

Package ‘BioTooltipR’

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Title Add Bio Tooltips to HTML Reports

Version 0.1.2

Description Provides lightweight helpers for adding gene and chemical tooltips to 'R Markdown', 'Quarto', 'shiny', 'pkgdown', and other HTML outputs. The package emits small HTML spans with module-specific data attributes and attaches the browser-side 'bio-tooltips' JavaScript and CSS assets through 'htmltools'. Entity lookup and rendering are handled in the browser by 'bio-tooltips'; this package does not query biological databases from R during package checks.

Language en-US

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URL <https://github.com/mattjmeier/BioTooltipR>

BugReports <https://github.com/mattjmeier/BioTooltipR/issues>

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auto_gene_tooltips	<i>Automatically wrap selected gene symbols in rendered HTML</i>
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Description

Experimental helper for reports where text has already been rendered. It injects a small browser script that scans selected DOM nodes and wraps a user-supplied vocabulary of gene symbols in Bio Tooltip spans.

Usage

```
auto_gene_tooltips(  
  genes,  
  species = "human",  
  selector = "p, li, td",  
  include_setup = TRUE,  
  class = NULL  
)
```

Arguments

- | | |
|---------------|--|
| genes | Character vector of gene symbols to wrap. |
| species | Species alias or NCBI taxonomy ID. |
| selector | CSS selector limiting where wrapping occurs. |
| include_setup | Include use_bio_tooltips() before the wrapping script. |
| class | Optional additional CSS class for generated spans. |

Details

This is intentionally opt-in and vocabulary-limited because many gene symbols are ambiguous in prose.

Value

An HTML tag list containing an optional setup tag and wrapping script.

Examples

```
auto_gene_tooltips(c("TP53", "BRCA1"), selector = ".results")
```

bio_tooltips_dependency

Bio Tooltips HTML dependency

Description

Creates the htmltools dependency for the browser-side Bio Tooltips bundle.

Usage

```
bio_tooltips_dependency(cdn = FALSE, version = "2.3.2", local_path = NULL)
```

Arguments

cdn	Use jsDelivr CDN assets instead of the vendored package assets. If FALSE, the package looks for local assets under inst/htmltools/bio-tooltips/ or local_path.
version	JavaScript package version. Use a pinned version for reproducible reports.
local_path	Optional path containing bio-tooltips.css and bio-tooltips.global.js.

Value

An `htmltools::htmlDependency` object.

bio_tooltip_span	Create a Bio Tooltip span
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Description

Low-level helper used by `gene_tt()` and `chem_tt()`. It emits an HTML `<span>` with the classes and `data-*` attributes expected by the JavaScript Bio Tooltips library.

Usage

```
bio_tooltip_span(  
  label,  
  type = c("gene", "chemical"),  
  query = NULL,  
  species = NULL,  
  scope = NULL,  
  lookup = NULL,  
  class = NULL  
)
```

Arguments

label	Character vector of visible labels.
type	Tooltip type. One of "gene" or "chemical".
query	Optional lookup query. Mostly useful for chemical identifiers.
species	Gene species alias or NCBI taxonomy ID.
scope	Chemical lookup scope, such as "pubchem", "chembl", "chebi", "drugbank", "unii", "inchikey", or "name".
lookup	Optional chemical lookup mode, such as "id" or "best-guess".
class	Optional additional CSS class or full class string. If NULL, the default module class is used.

Value

An HTML character vector with class `html`.

Examples

```
bio_tooltip_span("TP53", type = "gene", species = "human")  
bio_tooltip_span("aspirin", type = "chemical", query = "2244", scope = "pubchem")
```

bt_datatable	<i>Render a DT table with Bio Tooltips support</i>
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Description

Optional wrapper around `DT::datatable()` that disables HTML escaping by default and re-initializes tooltips when the table redraws.

Usage

```
bt_datatable(  
  data,  
  ...,  
  modules = c("gene", "chemical"),  
  include_setup = TRUE,  
  escape = FALSE  
)
```

Arguments

data	A data frame.
...	Passed to <code>DT::datatable()</code> . If callback is supplied, this helper will not override it.
modules	Tooltip modules to initialize.
include_setup	Include <code>use_bio_tooltips()</code> before the widget.
escape	Passed to <code>DT::datatable()</code> . Defaults to FALSE.

Value

A DT widget, optionally wrapped in an HTML tag list.

bt_deg_table	<i>Render a simple differential-expression style table</i>
--------------	--

Description

Convenience helper for common omics reports. It optionally sorts and truncates a results data frame, annotates the gene column, and renders an HTML table.

Usage

```
bt_deg_table(
  data,
  gene_col = "symbol",
  species = "human",
  sort_by = NULL,
  decreasing = FALSE,
  n = NULL,
  ...
)
```

Arguments

data	A data frame containing differential-expression results.
gene_col	Gene-symbol column name.
species	Species alias or NCBI taxonomy ID.
sort_by	Optional column name used for sorting.
decreasing	Sort direction.
n	Optional number of rows to keep after sorting.
...	Passed to bt_kable() .

Value

An HTML table with gene tooltip spans.

bt_kable	<i>Render a kable table with Bio Tooltips support</i>
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Description

Wrapper around [knitr::kable\(\)](#) that defaults to HTML output with escaping disabled and optionally prepends [use_bio_tooltips\(\)](#).

Usage

```
bt_kable(
  data,
  ...,
  modules = c("gene", "chemical"),
  include_setup = TRUE,
  format = "html",
  escape = FALSE
)
```

Arguments

data	A data frame or object accepted by <code>knitr::kable()</code> .
...	Passed to <code>knitr::kable()</code> .
modules	Tooltip modules to initialize when <code>include_setup = TRUE</code> .
include_setup	Include <code>use_bio_tooltips()</code> before the table.
format	Table format. Defaults to "html".
escape	Escape HTML? Defaults to FALSE so tooltip spans render.

Value

An HTML tag list when setup is included; otherwise the result of `knitr::kable()`.

Examples

```
top_genes <- data.frame(symbol = c("TP53", "BRCA1"))
top_genes <- gene_column(top_genes, symbol)
bt_kable(top_genes)
```

bt_plotly_gene_hover *Add Bio Tooltips gene hover behavior to a Plotly plot*

Description

`bt_plotly_gene_hover()` lets a Plotly widget use Bio Tooltips for gene hover cards. Map the gene symbol into Plotly's key aesthetic, then wrap the widget with this helper.

Usage

```
bt_plotly_gene_hover(
  plot,
  species = "human",
  gene_source = c("key", "customdata"),
  hide_plotly_hover = TRUE,
  include_setup = TRUE,
  class = NULL
)
```

Arguments

plot	A Plotly <code>htmlwidget</code> .
species	Species alias or NCBI taxonomy ID passed through to the generated gene tooltip anchor.
gene_source	Plotly point field containing the gene symbol. The default uses key, so build plots with <code>key = ~symbol</code> .

hide_plotly_hover	Suppress Plotly's native hover labels while keeping hover and click events active.
include_setup	Include <code>use_bio_tooltips()</code> before the widget. Set this to FALSE when the report already calls <code>use_bio_tooltips()</code> once.
class	Optional additional CSS class added to the generated gene anchor.

Details

Hover over a point on desktop, or tap a point on mobile. On screens at or below 600 CSS pixels wide, the tooltip opens as a persistent bottom drawer that stays open until another point is selected, the user taps outside the drawer, drags it closed, or activates its close button.

The helper attaches one [bio-tooltips](#) anchor with the programmatic `GeneTooltip.attach()` API and reuses it as the selected point changes, so repeated renders of the widget do not accumulate listeners.

Value

An HTML tag list containing the Plotly widget and a hidden, fixed-position Bio Tooltip anchor.

Examples

```
if (requireNamespace("plotly", quietly = TRUE)) {
  genes <- data.frame(symbol = c("TP53", "BRCA1"), x = 1:2, y = 2:3)
  plot <- plotly::plot_ly(
    genes,
    x = ~x,
    y = ~y,
    key = ~symbol,
    type = "scatter",
    mode = "markers"
  )
  bt_plotly_gene_hover(plot, include_setup = FALSE)
}
```

chem_column

Add chemical tooltip markup to a data-frame column

Description

Convenience wrapper around `tooltip_column()` for chemical labels.

Usage

```
chem_column(
  data,
  column,
  query_col = NULL,
```

```
scope = NULL,  
scope_col = NULL,  
lookup = NULL,  
class = NULL  
)
```

Arguments

data	A data frame.
column	Column to transform. May be unquoted or a single string.
query_col	Optional column containing stable lookup values.
scope	Chemical scope or scalar value recycled over rows.
scope_col	Optional column containing chemical scopes.
lookup	Optional chemical lookup mode.
class	Optional additional CSS class.

Value

data, with the selected column replaced by chemical tooltip HTML.

Examples

```
chemicals <- data.frame(name = "aspirin", cid = "2244")  
chem_column(chemicals, name, query_col = "cid", scope = "pubchem")
```

chem_tt	<i>Create chemical tooltip spans</i>
---------	--------------------------------------

Description

chem_tt() vectorizes over chemical labels and emits HTML spans understood by the Bio Tooltips MyChem.info module.

Usage

```
chem_tt(x, query = NULL, scope = NULL, lookup = NULL, class = NULL)  
  
chemical_tt(x, query = NULL, scope = NULL, lookup = NULL, class = NULL)  
  
chemical_tooltip(x, query = NULL, scope = NULL, lookup = NULL, class = NULL)
```

Arguments

x	Character vector of visible chemical labels.
query	Optional stable lookup value. For example, use a PubChem CID with scope = "pubchem".
scope	Optional lookup scope, such as "pubchem", "chembl", "chebi", "drugbank", "unii", "inchikey", or "name".
lookup	Optional lookup mode, such as "id" or "best-guess".
class	Optional additional CSS class.

Value

An HTML character vector with class html.

Examples

```
chem_tt("aspirin", query = "2244", scope = "pubchem")
chem_tt("caffeine", lookup = "best-guess")
```

gene_column

Add gene tooltip markup to a data-frame column

Description

Convenience wrapper around `tooltip_column()` for gene symbols.

Usage

```
gene_column(data, column, species = "human", class = NULL)
```

Arguments

data	A data frame.
column	Column to transform. May be unquoted or a single string.
species	Species alias or NCBI taxonomy ID.
class	Optional additional CSS class.

Value

data, with the selected column replaced by gene tooltip HTML.

Examples

```
top_genes <- data.frame(symbol = c("TP53", "BRCA1"))
gene_column(top_genes, symbol)
```

gene_tt	<i>Create gene tooltip spans</i>
---------	----------------------------------

Description

gene_tt() vectorizes over gene symbols and emits HTML spans understood by the Bio Tooltips MyGene.info module.

Usage

```
gene_tt(x, species = "human", class = NULL)

gene_tooltip(x, species = "human", class = NULL)
```

Arguments

x	Character vector of gene symbols or labels.
species	Species alias such as "human", "mouse", or a numeric NCBI taxonomy ID. Recycled over x.
class	Optional additional CSS class.

Value

An HTML character vector with class html.

Examples

```
gene_tt("TP53")
gene_tt(c("TP53", "BRCA1"), species = "human")
```

tooltip_column	<i>Add Bio Tooltip markup to a data-frame column</i>
----------------	--

Description

Replaces a selected column with HTML tooltip spans. This is useful before rendering with `knitr::kable(escape = FALSE)`, `bt_kable()`, or another HTML table system that can render unescaped HTML.

Usage

```
tooltip_column(
  data,
  column,
  type = c("gene", "chemical"),
  species = "human",
  query_col = NULL,
  scope = NULL,
  scope_col = NULL,
  lookup = NULL,
  class = NULL
)
```

Arguments

<code>data</code>	A data frame.
<code>column</code>	Column to transform. May be unquoted or a single string.
<code>type</code>	Tooltip type: "gene" or "chemical".
<code>species</code>	Species for gene tooltips.
<code>query_col</code>	Optional column containing chemical lookup values.
<code>scope</code>	Chemical scope or scalar value recycled over rows.
<code>scope_col</code>	Optional column containing chemical scopes.
<code>lookup</code>	Optional chemical lookup mode.
<code>class</code>	Optional additional CSS class.

Value

data, with the selected column replaced by HTML strings.

Examples

```
top_genes <- data.frame(symbol = c("TP53", "BRCA1"), padj = c(0.001, 0.02))
tooltip_column(top_genes, symbol, type = "gene")
```

use_bio_tooltips	<i>Attach and initialize Bio Tooltips</i>
------------------	---

Description

Use this once in an R Markdown, Quarto, Shiny UI, or other HTML-producing context. It attaches the Bio Tooltips CSS/JS dependency and initializes the selected modules after the DOM is ready.

Usage

```

use_bio_tooltips(
  modules = c("gene", "chemical"),
  cdn = FALSE,
  version = "2.3.2",
  theme = "auto",
  prefetch = "smart",
  gene_selector = ".gene-tooltip",
  chemical_selector = ".chemical-tooltip",
  visual_preload = NULL,
  debug_timings = FALSE,
  tooltip_width = NULL,
  tooltip_height = NULL,
  include_optional_visual_deps = "auto",
  d3_version = "7.9.0",
  ideogram_version = "1.53.0",
  local_path = NULL
)

```

Arguments

modules	Character vector containing "gene", "chemical", or both.
cdn	Use jsDelivr CDN assets instead of the vendored package assets. See bio_tooltips_dependency() .
version	JavaScript package version. Use a pinned version for reproducibility.
theme	Tooltip theme passed to Bio Tooltips.
prefetch	Prefetch strategy passed to Bio Tooltips.
gene_selector	CSS selector for gene tooltip elements.
chemical_selector	CSS selector for chemical tooltip elements.
visual_preload	Optional visual dependency warmup strategy for gene visuals. Passed as visualPreload.
debug_timings	Log Bio Tooltips timing diagnostics in the browser.
tooltip_width, tooltip_height	Optional tooltip dimensions.
include_optional_visual_deps	Include dependencies for D3 and Ideogram. The default, "auto", includes them when the gene module is initialized because Bio Tooltips gene visuals use these peer dependencies. Vendored files are used by default and CDN files are used when cdn = TRUE. Use FALSE to opt out, for example when gene visuals are disabled.
d3_version, ideogram_version	Versions used when optional visual dependencies are included.
local_path	Optional local path for vendored Bio Tooltips assets.

Value

An HTML tag list containing dependencies and an initialization script.

Examples

```
use_bio_tooltips()  
use_bio_tooltips(modules = "gene", theme = "light")
```

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