the cartoons with self-adjusted sizes, based on the size of the glycans, so that when glycans with different sizes are put together, they will look alike.

Usage

```
save_cartoon(cartoon, file, dpi = 300)
```

Arguments

`cartoon`	A ggplot2 object returned by `draw_cartoon()`.
`file`	File name of glycan cartoon.
`dpi`	Dots per inch, default = 300.

Examples

```
## Not run:
cartoon <- draw_cartoon("Gal(b1-3)GalNAc(a1-")
save_cartoon(cartoon, "p1.png", dpi = 300)

## End(Not run)
```

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