# Package 'BioTooltipR'

November 19, 2026

**Title** Add Bio Tooltips to HTML Reports

**Version** 0.2.0

**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

**License** MIT + file LICENSE

**URL** https://github.com/mattjmeier/BioTooltipR

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

**Encoding** UTF-8

**Depends** R (>= 4.1)

**Imports** htmltools, jsonlite, knitr, utils

**Suggests** DT, htmlwidgets, plotly, rmarkdown, testthat (>= 3.0.0)

**VignetteBuilder** knitr

**Config/testthat/edition** 3

**Config/roxygen2/version** 8.1.0

**NeedsCompilation** no

**Author** Matthew J. Meier [aut, cre]

**Maintainer** Matthew J. Meier <matthew.meier@hc-sc.gc.ca>

**Repository** CRAN

**Date/Publication** 2026-11-19 01:00:13 UTC

# Contents

auto_gene_tooltips . . . 2
bio_tooltips_dependency . . . 3
bio_tooltip_span . . . 4
bt_datatable . . . 5
bt_deg_table . . . 5
bt_kable . . . 6
bt_plotly_gene_hover . . . 7
chem_column . . . 8
chem_tt . . . 9
gene_column . . . 10
gene_tt . . . 11
tooltip_column . . . 11
use_bio_tooltips . . . 12

**Index** **15**

---

`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_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 = "2.4.2", 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*

## Description

Low-level helper used by `gene_tt()` and `chem_tt()`. It emits an HTML  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 *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 anchor. |
| 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 and click 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 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. On desktop, pinned tooltips stay open while you hover over or pin other points.

The helper uses the bio-tooltips `GeneTooltip.attach()` API to reuse a hover anchor and retain a separate anchor for each pinned tooltip. Repeated widget renders clean up the anchors and 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 *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 = "2.4.2",
  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")
```

# Index


auto_gene_tooltips, 2

bio-tooltips, *8*
bio_tooltip_span, 4
bio_tooltips_dependency, 3
bio_tooltips_dependency(), *13*
bt_datatable, 5
bt_deg_table, 5
bt_kable, 6
bt_kable(), *6*, *11*
bt_plotly_gene_hover, 7

chem_column, 8
chem_tt, 9
chem_tt(), *4*
chemical_tooltip *(*chem_tt*)*, 9
chemical_tt *(*chem_tt*)*, 9

DT::datatable(), *5*

gene_column, 10
gene_tooltip *(*gene_tt*)*, 11
gene_tt, 11
gene_tt(), *4*

knitr::kable(), *6, 7*

tooltip_column, 11
tooltip_column(), *8*, *10*

use_bio_tooltips, 12
use_bio_tooltips(), *2*, *5–8*