Package: BioTooltipR (via r-universe)

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Title Add Bio Tooltips to HTML Reports

Version 0.1.0

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

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Contents

`auto_gene_tooltips` *Automatically wrap selected gene symbols in rendered HTML*

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_tooltip_span` *Create a Bio Tooltip span*

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")
```

`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 = "1.1.1", 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.

`bt_datatable` *Render a DT table with Bio Tooltips support*

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 `DT::datatable()`. If `callback` is supplied, this helper will not override it.
`modules`	Tooltip modules to initialize.
`include_setup`	Include `use_bio_tooltips()` before the widget.
`escape`	Passed to `DT::datatable()`. Defaults to `FALSE`.

Value

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

`bt_deg_table` *Render a simple differential-expression style table*

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` *Render a kable table with Bio Tooltips support*

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 `knitr::kable()`.
`...`	Passed to `knitr::kable()`.
`modules`	Tooltip modules to initialize when `include_setup = TRUE`.
`include_setup`	Include `use_bio_tooltips()` 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 htmlwidget.
`species`	Species alias or NCBI taxonomy ID passed through to the generated gene tooltip span.
`gene_source`	Plotly point field containing the gene symbol. The default uses `key`, so build plots with `key = ~symbol`.
`hide_plotly_hover`	Suppress Plotly's native hover labels while keeping hover events active.
`include_setup`	Include `use_bio_tooltips()` before the widget. Set this to `FALSE` when the report already calls `use_bio_tooltips()` once.
`class`	Optional additional CSS class added to the generated gene span.

Value

An HTML tag list containing the Plotly widget and a cursor-following 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` *Create chemical tooltip spans*

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` *Create gene tooltip spans*

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` *Add Bio Tooltip markup to a data-frame column*

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

`data`	A data frame.
`column`	Column to transform. May be unquoted or a single string.
`type`	Tooltip type: `"gene"` or `"chemical"`.
`species`	Species for gene tooltips.
`query_col`	Optional column containing chemical 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 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` *Attach and initialize Bio Tooltips*

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 = "1.1.1",
  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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