# Package: BioTooltipR (via r-universe)

June 30, 2026

**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

**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** 8.0.0

**RoxygenNote** 7.3.2

**NeedsCompilation** no

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

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

**Repository** https://cran.r-universe.dev

**Date/Publication** 2026-06-30 10:10:09 UTC

**RemoteUrl** https://github.com/cran/BioTooltipR

**RemoteRef** HEAD

**RemoteSha** 172102ce5449fb6e00c4afcb686d968b8f0c8b68

# Contents

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

**Index** **14**

---

`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  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")
```

# Index


auto_gene_tooltips, 2

bio_tooltip_span, 3
bio_tooltips_dependency, 4
bio_tooltips_dependency(), *12*
bt_datatable, 4
bt_deg_table, 5
bt_kable, 6
bt_kable(), *6*, *11*
bt_plotly_gene_hover, 7

chem_column, 8
chem_tt, 9
chem_tt(), *3*
chemical_tooltip *(*chem_tt*)*, 9
chemical_tt *(*chem_tt*)*, 9

DT::datatable(), *4, 5*

gene_column, 10
gene_tooltip *(*gene_tt*)*, 10
gene_tt, 10
gene_tt(), *3*

knitr::kable(), *6*

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

use_bio_tooltips, 12
use_bio_tooltips(), *2*, *5–7*