Package: tabular (via r-universe)

June 12, 2026

Title Render Tables and Listings for Clinical Submissions

Version 0.1.1

Description Render clinical submission tables and listings to 'RTF', 'LaTeX', 'HTML', 'PDF', and 'DOCX' from pre-summarised data frames, with no external 'Java' or 'SAS' dependency. Features include decimal alignment via font metrics, multi-level column headers with passthrough leaves, predicate-targeted cell styling, footnotes, and group-aware pagination. Built for Clinical Data Interchange Standards Consortium (CDISC) Analysis Data Model (ADaM) workflows and regulatory submissions to agencies such as the Food and Drug Administration (FDA), European Medicines Agency (EMA), and Pharmaceuticals and Medical Devices Agency (PMDA).

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URL https://vthanik.github.io/tabular/, https://github.com/vthanik/tabular

BugReports https://github.com/vthanik/tabular/issues

Encoding UTF-8

Roxygen list(markdown = TRUE)

Depends R (>= 4.3.0)

Imports S7, cli, commonmark, rlang, xml2

Suggests testthat (>= 3.0.0), withr, digest, ggplot2, htmltools, knitr, quarto, pkgdown, rstudioapi, systemfonts, tibble, tinytex, webshot2, yaml

VignetteBuilder quarto

SystemRequirements Quarto command line tool (<https://github.com/quarto-dev/quarto-cli>), needed only to build the package vignettes.

Config/testthat/edition 3

Config/Needs/website pkgdown

LazyData true

Config/roxygen2/version 8.0.0

Config/pak/sysreqs libxml2-dev

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

Date/Publication 2026-06-08 21:53:55 UTC

RemoteUrl https://github.com/vthanik/tabular

RemoteRef HEAD

RemoteSha 4cf0ba1439c2ddb3389d9aa631ddc14ae177bcd2

Contents

`as.tags.tabular_spec` *Convert a* `tabular_spec` *to an* `htmltools` `tagList`

Description

Renders the spec to a self-contained HTML fragment and wraps it in an `htmltools::tagList` suitable for inline embedding in Quarto / Rmd chunks, RStudio / Positron viewer panes, pkgdown reference pages, and Shiny UIs.

Usage

```
## S3 method for class 'tabular_spec'
as.tags(x, ..., id = NULL)
```

Arguments

`x`	*The* `tabular_spec` *to convert.* `<tabular_spec>: required`.
`...`	*Reserved.* Ignored.
`id`	*Wrapping div id.* `<character(1) | NULL>: default NULL (auto-generate)`. Pass an explicit id when you need to target the table from external CSS or JavaScript.

Details

Fragment extraction. Tabular's HTML backend emits a full `<!DOCTYPE html>` document with a `<style>` block in the head and the table inside `<body>`. For inline embedding we extract the `<style>` and `<body>` content separately and re- wrap them in an `htmltools::tagList`:

```
<style>...table CSS...</style>
<div id="..." style="overflow-x:auto;max-width:100%;">
  ...table content...
</div>
```

The wrapping `<div>` gets a random unique `id` (so multiple tables on the same page have CSS-scopable hooks) and `overflow-x: auto` so wide tables get a horizontal scrollbar instead of overflowing their container.

Value

An `htmltools::tagList` containing a `<style>` block plus a wrapping `<div>` containing the table. Knitr, htmltools, and RStudio / Positron viewer panes all know how to render it.

See Also

Renders via: print.tabular_spec, knit_print().

Terminal verb: emit().

Examples

```
# `as.tags()` converts a spec into an htmltools tagList you can drop into
# a custom HTML page, a Shiny UI, or a Quarto / Rmd chunk. `print()` and
# `knit_print()` call it under the hood, so you seldom call it directly --
# but it is the seam for composing several tables into one container.
s1 <- tabular(cdisc_saf_demo, titles = "Demographics")
s2 <- tabular(cdisc_saf_ae, titles = "AE overall")

# Compose two tables into one parent tagList. Autoprinting `tables` in a
# Quarto / Rmd chunk renders both inline (via knit_print); embed it with
# htmltools::save_html() or a Shiny renderUI().
tables <- htmltools::tagList(
  htmltools::as.tags(s1),
  htmltools::as.tags(s2)
)

# The common path is autoprinting a spec: the viewer at an interactive
# prompt, an inline live table under pkgdown / knitr, and HTML source
# under R CMD check. This is the gt / flextable / tinytable convention --
# end on a bare table object and let the registered print method choose,
# with no browsable() / if (interactive()) wrapper, so R CMD check never
# launches a browser.
s1
```

---

as_grid *Resolve a* tabular_spec *into a* tabular_grid

Description

Runs the full engine pipeline against spec and returns the resolved tabular_grid — the same intermediate object emit() hands to a backend. Pure function: no files written, no global state touched. Use this during development to inspect what emit() will pass downstream, when building a custom backend, or when piping the resolved grid into a non-file consumer (e.g. an inline preview chunk in a Quarto notebook).

Usage

```
as_grid(.spec)
```

Arguments

.spec	*The* tabular_spec *to resolve.* <tabular_spec>: required. Built by the verb chain (tabular() -> cols() -> headers() -> sort_rows() -> style() -> paginate() -> preset()).

Details

Engine pipeline order is load-bearing. Phases run in this fixed order; the order matters because each phase reads the post- previous-phase state of the spec:

1. `engine_sort()` — apply the sort spec.
2. `engine_headers()` — validate the header tree and flatten it to a band grid.
3. `engine_style()` — evaluate every style predicate against the post-sort data grid. A predicate may reference any column in `spec@data`.
4. `engine_format()` — apply per-column formats, substitute `na_text`, and parse every cell / title / footnote / label through `parse_inline()` to its `inline_ast`.
5. `engine_decimal()` — column-wide decimal alignment for any column flagged `col_spec(align = "decimal")`. Operates on the formatted text; output is the same character matrix with NBSP padding inserted so the decimal marks line up.
6. `engine_paginate()` — split into pages (vertical row chunks + horizontal panel chunks). The plan drives the per-page slicing of cells / styles / ASTs below.

The grid is the backend contract. Every backend (`backend_md`, future `backend_html`, etc.) consumes a `tabular_grid` — never a `tabular_spec`. New backends only need to walk `grid@pages` and `grid@metadata`; the engine pipeline is a fixed dependency they never re-implement.

No I/O. `as_grid()` writes nothing to disk and touches no global state. It is safe to call repeatedly during interactive exploration; cost is roughly that of one `emit()` without the backend write step.

Value

A `tabular_grid` *S7 object.* Two slots:

- `@pages` — a list of one entry per display page. Each entry is a named list with pagination fields (`page_index`, `panel_index`, `is_continuation`, `continuation`, `show_titles`, `repeat_headers`, `show_footnotes_here`), row + column slice indices (`row_indices`, `col_indices`, `col_names`), the sliced cell text (`cells_text` — character matrix), sliced inline ASTs (`cells_ast` — list-matrix of `inline_ast`), sliced style nodes (`cells_style` — list-matrix of `style_node`), and the column-label ASTs for the visible columns (`col_labels_ast`).
- `@metadata` — per-table information backends consume once per render: `format` (the resolved backend tag, `NA_character_` for `as_grid()` calls), `rows_per_page`, `total_pages`, `total_panels`, `nrow_data`, `ncol_data`, `col_names`, `cols` (the original `col_spec()` entries keyed by column name), `headers` (the flattened header band grid), `titles`, `footnotes`, `titles_ast`, `footnotes_ast`, `col_labels_ast`, `pagehead_ast` / `pagefoot_ast` (resolved page-band content — `NULL` when the active preset declares no band, otherwise `list(left, center, right)` of length-N lists of `inline_ast` where N = row count and index 1 is the body-edge row).

See Also

I/O sibling: `emit()` writes the resolved grid to a file via a registered backend; `as_grid()` is the no-I/O entry into the same pipeline.

Build verbs the pipeline feeds from: `tabular()`, `cols()` / `col_spec()`, `headers()`, `sort_rows()`, `style()`, `paginate()`, `preset()`.

Inline formatting helpers: `md()`, `html()`.

Examples

```
# ---- Example 1: Demographics — inspect the resolved grid ----
#
# Resolve the canonical safety-pop demographics pipeline into a
# `tabular_grid` and inspect what `emit()` would hand a backend.
# The first page's `cells_text` matrix is the decimal-aligned
# output as the backend would render it; the metadata carries the
# pagination plan + header / title / footnote ASTs.
n <- stats::setNames(cdisc_saf_n$n, cdisc_saf_n$arm_short)

demo <- tabular(
  cdisc_saf_demo,
  titles = c(
    "Table 14.1.1",
    "Demographics and Baseline Characteristics",
    "Safety Population"
  ),
  footnotes = "Source: ADSL."
) |>
  cols(
    variable   = col_spec(usage = "group", label = "Characteristic"),
    stat_label = col_spec(label = "Statistic"),
    placebo  = col_spec(label = "Placebo\nN={n['placebo']}",  align = "decimal"),
    drug_50  = col_spec(label = "Drug 50\nN={n['drug_50']}",  align = "decimal"),
    drug_100 = col_spec(label = "Drug 100\nN={n['drug_100']}", align = "decimal"),
    Total    = col_spec(label = "Total\nN={n['Total']}",    align = "decimal")
  ) |>
  sort_rows(by = c("variable", "stat_label"))

demo_grid <- as_grid(demo)
demo_grid@metadata$total_pages
demo_grid@pages[[1]]$cells_text[1:3, c("stat_label", "placebo")]

# ---- Example 2: AE-by-SOC/PT paginated grid — verify the split ----
#
# Same shape as Example 1 plus pagination protecting the SOC
# grouping. With a tight font size the grid carries multiple page
# entries; concatenating each page's `row_indices` reconstructs
# the full data, and every page carries the full header band grid
# at `grid@metadata$headers` so backends can re-render the header
# on every continuation page.
n <- stats::setNames(cdisc_saf_n$n, cdisc_saf_n$arm_short)

ae_spec <- tabular(
  cdisc_saf_aesocpt,
  titles = c(
    "Table 14.3.1",
    "Adverse Events by SOC and Preferred Term",
    "Safety Population"
  ),
  footnotes = "Subjects counted once per SOC and once per PT."
) |>
```

```
  cols(
    label    = col_spec(label = "SOC / PT", indent = "indent_level"),
    soc      = col_spec(usage = "group", visible = FALSE,
                        group_display = "column_repeat"),
    row_type = col_spec(visible = FALSE),
    soc_n    = col_spec(visible = FALSE),
    n_total  = col_spec(visible = FALSE),
    placebo  = col_spec(label = "Placebo\nN={n['placebo']}",  align = "decimal"),
    drug_50  = col_spec(label = "Drug 50\nN={n['drug_50']}",  align = "decimal"),
    drug_100 = col_spec(label = "Drug 100\nN={n['drug_100']}", align = "decimal"),
    Total    = col_spec(label = "Total\nN={n['Total']}",    align = "decimal")
  ) |>
  sort_rows(by = c("soc_n", "n_total"), descending = c(TRUE, TRUE)) |>
  paginate(keep_together = "soc")

ae_grid <- as_grid(ae_spec)
length(ae_grid@pages)

# ---- Example 3: Subgroup partition — one page set per group ----
#
# When `subgroup()` is attached, `as_grid()` runs the resolve
# pipeline once per group and concatenates the pages. `cdisc_saf_subgroup`
# carries `sex` as a natural partition axis; inspect
# `@pages[[i]]$subgroup_index` and `@pages[[i]]$subgroup_line_ast`
# to confirm each page knows its group identity and banner text.
# `sex` auto-hides as the partition `by` column; no explicit
# `col_spec(visible = FALSE)` needed.
sg_spec <- tabular(cdisc_saf_subgroup) |>
  cols(
    sex_n      = col_spec(visible = FALSE),
    paramcd    = col_spec(visible = FALSE),
    param      = col_spec(usage = "group", label = "Parameter"),
    visit      = col_spec(usage = "group", label = "Visit"),
    stat_label = col_spec(label = "Statistic")
  ) |>
  subgroup("sex")

sg_grid <- as_grid(sg_spec)
length(sg_grid@pages)
vapply(sg_grid@pages, function(p) p$subgroup_index %||% NA_integer_, integer(1))

# ---- Example 4: Pre-flight inspection before emit() ----
#
# Resolve a spec to its grid without writing anywhere. Useful in
# tests, for snapshotting cell text under different presets, or
# for spec-introspection inside higher-level wrappers that need
# to know how many pages a render will produce.
n <- stats::setNames(cdisc_saf_n$n, cdisc_saf_n$arm_short)
demog_spec <- tabular(
  cdisc_saf_demo,
  titles = "Demographics"
) |>
  cols(
```

```
    variable   = col_spec(usage = "group", label = "Characteristic"),
    stat_label = col_spec(label = "Statistic"),
    placebo    = col_spec(
      label = "Placebo\nN={n['placebo']}",
      align = "decimal"
    ),
    drug_50    = col_spec(
      label = "Drug 50\nN={n['drug_50']}",
      align = "decimal"
    ),
    drug_100   = col_spec(
      label = "Drug 100\nN={n['drug_100']}",
      align = "decimal"
    ),
    Total      = col_spec(
      label = "Total\nN={n['Total']}",
      align = "decimal"
    )
  )
grid <- as_grid(demog_spec)
length(grid@pages)
dim(grid@pages[[1]]$cells_text)
```

---

brdr *Border-line specification*

Description

Build a small immutable record describing one border line — width, style, and colour. A `brdr()` value is the stroke you hand to the `preset()` `rules` knob (one entry per rule name, e.g. `rules = list(midrule = brdr(width = 0.75))`) or to `style()`'s border arguments (`style(border_top = brdr(...), .at = cells_table(side = "rows"))`). Successive `preset()` calls layer cleanly, so a one-off override composes onto a house-style template without disturbing the other rules.

Usage

```
brdr(width = "thin", style = "solid", color = "ink")

is_brdr(x)
```

Arguments

`width`	*Stroke width.* `<numeric(1) | character(1)>`: `default "thin"*. Either a numeric in points (>= 0`
`style`	*Line style.* `<character(1)>`: `default "solid"*. One of "solid", "dashed", "dotted", "double", "dashdot", "none"`.
`color`	*Stroke colour.* `<character(1)>`: `default "currentColor"*. Hex ("#RRGGBB"), CSS colour name, "currentColor"` to inherit the surrounding text colour.
`x`	*Any R object* — tested by `is_brdr()` for membership in the `tabular_brdr` S3 class.

Details

Surface. A single `tabular_brdr` value is a length-3 named list with class `"tabular_brdr"`: `list(style, width, color)`. The shape is identical to the bare triple `style()`'s per-side scalars accept, so the resolver in `R/borders.R` can ingest either form transparently. Construct with `brdr()`; test with `is_brdr()`.

Width keywords. `width` accepts either a numeric in points (typical clinical values: 0.25, 0.5, 1, 1.5) or one of the four named keywords:

keyword	points
`"hairline"`	0.25
`"thin"`	0.5
`"medium"`	1
`"thick"`	1.5

Keywords resolve to numeric points immediately; the constructed value carries a numeric `width`. Numeric inputs pass through unchanged after a non-negative check.

Style enum. `style` is one of `"solid"` (default), `"dashed"`, `"dotted"`, `"double"`, `"dashdot"`, `"none"`. `"none"` is the explicit clear-this-rule sentinel: setting a rule to `brdr(style = "none")` (or the bare string `"none"`) in `preset(rules = list(...))` suppresses the baseline rule that backend would otherwise draw.

Color. Hex (`"#212529"`), CSS colour name (`"black"`, `"slategray"`), the `"ink"` token (default; resolves to the primary rule ink `#212529`, decoupled from the surrounding text colour so a re-coloured header keeps a neutral rule), or `"currentColor"` (inherit the surrounding text colour per backend convention — `w:color="auto"` in DOCX, the document text colour in RTF, the CSS `currentColor` keyword in HTML).

Value

A `tabular_brdr` *S3 object* — a length-3 named list suitable for `preset(rules = list(<rule> = .))` or `style(border_* = .)`.

See Also

Where to attach: `preset()`'s `rules` knob (one brdr() per rule name) and `style()`'s `border_*` arguments.

Per-cell predicates: `style()` accepts the same per-side `border_<side>_{style,width,color}` triples without going through `brdr()`.

Resolver internals: `tabular_classes` (`style_node`'s 12 border scalars).

Examples

```
# ---- Example 1: A house-style rule set ----
#
# The `rules` knob takes one brdr() value per rule name. Here a
# thick column-label divider (midrule), a hairline dotted rule
# between body rows (rowrule), and the muted spanner rule dropped.
```

```
# Unlisted rules keep their booktabs defaults.
demo_n <- stats::setNames(cdisc_saf_n$n, cdisc_saf_n$arm_short)
tabular(
  cdisc_saf_ae,
  titles = c(
    "Table 14.3.1",
    "Overall Summary of Adverse Events",
    "Safety Population"
  ),
  footnotes = "Subjects counted once per category."
) |>
  cols(
    stat_label = col_spec(label = "Category"),
    placebo    = col_spec(label = "Placebo\nN={demo_n['placebo']}"),
    drug_50    = col_spec(label = "Drug 50\nN={demo_n['drug_50']}"),
    drug_100   = col_spec(label = "Drug 100\nN={demo_n['drug_100']}"),
    Total      = col_spec(label = "Total\nN={demo_n['Total']}")
  ) |>
  preset(
    rules = list(
      midrule  = brdr(width = "thick"),
      rowrule  = brdr(width = "hairline", style = "dotted"),
      spanrule = "none"
    )
  )

# ---- Example 2: Wrap a custom style into a reusable function ----
#
# The recommended way to share a rule style across many tables is to
# wrap the `preset()` call in a small function. A later `preset()` /
# `style()` call layers a one-off override cleanly on top.
custom_style <- function(spec) {
  spec |>
    preset(
      rules = list(
        toprule    = brdr(width = "thin", color = "#212529"),
        midrule    = brdr(width = "thin", color = "#212529"),
        bottomrule = brdr(width = "thin", color = "#212529")
      )
    )
}

tabular(cdisc_saf_n) |>
  custom_style() |>
  preset(rules = list(rowrule = brdr("hairline", "dashed")))

# ---- Example 3: Width keyword vs numeric, every style enum value ----
#
# Width accepts both the four named keywords and a bare numeric
# in points; style accepts six enum values. Use `is_brdr()` to
# confirm the constructor returned a valid `tabular_brdr` rather
# than a fallback list.
for (w in c("hairline", "thin", "medium", "thick")) {
```

```
  cat(w, "=", brdr(width = w)$width, "pt\n")
}
is_brdr(brdr(width = 0.75))

lapply(
  c("solid", "dashed", "dotted", "double", "dashdot", "none"),
  function(s) brdr(style = s)
)

# ---- Example 4: A full grid via the body-edge style() path ----
#
# The `rules` knob covers the named booktabs anatomy; for the body
# outer frame and inter-column separators, hand brdr() to
# `style(.at = cells_table(side = ...))`. Here a medium outer frame
# plus hairline column separators on a demographics table.
tabular(cdisc_saf_demo, titles = "Demographics with a full grid") |>
  cols(
    variable   = col_spec(usage = "group", label = "Characteristic"),
    stat_label = col_spec(label = "Statistic"),
    placebo    = col_spec(label = "Placebo",  align = "decimal"),
    drug_50    = col_spec(label = "Drug 50",  align = "decimal"),
    drug_100   = col_spec(label = "Drug 100", align = "decimal"),
    Total      = col_spec(label = "Total",    align = "decimal")
  ) |>
  style(border = brdr(width = "medium"), .at = cells_table(side = "outer")) |>
  style(border_left = brdr("hairline"), .at = cells_table(side = "cols"))
```

`cdisc_eff_estimates` *Treatment-effect estimates by model*

Description

Four competing efficacy models with their treatment-effect point estimate, 95% confidence-interval bounds, and nominal p-value. Shaped as a numeric-cell table (one row per model) rather than the usual pre-formatted character cells, so it exercises the `col_spec(format = ...)` + `col_spec(na_text = ...)` cascade. One row (`MMRM`) carries `NA` CI bounds to demonstrate `na_text`.

Usage

```
cdisc_eff_estimates
```

Format

A data frame with 4 rows and 5 columns:

`model` Model name (`"ANCOVA"`, `"MMRM"`, `"Cox PH"`, `"Bootstrap (1000 reps)"`).

`estimate` Numeric point estimate.

`lower_ci`, `upper_ci` Numeric 95% CI bounds. The MMRM row has `NA` bounds.

`p_value` Nominal p-value (numeric).

Source

Synthetic estimates following the `_archive/.../arframe-examples/tables/tte-summary.qmd` and `efficacy-bor.qmd` shapes. Not derived from any patient-level data — illustrative values only.

See Also

`col_spec()` for the formatting cascade these values exercise.

Examples

```
# Numeric-cell efficacy table — format = "%.2f" pins precision,
# na_text = "--" renders the MMRM row's NA bounds as dashes.
tabular(cdisc_eff_estimates, titles = "Treatment-effect estimates by model") |>
  cols(
    model    = col_spec(usage = "group",  label = "Model", valign = "top"),
    estimate = col_spec(label = "Estimate", align = "decimal",
                        format = "%.2f"),
    lower_ci = col_spec(label = "Lower\n95% CI", align = "decimal",
                        format = "%.2f", na_text = "--"),
    upper_ci = col_spec(label = "Upper\n95% CI", align = "decimal",
                        format = "%.2f", na_text = "--"),
    p_value  = col_spec(label = "p-value",  align = "decimal",
                        format = "%.4f")
  )
```

---

cdisc_eff_n *Efficacy-population BigN per arm*

Description

Per-arm subject counts (BigN) for the efficacy population used by `cdisc_eff_resp` / `eff_resp_card` — subjects with a `BOR` record in `pharmaverseadam::adrs_onco`. Same two-column naming convention as `cdisc_saf_n`; the totals differ from `cdisc_saf_n` because not every safety-pop subject contributes a best-overall-response record.

Usage

```
cdisc_eff_n
```

Format

A data frame with 4 rows and 3 columns; same schema as cdisc_saf_n (`arm`, `arm_short`, `n`).

Source

Derived in `data-raw/bundle-demo.R` from the per-arm BOR denominator computed inside the `cdisc_eff_resp` pipeline.

See Also

cdisc_saf_n for the safety-population counterpart.

Examples

```
# Efficacy BigN joined into column headers.
ne <- stats::setNames(cdisc_eff_n$n, cdisc_eff_n$arm_short)
col_spec(label = "Placebo\nN={ne['placebo']}")@label
```

---

cdisc_eff_resp *Best Overall Response and Response Rates*

Description

Pre-summarised efficacy table. Per-arm counts of best overall response (BOR) per CDISC category, plus derived ORR, CBR, and DCR rate rows each followed by an exact (Clopper-Pearson) 95% CI row. Four sections (Best Overall Response, Objective Response Rate, Clinical Benefit Rate, Disease Control Rate) are encoded via the `groupid` + `group_label` pair so a single `usage = "group"` / `group_display = "header_row"` on `group_label` synthesises one bold section band per groupid block; the body rows render below each band, auto-indented one level by the `"header_row"` section itself (the stub needs no `indent` — the section supplies it).

Usage

```
cdisc_eff_resp
```

Format

A data frame with 13 rows and 7 columns:

`stat_label` Row label (`"CR"`, `"PR"`, `"SD"`, `"NON-CR/NON-PD"`, `"PD"`, `"NE"`, `"MISSING"`, `"ORR (CR + PR)"`, `"95% CI (Clopper-Pearson)"`, `"CBR (CR + PR + SD)"`, `"95% CI (Clopper-Pearson)"`, `"DCR (CR + PR + SD + NON-CR/NON-PD)"`, `"95% CI (Clopper-Pearson)"`).

`row_type` `"category"` for BOR categorical rows, `"derived"` for ORR / CBR / DCR rate rows, `"ci"` for the paired confidence-interval rows. Hide via `col_spec(visible = FALSE)`.

`placebo`, `drug_50`, `drug_100` Per-arm cell text (`"n (pct)"` on rate rows, `"(lower, upper)"` on CI rows).

`groupid` Integer section id (1 = Best Overall Response, 2 = Objective Response Rate, 3 = Clinical Benefit Rate, 4 = Disease Control Rate). Hide via `col_spec(visible = FALSE)`; used as the section sort / partition key.

`group_label` Character section label, repeating across every row of its groupid block ("Best Overall Response" x7, "Objective Response Rate" x2, ...). Drives the engine's `usage = "group"` header_row synthesis when paired with `group_display = "header_row"`.

Source

Derived in `data-raw/bundle-demo.R` from `pharmaverseadam::adrs_onco` filtered to `PARAMCD == "BOR"`.

See Also

cdisc_eff_n for BigN denominators.

Examples

```
# 95% efficacy pattern: four bold section bands (Best Overall
# Response / Objective Response Rate / Clinical Benefit Rate /
# Disease Control Rate), each followed by indented stat rows. The
# source already ships in the right display order, so no sort step
# is needed; `group_label` repeats across every row of its section
# so the engine's `header_row` mode emits exactly one band per
# section.
ne <- stats::setNames(cdisc_eff_n$n, cdisc_eff_n$arm_short)
tabular(
  cdisc_eff_resp,
  titles = c(
    "Table 14.2.1",
    "Best Overall Response and Response Rates",
    "Efficacy Evaluable Population"
  )
) |>
  cols(
    group_label = col_spec(usage = "group", group_display = "header_row"),
    stat_label  = col_spec(label = "Response"),
    groupid     = col_spec(visible = FALSE),
    row_type    = col_spec(visible = FALSE),
    placebo     = col_spec(
      label = "Placebo\nN={ne['placebo']}",
      align = "decimal"
    ),
    drug_50     = col_spec(
      label = "Drug 50\nN={ne['drug_50']}",
      align = "decimal"
    ),
    drug_100    = col_spec(
      label = "Drug 100\nN={ne['drug_100']}",
      align = "decimal"
    )
  )
```

`cdisc_saf_ae` *Overall adverse-event summary, Safety Population*

Description

Pre-summarised wide-format AE overview. Two clinical blocks: high-level flag rows (any TEAE, any SAE, any treatment-related, any AE leading to death, any AE recovered / resolved) and maximum-severity rows (mild / moderate / severe). Severity rows are indented with two leading spaces in the data, so a plain `cols(stat_label = col_spec())` renders a flat overview with the severity rows nested under the flags, one row per category.

Usage

```
cdisc_saf_ae
```

Format

A data frame with 8 rows and 5 columns:

`stat_label` Row label (`"Any TEAE"`, `"Any Serious AE (SAE)"`, `"Any AE Related to Study Drug"`, `"Any AE Leading to Death"`, `"Any AE Recovered / Resolved"`, `" Maximum severity: Mild"`, `" Maximum severity: Moderate"`, `" Maximum severity: Severe"`).

`placebo` Placebo arm cell text (`"n (pct)"`).

`drug_50` Drug 50 arm cell text.

`drug_100` Drug 100 arm cell text.

`Total` Pooled-across-arms cell text.

Source

Derived in `data-raw/bundle-demo.R` from `pharmaverseadam::adae` filtered to `SAFFL == "Y"` and `TRTEMFL == "Y"`.

See Also

cdisc_saf_n for BigN denominators; cdisc_saf_aesocpt for the SOC / PT detail companion.

Examples

```
n <- stats::setNames(cdisc_saf_n$n, cdisc_saf_n$arm_short)
tabular(
  cdisc_saf_ae,
  titles = c(
    "Table 14.3.0",
    "Adverse Event Overview",
    "Safety Population"
  )
) |>
  cols(
    stat_label = col_spec(label = ""),
    placebo    = col_spec(
      label = "Placebo\nN={n['placebo']}",
      align = "decimal"
    ),
    drug_50    = col_spec(
      label = "Drug 50\nN={n['drug_50']}",
      align = "decimal"
    ),
    drug_100   = col_spec(
      label = "Drug 100\nN={n['drug_100']}",
      align = "decimal"
    ),
    Total      = col_spec(
```

```
      label = "Total\nN={n['Total']}",
      align = "decimal"
    )
  )
```

`cdisc_saf_aesocpt` *Adverse events by System Organ Class and Preferred Term*

Description

Pre-summarised AE-by-SOC/PT table. Interleaved row order: overall "any TEAE" row first, then per-SOC blocks where each SOC row is followed by its preferred-term detail rows. Top 10 SOCs and top 5 PTs per SOC are kept; `row_type` marks the role of each row and `indent_level` carries the canonical depth (0 for overall and SOC, 1 for PT) so the downstream pipeline drives the SOC -> PT indent via `col_spec(indent = "indent_level")` without reconstructing it in every script. The richer SOC × PT slice exercises `paginate()` and the engine's horizontal-panel splitter end-to-end on a realistic submission shell.

Usage

```
cdisc_saf_aesocpt
```

Format

A data frame with 61 rows and 10 columns:

`soc` System Organ Class label. Repeats across the SOC's PT rows; hide via `col_spec(visible = FALSE)` once `label` carries the same SOC text on SOC rows.

`label` The row's display label. Equal to `soc` on the overall and SOC-summary rows; equal to the preferred-term name on PT detail rows. Promoted to the primary display column — pair with `indent = "indent_level"` to drive the SOC -> PT indent.

`row_type` One of `"overall"`, `"soc"`, `"pt"`. Partition marker; hide via `col_spec(visible = FALSE)`.

`indent_level` Integer depth (0 on overall and SOC rows, 1 on PT rows). Consumed by `col_spec(indent = "indent_level")` on the `label` column; the engine auto-hides this column at resolve time.

`n_total` Integer. The row's own subject count — overall TEAE count on the overall row, the SOC's count on each SOC row, the PT's count on each PT row. Inner sort key.

`soc_n` Integer. The parent SOC's count, broadcast to every row in that SOC's cluster (SOC row + its PT children) so a descending sort on `soc_n` keeps PTs grouped under their parent. On the overall row, equal to the overall TEAE count. Outer sort key.

`placebo` Placebo arm cell text (`"n (pct)"`).

`drug_50`, `drug_100` Drug arms cell text.

`Total` Pooled-across-arms cell text.

Source

Derived in `data-raw/bundle-demo.R` from `pharmaverseadam::adae`. Filtered to the top 10 SOCs by total incidence and the top 5 PTs per SOC. Body rows are pre-sorted with the cards-style two-level rule (`arrange(desc(soc_n), soc, desc(n_total))`) so the canonical render order is already baked in; the render-time `sort_rows(by = c("soc_n", "n_total"), descending = c(TRUE, TRUE))` reproduces it via stable sort.

See Also

cdisc_saf_aesocpt_ard for the hierarchical long ARD; cdisc_saf_n for BigN denominators.

Examples

```
# 95% safety pattern: SOC/PT table where `label` carries SOC text
# on SOC rows and PT text on PT rows, indented by `indent_level`.
# `soc` / `row_type` / `n_total` / `soc_n` ride along as hidden
# partition + sort keys. `sort_rows(soc_n, n_total)` clusters PTs
# under their parent SOC and orders both levels by descending count.
n <- stats::setNames(cdisc_saf_n$n, cdisc_saf_n$arm_short)

tabular(
  cdisc_saf_aesocpt,
  titles = c(
    "Table 14.3.1",
    "Adverse Events by SOC and Preferred Term",
    "Safety Population"
  )
) |>
  cols(
    label    = col_spec(
      label = "SOC / PT",
      indent = "indent_level",
      align = "left"
    ),
    soc      = col_spec(visible = FALSE),
    row_type = col_spec(visible = FALSE),
    n_total  = col_spec(visible = FALSE),
    soc_n    = col_spec(visible = FALSE),
    placebo  = col_spec(
      label = "Placebo\nN={n['placebo']}",
      align = "decimal"
    ),
    drug_50  = col_spec(
      label = "Drug 50\nN={n['drug_50']}",
      align = "decimal"
    ),
    drug_100 = col_spec(
      label = "Drug 100\nN={n['drug_100']}",
      align = "decimal"
    ),
    Total    = col_spec(
      label = "Total\nN={n['Total']}",
```

```
    align = "decimal"
  )
) |>
sort_rows(
  by = c("soc_n", "n_total"),
  descending = c(TRUE, TRUE)
)
```

`cdisc_saf_aesocpt_ard` *Cards hierarchical ARD for AEs by SOC and PT*

Description

Long-format companion to `cdisc_saf_aesocpt`. Produced by `cards::ard_stack_hierarchical()` over `(AEBODSYS, AEDECOD)` with adsl-level denominators, sorted by descending overall incidence via `cards::sort_ard_hierarchical()`. Limited to the same top-10 SOC, top-5 PT subset as `cdisc_saf_aesocpt` so the two datasets describe the same slice of the data.

Usage

```
cdisc_saf_aesocpt_ard
```

Format

A `card`-classed tibble. Carries a hierarchical "overall" row (cards' internal `..ard_hierarchical_overall..` marker) that `pivot_across()` relabels to `"Overall"` (overridable via its `label` argument) and emits as the table's top `row_type = "overall"` row.

Details

This is the package's canonical **hierarchical ARD** demo (two grouping variables nested SOC -> PT). Its flat counterpart is cdisc_saf_demo_ard; together they cover both shapes `pivot_across()` must handle.

Source

Derived in `data-raw/bundle-demo.R` via `cards::ard_stack_hierarchical()` over `pharmaverseadam::adae` filtered to the top SOC / PT subset.

See Also

`pivot_across()` for the long-to-wide bridge; cdisc_saf_aesocpt for the wide companion.

Examples

```
# Hierarchical ARD pivot. pivot_across() recognises the
# ard_stack_hierarchical shape and emits soc / label / row_type.
n <- stats::setNames(cdisc_saf_n$n, cdisc_saf_n$arm_short)
cdisc_saf_aesocpt_ard |>
  pivot_across(statistic = "{n} ({p}%)") |>
  tabular(
    titles = c(
      "Table 14.3.1",
      "Adverse Events by SOC and PT",
      "Safety Population"
    )
  ) |>
  cols(
    label    = col_spec(label = "SOC / PT", align = "left"),
    soc      = col_spec(visible = FALSE),
    row_type = col_spec(visible = FALSE),
    `Placebo`              = col_spec(align = "decimal"),
    `Xanomeline Low Dose`  = col_spec(align = "decimal"),
    `Xanomeline High Dose` = col_spec(align = "decimal")
  )
```

`cdisc_saf_demo` *Demographics summary, Safety Population*

Description

Pre-summarised wide-format demographics suitable for direct passing into `tabular()`. One row per displayed statistic. Three parameter blocks — a deliberately minimal set covering both summary shapes:

Usage

```
cdisc_saf_demo
```

Format

A data frame with 11 rows and 6 columns:

`variable` Display-block label (`"Age (years)"`, `"Sex, n (%)"`, `"Race, n (%)"`). Driven by `cols(usage = "group")` to collapse repeat values at render.

`stat_label` Statistic or level label (`"n"`, `"Mean (SD)"`, `"Median"`, `"M"`, `"WHITE"`, ...).

`placebo` Placebo arm cell text.

`drug_50` Xanomeline Low Dose (50 mg) arm cell text.

`drug_100` Xanomeline High Dose (100 mg) arm cell text.

`Total` Pooled-across-arms cell text.

Details

- continuous: `Age (years)` — emitted as `n`, `Mean (SD)`, `Median`, `Q1, Q3`, `Min, Max`
- categorical: `Sex`, `Race` — each level rendered as `n (%)`

Shaped for the display-only contract: every cell is the final string that will appear in the rendered table.

Source

Derived in `data-raw/bundle-demo.R` from `pharmaverseadam::adsl` filtered to `SAFFL == "Y"` and the three CDISCPILOT01 treatment arms.

See Also

cdisc_saf_demo_ard for the long-format ARD companion; cdisc_saf_n for the matching BigN denominators.

Examples

```
# 95% safety pattern: demographics table with BigN-embedded
# column labels and CDISC-canonical statistic order.
n <- stats::setNames(cdisc_saf_n$n, cdisc_saf_n$arm_short)
tabular(
  cdisc_saf_demo,
  titles = c(
    "Table 14.1.1",
    "Demographics and Baseline Characteristics",
    "Safety Population"
  )
) |>
  cols(
    variable   = col_spec(usage = "group", label = "Parameter"),
    stat_label = col_spec(label = "Statistic"),
    placebo    = col_spec(
      label = "Placebo\nN={n['placebo']}",
      align = "decimal"
    ),
    drug_50    = col_spec(
      label = "Drug 50\nN={n['drug_50']}",
      align = "decimal"
    ),
    drug_100   = col_spec(
      label = "Drug 100\nN={n['drug_100']}",
      align = "decimal"
    ),
    Total      = col_spec(
      label = "Total\nN={n['Total']}",
      align = "decimal"
    )
  )
```

cdisc_saf_demo_ard *Cards ARD for demographics (flat ARD companion)*

Description

The same demographics summary as `cdisc_saf_demo`, but in the long Analysis Results Data (ARD) format produced by `cards::ard_stack()`. One row per (treatment arm, variable, statistic). Shipped as a teaching dataset that shows the upstream shape users typically have when they start from `cards`. Convert it to the wide form `tabular()` accepts via `pivot_across()` — tabular itself does **not** consume the long ARD format, since pre-summarised wide data is the package boundary.

Usage

```
cdisc_saf_demo_ard
```

Format

A `card`-classed tibble with columns `group1`, `group1_level`, `variable`, `variable_level`, `context`, `stat_name`, `stat_label`, `stat`. `group1 == "TRT01A"` and `group1_level` carries the original pharmaverseadam arm labels (`"Placebo"`, `"Xanomeline Low Dose"`, `"Xanomeline High Dose"`). `cards::ard_stack(.overall = TRUE)` adds overall rows with `group1_level = NA`; `pivot_across()` renders those into a `Total` column.

Details

Continuous variables: `AGE`, `WEIGHT`, `HEIGHT`, `BMI` (each emitting `N`, `mean`, `sd`, `median`, `p25`, `p75`, `min`, `max`). Categorical variables: `AGEGR1`, `SEX`, `RACE`, `ETHNIC`, `BMI_CAT` (each emitting `n`, `N`, `p`).

This is the package's canonical **flat ARD** demo. Its hierarchical counterpart is cdisc_saf_aesocpt_ard; together they cover both shapes `pivot_across()` must handle.

Source

Derived in `data-raw/bundle-demo.R` via `cards::ard_stack(.by = "TRT01A", .overall = TRUE)` over `pharmaverseadam::adsl`.

See Also

`pivot_across()` for the long-to-wide bridge; cdisc_saf_demo for the wide companion.

Examples

```
# 95% demographics pattern: cards ARD -> wide -> rendered table.
n <- stats::setNames(cdisc_saf_n$n, cdisc_saf_n$arm_short)
cdisc_saf_demo_ard |>
  pivot_across(
    statistic = list(
      continuous  = "{mean} ({sd})",
```

```
    categorical = "{n} ({p}%)"
  ),
  label = c(AGE = "Age (years)", SEX = "Sex", RACE = "Race")
) |>
tabular(
  titles = c(
    "Table 14.1.1",
    "Demographics",
    "Safety Population"
  )
)
```

`cdisc_saf_n` *Safety-population BigN per arm*

Description

Per-arm subject counts (BigN) for the safety population, plus a `Total` row. Use this table to embed BigN inline in column headers with a glue-style `{expr}` template against `cols(col_spec(label = ...))`; there is no dedicated BigN field on `col_spec` because the denominator already lives here in a discoverable, joinable form.

Usage

```
cdisc_saf_n
```

Format

A data frame with 4 rows and 3 columns:

`arm` Raw pharmaverseadam arm label (`"Placebo"`, `"Xanomeline Low Dose"`, `"Xanomeline High Dose"`, `"Total"`). Matches `group1_level` in the `_card` ARDs (so the pivot output's column names match a `setNames(cdisc_saf_n$n, cdisc_saf_n$arm)` lookup).

`arm_short` Renamed label (`"placebo"`, `"drug_50"`, `"drug_100"`, `"Total"`). Matches the column names of `cdisc_saf_demo`, `cdisc_saf_ae`, `cdisc_saf_aesocpt`, and `cdisc_saf_vital`.

`n` Integer subject count.

Details

Two arm-naming columns are shipped side by side so the same table can serve both the `_card` ARDs (raw pharmaverseadam labels in `group1_level`) and the renamed wide datasets (snake-cased arm column names).

Source

Derived in `data-raw/bundle-demo.R` from `pharmaverseadam::adsl` filtered to `SAFFL == "Y"` and the three CDISCPILOT01 arms.

See Also

cdisc_eff_n for the efficacy-population counterpart.

Examples

```
# Use cdisc_saf_n$arm_short when joining into the wide datasets
# (cdisc_saf_demo, cdisc_saf_ae, cdisc_saf_aesocpt, cdisc_saf_vital).
n <- stats::setNames(cdisc_saf_n$n, cdisc_saf_n$arm_short)
col_spec(label = "Placebo\nN={n['placebo']}")@label

# Use cdisc_saf_n$arm when joining into pivot_across() output
# (column names match the raw pharmaverseadam arm labels).
n_arm <- stats::setNames(cdisc_saf_n$n, cdisc_saf_n$arm)
col_spec(label = "Placebo\nN={n_arm['Placebo']}")@label
```

---

cdisc_saf_subgroup *Vital-signs subgroup summary by Sex, by Visit*

Description

Pre-summarised vital-signs stats partitioned by sex (F / M) across four visits (Baseline, Week 8, Week 16, End of Treatment). Two parameters (Systolic BP, Diastolic BP) emit four statistic rows each (n, Mean (SD), Median, Min, Max). A partition-constant sex_n BigN column rides alongside so banners can inline the denominator via subgroup(label = "Sex: {sex} (N = {sex_n})") without reaching for a separate lookup.

Usage

```
cdisc_saf_subgroup
```

Format

A data frame with 64 rows and 10 columns:

sex Factor (F / M).

sex_n Integer BigN — number of subjects in the partition row's sex (partition-constant; rides into the banner via {sex_n} template tokens).

paramcd CDISC parameter code (SYSBP / DIABP).

param Decoded parameter name ("Systolic BP (mmHg)", "Diastolic BP (mmHg)").

visit Analysis visit (Baseline, Week 8, Week 16, End of Treatment).

stat_label Statistic label (n, Mean (SD), Median, Min, Max).

placebo, drug_50, drug_100, Total Per-arm cell text.

Details

Designed for subgroup() and as_grid() examples: partition by sex (one page set per sex) and nest parameter then visit inside each page for the canonical by-visit CSR shape, or cross sex with visit for a multi-variable partition.

Source

Derived in `data-raw/bundle-demo.R` from `pharmaverseadam::advs` filtered to `SAFFL == "Y"`, the three CDISCPILOT01 arms, the `SYSBP` / `DIABP` parameters, and the four scheduled visits.

See Also

cdisc_saf_n for BigN denominators; `subgroup()` for the verb this dataset is designed for.

Examples

```
# 95% pattern: subgroup partition by sex with inline BigN, parameter
# nesting visit inside each sex page. `sex` and `sex_n` auto-hide
# from the body: `sex` because it is the partition `by` column;
# `sex_n` because the banner template references it. No explicit
# `col_spec(visible = FALSE)` needed.
tabular(cdisc_saf_subgroup, titles = "Vital Signs by Visit") |>
  cols(
    paramcd    = col_spec(visible = FALSE),
    param      = col_spec(usage = "group", label = "Parameter"),
    visit      = col_spec(usage = "group", label = "Visit"),
    stat_label = col_spec(label = "Statistic"),
    placebo    = col_spec(label = "Placebo",  align = "decimal"),
    drug_50    = col_spec(label = "Drug 50",  align = "decimal"),
    drug_100   = col_spec(label = "Drug 100", align = "decimal"),
    Total      = col_spec(label = "Total",    align = "decimal")
  ) |>
  subgroup(by = "sex", label = "Sex: {sex} (N = {sex_n})")
```

---

cdisc_saf_vital *Vital-signs summary*

Description

Pre-summarised vital-signs stats. Four parameters (SYSBP, DIABP, PULSE, TEMP) at four visits (Baseline, Week 8, Week 16, End of Treatment), each producing four statistic rows (`n`, `Mean (SD)`, `Median`, `Min, Max`). The 4 x 4 x 4 grid makes this dataset a natural fit for `paginate()` examples — 64 rows comfortably exceed a single page under typical clinical row-per-page settings.

Usage

```
cdisc_saf_vital
```

Format

A data frame with 64 rows and 7 columns:

`paramcd` CDISC parameter code (`SYSBP` / `DIABP` / `PULSE` / `TEMP`). Repeats across visit and statistic; use `col_spec(usage = "group")` to collapse.

`param` Decoded parameter name.

`visit` Analysis visit label (`"Baseline"` / `"Week 8"` / `"Week 16"` / `"End of Treatment"`).

`stat_label` Statistic label.

`placebo`, `drug_50`, `drug_100` Per-arm cell text.

Source

Derived in `data-raw/bundle-demo.R` from `pharmaverseadam::advs`.

See Also

cdisc_saf_n for BigN denominators.

Examples

```
n <- stats::setNames(cdisc_saf_n$n, cdisc_saf_n$arm_short)
tabular(
  cdisc_saf_vital,
  titles = c(
    "Table 14.4.1",
    "Vital Signs Summary at Baseline and End of Treatment",
    "Safety Population"
  )
) |>
  cols(
    paramcd    = col_spec(visible = FALSE),
    param      = col_spec(usage = "group", label = "Parameter"),
    visit      = col_spec(usage = "group", label = "Visit"),
    stat_label = col_spec(label = "Statistic"),
    placebo    = col_spec(
      label = "Placebo\nN={n['placebo']}",
      align = "decimal"
    ),
    drug_50    = col_spec(
      label = "Drug 50\nN={n['drug_50']}",
      align = "decimal"
    ),
    drug_100   = col_spec(
      label = "Drug 100\nN={n['drug_100']}",
      align = "decimal"
    )
  )
```

---

cells *Cell-location constructors for* `style()`

Description

Build a `tabular_location` value naming one region of the rendered table; pass the result to `style()`'s `at` argument. Each constructor targets one surface (body, headers, footnotes, ...); optional `i` / `j` / `where` / `level` / `labels` filters narrow the target within that surface.

Usage

```
cells_body(i = NULL, j = NULL, where = NULL)

cells_headers(level = NULL, labels = NULL, j = NULL)

cells_group_headers(j = NULL, where = NULL)

cells_title()

cells_subgroup_labels()

cells_footnotes()

cells_pagehead(slot = NULL)

cells_pagefoot(slot = NULL)

cells_table(side = NULL, i = NULL, j = NULL)

is_tabular_location(x)
```

Arguments

i	*Row index filter.* <integer | logical | character | NULL>. Integer = 1-based row numbers; logical = length-nrow mask (broadcasts from scalar TRUE/FALSE); character = matches the visible row labels. NULL (default) = no filter (every row).
j	*Column index filter.* <integer | character | NULL>. Integer = 1-based column positions; character = matches column names in spec@data. NULL (default) = every column.
where	*Predicate.* An unquoted expression evaluating to a length-nrow logical vector when run against the data grid. Captured as an rlang quosure (so pvalue < 0.05 works without needing to wrap in vars() or similar). Mutually exclusive with i.
level	*Header-band depth (for* cells_headers*).* <integer(1) | NULL>. 1 = topmost spanner band; increasing integers walk toward the leaves. -1 = the leaf band (per-column labels built from col_spec@label). NULL (default) = every band at every depth.
labels	*Header-band labels (for* cells_headers*).* <character | NULL>. Targets header_node(s) whose @label matches, at any depth. Mutually exclusive with level.
slot	*Band slot (for* cells_pagehead / cells_pagefoot*).* <character(1) | NULL>. One of "left", "center", "right", or NULL for every slot.
side	*Table edge / separator (for* cells_table*).* <character(1) | NULL>. One of "outer" (all four outer edges), "outer_top", "outer_bottom", "outer_left", "outer_right", "rows" (horizontal separator between body rows), "cols"

(vertical separator between body columns), or NULL for whole-body (same as cells_body()).

x — *Any R object* — tested by is_tabular_location() for membership in the tabular_location S3 class.

Details

One surface per location. A tabular_location always names exactly one of: body, headers, group_headers, title, subgroup_labels, footnotes, pagehead, pagefoot, table. Cross-surface styling layers in via multiple chained style() calls (one per location).

Index vocabulary. Where supported, the i (rows) and j (columns) arguments accept integer, logical, or character vectors — matching the convention established by **flextable** (bold(ft, i, j)) and **tinytable** (style_tt(i, j)). Character vectors match against the data frame's column names (j) or row labels (i); integers are 1-based positions; logicals broadcast to nrow / ncol.

Predicate vocabulary. cells_body(where = pvalue < 0.05) is the canonical data-driven filter — where is captured as an rlang quosure and evaluated at engine time against the post-sort grid. Mutually exclusive with i (you target *either* by index *or* by predicate, not both).

Why cells_headers not cells_column_spanners. The verb that builds the multi-level header tree is named headers(). The location follows the same vocabulary: one word ("headers") covers the entire column-header section — inner spanner bands AND the leaf band of per-column labels. Pass level or labels to narrow.

Value

A tabular_location S3 list with slots surface, i, j, where, labels, level, slot, side (unused slots are NULL). Pass to style()'s at argument.

Surface filters

constructor	filters
cells_body(i, j, where)	row index / col index / predicate
cells_headers(level, labels, j)	band depth / spanner label / cols
cells_group_headers(j, where)	injected section rows
cells_title()	(no filter — whole block)
cells_subgroup_labels()	(no filter)
cells_footnotes()	(no filter)
cells_pagehead(slot)	"left" / "center" / "right"
cells_pagefoot(slot)	"left" / "center" / "right"
cells_table(side, i, j)	outer edge / row separator / etc.

See Also

Verb that consumes locations: style().

Border value type: brdr().

Reusable house style: style_template().

Examples

```
# Whole body cells (the default for style())
cells_body()

# Row index 1:3, column "Total"
cells_body(i = 1:3, j = "Total")

# Data-driven subset
cells_body(where = stat_label == "Mean (SD)")

# Topmost spanner band only
cells_headers(level = 1)

# Leaf band (per-column labels)
cells_headers(level = -1)

# A specific spanner by label
cells_headers(labels = "Treatment Group")

# Section-header rows for col_spec(group_display = "header_row")
cells_group_headers()

# Title / footnotes blocks
cells_title()
cells_footnotes()

# Page-header / page-footer slots
cells_pagehead(slot = "left")
cells_pagefoot(slot = "right")

# Outer table frame
cells_table(side = "outer")

# Horizontal rules between body rows
cells_table(side = "rows")
```

---

check_fonts *Check font availability across backends*

Description

Walks the resolved font fallback chain for each backend and reports which entries the local machine can find. Useful for answering "is the preview I'm seeing the same fonts the downstream reviewer will see?".

Usage

```
check_fonts(.spec)
```

Arguments

.spec	*A* tabular_spec *or* preset_spec. <tabular_spec | preset_spec>: required. The spec whose effective preset determines which font chain to walk.

Details

The diagnostic does NOT change what emit() writes to the file. Tabular's backends emit font *names* (CSS strings, LaTeX \setmainfont commands, RTF font-table entries); the consuming application (browser, LaTeX engine, Word, Adobe Reader) on the opening machine resolves those names against its own installed fonts. check_fonts() is purely informational — it tells you which entries of the cross-platform fallback chain you can see on this machine, so you can predict drift.

Status markers:

- v — font is installed on this machine (via systemfonts).
- o — font is a CSS / LaTeX generic; always resolvable by the consuming application.
- x — font is not installed on this machine; the consuming app on a different machine may or may not have it.

Requires the systemfonts package (in Suggests); call install.packages("systemfonts") first if it isn't installed.

Value

Invisibly returns the resolved per-backend chains as a named list of character vectors. Side effect: prints a cli tree showing the availability marker for every entry.

See Also

Builds the spec: tabular(), preset().

Resolves the spec: as_grid(), emit().

Examples

```
# ---- Example 1: Inspect default font resolution ----
#
# Build a spec with the default font_family ("mono") and ask
# which entries in the cross-platform chain are findable
# locally. Useful before sharing a render with downstream
# reviewers who may be on a different OS.
spec <- tabular(
  cdisc_saf_demo,
  titles = "Demographics"
)
if (requireNamespace("systemfonts", quietly = TRUE)) {
  check_fonts(spec)
}

# ---- Example 2: Diagnose a Courier New request ----
#
# A request for "Courier New" (a specific named font) renders
```

```
# on macOS / Windows but may fall back to a serif on Linux.
# `check_fonts()` flags this so the user knows to switch to
# the "mono" generic for portable output.
spec_mono <- tabular(
  cdisc_saf_demo,
  titles = "Mono request"
) |>
  preset(font_family = "Courier New")
if (requireNamespace("systemfonts", quietly = TRUE)) {
  check_fonts(spec_mono)
}

# ---- Example 3: Explicit cross-platform stack ----
#
# A length>1 input is treated as an explicit fallback chain and
# emitted verbatim — no alias lookup, no fabrication. Use this
# when the first choice is a sponsor / brand face that needs an
# honest fallback for reviewers who don't have it installed.
spec_brand <- tabular(cdisc_saf_demo) |>
  preset(font_family = c("Inter", "Liberation Sans", "Arial", "sans"))
if (requireNamespace("systemfonts", quietly = TRUE)) {
  check_fonts(spec_brand)
}

# ---- Example 4: Compare serif vs sans fallback chains ----
#
# Side-by-side check of the two generic families. Useful when
# deciding the house-style default: the serif chain leads with
# Liberation Serif (Linux-server-first); the sans chain leads
# with Liberation Sans. Both close with the backend's native
# fallback layer (CSS generic on HTML, Latin Modern on LaTeX).
if (requireNamespace("systemfonts", quietly = TRUE)) {
  tabular(cdisc_saf_demo) |>
    preset(font_family = "serif") |>
    check_fonts()

  tabular(cdisc_saf_demo) |>
    preset(font_family = "sans") |>
    check_fonts()
}
```

`check_latex` *Check LaTeX-package availability for PDF output*

Description

Reports, for every TeX package the LaTeX / PDF backend can emit, whether it is present in the local TeX tree, and prints the exact `tinytex::tlmgr_install()` call that installs any that are missing. Run this before `emit(spec, "out.pdf")` on a fresh machine to turn a cryptic mid-compile `File 'tabularray.sty' not found` into an up-front, actionable checklist.

Usage

```
check_latex(quiet = FALSE)
```

Arguments

quiet	*Suppress the printed cli report.* <logical(1)>: default FALSE. When TRUE, runs the checks and returns the result invisibly without printing. Use in scripts that branch on the return value.

Details

The required set is a superset of every \\usepackage{} / \\UseTblrLibrary{} directive the backend emits, across all conditional branches (running headers / footers pull fancyhdr + lastpage; xelatex pulls fontspec; pdflatex pulls the classic font bundles). The check is informational, it does not install anything.

OS-managed TeX Live gotcha. On Linux distributions that ship TeX Live through the system package manager (RHEL / Fedora via dnf, Debian / Ubuntu via apt), tlmgr is locked against user installs and tlmgr_install() will fail. The fix is to install a user-space TinyTeX with tinytex::install_tinytex() and let that tree own the packages. Never force a locked tlmgr with --ignore-warning: it leaves the system tree half-written.

Slow / stuck install (often Windows). The default CTAN repository mirror.ctan.org redirects to a random mirror on every call, and a slow or stale one makes tinytex::tlmgr_install() appear to hang. Pin a concrete mirror once with tinytex::tlmgr_repo()("auto") (it follows the redirect a single time and remembers the result), then retry the install.

Status markers:

- v — package is installed in the local TeX tree.
- x — package is missing; the tlmgr_install() line at the bottom of the report installs every missing package at once.
- ? — availability could not be determined (no tinytex, or tlmgr not reachable); treated as missing for remediation.

Requires the tinytex package (in Suggests); call install.packages("tinytex") first if it isn't installed.

Value

Invisibly returns a data frame with one row per required package and columns package (<character>) and installed (<logical>, NA when undeterminable). Side effect: prints a cli report with a per-package status marker and, when anything is missing, the exact tlmgr_install() remedy.

See Also

Companion diagnostic: check_fonts().

Consumes the result: emit().

Examples

```
# ---- Example 1: Audit the PDF toolchain before emitting ----
#
# Run check_latex() on a fresh machine to confirm every LaTeX
# package the PDF backend needs is present. The call prints a
# status line per package and, if any are missing, the exact
# tinytex::tlmgr_install() command to fix them in one shot. It is
# guarded on tinytex so it is a no-op where TeX is unavailable.
if (requireNamespace("tinytex", quietly = TRUE)) {
  check_latex()
}
```

`col_spec` *Per-column display specification*

Description

Build a single column's display attributes — usage, label, format, visibility, width, alignment, NA text. The result feeds `cols()`, which stamps the input column name onto the spec from its named-argument position and attaches it to the parent `tabular_spec`.

Usage

```
col_spec(
  usage = NULL,
  label = NA_character_,
  format = NULL,
  visible = NA,
  width = "auto",
  group_display = NA,
  group_skip = NA,
  align = NULL,
  valign = NULL,
  na_text = NA_character_,
  indent = NA
)
```

Arguments

`usage` *Engine role.* `<character(1) | NULL>: default NULL`. One of:

- `"display"` (default in `cols()`) — pass-through.
- `"group"` — row-label with repeat-suppression and continuation-page repeat keys. Use for `variable`, `soc`, `stat_label`. (Cosmetic indent depth is the separate `indent` argument, not a usage role.)

- `"id"` — a row-identifier column. Renders like `"display"` (one value per row, never collapses) but joins the *stub*: it repeats on every horizontal panel (`paginate(panels = N)`) and shows once on the left when a continuous backend (HTML / Markdown) collapses the panels into one table. The PROC REPORT `ID` role, orthogonal to grouping. Use for a per-row statistic label (`"n"`, `"Mean"`, `"SD"`) that must stay legible on every panel of a wide demographics or efficacy table.
- `NULL` / `NA` — the unset sentinel; resolves to `"display"` at render. `NA` is mergeable, so an explicit `"display"` on a later `cols()` call can override a prior `"group"` / `"id"`.

```
# Two row-label columns and four arm columns.
cols(
  variable   = col_spec(usage = "group"),
  stat_label = col_spec(usage = "group"),
  placebo    = col_spec(),
  drug_50    = col_spec()
)

# Section-band table: the `group_label` column drives section
# headers; `stat_label` body rows auto-indent under each header
# without an explicit depth column.
cols(
 group_label = col_spec(usage = "group", group_display = "header_row"),
  stat_label  = col_spec(label = "Response"),
  placebo     = col_spec(align = "decimal")
)

# End-to-end ARD → wide → tabular pipeline. The cards ARD
# `cdisc_saf_demo_ard` is the long upstream input; `pivot_across()`
# widens to one column per arm and stamps an internal marker
# so [`sort_rows()`] can reject sort keys on those arm columns.
# `cols()` then attaches per-column display rules.
wide <- pivot_across(
  cdisc_saf_demo_ard,
  statistic = list(
    continuous  = c(N = "{N}", "Mean (SD)" = "{mean} ({sd})"),
    categorical = "{n} ({p}%)"
  )
)
tabular(wide, titles = "Demographics") |>
  cols(
    variable                = col_spec(
      usage = "group", label = "Characteristic"
    ),
    stat_label              = col_spec(
      usage = "group", label = "Statistic"
    ),
    Placebo                 = col_spec(align = "decimal"),
    `Xanomeline High Dose`  = col_spec(
```

```
    label = "High Dose", align = "decimal"
  ),
  `Xanomeline Low Dose`    = col_spec(
    label = "Low Dose", align = "decimal"
  ),
  Total                    = col_spec(align = "decimal")
)
```

label — *Display label for the column header.* <character(1)>: default NA_character_. Embed \n for multi-line headers (arm name on row 1, BigN denominator on row 2 is the clinical convention). NA_character_ means use the input column name verbatim.

Restriction: Empty string and whitespace-only labels are accepted here, unlike headers() band labels which are strict.

Supports glue-style {expr} interpolation: braces are evaluated as R code in the calling environment at build time, so a BigN value folds inline, label = "Placebo (N={n['placebo']})". Double a brace ({{ or }}) for a literal one. An md() / html() label is passed through without interpolation.

Per-column token. {.name} (alias {.col}) inside a {expr} is *deferred* and resolved to the matched column's name when the spec is stamped by cols() / cols_apply(), so one spec can carry a variable-N arm header. See cols_apply() for the loop-free idiom.

```
# Two-line header with arm name and BigN from cdisc_saf_n.
n <- stats::setNames(cdisc_saf_n$n, cdisc_saf_n$arm_short)
col_spec(
  label = "Placebo\nN={n['placebo']}",
  align = "decimal"
)
```

format — *Post-cell formatter.* <character(1) | function | NULL>: default NULL. A sprintf template applied per cell, OR a unary function(x) -> character of the same length, OR NULL for backend default.

Restriction: Character templates are probed with sprintf(format, 0) at construction; malformed templates fail fast. **Tip:** Use a function for non-sprintf formatting (locale- aware numbers, thousand separators, conditional symbols).

```
# sprintf template vs. function form.
col_spec(format = "%.1f")
col_spec(format = function(x) formatC(x, format = "f", digits = 1, big.mark = ","))
```

visible — *Whether the column renders.* <logical(1)>: default NA. FALSE hides the column from output but keeps it in spec@data so sort_rows() and style() predicates can still reference it. NA (default) is the merge "unset" sentinel — it resolves to visible at render and, crucially, is mergeable: a later cols() call with visible = TRUE can **re-show** a column an earlier call hid.

Interaction: Hidden columns are the standard pattern for sort-key helpers (row_type, n_total) and for the numeric counts behind formatted-text percentage cells.

Auto-hide. The depth column named by a character indent and every column named by subgroup(by = ...) or referenced via a {col} placeholder in

the subgroup banner template are flipped to `visible = FALSE` automatically at engine time — restating it here is redundant.

Break-only group column. A hidden `usage = "group"` column emits no header rows and no in-column text; it contributes only its `group_skip` transitions, so `group_display` is ignored while hidden. This is the canonical "spacer" that drops a blank line wherever a marker value changes (e.g. continuous stats vs. categorical groups inside one characteristic): `col_spec(usage = "group", group_skip = TRUE, visible = FALSE)`.

`width` *Column width — auto-sized, pinned, or proportional.* `<character(1) | numeric(1)>: default "auto"`

- `"auto"` *(default)* — engine measures the widest cell (header + body) using bundled Adobe AFM Core 13 glyph metrics and distributes against the available content width. The **header** is sized to its widest *word*, so a multi-word header (e.g. `"n, median"`) wraps at spaces; a non-breaking space ( ) keeps a run whole. The **body** is sized to its widest *line* and never wraps, so numeric values stay intact. Pin a numeric width to wrap the body too.
- `<number>` — pinned in inches. Backends wrap content inside the pinned width (tabularray `Q[wd=...]`, HTML `style="width:..."`, RTF / DOCX after twips conversion).
- `"2.5in"` / `"60mm"` / `"4cm"` / `"30pt"` / `"5pc"` — pinned dimension with an explicit TeX unit. Same behaviour as a bare numeric.
- `"30%"` — proportional width, percent of available content width. Resolved at engine time against the printable area.

Tip: Mix freely. Pinned and percent widths take priority; `"auto"` columns distribute whatever space remains. If pinned widths together exceed the available content width, the engine warns and leaves `"auto"` columns at their natural fit (layout may overflow).

Restriction: Must be positive. Percent values must fall in `[0, 100]`. Font-relative units (`em`, `ex`, `rem`) are rejected (no font-size context at parse time).

Cross-format semantics (gt convention). The width value is the user's source-of-truth. HTML emits it verbatim into `<col style="width:...">` (CSS accepts every unit: `%`, `in`, `px`, `pt`, `cm`, `mm`). Paper backends (LaTeX / RTF / PDF / DOCX) convert to their native unit via the AFM / distribute-widths pipeline. HTML is unconditionally responsive: when `width = "auto"` (default), the browser auto-sizes the column and cells wrap when the viewport narrows.

Note: `NA` and `NULL` are rejected. In pre-v0.1.0 tabular `NA` deferred to backend auto-fit; that path was inconsistent across backends and is replaced by the `"auto"` default, which produces identical widths across RTF / LaTeX / HTML.

Merge sentinel. For the field-merge across repeated `cols()` / `cols_apply()` calls, `"auto"` is treated as the default: a later call carrying `width = "auto"` leaves a previously pinned width intact, and only an explicit non-`"auto"` width overrides.

`group_display` *How* `usage = "group"` *values render in the body.* `<character(1)>: default NA`. Active only when `usage = "group"` — setting it on a non-group column is ignored and warns. `NA` (default) is the merge "unset" sentinel and resolves to `"header_row"` at render; an explicit value is mergeable, so a later `cols()` call can reset it back to `"header_row"`.

- `"header_row"` *(default)* — each unique value emits as a section header row above its block of data rows, and **the body rows beneath are automatically indented one level**. The section header itself sits flush left at depth 0; its child rows render one indent level in. Because the section already supplies that indent, the stub column needs **no** `indent` — adding `indent = 1` there overrides (does not stack) the auto-indent, leaving a single level. The source column is hidden from the visible body. Matches the canonical submission shape used by clinical TFL house templates (Disposition, Demographics, Statistical Report sections).
- `"column"` — column stays visible; repeated values are suppressed (only the first row of each value shows the label). PROC REPORT's default for grouping variables.
- `"column_repeat"` — column stays visible; every row repeats the value (no suppression). The shape R's `print.data.frame` produces.

Composition under multiple group columns. When more than one `usage = "group"` column is declared, the FIRST one encountered in `cols()` order is the outer group; subsequent group columns nest inside it. Each column's `group_display` choice is independent — a common clinical pattern is the outer `variable` as `"header_row"` plus the inner `stat_label` as `"column"` (visible row labels under each section header).

```
# Demographics layout: variable as section header, stat_label
# as visible suppressed column.
cols(
 variable  = col_spec(usage = "group", group_display = "header_row"),
 stat_label = col_spec(usage = "group", group_display = "column"),
  placebo    = col_spec(label = "Placebo", align = "decimal")
)
```

`group_skip` *Insert a blank row between consecutive groups.* `<logical(1)>: default NA`. Active only when `usage = "group"` — setting it on a non-group column is ignored and warns. Three values:

- `TRUE` — engine injects one blank row immediately before each value transition on this column (PROC REPORT's `BREAK AFTER var / SKIP` semantics, lifted to per-column control). Never trails the final group.
- `FALSE` — never insert a blank row for this column.
- `NA` *(default)* — follow `group_display`: `TRUE` when `group_display = "header_row"`, `FALSE` when `"column"` or `"column_repeat"`. Picks the canonical shape without an extra knob to set.

Interaction: When two or more columns have an effective `group_skip = TRUE` and their value transitions coincide on the same row, the engine emits ONE blank row at that boundary, not one per column. Transition row indices are unioned across all contributing group columns.

```
# Default: header_row mode auto-injects blanks between sections.
col_spec(usage = "group", group_display = "header_row")

# Override: keep the column visible (suppressed-value mode) but
```

```
# still insert blank-row separators between value changes.
col_spec(usage = "group", group_display = "column", group_skip = TRUE)

# Override: section headers without the blank-row separator
# (denser layout, used when vertical space is tight).
col_spec(usage = "group", group_display = "header_row", group_skip = FALSE)

# Break-only "spacer": pairs with visible = FALSE to drop a blank
# line wherever a hidden marker changes, without rendering the
# column or any header row. group_display is ignored when hidden.
col_spec(usage = "group", group_skip = TRUE, visible = FALSE)
```

`align` *Horizontal alignment within the column.* `<character(1) | NULL>`: default `NULL`. One of:

- `"left"` — character columns; row labels.
- `"center"` — column-header band; rarely on data cells.
- `"right"` — numeric content without decimals.
- `"decimal"` — numeric or mixed-format cells aligned on the decimal mark. Use for `"5 (3.2%)"` next to `"54 (32.1%)"`.
- `NULL` (default) — falls through to `preset(alignment = list(body_halign = ...))` and then to the baked default `"left"`.

Tip: `"decimal"` pads numerics with non-breaking spaces so the decimal mark falls on a single column-wide anchor. The active preset's `decimal_metrics` knob is reserved for future em-aware padding refinement (see `preset()`); the current engine pads by character count.

Default behaviour. When `align` is unset (`NULL` / `NA`), every column emits with body left-aligned and header centred, regardless of the column's R data type. tabular's canonical input is pre-summarised wide data frames where numeric content is already formatted as character strings (e.g. `"52 (60.5)"`), so `is.numeric()`-based auto-detection would mis-classify those columns as text and align them left — the opposite of intent. Use explicit `align = "decimal"` for NBSP-padded numeric columns (centred header over the padded centroid) or `align = "right"` for plain right-aligned numeric columns. The default cascade is body → `preset(alignment = list( body_halign = ...))` → CSS `text-align: left`; header → `preset(alignment = list(header_halign = ...))` → CSS `text-align: center`.

`valign` *Vertical alignment within the cell.* `<character(1) | NULL>`: default `NULL`. One of `"top"`, `"middle"`, `"bottom"`. `NULL` falls through to `preset(alignment = list(body_valign = ...))` (baked default `"top"`). Per-cell overrides via `style(valign = ...)` still win over the column setting.

Tip: Set `"middle"` on the row-label column of a banded- row table so the label stays centred against the multi-line stat-block in the adjacent cell.

`na_text` *Text substituted for* `NA` *cells.* `<character(1) | NA>`: default `NA`. Substituted BEFORE the `format` step, so `format` does not need to anticipate `NA`. `NA` (default) inherits the preset's table-wide `na_text`; any string overrides it for this column, including `""` to force blank cells even when the preset uses a non-empty token.

Tip: Use a sentinel (`"-"`, `"NR"`, `"."`) when blank cells would be ambiguous, e.g. when "not applicable" and "not reported" both render blank.

`indent` *Cosmetic indent depth on this column.* `<numeric(1) | character(1) | NA>: default NA`. Two modes by type:

- **A non-negative whole number** — every body row of this column is indented that many levels (each level is `preset@indent_size` space-widths). `indent = 1` is the common "nudge this stub in one level" case; `indent = 0` is a real value that flattens children under a `"header_row"` section.
- **A column name (character)** — per-row depth: the engine reads `spec@data[[indent]]`, coerces each row to a non-negative integer, and prefixes that row's text + AST with `strrep(" ", preset@indent_size * depth)`. The referenced depth column is auto-hidden — no need to set `visible = FALSE` on it.

`NA` (default) means no indent. Backends with native padding-left (HTML / LaTeX / RTF / DOCX / PDF) emit the depth as cell padding so wrapped continuation lines align with the indented baseline; Markdown carries the literal space-prefix. Synthesised group-header rows are never indented — they are the parent at depth 0.

Interaction: an explicit `indent` on a `group_display = "header_row"` host **suppresses** that section's automatic one-level child indent (you take control of the depth) — so a stub under a section needs no `indent` at all, and adding `indent = 1` there yields a single, not double, indent.

Per-row SOC / PT pattern (the bundled `cdisc_saf_aesocpt` ships the canonical depth column, so no upstream construction is needed):

```
cols(
 label   = col_spec(label = "Category", indent = "indent_level"),
  soc      = col_spec(visible = FALSE),
  row_type = col_spec(visible = FALSE)
)
```

Depth-column values `c(0L, 1L, 2L, ...)` produce `0`, `1`, `2`, ... levels. Negative values clamp to 0 (warn); fractional numerics floor (warn); NA → 0 (silent). Works in flat listings too — a character `indent` does not require any `usage = "group"` columns.

Details

Constructor-only. `col_spec()` does not know which input column it belongs to until `cols()` stamps the name. Build reusable specs as ordinary R objects (e.g. `arm_col <- col_spec(align = "decimal")`) and apply them to multiple inputs without restating the name.

Merge semantics across repeated `cols()` calls. When `cols()` is called twice for the same column, the engine merges field-by-field: any field set to a non-default value on the new spec overrides; a field left at its "unset" sentinel (`NA` / `NULL` / `"auto"`) leaves the existing value intact. Because every mergeable field has a genuine unset sentinel, a later call can also *restore* a default — e.g. `visible = TRUE` re-shows a column an earlier call hid. Build a column's spec in stages without re-stating earlier attributes.

Validation timing. Argument shapes are validated eagerly — a malformed `sprintf` template is probed at construction (`sprintf(format, 0)`) and fails fast at write time, not at render time.

Value

A `col_spec` *S7 object.* Pass it to `cols()` keyed by the input column name; the constructor itself does not stamp a name.

See Also

Companion verb: `cols()` attaches `col_spec` entries to a `tabular_spec` keyed by input column name.

Sibling build verbs: `headers()`, `sort_rows()`, `style()`, `paginate()`, `preset()`.

Entry / terminal verbs: `tabular()`, `emit()`, `as_grid()`.

Inline label formatting: `md()`, `html()`.

Examples

```
# ---- Example 1: Demographics with every col_spec field exercised ----
#
# Demographics table where every `col_spec` field is in play:
# the row-label columns are pinned to a fixed width and aligned
# left, the four arm columns embed BigN inline in the header,
# decimal-align numeric content, and render `NA` cells as "-".
n <- stats::setNames(cdisc_saf_n$n, cdisc_saf_n$arm_short)

tabular(
  cdisc_saf_demo,
  titles = c(
    "Table 14.1.1",
    "Demographics and Baseline Characteristics",
    "Safety Population"
  ),
  footnotes = "Percentages based on N per treatment group."
) |>
  cols(
    variable   = col_spec(
      usage = "group", label = "Parameter",
      width = 2.0,     align = "left"
    ),
    stat_label = col_spec(label = "Statistic", align = "left"),
    placebo  = col_spec(
      label = "Placebo\nN={n['placebo']}",
      align = "decimal", na_text = "-"
    ),
    drug_50  = col_spec(
      label = "Drug 50\nN={n['drug_50']}",
      align = "decimal", na_text = "-"
    ),
    drug_100 = col_spec(
      label = "Drug 100\nN={n['drug_100']}",
      align = "decimal", na_text = "-"
    ),
    Total    = col_spec(
```

```
      label = "Total\nN={n['Total']}",
      align = "decimal", na_text = "-"
    )
  ) |>
  sort_rows(by = c("variable", "stat_label"))

# ---- Example 2: AE table with indented label + hidden helpers ----
#
# AE-by-SOC/PT table where `label` carries both the SOC and the PT
# text in one column, each PT indented one level under its parent
# SOC via `indent_level`. The hidden numeric helpers `soc_n` (the
# parent SOC's count, broadcast across its PT children) and
# `n_total` (each row's own count) drive the sort: ordering by
# `soc_n` descending keeps every SOC cluster together, and the
# `n_total` descending tiebreak floats the SOC summary row above
# its PTs, so the table reads SOC then its PTs, next SOC then its
# PTs. Demonstrates `indent` plus `visible = FALSE` for sort-only
# columns, fixed width on the wide label column, and decimal
# alignment on all four arm columns.
n <- stats::setNames(cdisc_saf_n$n, cdisc_saf_n$arm_short)

tabular(
  cdisc_saf_aesocpt,
  titles = c(
    "Table 14.3.1",
    "Adverse Events by SOC and Preferred Term",
    "Safety Population"
  )
) |>
  cols(
    label    = col_spec(label = "SOC / Preferred Term",
                        indent = "indent_level", width = 2.5),
    soc      = col_spec(visible = FALSE),
    row_type = col_spec(visible = FALSE),
    soc_n    = col_spec(visible = FALSE),
    n_total  = col_spec(visible = FALSE),
    placebo  = col_spec(label = "Placebo\nN={n['placebo']}",  align = "decimal"),
    drug_50  = col_spec(label = "Drug 50\nN={n['drug_50']}",  align = "decimal"),
    drug_100 = col_spec(label = "Drug 100\nN={n['drug_100']}", align = "decimal"),
    Total    = col_spec(label = "Total\nN={n['Total']}",    align = "decimal")
  ) |>
  sort_rows(by = c("soc_n", "n_total"), descending = c(TRUE, TRUE))

# ---- Example 3: Format string + na_text for clean numeric display ----
#
# `cdisc_eff_estimates` ships four competing efficacy models with
# pre-computed numeric estimates, 95% CI bounds (NA on the MMRM
# row), and a nominal p-value. `format =` pins the printed
# precision; `na_text` renders the missing CI bounds as a dash
# rather than a literal "NA". `valign = "top"` keeps the multi-
# line cell text aligned to the top.
tabular(cdisc_eff_estimates, titles = "Treatment-effect estimates by model") |>
  cols(
```

```
    model    = col_spec(usage = "group",  label = "Model",   valign = "top"),
    estimate = col_spec(label = "Estimate", align = "decimal", format = "%.2f"),
    lower_ci = col_spec(
      label   = "Lower\n95% CI",
      align   = "decimal",
      format  = "%.2f",
      na_text = "--"
    ),
    upper_ci = col_spec(
      label   = "Upper\n95% CI",
      align   = "decimal",
      format  = "%.2f",
      na_text = "--"
    ),
    p_value  = col_spec(
      label   = "p-value",
      align   = "decimal",
      format  = "%.4f"
    )
  )

# ---- Example 4: Per-column width + halign override for vitals ----
#
# `width` accepts a numeric (inches), a CSS-style string ("1.5in",
# "20%"), or `"auto"`. Centering the visit column under a wider
# group-column setup demonstrates the alignment cascade —
# col_spec@align beats the engine default but yields to a more
# specific style() rule downstream.
n <- stats::setNames(cdisc_saf_n$n, cdisc_saf_n$arm_short)
tabular(
  cdisc_saf_vital,
  titles = "Vital Signs at Baseline and End of Treatment"
) |>
  cols(
    paramcd    = col_spec(visible = FALSE),
    param      = col_spec(usage = "group", label = "Parameter",
                          width = "1.6in"),
    visit      = col_spec(usage = "group", label = "Visit",
                          width = "1.2in", align = "center"),
    stat_label = col_spec(label = "Statistic", width = "1.0in"),
    placebo    = col_spec(
      label = "Placebo\nN={n['placebo']}",
      align = "decimal", width = "0.9in"
    ),
    drug_50    = col_spec(
      label = "Drug 50\nN={n['drug_50']}",
      align = "decimal", width = "0.9in"
    ),
    drug_100   = col_spec(
      label = "Drug 100\nN={n['drug_100']}",
      align = "decimal", width = "0.9in"
    )
  )
```

```
# ---- Example 5: Non-collapsing `id` stub for a panelled table ----
#
# `usage = "id"` marks `stat_label` ("n", "Mean", "SD", ...) as a
# row identifier: like `display` it shows on every row, but it also
# joins the stub, so it repeats on each horizontal panel created by
# `paginate(panels = 2)`. On HTML / Markdown (no page width) the
# panels collapse into one scrollable table with a "Panel 1 / Panel
# 2" header note; on RTF / Word each panel is its own page with the
# `variable` + `stat_label` stub repeated.
n <- stats::setNames(cdisc_saf_n$n, cdisc_saf_n$arm_short)
tabular(
  cdisc_saf_demo,
  titles = c("Table 14.1.1", "Demographics", "Safety Population")
) |>
  cols(
    variable   = col_spec(usage = "group", group_display = "column",
                          label = "Parameter"),
    stat_label = col_spec(usage = "id", label = "Statistic"),
    placebo    = col_spec(label = "Placebo\nN={n['placebo']}",  align = "decimal"),
    drug_50    = col_spec(label = "Drug 50\nN={n['drug_50']}",  align = "decimal"),
    drug_100   = col_spec(label = "Drug 100\nN={n['drug_100']}", align = "decimal"),
    Total      = col_spec(label = "Total\nN={n['Total']}",    align = "decimal")
  ) |>
  paginate(panels = 2)
```

`cols` *Attach per-column specifications*

Description

Add `col_spec()` entries to a `tabular_spec`. Each named argument is one column: the name is the input column in `.spec@data` and the value is the `col_spec` carrying that column's display attributes (usage, label, format, alignment, width, visibility, NA text). Columns not mentioned get a default `col_spec()` (usage = display) at engine-validate time.

Usage

```
cols(.spec, ..., .default = NULL)
```

Arguments

`.spec`	*The* `tabular_spec` *to extend.* `<tabular_spec>: required`. Dot-prefixed so R's partial argument matching cannot accidentally bind a short user-supplied name (e.g. `s`, `sp`) in `...` to the spec slot. Pipe input (`tabular(...) |> cols(...)`) works the normal way — the spec is supplied positionally.

`...` *Named* `col_spec` *objects, one per column.* Each name is the input column name in `.spec@data`. Names must match an existing column — pre-compute derived columns upstream with `dplyr::mutate()` (or equivalent) before `tabular()`.

Restriction: Names must be unique within a single `cols()` call (duplicates warn; "last value wins"). **Tip:** To override an attribute already declared, use a second `cols()` call downstream and let the merge rule apply.

`.default` *Fallback* `col_spec` *for unmentioned columns.* `<col_spec | NULL>: default NULL`. When a `col_spec`, it is field-merged onto every data column that is NOT named in `...` and does not already carry a spec from an earlier `cols()` call. `NULL` (default) leaves unmentioned columns to the engine-time default. Use it to set one alignment / format across a variable number of arm columns in a single call.

Interaction: Explicit `...` specs always win — `.default` only fills the gaps. A column carried over from a prior `cols()` call is treated as already specified and is left untouched.

```
# Decimal-align every arm column without listing each by name.
tabular(cdisc_saf_demo) |>
  cols(
    variable   = col_spec(usage = "group", label = "Parameter"),
    stat_label = col_spec(label = "Statistic"),
    .default   = col_spec(align = "decimal")
  )
```

Details

Sparse declaration. Declare only the columns whose attributes differ from the default — a typical pipeline uses one `cols()` call with one entry per non-default column.

Layout order follows the data frame, not `cols()`. The left-to-right column order in the rendered table is the column order of `.spec@data`; the order of the named `...` arguments here is irrelevant (they are a lookup keyed by name). To move a column, reorder the data frame upstream — a column derived with `df$new <- ...` is appended last and will render last unless you reorder.

Within-call duplicates warn. A duplicate name inside one `cols()` call warns and "last value wins". To intentionally override an attribute, use a second `cols()` call downstream and let the merge rule below apply.

Value

The updated `tabular_spec`. Continue chaining with `headers()`, `sort_rows()`, `style()`.

Repeat-call merge semantics

When `cols()` is called more than once for the same column, the engine merges the new `col_spec` into the existing one field-by- field. A field set to a non-default value on the new spec overrides; a field left at its "unset" sentinel leaves the existing value intact. Every mergeable field has a genuine unset sentinel, so a later call can also *restore* a default (e.g. `visible = TRUE` re-shows a hidden column, `group_display = "header_row"` resets a prior `"column"`). This lets you build a column's spec in stages — declare the label-and-alignment block up front, add the width once you know it fits, then attach a sort key, all without re-stating earlier attributes. Essential when generating specs programmatically (looping over arms, layering a house-style helper).

Unset sentinels — a field left at this value does NOT override the existing field (every other value, including a default like `visible = TRUE`, overrides):

field	unset sentinel
usage	NA
label	NA_character_
format	NULL
visible	NA
width	"auto"
group_display	NA
group_skip	NA
align	NA_character_
valign	NA_character_
na_text	NA_character_ (inherit preset)
indent	NA

```
# Three-stage build: label/usage first, alignment second, width
# third. Each stage leaves earlier fields intact.
tabular(cdisc_saf_demo) |>
  cols(variable = col_spec(usage = "group", label = "Parameter")) |>
  cols(variable = col_spec(align = "left")) |>
  cols(variable = col_spec(width = 2.0))
# Result: variable has usage="group", label="Parameter",
#         align="left", width=2.0 — all four fields set.
```

See Also

Companion constructor: `col_spec()` builds the per-column DSL object that `cols()` attaches.

Sibling build verbs: `headers()`, `sort_rows()`, `style()`, `paginate()`, `preset()`.

Entry / terminal verbs: `tabular()`, `emit()`, `as_grid()`.

Examples

```
# ---- Example 1: Demographics with arm BigN inline in headers ----
#
# Demographics table where the row-label columns sit on the left
# and the four treatment-arm columns embed BigN in the header
# label (drawn inline from the bundled `cdisc_saf_n` data frame). Every
# arm column is decimal-aligned so mixed-format cells like
# "5 (3.2%)" line up on the decimal mark.
n <- stats::setNames(cdisc_saf_n$n, cdisc_saf_n$arm_short)

tabular(
  cdisc_saf_demo,
  titles = c(
    "Table 14.1.1",
    "Demographics and Baseline Characteristics",
    "Safety Population"
  ),
```

```
  footnotes = "Percentages based on N per treatment group."
) |>
  cols(
    variable   = col_spec(usage = "group", label = "Parameter"),
    stat_label = col_spec(label = "Statistic"),
    placebo    = col_spec(label = "Placebo\nN={n['placebo']}",  align = "decimal"),
    drug_50    = col_spec(label = "Drug 50\nN={n['drug_50']}",  align = "decimal"),
    drug_100   = col_spec(label = "Drug 100\nN={n['drug_100']}", align = "decimal"),
    Total      = col_spec(label = "Total\nN={n['Total']}",    align = "decimal")
  ) |>
  sort_rows(by = c("variable", "stat_label"))

# ---- Example 2: BOR table with CDISC factor ordering and hidden helper ----
#
# Best Overall Response table where `stat_label` carries the
# canonical CDISC factor levels (driving the sort) and `row_type`
# is hidden — present in the data for the sort, absent from the
# rendered output via `col_spec(visible = FALSE)`.
bor_levels <- c(
  "CR", "PR", "SD", "NON-CR/NON-PD", "PD", "NE", "MISSING",
  "ORR (CR + PR)", "CBR (CR + PR + SD)",
  "DCR (CR + PR + SD + NON-CR/NON-PD)", "95% CI (Clopper-Pearson)"
)
eff <- cdisc_eff_resp
eff$stat_label <- factor(eff$stat_label, levels = bor_levels)
ne <- stats::setNames(cdisc_eff_n$n, cdisc_eff_n$arm_short)

tabular(
  eff,
  titles = c(
    "Table 14.2.1",
    "Best Overall Response and Response Rates",
    "Efficacy Evaluable Population"
  ),
  footnotes = "Response per RECIST 1.1, investigator assessment."
) |>
  cols(
    stat_label  = col_spec(label = "Response"),
    row_type    = col_spec(visible = FALSE),
    groupid     = col_spec(visible = FALSE),
    group_label = col_spec(visible = FALSE),
    placebo    = col_spec(label = "Placebo\nN={ne['placebo']}",  align = "decimal"),
    drug_50    = col_spec(label = "Drug 50\nN={ne['drug_50']}",  align = "decimal"),
    drug_100   = col_spec(label = "Drug 100\nN={ne['drug_100']}", align = "decimal")
  ) |>
  sort_rows(by = c("groupid", "stat_label"))

# ---- Example 3: AE-by-SOC/PT with indented label + repeat-call merge ----
#
# `label` carries SOC text on SOC rows and PT text on PT rows;
# `indent = "indent_level"` indents the PT rows one level under
# their SOC. `soc`, `row_type`, and `n_total` ride along as hidden
# sort keys. A second `cols()` call later in the chain adds widths
```

```
# once the user knows the page geometry; the repeat-call merge
# preserves prior attributes (label, indent, align, visible)
# without restating them.

tabular(
  cdisc_saf_aesocpt,
  titles = c("Table 14.3.1", "Adverse Events by SOC and Preferred Term")
) |>
  cols(
    label    = col_spec(label = "SOC / PT", indent = "indent_level"),
    soc      = col_spec(visible = FALSE),
    row_type = col_spec(visible = FALSE),
    soc_n    = col_spec(visible = FALSE),
    n_total  = col_spec(visible = FALSE),
    placebo  = col_spec(label = "Placebo",  align = "decimal"),
    drug_50  = col_spec(label = "Drug 50",  align = "decimal"),
    drug_100 = col_spec(label = "Drug 100", align = "decimal"),
    Total    = col_spec(label = "Total",    align = "decimal")
  ) |>
  sort_rows(by = c("soc_n", "n_total"), descending = c(TRUE, TRUE)) |>
  # Second `cols()` call: add widths after the rest of the spec
  # is built. Repeat-call merge preserves prior attributes.
  cols(
    label    = col_spec(width = "2.5in"),
    placebo  = col_spec(width = "0.9in"),
    drug_50  = col_spec(width = "0.9in"),
    drug_100 = col_spec(width = "0.9in"),
    Total    = col_spec(width = "0.9in")
  )

# ---- Example 4: Compact AE-overall with pre-derived Active column ----
#
# Drop the per-arm columns and surface only the Total. Pre-compute
# the pooled "Active" column upstream (here `paste0(drug_50, " / ",
# drug_100)`) before piping into `tabular()`; `cols()` then just
# declares each column's display role. The same pattern handles
# any post-pivot derivation (`pivot_across() |> mutate(...) |>
# tabular()`).
#
# Column LAYOUT order follows the data frame, not the `cols()`
# argument order. A derived column appended with `ae$active <- ...`
# would render last, so reorder the frame to place it where it
# should display (here between Placebo and Total).
ae <- cdisc_saf_ae
ae$active <- paste0(ae$drug_50, " / ", ae$drug_100)
ae <- ae[c("stat_label", "placebo", "active", "Total", "drug_50", "drug_100")]

tabular(
  ae,
  titles = c("Table 14.3.0", "Adverse Event Overview"),
  footnotes = "Active = pooled Drug 50 + Drug 100 columns."
) |>
  cols(
```

```
  stat_label = col_spec(label = ""),
  placebo    = col_spec(label = "Placebo",  align = "decimal"),
  active     = col_spec(label = "Active arms"),
  drug_50    = col_spec(visible = FALSE),
  drug_100   = col_spec(visible = FALSE),
  Total      = col_spec(label = "Total", align = "decimal")
)
```

`cols_apply` *Apply one column spec to many columns*

Description

Field-merge a single `col_spec()` onto every column matched by name or by a predicate. The vectorized companion to `cols()` for the common case of a variable number of treatment-arm columns that all share the same display rule (decimal alignment, a numeric format), so you avoid `do.call()` / `!!!` splicing one named argument per arm.

Usage

```
cols_apply(.spec, .cols, .col_spec)
```

Arguments

`.spec`	*The* `tabular_spec` *to extend.* `<tabular_spec>: required`. Dot-prefixed so partial matching cannot bind a user name in another slot.
`.cols`	*Columns to match.* `<character | function>: required`. Either a character vector of input column names in `.spec@data`, or a predicate `function(names) -> logical` evaluated against `names(.spec@data)` (one logical per column, same length). **Restriction:** Named columns must exist in `.spec@data`. A predicate must return a logical vector the length of `names(.spec@data)`. **Tip:** No tidyselect helpers ship; pass a base vector (`grep("^ARM", names(df), value = TRUE)`) or a predicate (`\(nm) startsWith(nm, "ARM")`).
`.col_spec`	*The spec to field-merge onto every match.* `<col_spec>: required`. Built with `col_spec()`.

Details

Field-merge, not replace. `cols_apply()` reuses the same field-by-field merge as repeated `cols()` calls: a non-default field on `.col_spec` overrides; a default-valued field leaves any prior attribute on the matched column intact. Set the shared rule across arms first, then refine an individual arm with a later `cols()` call (or the reverse).

Per-column label token. A `label` that references `{.name}` (or its alias `{.col}`) inside a `{expr}` is resolved *per matched column*, with `.name` and `.col` both bound to that column's name. This makes a variable-N arm header a single declarative call instead of a hand-written loop. The rest of the `{expr}` evaluates in the calling environment, so a per-arm BigN looked up from a named vector works directly:

```
n <- c(placebo = 86, drug_50 = 84, drug_100 = 84)
cols_apply(
  spec, c("placebo", "drug_50", "drug_100"),
  col_spec(label = "{.name}\n(N={n[.name]})", align = "decimal")
)
# placebo  -> "placebo\n(N=86)" ; drug_50 -> "drug_50\n(N=84)" ; ...
```

The token is a plain-string feature; a label wrapped in `md()` / `html()` is parsed eagerly and does not interpolate. A failing token expression aborts naming the offending column.

`width` **merge.** `width`'s default sentinel for the merge is `"auto"`: a later `cols()` / `cols_apply()` call carrying the default `width = "auto"` leaves a previously pinned width intact (only an explicit non-`"auto"` width overrides). Apply a shared width last to broadcast it across arms.

Value

The updated `tabular_spec`. Continue chaining with `headers()`, `sort_rows()`, `style()`.

See Also

Companion verbs: `cols()` attaches per-column specs by name; `col_spec()` builds the spec.

Sibling build verbs: `headers()`, `sort_rows()`, `style()`, `paginate()`, `preset()`.

Examples

```
# ---- Example 1: Decimal-align every arm column by name vector ----
#
# Demographics table whose treatment-arm columns are selected by a
# name vector (`grep()` against the data) and given one shared
# decimal-alignment spec, while the two row-label columns keep
# their own roles set with `cols()`.
arm_cols <- grep("^placebo$|^drug_|^Total$", names(cdisc_saf_demo), value = TRUE)

tabular(
  cdisc_saf_demo,
  titles = c(
    "Table 14.1.1",
    "Demographics and Baseline Characteristics",
    "Safety Population"
  )
) |>
  cols(
    variable   = col_spec(usage = "group", label = "Parameter"),
    stat_label = col_spec(label = "Statistic")
  ) |>
  cols_apply(arm_cols, col_spec(align = "decimal")) |>
  sort_rows(by = c("variable", "stat_label"))

# ---- Example 2: Select arm columns with a predicate ----
#
# Best Overall Response table. The arm columns are matched with a
# predicate over the column names; the hidden sort helpers and the
```

```
# response label are declared with `cols()`. The predicate scales
# to any number of arms without editing the call.
bor_levels <- c(
  "CR", "PR", "SD", "NON-CR/NON-PD", "PD", "NE", "MISSING",
  "ORR (CR + PR)", "CBR (CR + PR + SD)",
  "DCR (CR + PR + SD + NON-CR/NON-PD)", "95% CI (Clopper-Pearson)"
)
eff <- cdisc_eff_resp
eff$stat_label <- factor(eff$stat_label, levels = bor_levels)

tabular(
  eff,
  titles = c(
    "Table 14.2.1",
    "Best Overall Response and Response Rates",
    "Efficacy Evaluable Population"
  )
) |>
  cols(
    stat_label  = col_spec(label = "Response"),
    row_type    = col_spec(visible = FALSE),
    groupid     = col_spec(visible = FALSE),
    group_label = col_spec(visible = FALSE)
  ) |>
  cols_apply(
    \(nm) nm %in% c("placebo", "drug_50", "drug_100"),
    col_spec(align = "decimal")
  ) |>
  sort_rows(by = c("groupid", "stat_label"))
```

`emit` *Render a* `tabular_spec` *to a file*

Description

Resolve spec through the engine pipeline, dispatch to the backend registered for the chosen format, and (optionally) write a QC data file and a CDISC ARS audit manifest alongside the rendered artefact. `emit()` is the package's terminal verb — it returns `file` invisibly so the call can sit at the bottom of a pipe without losing the path.

Usage

```
emit(
  .spec,
  file,
  format = NULL,
  data_file = NULL,
  manifest = FALSE,
  create_dir = FALSE
)
```

Arguments

`.spec`	*The* `tabular_spec` *to render.* `<tabular_spec>: required`. The full verb chain (`tabular()` -> `cols()` -> `headers()` -> `sort_rows()` -> `style()` -> `paginate()` -> `preset()`) feeds into `emit()`'s first argument by pipe.
`file`	*Destination path for the rendered artefact.* `<character(1)>: required`. Extension drives the backend (see the dispatch table in the Details section). The parent directory must already exist; `emit()` does not auto-create directories. **Tip:** Use `tempfile(fileext = ".md")` inside vignettes and examples so the example runs in `R CMD check` without polluting the package directory.
`format`	*Explicit backend override.* `<character(1) | NULL>: default NULL`. When set, wins over the file extension. Useful for writing `.txt` files that should contain RTF, for round-trip testing, or when the user has a custom backend registered under a non-standard name.

`data_file`	*QC artefact writer.* `<character(1) | function(file) -> character(1) | NULL>: default NULL`. When set, writes the resolved wide data frame alongside the render. A character path writes there directly; a lambda receives the render path and returns the data file path (typical for sponsor-flexible naming).
	Restriction: Returned-path extension must be `.csv`, `.tsv` / `.txt`, or `.rds`. **Tip:** The data frame the lambda governs is pre-backend — the same CSV is emitted regardless of whether `file` is RTF, PDF, or DOCX.
	`# Three canonical sponsor patterns for the lambda.`
	`data_file = \(f) paste0(tools::file_path_sans_ext(f), "_qc.csv")`
	`data_file = \(f) file.path(`
	`  "validation",`
	`  paste0("val_", basename(tools::file_path_sans_ext(f)), ".csv")`
	`)`
	`data_file = \(f) file.path(`
	`  "rd",`
	`  paste0("rd_", basename(tools::file_path_sans_ext(f)), ".rds")`
	`)`

`manifest`	*Emit the CDISC ARS audit manifest sidecar.* `<logical(1)>: default FALSE`. `TRUE` writes `<file>.audit.yml` with verbatim CDISC ARS LDM v1.0 Output keys; see the `manifest = TRUE` invariant in the Details section for what the file contains and the determinism contract it satisfies.
`create_dir`	*Create the destination directory if it is missing.* `<logical(1)>: default FALSE`. When `TRUE`, the parent directory of `file` (and any missing ancestors) is created recursively before rendering, instead of aborting. The default `FALSE` keeps the safe behaviour of erroring on a missing parent.

Details

Validation before I/O. Every argument is validated and the backend is resolved BEFORE the engine runs. An unsupported extension, a malformed `data_file` path, or a missing backend raises `tabular_error_input` without writing any file. A spec that resolves cleanly but whose backend errors mid-write may leave a partial file behind; this is the only failure mode that touches disk.

Backend dispatch. The effective backend is resolved from the file extension via the table below; the `format` argument always wins when both are supplied. Each backend lives in its own `R/backend_<fmt>.R` file and self-registers at package load time.

extension(s)	format	backend
`.md`, `.markdown`	`md`	GFM pipe table (Step 15; shipped)
`.html`, `.htm`	`html`	self-contained Bootstrap 5 (planned)
`.tex`, `.latex`	`latex`	tabularray (planned)
`.pdf`	`pdf`	tinytex compile of LaTeX (planned)
`.rtf`	`rtf`	RTF 1.9.1, native (shipped)
`.docx`	`docx`	OOXML native, no JVM (planned)

Unknown extensions, missing extensions, and formats with no registered backend all raise `tabular_error_input`. The error message lists the currently registered formats so the failure is actionable.

`data_file` **is sponsor-neutral.** Pass an explicit path (`"out/qc.csv"`) for a fixed location, or a lambda (`function(file) -> path`) for sponsor-flexible naming. The lambda receives the resolved render path so it can derive the QC file from it (suffix, sibling folder, separate sponsor-styled name). Recognised extensions on the returned path are `.csv`, `.tsv` (alias: `.txt`), and `.rds`; anything else raises `tabular_error_input`. The written data frame is the post- `sort_rows()` / post-`engine_decimal()` wide grid — exactly the cell text the backend wrote.

`manifest = TRUE` **writes a sidecar.** The audit manifest is written to `<file>.audit.yml` next to the render (e.g. `out.md` -> `out.audit.yml`). Keys are CDISC ARS LDM v1.0 Output verbatim: `id`, `name`, `programmingCode` (best-effort git + R + platform

- timestamp), `fileSpecifications` (sha256 of every emitted artefact including `data_file`), `displays/displaySections` (Title / Header / Body / Footnote), `referencedAnalyses` (empty in v0.1; reserved for the mintverse handoff), `x-tabular` (rendering geometry, pagination, style trace, input provenance). Determinism contract: two consecutive `emit()` calls are byte-identical except for the `rendered_at` parameter timestamp; the YAML round-trips through `yaml::read_yaml()` + `yaml::write_yaml()`.

Pure dispatcher. `emit()` does not do any rendering itself; it composes `as_grid()` with a backend writer. To inspect the resolved grid without writing a file (during development, or to build a custom downstream consumer), call `as_grid()` directly.

Value

The `file` *path, invisibly.* Use this when chaining `emit()` into a downstream consumer that needs the resolved path (e.g. printing the link in a Quarto chunk, copying the sidecar manifest into an archive, attaching the render to a submission folder builder).

See Also

No-I/O sibling: `as_grid()` returns the resolved grid without writing a file — use during development to inspect what `emit()` would hand a backend.

Build verbs the pipeline feeds from: `tabular()`, `cols()` / `col_spec()`, `headers()`, `sort_rows()`, `style()`, `paginate()`, `preset()`.

Inline formatting helpers: `md()`, `html()` (titles, footnotes, labels, cell text).

Examples

```
# ---- Example 1: Render demographics to Markdown ----
#
# Smallest possible emit: spec in, .md out. The backend is chosen
# from the file extension; the engine pipeline runs internally,
# then the registered md backend writes a GFM pipe table you can
# preview in any Markdown renderer. tempfile() keeps the example
# clean for `R CMD check`.
n <- stats::setNames(cdisc_saf_n$n, cdisc_saf_n$arm_short)

demo <- tabular(
  cdisc_saf_demo,
  titles = c(
    "Table 14.1.1",
    "Demographics and Baseline Characteristics",
    "Safety Population"
  ),
  footnotes = "Source: ADSL."
) |>
  cols(
    variable   = col_spec(usage = "group", label = "Characteristic"),
    stat_label = col_spec(label = "Statistic"),
    placebo  = col_spec(label = "Placebo\nN={n['placebo']}",  align = "decimal"),
    drug_50  = col_spec(label = "Drug 50\nN={n['drug_50']}",  align = "decimal"),
    drug_100 = col_spec(label = "Drug 100\nN={n['drug_100']}", align = "decimal"),
    Total    = col_spec(label = "Total\nN={n['Total']}",    align = "decimal")
  ) |>
  sort_rows(by = c("variable", "stat_label"))

demo_md <- tempfile(fileext = ".md")
emit(demo, demo_md)

# ---- Example 2: Render + QC data + CDISC audit manifest ----
#
# The clinical double-programming pattern: render the table,
# write a QC CSV alongside it for an independent programmer to
# verify cell-for-cell, and emit the CDISC ARS audit manifest
# for submission packaging. The lambda derives the QC path from
# the render path so the sponsor's naming convention lives in one
# place.

ae_spec <- tabular(
  cdisc_saf_aesocpt,
  titles = c(
    "Table 14.3.1",
    "Adverse Events by SOC and Preferred Term",
    "Safety Population"
  ),
  footnotes = "Subjects counted once per SOC and once per PT."
) |>
  cols(
    label    = col_spec(label = "SOC / PT", indent = "indent_level"),
```

```
    soc      = col_spec(visible = FALSE),
    row_type = col_spec(visible = FALSE),
    soc_n    = col_spec(visible = FALSE),
    n_total  = col_spec(visible = FALSE),
    placebo  = col_spec(label = "Placebo\nN={n['placebo']}",  align = "decimal"),
    drug_50  = col_spec(label = "Drug 50\nN={n['drug_50']}",  align = "decimal"),
    drug_100 = col_spec(label = "Drug 100\nN={n['drug_100']}", align = "decimal"),
    Total    = col_spec(label = "Total\nN={n['Total']}",    align = "decimal")
  ) |>
  sort_rows(by = c("soc_n", "n_total"), descending = c(TRUE, TRUE))

ae_md <- tempfile(fileext = ".md")
emit(
  ae_spec,
  ae_md,
  data_file = \(f) paste0(tools::file_path_sans_ext(f), "_qc.csv"),
  manifest  = TRUE
)

# ---- Example 3: Same spec, four backends — one-loop fan-out ----
#
# `emit()` dispatches by file extension, so the same spec can
# render to every backend in one loop. Useful for visual diffs
# across formats during development and for shipping a build
# artefact set (RTF for submission, HTML for review, PDF for the
# CSR appendix).
eff_spec <- tabular(cdisc_eff_resp, titles = "Best Overall Response") |>
  cols(
    stat_label  = col_spec(usage = "id", label = "Response"),
    row_type    = col_spec(visible = FALSE),
    groupid     = col_spec(visible = FALSE),
    group_label = col_spec(visible = FALSE),
    placebo     = col_spec(label = "Placebo",  align = "decimal"),
    drug_50     = col_spec(label = "Drug 50",  align = "decimal"),
    drug_100    = col_spec(label = "Drug 100", align = "decimal")
  )

out_dir <- tempfile()
dir.create(out_dir)
for (ext in c(".html", ".rtf", ".tex", ".docx", ".md")) {
  emit(eff_spec, file.path(out_dir, paste0("eff", ext)))
}
list.files(out_dir)

# ---- Example 4: QC artefact via data_file alongside the render ----
#
# `emit(data_file = ...)` writes the resolved post-engine wide
# data frame alongside the rendered table. The sponsor's QC
# programmer picks up the side-car .csv (or .rds) and validates
# cell values without parsing the rendered RTF.
rtf_out  <- tempfile(fileext = ".rtf")
data_out <- tempfile(fileext = ".csv")
emit(eff_spec, rtf_out, data_file = data_out)
```

```
file.exists(rtf_out)
file.exists(data_out)

# ---- Example 5: Render into a not-yet-existing output folder ----
#
# `create_dir = TRUE` builds the destination directory tree on the
# fly, so a submission-folder layout can be written in one pass
# without a separate `dir.create()` step.
nested <- file.path(tempfile(), "tables", "safety", "eff.md")
emit(eff_spec, nested, create_dir = TRUE)
file.exists(nested)
```

`footnote` *Attach an auto-numbered footnote to a table location*

Description

Anchor a footnote to a cell, column header, title line, or any other `cells_*()` location. The engine assigns the marker, places a superscript at every matching anchor, and emits the marked-footnote line at the foot of the table. Markers are assigned **once**, in reading order, deduped by `id`, and are byte-identical across every backend (RTF / LaTeX / PDF / HTML / DOCX) and every page, so the marker at the anchor can never desynchronise from its note.

Usage

```
footnote(.spec, text, .at = cells_body(), id = NULL, symbol = NULL)
```

Arguments

`.spec`	*The* `tabular_spec` *to annotate.* `<tabular_spec>: required`.
`text`	*The footnote text.* `<character(1)> | md() | html()`. Wrap in `md()` / `html()` for inline markup; plain strings are shown verbatim. A plain string supports glue-style `{expr}` interpolation, evaluated as R code in the calling environment at build time (double a brace for a literal one); an `md()` / `html()` value is passed through without interpolation.
`.at`	*Where the marker is placed.* `<tabular_location>: default [cells_body()]`. Any `cells_*()` location: a body-cell predicate (`cells_body(where = ...)`), a column header (`cells_headers()`), a title line (`cells_title()`), and so on.

```
# data-driven body anchor: mark every high-frequency preferred term
footnote(spec, "Includes events of any severity.",
         .at = cells_body(where = n_total >= 50, j = "label"))

# column-header anchor: mark the analysis-population denominator
footnote(spec, "Safety population.",
         .at = cells_headers(j = "Total"))
```

Note: the styling argument is `.at`, never `at`.

`id` — *Stable identifier for sharing one marker across anchors.* `<character(1)> | NULL`. Two `footnote()` calls with the same `id` share a single marker and a single note line. `NULL` (default) makes each call its own note.

`symbol` — *Pin an explicit marker glyph.* `<character(1)> | NULL`. Overrides the auto-allocated marker for this note (e.g. `"*"`). A pinned symbol is reserved and skipped by the auto-allocator, so it never collides. `NULL` (default) auto-allocates from the preset scheme.

Details

Engine-assigned, never hand-typed. Unlike a literal `^a^` typed into both a cell and the `footnotes` argument, a `footnote()` marker is allocated by the resolve engine after decimal alignment, so it never disturbs column alignment and never drifts out of sync. The scheme (`letters` / `numbers` / `symbols`) and the block-line format come from the active preset (`footnote_markers`, `footnote_label`).

Dedup by id. Give two anchors the same `id` to share one marker and one note line. Without an `id`, each `footnote()` call is its own note.

Coexists with `footnotes`. Manual `footnotes` lines render first; the auto-numbered block follows. The two systems do not cross-dedup, so do not mix a hand-typed marker with an engine one for the same note.

Value

A `tabular_spec`. Pipe it onward to more verbs or to `emit()`.

See Also

Manual footnote lines: the `footnotes` argument to `tabular()`.

Location helpers: `cells_body()`, `cells_headers()`, `cells_title()`.

Inline markup: `md()`, `html()`.

Examples

```
# ---- Example 1: a denominator note on a column header ----
#
# AE-by-SOC/PT table whose Total column header carries the analysis-
# population note. The engine drops a superscript "a" on the header
# and prints "a <text>" beneath the table.
n <- stats::setNames(cdisc_saf_n$n, cdisc_saf_n$arm_short)
tabular(cdisc_saf_aesocpt) |>
  cols(
    label    = col_spec(label = "SOC / PT", indent = "indent_level"),
    soc      = col_spec(visible = FALSE),
    row_type = col_spec(visible = FALSE),
    soc_n    = col_spec(visible = FALSE),
    n_total  = col_spec(visible = FALSE),
    placebo  = col_spec(label = "Placebo\nN={n['placebo']}"),
    drug_50  = col_spec(label = "Drug 50\nN={n['drug_50']}"),
    drug_100 = col_spec(label = "Drug 100\nN={n['drug_100']}"),
```

```
    Total    = col_spec(label = "Total\nN={n['Total']}")
  ) |>
  footnote(
    "Safety population: all randomised subjects who took study drug.",
    .at = cells_headers(j = "Total")
  )

# ---- Example 2: a data-driven note shared across cells ----
#
# A single note marks every high-frequency preferred term (n >= 50 in
# the Total column) in the SOC/PT stub. Sharing one `id` keeps it to
# one marker and one line; the marker lands on each matching cell.
tabular(cdisc_saf_aesocpt) |>
  cols(
    label    = col_spec(label = "SOC / PT", indent = "indent_level"),
    soc      = col_spec(visible = FALSE),
    row_type = col_spec(visible = FALSE),
    soc_n    = col_spec(visible = FALSE),
    n_total  = col_spec(visible = FALSE),
    placebo  = col_spec(label = "Placebo"),
    drug_50  = col_spec(label = "Drug 50"),
    drug_100 = col_spec(label = "Drug 100"),
    Total    = col_spec(label = "Total")
  ) |>
  footnote(
    md("Includes events of *any* severity."),
    .at = cells_body(where = n_total >= 50, j = "label"),
    id = "anysev"
  )
```

`get_preset` *Get the active session-default preset*

Description

Return the `preset_spec` last attached via `set_preset()`, or `NULL` when no session default has been set. The cascade resolver calls this internally; users call it for diagnostics ("what is my session inheriting?") or to copy the active default into a per-spec override via `preset()`.

Usage

```
get_preset()
```

Value

A `preset_spec`, or `NULL` when no session default is active.

See Also

Session-scope setter: set_preset().

Per-spec partner: preset().

Entry / terminal verbs: tabular(), emit(), as_grid().

Examples

```
# ---- Example 1: Inspect after setting a session default ----
#
# `get_preset()` returns NULL before any session default has been
# attached, then returns the `preset_spec` after `set_preset()`.
get_preset()  # NULL

set_preset(font_size = 8, orientation = "landscape")

active <- get_preset()
is_preset_spec(active)     # TRUE
active@font_size            # 8
active@orientation          # "landscape"

# ---- Example 2: Copy the session default into a per-spec override ----
#
# Read the session preset, tweak one knob for a single table, and
# attach as a per-spec override without disturbing the session.
set_preset(font_size = 9, paper_size = "letter")

# Read-tweak-attach without mutating the session default.
base_knobs <- get_preset()
tabular(cdisc_saf_n) |>
  preset(
    font_size   = base_knobs@font_size,
    paper_size  = base_knobs@paper_size,
    orientation = "landscape"
  )

# Reset the session default so subsequent examples / R sessions
# are not affected.
set_preset(.reset = TRUE)
```

---

headers *Attach multi-level column headers*

Description

Build the column-header band(s) above the rendered table. Each named argument is one band; the value is either a character vector of column names (leaf band) or a named list of further bands (inner band). Nesting depth is arbitrary — the engine renders one band row per depth level, with each cell spanning the columns of its leaves.

Usage

```
headers(.spec, ...)
```

Arguments

`.spec`	*The* `tabular_spec` *to attach the header tree to.* `<tabular_spec>: required`. Dot-prefixed so R's partial argument matching cannot accidentally bind a short user-supplied band label in `...` to the spec slot.
`...`	*Named header bands.* Each name is the band label (must be non-blank); each value is either: • a **character vector** of data-column names — leaf band, or • a **named list** whose entries follow the same recursive pattern — inner band. Inside a nested-list value, an unnamed character-vector entry declares a passthrough leaf (see the Passthrough section below). **Restriction:** Every column referenced must exist in `.spec@data`. A column may appear under at most one leaf. Names must be unique within one `headers()` call. **Tip:** Pass `headers()` with no arguments to clear the tree. **Interaction:** Band labels support glue-style `{expr}` interpolation, evaluated as R code in the calling environment at build time (double a brace for a literal one). The non-blank and uniqueness checks apply to the raw author-typed name, before interpolation.

Details

Replace, not stack. A second `headers()` call REPLACES the prior tree — header structure is a single spec, not a stackable list. Call with no arguments to clear the tree.

Strict label rule. Every declared band label must carry visible text — empty strings, NA, and whitespace-only labels are rejected at every nesting level. This is stricter than `col_spec()`, which DOES accept empty labels (a row-label column with no header text is a legitimate clinical case). A silently-blank band would be a layout artefact.

Uncovered columns render naked. Columns not referenced under any band render with their `col_spec.label` only — no extra band row above them. This is the canonical pattern for row-label columns (`variable`, `soc`, `stat_label`).

Multi-line band labels. Embed `\n` in a band label for a two-line band cell (arm name on row 1, BigN on row 2).

Spanner underline trim (backend limitation). Each spanner's underline is trimmed at both ends, booktabs `\cmidrule(lr)` style, so adjacent spanners are separated by a visible gap rather than merging into one continuous line. PDF / LaTeX (tabularray `leftpos/rightpos`) and HTML (an inset rule) render the trim natively. RTF and DOCX cannot inset a cell border horizontally, so there the spanner underline spans the full band width (adjacent spanner rules abut). This is a known, documented limitation of the OOXML / RTF cell-border model, not a bug.

Value

The updated `tabular_spec`. Continue chaining with `sort_rows()`, `style()`.

Passthrough leaves inside a nested band

Inside a nested-list value, a child entry may be **unnamed** — the entry is then a character vector of column names that sit directly under the parent with no intermediate band at this depth. Use this when one column under a band has no sub-grouping while its siblings do. The strict-label rule still applies to every declared band; an unnamed passthrough is NOT a band with a missing label — it is "no band declared at this depth for this column."

See Also

Companion verb: `cols()` / `col_spec()` sets per-column labels — the leaf-row header text that sits below the band rows this verb builds.

Sibling build verbs: `sort_rows()`, `style()`, `paginate()`, `preset()`.

Entry / terminal verbs: `tabular()`, `emit()`, `as_grid()`.

Inline label formatting: `md()`, `html()`.

Examples

```
# ---- Example 1: Single "Treatment Group" band over four arms ----
#
# AE-by-SOC/PT table with one flat band labelled "Treatment Group"
# spanning the four arm columns and the Total column. The
# row-label column (`soc`) sits to the left of the band with no
# header covering it — the canonical clinical layout.
n <- stats::setNames(cdisc_saf_n$n, cdisc_saf_n$arm_short)

tabular(
  cdisc_saf_aesocpt,
  titles = c(
    "Table 14.3.1",
    "Adverse Events by System Organ Class and Preferred Term",
    "Safety Population"
  ),
  footnotes = "Subjects are counted once per SOC and once per PT."
) |>
  cols(
    label    = col_spec(label = "SOC / PT", indent = "indent_level"),
    soc      = col_spec(visible = FALSE),
    row_type = col_spec(visible = FALSE),
    soc_n    = col_spec(visible = FALSE),
    n_total  = col_spec(visible = FALSE),
    placebo  = col_spec(label = "Placebo\nN={n['placebo']}"),
    drug_50  = col_spec(label = "Drug 50\nN={n['drug_50']}"),
    drug_100 = col_spec(label = "Drug 100\nN={n['drug_100']}"),
    Total    = col_spec(label = "Total\nN={n['Total']}")
  ) |>
  headers(
    "Treatment Group" = c("placebo", "drug_50", "drug_100", "Total")
  ) |>
  sort_rows(by = c("soc_n", "n_total"), descending = c(TRUE, TRUE))
```

```
# ---- Example 2: Two-level nested band — Control vs Active arms ----
#
# Efficacy BOR table where the active arms are grouped under an
# "Active" sub-band and the placebo arm under a "Control"
# sub-band, both under a single "Treatment Group" parent.
# Demonstrates the named-list value form for arbitrary-depth
# nesting.
bor_levels <- c(
  "CR", "PR", "SD", "NON-CR/NON-PD", "PD", "NE", "MISSING",
  "ORR (CR + PR)", "CBR (CR + PR + SD)",
  "DCR (CR + PR + SD + NON-CR/NON-PD)", "95% CI (Clopper-Pearson)"
)
eff <- cdisc_eff_resp
eff$stat_label <- factor(eff$stat_label, levels = bor_levels)
ne <- stats::setNames(cdisc_eff_n$n, cdisc_eff_n$arm_short)

tabular(
  eff,
  titles = c(
    "Table 14.2.1",
    "Best Overall Response and Response Rates",
    "Efficacy Evaluable Population"
  ),
  footnotes = "Response per RECIST 1.1, investigator assessment."
) |>
  cols(
    stat_label  = col_spec(label = "Response"),
    row_type    = col_spec(visible = FALSE),
    groupid     = col_spec(visible = FALSE),
    group_label = col_spec(visible = FALSE),
    placebo    = col_spec(label = "Placebo\nN={ne['placebo']}"),
    drug_50    = col_spec(label = "Drug 50\nN={ne['drug_50']}"),
    drug_100   = col_spec(label = "Drug 100\nN={ne['drug_100']}")
  ) |>
  headers(
    "Treatment Group" = list(
      "Control" = "placebo",
      "Active"  = c("drug_50", "drug_100")
    )
  ) |>
  sort_rows(by = c("groupid", "stat_label"))

# ---- Example 3: Multiple peer bands side by side ----
#
# Vital-signs summary where the parameter columns (param,
# paramcd, visit, stat_label) sit on the left under a "Variable"
# band, and the arm columns sit on the right under "Treatment
# Group". Demonstrates multiple top-level bands in one call --
# bands render side by side in the order declared.
vit <- cdisc_saf_vital
tabular(vit, titles = c("Table 14.4.1", "Vital Signs Summary")) |>
  cols(
    param      = col_spec(usage = "group", label = "Parameter"),
```

```
    paramcd    = col_spec(visible = FALSE),
    visit      = col_spec(usage = "group", label = "Visit"),
    stat_label = col_spec(label = "Statistic"),
    placebo    = col_spec(label = "Placebo",  align = "decimal"),
    drug_50    = col_spec(label = "Drug 50",  align = "decimal"),
    drug_100   = col_spec(label = "Drug 100", align = "decimal")
  ) |>
  headers(
    "Variable"        = c("param", "paramcd", "visit", "stat_label"),
    "Treatment Group" = c("placebo", "drug_50", "drug_100")
  )

# ---- Example 4: Three-tier band over efficacy arms + Total ----
#
# Demographics-style three-tier nesting: top band labels the
# whole arm strip, middle band splits Active vs Placebo, leaf
# bands carry the per-arm column labels. Each child within a
# `list(...)` may itself be a `list(...)` — bands nest to
# arbitrary depth using nested list literals.
n <- stats::setNames(cdisc_saf_n$n, cdisc_saf_n$arm_short)
tabular(cdisc_saf_demo, titles = "Demographics, hierarchical headers") |>
  cols(
    variable   = col_spec(usage = "group", label = "Characteristic"),
    stat_label = col_spec(label = "Statistic"),
    placebo    = col_spec(label = "N={n['placebo']}"),
    drug_50    = col_spec(label = "N={n['drug_50']}"),
    drug_100   = col_spec(label = "N={n['drug_100']}"),
    Total      = col_spec(label = "N={n['Total']}")
  ) |>
  headers(
    "Treatment Group" = list(
      "Control" = "placebo",
      "Active"  = list(
        "Drug 50"  = "drug_50",
        "Drug 100" = "drug_100"
      ),
      "Pooled"  = "Total"
    )
  )
```

`html` *Mark a string as HTML for inline formatting*

Description

Wrap a length-1 character vector so `tabular()`, `col_spec()`, and similar string slots interpret it as a constrained HTML subset at render time. Use when CommonMark cannot express the formatting (custom CSS via `<span style="...">`, raw destination codes via `<span data-rtf="...">`).

Usage

```
html(text)
```

Arguments

text	*The HTML fragment.* <character(1)>: required. Length-1 character vector. NA is rejected.

Details

Recognised tag whitelist. <p>,
 /
, , <b>, , <i>, <sup>, <sub>, <code>, <a href>, <span style>. Tags outside this set drop their wrapper and keep their text content (no arbitrary HTML attack surface).

Span styles. x parses the style attribute into a named character vector (c(color = "red", "font-weight" = "bold")). Backends translate CSS keys to destination-specific markup (RTF \cf, LaTeX \textcolor, DOCX <w:color>, HTML inline style).

Backend-specific raw codes. A span with data-rtf, data-latex, data-html, or data-docx attributes carries per-backend raw markup. The matching backend emits its data value verbatim and ignores the others; non-matching backends render the span's text content as plain. Use for cases the AST cannot express portably.

Value

A length-1 character vector classed c("from_html", "character"). Pass it directly into any string-bearing slot (tabular() titles / footnotes, col_spec() label, style() pretext / posttext); the resolve engine calls parse_inline() internally and backends walk the resulting inline_ast.

See Also

Sibling helper: md() — Markdown wrapper for the common case.

String slots that consume the wrapper: tabular() (titles, footnotes), col_spec() (label), style() (pretext, posttext).

Entry / terminal verbs: tabular(), emit(), as_grid().

Examples

```
# ---- Example 1: Colour-styled span in a title ----
#
# Demographics table title with the population subset shaded
# red. The HTML wrapper carries an inline CSS style; backends
# translate (RTF: \cf, LaTeX: \textcolor, HTML: inline style).
n <- stats::setNames(cdisc_saf_n$n, cdisc_saf_n$arm_short)

tabular(
  cdisc_saf_demo,
  titles = c(
    "Table 14.1.1",
    "Demographics",
```

```
    html(sprintf("Safety Pop <span style='color:red'>(N=%d)</span>", n["Total"]))
  )
)

# ---- Example 2: HTML link plus superscript footnote marker ----
#
# AE table footnote with an HTML link and a superscript marker.
# `html()` lets the user write tags directly when CommonMark
# would be awkward (e.g. attributes that Markdown does not
# surface).
tabular(
  cdisc_saf_ae,
  titles = c("Table 14.3.0", "Overall Adverse Event Summary"),
  footnotes = c(
    html('See <a href="https://www.meddra.org/">MedDRA</a> coding<sup>1</sup>.')
  )
) |>
  cols(stat_label = col_spec(label = "Category"))
```

`md` *Mark a string as Markdown for inline formatting*

Description

Wrap a length-1 character vector so `tabular()`, `col_spec()`, `style()` pretext / posttext, and similar string slots interpret it as CommonMark Markdown at render time. Supports the GitHub-flavoured plus Pandoc-style superscript (`^sup^`) and subscript (`~sub~`) extensions; raw HTML inside Markdown passes through to the constrained tag set documented under `html()`.

Usage

```
md(text)
```

Arguments

`text`	*The Markdown string.* `<character(1)>: required`. Length-1 character vector. `NA` is rejected; the empty string `""` renders as no content.

Details

Convention adopted from gt. Marking strings with `md()` and `html()` mirrors the well-tested gt convention. Plain (unwrapped) strings render as plain text — a stray `**` will NOT silently bold the surrounding span. Wrap explicitly to opt in.

Recognised Markdown. `**bold**`, `*italic*`, `` `code` ``, `[link text](url)`, hard line break (two trailing spaces + `\n` or `\\` + `\n`), Pandoc `^sup^` and `~sub~`. Single embedded `\n` (a "soft break" in CommonMark) renders as a space in HTML; tabular preserves it as a line break for clinical-table use where multi-line cells / titles are routine.

HTML pass-through. Raw HTML in Markdown (e.g. `md("Drug A <span style='color:red'>warning</span>")`) is parsed as HTML using the same tag whitelist as `html()`. Tags outside the whitelist drop their wrapper and keep their text content.

Composition with plain strings. `md()` and `html()` wrap the input with an internal control-character prefix that survives `c()` concatenation, so you can freely mix plain and marked strings in a single character vector: `c("Table 14.3.1", md("**Drug A**"), "third")`. Backends strip the marker before rendering; users never see it.

Value

A length-1 character vector classed `c("from_markdown", "character")`. Pass it directly into any string-bearing slot (`tabular()` titles / footnotes, `col_spec()` label, `style()` pretext / posttext); the resolve engine calls `parse_inline()` internally and backends walk the resulting `inline_ast`.

See Also

Sibling helper: `html()` — same wrapper pattern for raw HTML when Markdown cannot express the formatting.

String slots that consume the wrapper: `tabular()` (`titles`, `footnotes`), `col_spec()` (`label`), `style()` (`pretext`, `posttext`).

Entry / terminal verbs: `tabular()`, `emit()`, `as_grid()`.

Examples

```
# ---- Example 1: Italic title qualifier with Pandoc footnote marker ----
#
# AE-by-SOC/PT table. Title lines are bold by default, so the third
# line italicises "Safety Population" via `md("*...*")` for a visible
# contrast; the first footnote carries a Pandoc-style superscript
# marker `^a^` that the backends render as a true superscript.
n <- stats::setNames(cdisc_saf_n$n, cdisc_saf_n$arm_short)

tabular(
  cdisc_saf_aesocpt,
  titles = c(
    "Table 14.3.1",
    "Adverse Events by System Organ Class and Preferred Term",
    md("*Safety Population*")
  ),
  footnotes = c(
    md("^a^ Subjects counted once per SOC and once per PT.")
  )
) |>
  cols(
    label    = col_spec(label = "SOC / PT", indent = "indent_level"),
    soc      = col_spec(visible = FALSE),
    row_type = col_spec(visible = FALSE),
    soc_n    = col_spec(visible = FALSE),
    n_total  = col_spec(visible = FALSE),
    placebo  = col_spec(label = "Placebo\nN={n['placebo']}",  align = "decimal"),
```

```
    drug_50  = col_spec(label = "Drug 50\nN={n['drug_50']}",  align = "decimal"),
    drug_100 = col_spec(label = "Drug 100\nN={n['drug_100']}", align = "decimal"),
    Total    = col_spec(label = "Total\nN={n['Total']}",    align = "decimal")
  )

# ---- Example 2: Markdown link in a footnote ----
#
# Efficacy BOR table that footnotes the response criteria with
# a Markdown link. HTML / PDF / DOCX render as clickable; RTF /
# LaTeX render the link text with the URL inline (backend
# decides).
ne <- stats::setNames(cdisc_eff_n$n, cdisc_eff_n$arm_short)

tabular(
  cdisc_eff_resp,
  titles = c(
    "Table 14.2.1",
    "Best Overall Response",
    "Efficacy Evaluable Population"
  ),
  footnotes = c(
    md("Response per [RECIST 1.1](https://recist.eortc.org/), investigator assessment.")
  )
) |>
  cols(
    stat_label  = col_spec(usage = "id", label = "Response"),
    row_type    = col_spec(visible = FALSE),
    groupid     = col_spec(visible = FALSE),
    group_label = col_spec(visible = FALSE),
    placebo     = col_spec(label = "Placebo\nN={ne['placebo']}",  align = "decimal"),
    drug_50     = col_spec(label = "Drug 50\nN={ne['drug_50']}",  align = "decimal"),
    drug_100    = col_spec(label = "Drug 100\nN={ne['drug_100']}", align = "decimal")
  )
```

`paginate` *Configure pagination*

Description

Attach a `pagination_spec` to a `tabular_spec`. The engine uses the spec at render time to decide where page breaks fall, how wide tables split into horizontal panels, and what continuation marker (if any) prints on continued pages. The row budget per page is computed by the engine from the active preset (paper, orientation, margins, font size) and the chrome rows consumed by titles, column headers, and footnotes — you do not set rows-per-page directly.

Usage

```
paginate(
  .spec,
```

```
  keep_together = character(),
  panels = 1,
  orphan_floor = 3,
  widow_floor = 2,
  repeat_content = c("titles", "headers", "footnotes"),
  continuation = NULL
)
```

Arguments

`.spec`	*The* `tabular_spec` *to attach pagination to.* `<tabular_spec>: required`.

`keep_together`	*Group columns whose runs of identical values must not be split across a page break.* `<character>: default character()`. Every entry must be a `usage = "group"` column declared in `cols()`.
	Interaction: A run too tall to fit in the computed row budget less `orphan_floor` is split anyway; pagination is best-effort, not a hard contract.
	
	`# Protect the SOC-level grouping in an AE-by-SOC/PT table.`
	`paginate(keep_together = "soc")`

`panels`	*Number of horizontal panels for wide tables.* `<integer(1)>: default 1`. With `1`, every column is on every page (single vertical scroll). With `N > 1`, the engine splits non-group columns into `N` chunks and repeats every group column on every panel.
`orphan_floor`	*Minimum rows on a continued-from page.* `<integer(1)>: default 3`. When `keep_together` would move a page break back so far that fewer than `orphan_floor` rows would ride on the current page, the engine splits the protected run anyway. Acts as the escape valve for groups too tall to fit.
`widow_floor`	*Minimum rows on the final page.* `<integer(1)>: default 2`. If the last page would carry fewer than `widow_floor` rows, the engine merges those rows back onto the previous page (page overflow accepted). Avoids the "one-row-orphaned-on-page-N" look without complicating the primary split rule.
`repeat_content`	*Which page chrome repeats on every page.* `<character>: default c("titles", "headers", "footno` A subset of those three values; each is governed independently: • `"titles"` — title block on every page (else page 1 only). • `"headers"` — column-header band on every page (else page 1 only). • `"footnotes"` — footnote block on every page (else last page only). The default repeats all three so each page is self-contained per the submission layout contract. Pass a subset to drop one (e.g. `c("headers", "footnotes")` keeps the title on page 1 only), or `character()` to repeat nothing. **Note:** Footnotes are always anchored to the page foot when present; membership only chooses every-page vs last-page-only, never table-body placement. **HTML / MD:** ignored. HTML renders one continuous `<table>` and browsers natively repeat `<thead>` on print; MD has no print model. Effective only for the page-oriented backends (RTF, PDF, LaTeX, DOCX).

`continuation` *Marker text appended after a continuing table's title block.* `<character(1) | NULL>: default NULL`. `NULL` (the default) renders no marker — pick the wording your submission style guide expects (e.g. `"(continued)"`, `"(Cont'd)"`, `"Page %d of %d"`) and pass it explicitly.

Backend support is uneven — verify against your render target:

- **PDF / LaTeX** — full: the marker prints on every continuation page (both vertical page overflow and horizontal panels).
- **RTF** — horizontal continuation *panels* only (`paginate(panels = N)`); the marker does NOT appear on vertical page-overflow continuations.
- **DOCX** — not marked. DOCX paginates natively but emits no continuation marker.
- **HTML / MD** — ignored. With one continuous document on screen there is no continuing-page boundary to mark.

Details

Replace, not stack. A second `paginate()` call REPLACES the prior spec — pagination is a single configuration block, not a stackable list. Call with all defaults to clear back to the engine's auto behaviour.

Rows per page are computed, not configured. The engine takes the paper height for the active orientation (`letter`, `a4`) and subtracts the top + bottom margins, the title block height (number of title lines + a blank separator), the column-header band height (max embedded `\n` line count across visible column labels, plus any spanning header levels), and the footnote block height (number of footnote lines + a blank separator). The remainder, divided by the row height for the active font size, gives the body-row budget per page. Landscape pages naturally carry fewer rows than portrait at the same paper size; smaller fonts carry more.

`keep_together` **protects group runs.** When a page break would fall in the middle of a contiguous run of identical values in a `usage = "group"` column listed in `keep_together`, the engine moves the break BACK to the start of the run so the whole run rides on the next page. Single rule of escape: if moving the break back would leave fewer than `orphan_floor` rows on the current page, the engine splits the run anyway (a single group too tall to fit on one page cannot be kept together).

`panels` **and group stickiness.** With `panels > 1`, the engine splits the NON-group columns into approximately equal slices and repeats every `usage = "group"` column on every panel for row context.

Value

The updated `tabular_spec`. Continue chaining with `style()`, `preset()`, then render via `emit()` (or resolve without I/O via `as_grid()`).

See Also

Render-geometry partner: `preset()` / `set_preset()` — the preset's paper, orientation, margins, and font size feed the per-page row budget this verb depends on.

Sibling build verbs: `cols()` / `col_spec()`, `headers()`, `sort_rows()`, `style()`.

Entry / terminal verbs: `tabular()`, `emit()`, `as_grid()`.

Examples

```
# ---- Example 1: AE table paginated by SOC ----
#
# AE-by-SOC/PT table that may run several pages. The SOC column is
# protected by `keep_together` so a page break never lands in the
# middle of one SOC's PT rows. The engine derives the row budget
# from the preset's orientation + font_size + paper size and from
# the title / footnote / header line counts on the spec — no
# manual rows-per-page knob to keep in sync.
n <- stats::setNames(cdisc_saf_n$n, cdisc_saf_n$arm_short)

tabular(
  cdisc_saf_aesocpt,
  titles = c(
    "Table 14.3.1",
    "Adverse Events by System Organ Class and Preferred Term",
    "Safety Population"
  ),
  footnotes = "Subjects are counted once per SOC and once per PT."
) |>
  cols(
    label    = col_spec(label = "SOC / PT", indent = "indent_level"),
    soc      = col_spec(usage = "group", visible = FALSE,
                        group_display = "column_repeat"),
    row_type = col_spec(visible = FALSE),
    soc_n    = col_spec(visible = FALSE),
    n_total  = col_spec(visible = FALSE),
    placebo  = col_spec(label = "Placebo\nN={n['placebo']}"),
    drug_50  = col_spec(label = "Drug 50\nN={n['drug_50']}"),
    drug_100 = col_spec(label = "Drug 100\nN={n['drug_100']}"),
    Total    = col_spec(label = "Total\nN={n['Total']}")
  ) |>
  headers("Treatment Group" = c("placebo", "drug_50", "drug_100", "Total")) |>
  sort_rows(by = c("soc_n", "n_total"), descending = c(TRUE, TRUE)) |>
  paginate(
    keep_together = "soc",
    repeat_content = c("titles", "headers", "footnotes"),
    continuation = "(continued)"
  )

# ---- Example 2: Wide ACROSS-style efficacy table split across 2 panels ----
#
# BOR table where the four-arm column block is too wide for portrait
# paper. Split into 2 horizontal panels; the group column
# (`stat_label`) repeats on every panel for row context. Vertical
# pagination still applies, so on a tall table you would see panel A
# pages 1-2, then panel B pages 1-2.
bor_levels <- c(
  "CR", "PR", "SD", "NON-CR/NON-PD", "PD", "NE", "MISSING",
  "ORR (CR + PR)", "CBR (CR + PR + SD)",
  "DCR (CR + PR + SD + NON-CR/NON-PD)", "95% CI (Clopper-Pearson)"
)
```

```
eff <- cdisc_eff_resp
eff$stat_label <- factor(eff$stat_label, levels = bor_levels)
ne <- stats::setNames(cdisc_eff_n$n, cdisc_eff_n$arm_short)

tabular(
  eff,
  titles = c(
    "Table 14.2.1",
    "Best Overall Response and Response Rates",
    "Efficacy Evaluable Population"
  ),
  footnotes = "Response per RECIST 1.1, investigator assessment."
) |>
  cols(
    stat_label  = col_spec(usage = "id", label = "Response"),
    row_type    = col_spec(visible = FALSE),
    groupid     = col_spec(visible = FALSE),
    group_label = col_spec(visible = FALSE),
    placebo    = col_spec(label = "Placebo\nN={ne['placebo']}"),
    drug_50    = col_spec(label = "Drug 50\nN={ne['drug_50']}"),
    drug_100   = col_spec(label = "Drug 100\nN={ne['drug_100']}")
  ) |>
  sort_rows(by = c("groupid", "stat_label")) |>
  paginate(panels = 2, repeat_content = c("titles", "headers", "footnotes"))

# ---- Example 3: Orphan / widow floors + continuation marker ----
#
# Long vital-signs table with two safeguards: orphan_floor = 4
# prevents fewer than 4 rows of a group landing alone at the
# bottom of a page; widow_floor = 2 prevents fewer than 2 rows of
# a group landing alone at the top of the next page; the
# continuation marker prints on every page after the first.
tabular(
  cdisc_saf_vital,
  titles = c("Table 14.4.1", "Vital Signs Summary at Each Visit")
) |>
  cols(
    param      = col_spec(usage = "group", label = "Parameter"),
    paramcd    = col_spec(visible = FALSE),
    visit      = col_spec(usage = "group", label = "Visit"),
    stat_label = col_spec(label = "Statistic"),
    placebo    = col_spec(label = "Placebo",  align = "decimal"),
    drug_50    = col_spec(label = "Drug 50",  align = "decimal"),
    drug_100   = col_spec(label = "Drug 100", align = "decimal")
  ) |>
  paginate(
    keep_together = "param",
    orphan_floor  = 4L,
    widow_floor   = 2L,
    continuation  = "(continued)"
  )

# ---- Example 4: Many-arm horizontal pagination via column-fit ----
```

```
#
# Wide AE-by-SOC/PT table where the column strip itself does not
# fit on a single page. The engine slices columns into groups
# (each group keeping the `usage = "group"` columns repeated on
# every horizontal page) so the SOC / PT label band re-appears
# alongside whichever arm columns land on each panel.
tabular(
  cdisc_saf_aesocpt,
  titles = c("Table 14.3.1", "AEs by SOC and PT (wide-page split)")
) |>
  cols(
    label    = col_spec(label = "SOC / PT", indent = "indent_level",
                        width = "2.5in"),
    soc      = col_spec(usage = "group", visible = FALSE,
                        group_display = "column_repeat"),
    soc_n    = col_spec(visible = FALSE),
    n_total  = col_spec(visible = FALSE),
    row_type = col_spec(visible = FALSE),
    placebo  = col_spec(label = "Placebo",  align = "decimal",
                        width = "2.0in"),
    drug_50  = col_spec(label = "Drug 50",  align = "decimal",
                        width = "2.0in"),
    drug_100 = col_spec(label = "Drug 100", align = "decimal",
                        width = "2.0in"),
    Total    = col_spec(label = "Total",    align = "decimal",
                        width = "2.0in")
  ) |>
  paginate(keep_together = "soc")
```

`pivot_across` *Convert a cards ARD to a wide display data.frame*

Description

`pivot_across()` is tabular's input-side helper: it consumes a long Analysis Results Data (ARD) data frame (typically produced by `cards::ard_stack()` or `cards::ard_stack_hierarchical()`) and returns a wide display data.frame ready to pass to `tabular()`.

Usage

```
pivot_across(
  data,
  statistic = list(continuous = "{mean} ({sd})", categorical = "{n} ({p}%)"),
  column = NULL,
  row_group = NULL,
  label = NULL,
  overall = "Total",
  decimals = NULL,
  fmt = NULL
)
```

Arguments

`data` *Long ARD input data.* `<data.frame>: required`. At minimum needs `stat_name` and `stat`. Cards-style group columns (`group1`, `group1_level`, ...) and `variable` / `variable_level` are auto-detected. Tibbles / `card` objects / arrow tables are coerced via `as.data.frame()`.

`statistic` *Format spec for cell composition.* `<character(1) | named list>: required`. Combines one or more ARD stats into one display cell. Three accepted forms — each illustrated below. Inside a format string, `{stat_name}` substitutes that stat's value from the ARD (for example, `"{n} ({p}%)"` interpolates the `n` and `p` stats into a `"53 (62%)"` cell). The lookup order when a value is needed for a variable is: per-variable -> per-context -> `default` -> the literal `"{n}"`.

Form 1: single string:
One format string applied to every variable regardless of context. Use when your ARD is homogeneous (e.g. all categorical).

```
# Every variable rendered as "n (p%)" — categorical-only slice.
cat_only <- cdisc_saf_demo_ard[cdisc_saf_demo_ard$context == "categorical", ]
pivot_across(
  cat_only,
  statistic = "{n} ({p}%)"
)
```

Form 2: named list by context:
Different formats per context. This is the typical clinical-table form because demographics mix continuous and categorical variables.
The list names must match the values in the ARD's `context` column verbatim. Which strings appear there depends on how the ARD was built:

- `cards::ard_continuous()` / `ard_categorical()` emit `"continuous"` / `"categorical"`.
- `cards::ard_summary()` / `ard_tabulate()` emit `"summary"` / `"tabulate"`.

So an ARD assembled with `ard_stack(ard_summary(...), ard_tabulate(...))` is keyed `summary` / `tabulate`, not `continuous` / `categorical`. Inspect `unique(ard$context)` when unsure.

```
# AGE (continuous) -> "75.2 (8.59)"; SEX (categorical) -> "53 (62%)"
pivot_across(
  cdisc_saf_demo_ard,
  statistic = list(
    continuous  = "{mean} ({sd})",
    categorical = "{n} ({p}%)"
  )
)
```

Form 3: named list by variable:
Override on a per-variable basis; fall back to `default` or context. Use when one variable needs a custom format.

```
# AGE shows just the mean; SEX / RACE keep the categorical default.
pivot_across(
  cdisc_saf_demo_ard,
  statistic = list(
```

```
    AGE         = "{mean}",
    categorical = "{n} ({p}%)",
    default     = "{mean} ({sd})"
  )
)
```

Multi-row continuous spec:
Any single entry can itself be a **named character vector** — each element becomes one display row, with the name as the row label. Use for `N / Mean (SD) / Median / Min, Max`-style blocks.

```
pivot_across(
  cdisc_saf_demo_ard,
  statistic = list(
    continuous = c(
      N           = "{N}",
      "Mean (SD)" = "{mean} ({sd})",
      Median      = "{median}",
      "Min, Max"  = "{min}, {max}"
    ),
    categorical = "{n} ({p}%)"
  )
)
```

`column` *Grouping column whose unique values become arms.* `<character(1) | NULL>: default NULL`. `NULL` auto-detects from the ARD's `group1` value or — for renamed input — picks the single non-standard column. Pass a string when multiple group columns exist.

`row_group` *Second, non-column grouping dimension.* `<character(1) | NULL>: default NULL`. Names the non-arm group variable of a two-variable `.by` (e.g. `SEX` in `ard_stack(.by = c(ARM, SEX))`). It widens into a leading row column (not a pivoted arm column), so the result composes with `subgroup(by = ...)` or `col_spec(usage = "group")` downstream.

Why it is required. cards encodes a crossing factor and a SOC/PT hierarchy identically (the second group variable appears in `variable` on its by-marginal rows), so the two cannot be told apart automatically. Naming `row_group` declares "this is a crossing factor": the by-marginal rows are dropped and the flat path is used. Leave it `NULL` for a genuine hierarchy.

Restriction: Must name a second grouping variable present in the ARD and must differ from `column`.

`label` *Variable-name to display-label map.* `<character> | NULL: default NULL`. Named character vector mapping variable names to display labels (e.g. `c(AGE = "Age (years)", SEX = "Sex")`). Applies to `variable`, `soc`, and `label` columns of the output. `NULL` leaves the upstream variable names verbatim.

Renaming the hierarchical "overall" row. A `cards::ard_stack_hierarchical(overall = TRUE)` ARD carries an internal `..ard_hierarchical_overall..` sentinel for the grand-total ("any event") row. It is relabelled to `"Overall"` by default; map the sentinel key to override, e.g. `label = c("..ard_hierarchical_overall.." = "TOTAL SUBJECTS WITH AN EVENT")`. The raw sentinel never reaches the output at any hierarchy depth.

`overall` *Column name for* `NA`*-arm (overall / total) rows.* `<character(1) | NULL>: default "Total"`. Pass `NULL` to drop overall rows entirely (per-arm only output).

`decimals` *Per-stat decimal precision.* `<named integer | named list>: default c()`". Accepts two forms:

- **named integer vector** — global per-stat overrides (`c(mean = 1, sd = 2, p = 0)`).
- **named list** — per-variable plus `.default` (`list(AGE = c(mean = 2), .default = c(p = 1))`).

Built-in defaults apply when neither sets a stat.

`fmt` *Per-stat custom formatter functions.* `<named list of function>: default list()`". Each function takes a numeric value and returns a character string; overrides built-ins and `decimals` for that stat. Useful for p-value styling and other domain-specific formatting.

```
# p-value formatter: render below-threshold values as "<0.001".
fmt = list(
  p.value = function(x) {
    ifelse(x < 0.001, "<0.001", sprintf("%.3f", x))
  }
)
```

Details

tabular's package boundary is **display-only**: pre-summarised data in, rendered file out. `pivot_across()` is the canonical bridge between the cards aggregation backend and that boundary. It does not aggregate — it pivots arms to columns, interpolates per-cell display strings from the stat values, and applies decimal precision. Filtering, weighting, and aggregation happen upstream in cards or your own data-prep step.

Key `statistic` by the ARD `context`:

`statistic` (and `fmt`) are matched against the ARD's `context` column verbatim, and that value differs per generating function. Keying by the wrong name silently drops the format. Inspect `unique(ard$context)` first and key to match (or pass a single format string / `default =` to cover everything). When an explicitly-supplied `statistic` matches no context at all, `pivot_across()` warns rather than silently emitting `{n}`.

Generating function	`context` to key on
`cards::ard_summary()`	`summary`
`cards::ard_tabulate()`	`tabulate`
`cards::ard_continuous()`	`continuous`
`cards::ard_categorical()`	`categorical`
`cards::ard_stack_hierarchical()`	`tabulate` + `hierarchical`
`cardx::ard_categorical_ci()`	`proportion_ci`
`cardx::ard_continuous_ci()`	`continuous_ci`

Indentation of `stat_label`:

Categorical levels and the multi-row continuous stat labels come back already indented with two leading spaces, ready to render as a plain display column. Do **not** also set `col_spec(indent =`

`...)` on `stat_label` — that stacks the engine indent on top of the string indent (a double indent). Use one or the other.

Zero-suppression (always-on default):

A row whose `n` value equals zero renders the whole cell as the bare `n` value instead of fully interpolating the format string. For a categorical level with `n = 0`, the cell shows `"0"`, not `"0 (0.0%)"`. This is clinical convention — empty cells should read as a single zero, not advertise a meaningless rate.

How the default fires (chain of events). During cell assembly, before format-string interpolation, the engine checks the row's `n` stat. If it is zero, the engine short-circuits and returns the formatted `n` value (`"0"`) as the entire cell — `{p}` is never substituted, so the `(0.0%)` half of the format string is dropped.

How to opt out: supply a custom `fmt$n`. Setting any function under `fmt$n` is the engine's signal that the user owns the `n` rendering. The short-circuit is disabled for the whole table; for every row the full format string interpolates, so `{n}` becomes your formatter's output and `{p}` becomes the standard percentage. For `n = 0`, that's `"0 (0.0%)"`.

```
# Force "0 (0.0%)" for n = 0 rows by attaching a custom n formatter.
# The body of fmt$n can be the default integer rendering — its
# presence alone is what disables the zero-suppression branch.
pivot_across(
  cdisc_saf_demo_ard,
  statistic = list(
    continuous  = "{mean} ({sd})",
    categorical = "{n} ({p}%)"
  ),
  fmt = list(n = function(x) sprintf("%d", as.integer(x)))
)
```

Pharma rounding (always-on default):

A percentage that would otherwise round to `0` (when the value is positive but smaller than the chosen precision) renders as `<0.1`; one that would round to `100` (positive but smaller than 100) renders as `>99.9`. The threshold is precision-aware: `decimals = c(p = 2)` produces `<0.01` / `>99.99`. This matches the pharma convention of never claiming exactly `0%` or `100%` when at least one subject contributed.

Override per-stat via `fmt`:

```
# Show exact rounded percentages even at the extremes
pivot_across(
  data,
  statistic = "{n} ({p}%)",
  decimals  = c(p = 1),
  fmt = list(p = function(x) sprintf("%.1f", x * 100))
)
```

Your `fmt$p` receives the raw stat value (a proportion between 0 and 1) and returns the displayed string. The pharma-threshold branch only fires inside the built-in `p` formatter and the `decimals`-driven path, so any custom `fmt$p` bypasses it.

Value

A wide `data.frame` *ready for* `tabular()`. Schema:

- `variable` — variable name (or label after `label = ...`).
- `stat_label` — display-row label.
- One column per arm level (named after the `group1_level` values or the renamed arm column).
- `Total` (or whatever `overall` is set to) when applicable.
- A leading column named after `row_group` when set (the second grouping dimension).
- Hierarchical ARD adds `soc`, `label`, `row_type` instead of `variable`.

Pass the result straight into `tabular()` to start the render pipeline.

See Also

Pipeline entry consumer: `tabular()` — wraps the wide data frame this helper returns.

Downstream spec-build verbs: `cols()` / `col_spec()`, `headers()`, `sort_rows()`, `style()`, `paginate()`, `preset()`.

Terminal verbs: `emit()`, `as_grid()`.

Examples

```
# ---- Example 1: Demographics — long ARD to rendered spec ----
#
# Full pipeline from a `cards::ard_stack()`-style long ARD to a
# sorted `tabular_spec`. The multi-row continuous block (N /
# Mean (SD) / Median / Min, Max) sits above each categorical
# block; decimals are set per-stat (mean 1, sd 2, p 1) to match
# the CDISC convention.
n <- stats::setNames(cdisc_saf_n$n, cdisc_saf_n$arm_short)

cdisc_saf_demo_ard |>
  pivot_across(
    statistic = list(
      continuous = c(
        N           = "{N}",
        "Mean (SD)" = "{mean} ({sd})",
        Median      = "{median}",
        "Min, Max"  = "{min}, {max}"
      ),
      categorical = "{n} ({p}%)"
    ),
    decimals = c(mean = 1, sd = 2, p = 1, median = 1, min = 0, max = 0),
    label    = c(AGE = "Age (years)", SEX = "Sex", RACE = "Race")
  ) |>
  tabular(
    titles = c(
      "Table 14.1.1",
      "Demographics and Baseline Characteristics",
      "Safety Population"
```

```
    ),
    footnotes = "Percentages based on N per treatment group."
  ) |>
  cols(
    variable   = col_spec(usage = "group", label = "Parameter"),
    stat_label = col_spec(label = "Statistic"),
    Placebo    = col_spec(
      label = "Placebo\nN={n['placebo']}",
      align = "decimal"
    ),
    `Xanomeline Low Dose` = col_spec(
      label = "Drug 50\nN={n['drug_50']}",
      align = "decimal"
    ),
    `Xanomeline High Dose` = col_spec(
      label = "Drug 100\nN={n['drug_100']}",
      align = "decimal"
    ),
    Total = col_spec(
      label = "Total\nN={n['Total']}",
      align = "decimal"
    )
  )

# ---- Example 2: Hierarchical SOC/PT AE table ----
#
# Hierarchical `cards::ard_stack_hierarchical()` output threaded
# through `pivot_across()`. The hierarchical ARD emits a
# (soc, label, row_type) triple plus one stat row per (arm, SOC, PT);
# `pivot_across()` folds the arm dimension to columns and preserves
# the hierarchy markers. Derive `indent_level` from `row_type` so
# `col_spec(indent = "indent_level")` drives the SOC -> PT
# indent on the `label` column.
wide <- cdisc_saf_aesocpt_ard |>
  pivot_across(statistic = "{n} ({p}%)")
wide$indent_level <- as.integer(wide$row_type == "pt")

tabular(
  wide,
  titles = c(
    "Table 14.3.1",
    "Adverse Events by System Organ Class and Preferred Term",
    "Safety Population"
  ),
  footnotes = c(
    "Subjects are counted once per SOC and once per PT.",
    "Percentages based on N per treatment group."
  )
) |>
  cols(
    label    = col_spec(label = "SOC / PT", indent = "indent_level"),
    soc      = col_spec(visible = FALSE),
    row_type = col_spec(visible = FALSE),
```

```
    Placebo  = col_spec(
      label = "Placebo\nN={n['placebo']}",
      align = "decimal"
    ),
    `Xanomeline Low Dose` = col_spec(
      label = "Drug 50\nN={n['drug_50']}",
      align = "decimal"
    ),
    `Xanomeline High Dose` = col_spec(
      label = "Drug 100\nN={n['drug_100']}",
      align = "decimal"
    )
  )

# ---- Example 3: Hierarchical ARD (SOC / PT) ----
#
# `cdisc_saf_aesocpt_ard` carries an `ard_stack_hierarchical` shape with
# two grouping variables (AEBODSYS / AEDECOD). `pivot_across()`
# recognises the hierarchical structure and emits dedicated `soc`,
# `label`, and `row_type` columns so the SOC -> PT nesting survives
# the pivot. The result is ready for `tabular()` plus `sort_rows()`.
head(cdisc_saf_aesocpt_ard, 3)

wide <- cdisc_saf_aesocpt_ard |>
  pivot_across(statistic = "{n} ({p}%)")
head(wide, 3)

# ---- Example 4: Multi-row continuous spec + label re-labelling ----
#
# `statistic = c(<label> = <template>, ...)` produces one display
# row per named entry — the canonical "N / Mean (SD) / Median /
# Min, Max" block for continuous variables. `label = c(...)`
# renames the variable headings emitted into the wide output.
cdisc_saf_demo_ard |>
  pivot_across(
    statistic = list(
      continuous = c(
        N            = "{N}",
        "Mean (SD)"  = "{mean} ({sd})",
        Median       = "{median}",
        "Q1, Q3"     = "{p25}, {p75}",
        "Min, Max"   = "{min}, {max}"
      ),
      categorical = "{n} ({p}%)"
    ),
    label = c(
      AGE    = "Age (years)",
      WEIGHT = "Weight (kg)",
      HEIGHT = "Height (cm)",
      BMI    = "BMI (kg/m^2)"
    )
  )
```

```
# ---- Example 5: ARD keyed by summary / tabulate contexts ----
#
# The `statistic` list names must match the ARD's `context` column
# verbatim. `cards::ard_summary()` / `ard_tabulate()` emit `"summary"` /
# `"tabulate"` (not the `"continuous"` / `"categorical"` of
# `ard_continuous()` / `ard_categorical()`), so a list keyed
# `continuous`/`categorical` would silently match nothing. Always check
# `unique(ard$context)` first. Here the bundled `cdisc_saf_demo_ard` is
# relabelled to mimic `ard_summary()` + `ard_tabulate()` output; the
# by-variable's own row drops automatically and both the summary and
# the tabulate variables survive.
card_st <- cdisc_saf_demo_ard
card_st$context[card_st$context == "continuous"] <- "summary"
card_st$context[card_st$context == "categorical"] <- "tabulate"
pivot_across(
  card_st,
  statistic = list(
    summary  = "{mean} ({sd})",
    tabulate = "{n} ({p}%)"
  )
)
```

`preset` *Override the render preset on a spec*

Description

Attach a `preset_spec` to a `tabular_spec`, carrying page-geometry knobs (paper, orientation, margins, body font_size + family, h-rule policy, decimal metric, typography defaults). The engine consults the per-spec preset first when computing the per-page row budget, decimal-aligned column widths, and the chrome that the backend renders around the body grid.

Usage

```
preset(.spec, ..., .template = NULL, .style = NULL, .reset = FALSE)
```

Arguments

`.spec`	*The* `tabular_spec` *to attach the preset to.* `<tabular_spec>: required`. Dot-prefixed so R's partial argument matching cannot accidentally bind a knob name in `...` to the spec slot.
`...`	*Named preset knobs.* Any subset of the preset knobs the `preset_spec` class carries. Knob values are validated against the class's enum / length / type rules; bad values raise `tabular_error_input`. Unknown knob names raise `tabular_error_input` with the recognised set listed. Recognised knobs: • `font_size` — body point size. `<numeric(1)>`.

- font_family — body font family. <character | character(1)>. Default "mono". Three accepted shapes:
  1. **Generic family** — "mono" (default), "serif", "sans" (CSS aliases "monospace" / "sans-serif" also recognised). The resolver expands to a per-backend chain that leads with the Linux-installed **Liberation** face (Posit Workbench / Domino / Citrix / RStudio Server), then the Microsoft Office face (Courier New / Times New Roman / Arial) for desktop Win / Mac consumers, then TeX Gyre for LaTeX compile, then the CSS generic for HTML. Liberation Mono / Serif / Sans are metric-compatible with Courier New / TNR / Arial, so layout, line breaks, and decimal alignment hold across every render context. The mono default matches the dominant submission-TFL convention where deterministic glyph widths drive n (%) cell alignment.
  2. **Named alias** — "Times", "Times New Roman", "Arial", "Helvetica", "Courier", "Courier New". These PostScript-era names alias to the appropriate generic family (Times -> serif, Arial / Helvetica -> sans, Courier -> mono) and emit the same expanded chain. Honours the user's intent ("I want Times-like rendering") on every OS instead of hard-erroring on a Linux server with no TNR installed.
  3. **Named font** — "Inter", "JetBrains Mono", "Source Serif Pro", sponsor-specific face, etc. Emitted verbatim with no fallback fabricated. The consuming app (browser, xelatex, Word, LibreOffice) resolves the name against its own font matcher. RTF and DOCX fall back to the consuming app's substitution table when the name is missing; xelatex hard-errors at compile time; HTML browsers fall through to the browser's default font (not necessarily class-matched).
  4. **Explicit stack** — c("Inter", "Helvetica", "sans"). User owns the chain. Returned verbatim — alias lookup is **bypassed**, so c("Times", "Times") honours the exact name with no chain expansion (escape hatch for users who genuinely want exact-name semantics).

  Note: Adobe Source Pro is no longer the default lead. Source Pro is not pre-installed on production Linux servers, so leading with it walks through 2-3 missing names before resolving. Users who installed Source Pro can opt in via the explicit-stack form (c("Source Serif Pro", "serif")).
  What you see in Word's font dropdown vs. what renders. When you open a tabular-generated .rtf in Word on macOS or Windows, the font dropdown displays the file's *requested* face — "Liberation Mono" by default (the Linux-server-installed face). The rendered text on screen is whatever Word's *\\falt substitution resolved to — typically Courier New on macOS / Windows. This is correct: Liberation Mono and Courier New are metric-compatible by design, so the rendered layout (line breaks, decimal alignment, page breaks) is identical regardless of which face Word actually used to render. The same *\\falt substitution model applies to serif (Liberation Serif -> Times New Roman) and sans (Liberation Sans -> Arial).
  How to force Office names as the primary. If reviewers will be confused by seeing "Liberation Mono" in the Word font dropdown (cosmetic concern; doesn't affect rendering), pass an explicit length>1 stack with the Of-

fice name first. The resolver returns the vector verbatim — no alias lookup, no chain expansion — so the RTF file then names the Office face as primary and your chosen alternate as `\\*\\falt`:

```
preset(font_family = c("Courier New", "Courier", "Liberation Mono"))
```

This is the canonical escape hatch for authors who know their consumer audience is Mac / Windows Word users and want the dropdown to show the Office face directly.

- `orientation` — page orientation. `<character(1)>`. One of `"landscape"` (default), `"portrait"`.
- `paper_size` — paper key. `<character(1)>`. One of `"letter"` (default), `"a4"`.
- `margins` — page margins in inches. `<numeric(1) | numeric(4)>`. Length 1 = all four sides; length 4 = top, right, bottom, left.
- `pagehead`, `pagefoot` — per-page header / footer band content. `<list>`. Each band is a named list with slots from `left` / `center` / `right`; every other slot name is rejected. Each slot accepts `NULL` (omit), a character scalar, a character vector (multi-row content), or an `inline_ast`. Empty `list()` (the default) -> no band emitted.
  Single-row form (scalar slots):

  ```
  pagehead = list(
    left   = "Protocol: ABC-123",
    center = "Draft",
    right  = "Page {page} of {npages}"
  )
  ```

  Multi-row form (vector slots, index-aligned):

  ```
  pagehead = list(
    left  = c("Protocol: ABC-123", "Analysis Set: Safety"),
   right = "Page {page} of {npages}"  # scalar -> body-edge row
  )
  ```

  Growth direction. Vector index 1 = body edge; index N = far from body. `pagehead` rows stack **upward** away from the table (the row closest to the table is index 1). `pagefoot` rows stack **downward** away from the table (the row closest to the table is index 1). Shorter slots pad with `""` at the FAR end (high index), so a scalar slot naturally lands on the body-edge row.
  Token vocabulary — substituted into slot text:

Token	Phase	Expansion
`{page}`	backend	current page number (field code)
`{npages}`	backend	total page count (field code)
`{program}`	engine	calling script's base name
`{program_path}`	engine	calling script's full path
`{datetime}`	engine	`DDMMMYYYY HH:MM:SS` UTC (render time)

`{program}`, `{program_path}`, and `{datetime}` resolve once per render (at `as_grid()` / `emit()`); `{page}` and `{npages}` resolve per page (filled in by Word / xelatex / the browser's print engine at view time). The program

tokens walk a 5-mode detection chain — RStudio API, source() frame, Rscript / R CMD BATCH commandArgs (covers Domino + Linux batch + CI), knitr current_input, fallback "<interactive>".

- rules — the single border vocabulary (replaces the old borders knob). String sugar "booktabs" (default, the clinical baseline), "grid", "frame", "none"; a single brdr() broadcast to every active rule; or a named list keyed by the nine rule names (toprule, midrule, bottomrule, spanrule, rowrule, footnoterule, leftrule, rightrule, colrule) — unlisted rules keep their default, and the bare string "none" drops one. rules = list(rowrule = brdr()) reproduces the old hlines = "all".
  bottomrule **vs** footnoterule**.** These are mutually exclusive: exactly one rule sits at the data -> footnote boundary. The default is bottomrule (the table's bottom edge); footnoterule (a table-width rule opening the footnote section) is OFF by default. As a distinct footnote-section rule, footnoterule is drawn only by the paginated backends — **RTF, LaTeX / PDF, and DOCX**. The **HTML** backend is continuous (non-paginated) and has no separate footnote section, so it folds both into one rule: whichever of bottomrule / footnoterule is active becomes the table's bottom edge (bottomrule wins when both are set). Setting footnoterule therefore still draws a closing rule on HTML — rendered as the bottomrule.
- spacing — region-keyed blank-line control. A named list keyed by title / body / subgroup / footnote, each a named numeric c(above = , below =) (footnote: above only). Default is the one blank line above and below the title block. Two adjoining region-sides that target the same physical gap resolve to the MAX (never the sum), so a gap is never accidentally doubled.
- stripe — zebra body-row fills. A single colour (applied to even rows) or a named c(odd = , even =); NULL (default) is off.
- indent_size — row-label indent width, in monospace- space units. <integer(1)>. Default 2L. Each indent level adds this many space-widths of left padding to the cell. 0L disables the indent prefix entirely. Backends with native padding-left semantics (HTML / LaTeX / RTF / DOCX / PDF) emit this as cell padding so wrapped continuation lines align with the indented baseline; Markdown carries the literal space-prefix. Block alignment for the title / footnote / header / subgroup / body surfaces is set via the alignment named-list knob (alignment = list(title_halign = "left", ...)), not a scalar knob; blank-line spacing is set via spacing (above).
- na_text — global NA fallback. <character(1)>.
- decimal_metrics — decimal-padding metric. <character(1)>. Only "chars" (default); the engine pads decimal columns by character count.
- decimal_markers — missing-value tokens recognised by col_spec(align = "decimal"). <character>. Default c("NR", "NE", "NC", "ND", "BLQ"). A cell whose trimmed value is one of these is treated as a non-numeric *marker*: it is shown and right-aligned in the column rather than parsed as a number, and a marker appearing inside a compound (e.g. the upper bound of 14.3 (11.2, NR)) is preserved and slot-aligned. Excludes "-", "NA", and "INF"/"-INF" by default: "-" collides with range separators, "NA" is handled by na_text, and infinities are real values. Set to character(0) to disable marker handling.

- `width_mode` — table-level column-sizing policy. Mirrors Word's Table Layout menu. `<character(1)>`. One of:
  - `"content"` *(default)* — Each column auto-sized to `max(body, header)`. The table doesn't fill the page. Word's "Auto-fit Contents".
  - `"window"` — Auto-sized columns expand to share the residual page width equally. Pinned and percent columns keep their pins. Word's "Auto-fit Window".
  - `"fixed"` — Only explicit per-column widths drive the layout. Auto-sized columns collapse to a minimum sliver. Word's "Fixed Column Width".

  Interaction: Pair with `col_spec(width = ...)` pins to drive the layout under `"window"` / `"fixed"`. Under `"content"`, pins still take priority over auto columns.
  HTML backend. `width_mode` drives paper backends (LaTeX / RTF / PDF / DOCX) only. HTML is unconditionally responsive — the table always fills its parent and columns wrap when the viewport narrows, regardless of `width_mode`. Per-column widths (`col_spec(width)`) emit verbatim into the HTML colgroup per the gt convention.
- `whitespace` — how significant ASCII spaces in labels and cells render. `<character(1)>`. One of:
  - `"preserve"` *(default)* — leading, trailing, and interior runs of 2+ spaces become the backend non-breaking token (` ` / `~` / `\~`; DOCX preserves via `xml:space`), so a hand-built indent like `col_spec(label = "  Placebo")` renders verbatim across every backend. A single interior space stays breakable, so cells still wrap.
  - `"collapse"` — leave the backend's native run-folding in place (HTML / md / LaTeX collapse runs to one space).

  Note: never affects `col_spec(align = "decimal")` padding, which uses U+00A0 and is preserved unconditionally.
- `footnote_markers` — the glyph scheme for `footnote()` markers, which the engine allocates once in reading order. `<character(1)>`. One of:
  - `"letters"` *(default)* — a, b, ..., z, aa, ab, ... (bijective base-26).
  - `"numbers"` — 1, 2, 3, ...
  - `"symbols"` — Lamport's sequence *, †, ‡, §, ¶, ‖, then doubled (**, ††, ...) once it spills past the sixth.

  Interaction: a note's *anchor* is fixed by `footnote()`; its *scheme* (this knob) and *label* (`footnote_label`) are resolved from the active preset at render, so flipping either re-letters every marker at once.
- `footnote_label` — block-line template for a `footnote()` marker. `<character(1)>`. Default `"{m}"`; the `{m}` token is replaced by the allocated marker, so `"[{m}]"` prints `[a]` ahead of the note text on the footnote line.
- `cell_padding` — cell padding in points, CSS shorthand of length 1 / 2 / 4 (`all | vertical horizontal | top right bottom left`), parsed by the same length rule as `margins`. `<numeric>: default c(0, 5.4)` (vertical 0, horizontal 5.4pt). The single source of truth for both auto column-width measurement (left + right) and every backend's cell margin, so measured and rendered widths agree.

Interaction: A body per-side padding override (`preset(padding = list(body = ...))` or `style(.at = cells_body(), padding = ...)`) takes precedence at both measurement and render.
Note: DOCX and LaTeX render left / right exactly; RTF (`\\trgaph` is one symmetric gap) renders the average, so the total width still matches but the two sides look equal.

```
# Landscape A4, 8pt body, slim margins for one wide table.
preset(
  orientation = "landscape",
  paper_size  = "a4",
  font_size   = 8,
  margins     = c(0.75, 0.5, 0.75, 0.5)
)
```

`.template` *A* `preset_spec` *to bulk-apply before* `...`. `<preset_spec | NULL>: default NULL`. When supplied, every knob the template has set away from its factory default feeds in as the base layer; user-supplied `...` knobs then merge on top. List-valued knobs (`rules`, `fonts`, `colors`, `padding`, `alignment`) shallow-merge per key; scalars replace. Use this to layer a house-style `preset_spec` onto a chain without restating its knobs.

`.style` *A* `style_template()` *to layer onto the cascade.* `<style_template | NULL>: default NULL`. When supplied, every layer the template has accumulated via `style()` is replayed in order at engine time, after the per-spec `style()` layers on `.spec`. Use this to attach a sponsor's reusable house style to a chain without restating every per-region rule.

`.reset` *Discard the spec's existing preset before applying* `...`. `<logical(1)>: default FALSE`. When `TRUE`, the spec's prior `preset_spec` (if any) is dropped and `...` knobs are merged onto fresh `preset_spec()` defaults. With no knobs, the per-spec preset is cleared back to NULL (the spec falls through to `set_preset()` or `preset_spec()` defaults).

Details

Per-spec, chained. `preset()` is the per-spec override — a verb that returns a modified spec, composable on the pipe alongside `cols()` / `headers()` / `paginate()`. Use it when a single table needs a one-off geometry (e.g. landscape A4 for one wide efficacy summary inside a portfolio of portrait letter tables).

Merge, not replace. A second `preset()` call merges its scalar knobs onto the spec's existing preset; unspecified knobs keep their prior value. The five named-list knobs (`alignment` / `rules` / `fonts` / `colors` / `padding`) lower to `style_layer` records on `preset@style` via `.preset_args_to_layers()` (internal) and append in call order; layer order is precedence within the engine cascade, so a later `preset()` call's lowered attribute wins over an earlier one at the cell. Pass `.reset = TRUE` to discard the existing knobs and start from `preset_spec()` defaults. `preset(.spec, .reset = TRUE)` with no knobs clears the per-spec override entirely (the spec then falls through to `set_preset()` or `preset_spec()` defaults at render time).

Direct `preset_spec()` calls bypass lowering. The five named-list knobs are no longer slots on the `preset_spec` S7 class — they exist only as `preset()` / `set_preset()` arguments that lower into

`@style`. `preset_spec(rules = list(...))` (and analogous direct calls) raise "unused argument". Wrap such calls in `tabular(...) |> preset(...)` so the lowering helper fires and the layers land on `@style`.

Cascade with `set_preset()`. The engine resolves the active preset in this order: (1) the spec's per-call preset (this verb), (2) the session default attached via `set_preset()`, (3) `preset_spec()` factory defaults. The first non-NULL layer wins; layers are not field-merged across the cascade.

Value

The updated `tabular_spec`. Continue chaining with `paginate()`, `style()`, then render via `emit()` (or resolve without I/O via `as_grid()`).

See Also

Session-scope partners: `set_preset()`, `get_preset()`.

Render-geometry consumer: `paginate()` derives the per-page row budget from the active preset's paper, orientation, margins, and font size.

Sibling build verbs: `cols()` / `col_spec()`, `headers()`, `sort_rows()`, `style()`.

Entry / terminal verbs: `tabular()`, `emit()`, `as_grid()`.

Examples

```
# ---- Example 1: Landscape A4 for a wide efficacy table ----
#
# BOR table where the four-arm column block fits portrait letter
# with a smaller body font, but the sponsor wants A4 landscape at
# 8pt for visual breathing room. `preset()` attaches the geometry;
# `paginate()` reads it later to size the per-page row budget.
bor_levels <- c(
  "CR", "PR", "SD", "NON-CR/NON-PD", "PD", "NE", "MISSING",
  "ORR (CR + PR)", "CBR (CR + PR + SD)",
  "DCR (CR + PR + SD + NON-CR/NON-PD)", "95% CI (Clopper-Pearson)"
)
eff <- cdisc_eff_resp
eff$stat_label <- factor(eff$stat_label, levels = bor_levels)
ne <- stats::setNames(cdisc_eff_n$n, cdisc_eff_n$arm_short)

tabular(
  eff,
  titles = c(
    "Table 14.2.1",
    "Best Overall Response and Response Rates",
    "Efficacy Evaluable Population"
  ),
  footnotes = "Response per RECIST 1.1, investigator assessment."
) |>
  cols(
    stat_label  = col_spec(label = "Response"),
    row_type    = col_spec(visible = FALSE),
    groupid     = col_spec(visible = FALSE),
```

```
    group_label = col_spec(visible = FALSE),
    placebo    = col_spec(label = "Placebo\nN={ne['placebo']}"),
    drug_50    = col_spec(label = "Drug 50\nN={ne['drug_50']}"),
    drug_100   = col_spec(label = "Drug 100\nN={ne['drug_100']}")
  ) |>
  sort_rows(by = c("groupid", "stat_label")) |>
  preset(
    orientation = "landscape",
    paper_size  = "a4",
    font_size   = 8
  ) |>
  paginate()

# ---- Example 2: Per-spec override with per-page chrome ----
#
# The submission session sets a portrait letter 9pt default (typical
# safety-table geometry). One particular AE table needs landscape
# for a long PT label band; the per-spec `preset()` overrides only
# orientation. The same per-spec call wires the canonical
# per-page header band (protocol on the left, page X of Y on the
# right) and a footer band that auto-resolves the calling
# script's name and the current render timestamp via the
# `{program}` and `{datetime}` tokens.
set_preset(font_size = 9, paper_size = "letter")

n <- stats::setNames(cdisc_saf_n$n, cdisc_saf_n$arm_short)

tabular(
  cdisc_saf_aesocpt,
  titles = c(
    "Table 14.3.1",
    "Adverse Events by System Organ Class and Preferred Term",
    "Safety Population"
  ),
  footnotes = "Subjects are counted once per SOC and once per PT."
) |>
  cols(
    label    = col_spec(label = "SOC / PT", indent = "indent_level"),
    soc      = col_spec(usage = "group", visible = FALSE,
                        group_display = "column_repeat"),
    row_type = col_spec(visible = FALSE),
    soc_n    = col_spec(visible = FALSE),
    n_total  = col_spec(visible = FALSE),
    placebo  = col_spec(label = "Placebo\nN={n['placebo']}"),
    drug_50  = col_spec(label = "Drug 50\nN={n['drug_50']}"),
    drug_100 = col_spec(label = "Drug 100\nN={n['drug_100']}"),
    Total    = col_spec(label = "Total\nN={n['Total']}")
  ) |>
  headers("Treatment Group" = c("placebo", "drug_50", "drug_100", "Total")) |>
  sort_rows(by = c("soc_n", "n_total"), descending = c(TRUE, TRUE)) |>
  preset(
    orientation = "landscape",
    pagehead = list(
```

```
      left  = "Protocol: ABC-123",
      right = "Page {page} of {npages}"
    ),
    pagefoot = list(
      left  = "{program}",
      right = "{datetime}"
    )
  ) |>
  paginate(keep_together = "soc")

# Reset the session default so subsequent examples / R sessions
# are not affected.
set_preset(.reset = TRUE)
```

`preset_minimal` *Minimal theme: one header rule, normal weight throughout*

Description

Apply the stripped-down table look in one verb. The column-label divider (`midrule`) becomes the only rule drawn, and every bold-by-default surface renders in normal weight: the title block, the column-header band, the subgroup banner, and the section-header rows synthesized for `usage = "group"` columns. The analogue of ggplot2's `theme_minimal()`, composable on the pipe between the build verbs and the terminal `emit()` / `as_grid()`.

Usage

```
preset_minimal(.spec, ...)
```

Arguments

`.spec`	*The* `tabular_spec` *to apply the minimal theme to.* `<tabular_spec>: required`. Dot-prefixed so partial matching cannot bind a `...` knob to the spec slot.
`...`	*Named preset knobs.* Forwarded verbatim to `preset()` (e.g. `font_size`, `font_family`, `orientation`, `paper_size`, `margins`), so a single call sets both the minimal look and the page geometry. **Restriction:** the `rules` (and legacy `borders`) knob is owned by this helper and may not be passed here; call `preset()` directly for a custom rule set.

Details

What it sets, both at theme (lowest) precedence so an explicit later `style()` wins:

1. **Rules.** Drops the booktabs `toprule` and `bottomrule` (the outer frame), keeping the `midrule` under the column labels and the muted column-spanner `spanrule`. Equivalent to `preset(rules = list(toprule = "none", bottomrule = "none"))`.

2. **Weight.** Sets `bold = FALSE` on the title, column-header, subgroup-label, and group-header surfaces. The HTML backend overrides its `font-weight: 600` class default with an inline `font-weight: normal`; the paginated backends (RTF / LaTeX / PDF / DOCX) suppress the surface's bold run.

Last verb wins. Because the weight layers ride the theme tier, a later explicit `style(bold = TRUE, .at = cells_title())` (or any surface) re-bolds it. Treat `preset_minimal()` as the theme baseline and override individual surfaces afterwards.

Markdown. GFM cannot represent colour / background / font on a surface; rendering a styled surface to `.md` emits a one-time `tabular_warning_fidelity` and degrades gracefully. Weight (bold) and italic carry through.

Value

The updated `tabular_spec`. Continue chaining with `paginate()` / `style()`, then render via `emit()` (or resolve without I/O via `as_grid()`).

See Also

Underlying verbs: `preset()` (the rule presets `"booktabs"` / `"grid"` / `"frame"` / `"none"` live there as `rules` string sugar), `style()`.

Target the surfaces it touches: `cells_title()`, `cells_headers()`, `cells_subgroup_labels()`, `cells_group_headers()`.

Entry / terminal verbs: `tabular()`, `emit()`, `as_grid()`.

Examples

```
# ---- Example 1: Minimal AE overall summary ----
#
# The overall adverse-event summary with a single rule under the
# column labels and no bold anywhere. `preset_minimal()` is the theme
# baseline; the page stays at the session default geometry.
demo_n <- stats::setNames(cdisc_saf_n$n, cdisc_saf_n$arm_short)

tabular(
  cdisc_saf_ae,
  titles = c(
    "Table 14.3.1",
    "Overall Summary of Adverse Events",
    "Safety Population"
  ),
  footnotes = "Subjects counted once per category."
) |>
  cols(
    stat_label = col_spec(label = "Category"),
    placebo    = col_spec(label = "Placebo\nN={demo_n['placebo']}"),
    drug_50    = col_spec(label = "Drug 50\nN={demo_n['drug_50']}"),
    drug_100   = col_spec(label = "Drug 100\nN={demo_n['drug_100']}"),
    Total      = col_spec(label = "Total\nN={demo_n['Total']}")
  ) |>
  preset_minimal()
```

```
# ---- Example 2: Flat AE table under the minimal theme, then tint ----
#
# AE by SOC / PT rendered flat: the SOC subtotal row and its PT rows
# share the `label` stub, indented by `indent_level` (SOC at depth 0,
# PT at depth 1), so each SOC name appears once. `preset_minimal()`
# strips the outer frame and leaves the column-header band plain; a
# trailing `style()` tints just that band, showing a per-table
# override composing on top of the theme, and `font_size` forwards
# through `...`.

tabular(
  cdisc_saf_aesocpt,
  titles = c("Table 14.3.2", "Adverse Events by SOC and Preferred Term"),
  footnotes = "Subjects counted once per SOC and once per PT."
) |>
  cols(
    label    = col_spec(label = "SOC / PT", indent = "indent_level"),
    soc      = col_spec(visible = FALSE),
    row_type = col_spec(visible = FALSE),
    soc_n    = col_spec(visible = FALSE),
    n_total  = col_spec(visible = FALSE),
    placebo  = col_spec(label = "Placebo\nN={demo_n['placebo']}"),
    drug_50  = col_spec(label = "Drug 50\nN={demo_n['drug_50']}"),
    drug_100 = col_spec(label = "Drug 100\nN={demo_n['drug_100']}"),
    Total    = col_spec(label = "Total\nN={demo_n['Total']}")
  ) |>
  preset_minimal(font_size = 8) |>
  style(background = "#DBE4F0", .at = cells_headers())
```

`print.tabular_spec` *Print a* `tabular_spec`

Description

Renders a `tabular_spec` interactively. The default behaviour mirrors `gt::gt()`: convert the spec to an `htmltools` tag list and let htmltools dispatch — RStudio + Positron viewer panes, Quarto / Rmd notebook inline, Databricks `displayHTML`, and plain-console `cat()` are all handled without any IDE- specific branching.

Arguments

`x`	*The* `tabular_spec` *to render.* `<tabular_spec>: required`. The same object you'd hand to `emit()`.
`...`	*Forwarded to* `htmltools::print / as.tags()`. Use this to pass `id`, `style`, `class` overrides to the wrapping `<div>`.

`view` *Open the viewer?* `<logical(1)>: default interactive()`“. Same role as `gt::gt`’s ‘view‘ argument: passes through to htmltools as ‘browse = view‘. Set ‘view = FALSE‘ to suppress the viewer for one call (e.g. to capture the HTML string without launching a window).

`output` *Force a specific preview format.* `<character(1) | NULL>: default NULL (auto)`. See the `output` **argument** section below for the full list. The session default can be set via `options(tabular_print_output = "cli")` for users who prefer the structural summary over the HTML preview.

Details

Dispatch. `print()` delegates to `as.tags.tabular_spec()` which returns an `htmltools::tagList`. That tag list is handed to `htmltools`’s own print method with `browse = view`: htmltools opens the IDE viewer when one is registered, inlines under a Quarto / Rmd chunk when running inside one, or `cat()`s the HTML when neither applies. No `is_rstudio()` / `is_positron()` / `is_notebook()` heuristics — htmltools already knows.

`view` **argument.** Defaults to `interactive()`, the same universal off-switch `gt::gt()` uses. Non-interactive contexts (`Rscript`, `R CMD check`, CI, devtools::test) bypass the viewer automatically. Pass `view = FALSE` explicitly at an interactive prompt to suppress the viewer for a single call.

`output` **argument.** Forces a specific preview format instead of the default HTML-via-htmltools path. One of:

- `"html"` — same as the default, but explicit.
- `"md"` / `"markdown"` — `cat()` the markdown source to the console (round-trips through `backend_md`).
- `"latex"` — `cat()` the markdown source as a temporary placeholder (real LaTeX preview lands with `backend_latex`).
- `"rtf"` / `"docx"` / `"pdf"` — render an HTML preview and emit a cli note pointing at `emit()` for the real artefact. The viewer pane cannot render RTF / OOXML, and we deliberately do *not* compile through tinytex on every autoprint.
- `"cli"` — print the structural cli-tree summary (props, headers, sort, pagination, preset). Useful for debugging spec composition without paying the HTML render cost.

Robustness. The HTML render is wrapped in `tryCatch`; if rendering fails for any reason the printer falls back to the cli-tree summary and a `cli::cli_warn()` describing the failure, so a broken spec never crashes the REPL.

Tempdir. Preview HTML files live under `getOption("tabular_preview_dir", default = tempdir())`. Override the option to keep them in a stable location (handy on Linux distros where browsers don’t have read access to `/tmp/`).

Value

Invisibly returns `x`. Side effect: opens the viewer, inlines under a chunk, or `cat()`s output.

See Also

Tag conversion: `as.tags.tabular_spec()` — the htmltools tag list that `print()` delegates to. Call it directly to embed the table in a custom `htmltools::tagList` or Shiny UI.

Terminal verb: `emit()` writes the resolved artefact to disk; `print()` is for in-session preview only.

Pipeline shape: `as_grid()` resolves the engine pipeline to a `tabular_grid` without I/O.

Examples

```
# ---- Example 1: Build + autoprint (HTML preview) ----
#
# Build a spec and let autoprint render it. Inside RStudio /
# Positron the HTML lands in the viewer pane; inside a
# Quarto / Rmd chunk it inlines under the chunk; at a plain
# console the HTML source is `cat()`-ed.
tabular(
  cdisc_saf_demo,
  titles = c("Table 14.1.1", "Demographics"),
  footnotes = "Safety Population."
)

# ---- Example 2: Force the cli-tree structural view ----
#
# The cli-tree summary shows props at a glance. Useful for
# debugging spec composition without paying the HTML render
# cost.
spec <- tabular(cdisc_saf_demo, titles = "Demographics") |>
  cols(variable = col_spec(usage = "group", label = "Characteristic"))

print(spec, output = "cli")
```

`set_preset` *Set or clear the session default preset*

Description

Stash a `preset_spec` in the package-internal session environment. Every subsequent `tabular()` chain that does not attach its own `preset()` inherits these knobs at render time. Mirrors ggplot2's `ggplot2::theme_set()`: one call up front, many tables downstream.

Usage

```
set_preset(new = NULL, ..., .template = NULL, .style = NULL, .reset = FALSE)
```

Arguments

new	*A* `preset_spec` *to install wholesale.* `<preset_spec | NULL>: default NULL.` When non-`NULL`, replaces the session preset in one call without touching knobs. The primary use is the save/restore round-trip (`old <- set_preset(...); set_preset(old)`) — `new` accepts any `preset_spec` previously returned by `set_preset()` or `get_preset()`. Mutually exclusive with `...`, `.template`, `.style`, `.reset`: passing any of those alongside a non-`NULL` `new` raises `tabular_error_input`.

`...`	*Named preset knobs.* Same shape as `preset()`; see that verb for the full list of 13 recognised knobs. Unknown names raise `tabular_error_input`. Mutually exclusive with a non-`NULL` `new`.
`.template`	*A* `preset_spec` *to bulk-apply before* `...`. `<preset_spec | NULL>: default NULL`. Same semantics as `preset()`'s `.template`: every knob set away from its factory default feeds in as the base layer; user-supplied `...` knobs then merge on top with shallow-merge per list-valued knob.
`.style`	*A* `style_template()` *to layer into the session default.* `<style_template | NULL>: default NULL`. Same semantics as `preset()`'s `.style`: the template's accumulated layers feed in as session-default style, layered before any per-spec `style()` calls.
`.reset`	*Discard the existing session preset before applying* `...`. `<logical(1)>: default FALSE`. With no knobs, clears the session default back to NULL.

Details

Persistence. The session preset lives in a package-internal environment populated when `tabular` is loaded and emptied when the namespace unloads. There is no on-disk persistence; set the default at the top of each analysis script (or in a project-level `.Rprofile`) when a sticky house style is needed.

Merge, not replace. A second `set_preset()` call merges its knobs onto the existing session preset; unspecified knobs keep their prior value. Pass `.reset = TRUE` to discard the existing session preset and start from `preset_spec()` defaults. `set_preset(.reset = TRUE)` with no knobs clears the session default back to NULL.

Save and restore. Every call returns the *previous* session preset invisibly, the same primitive ggplot2's `ggplot2::theme_set()` ships. Capture it once, render, and restore by passing the saved value back as the positional `new` argument:

```
old <- set_preset(font_size = 10, paper_size = "a4")
# ... one renegade render at 10pt A4 ...
set_preset(old)        # restore
```

When the prior was `NULL` (no session preset ever attached), the restore is `set_preset(.reset = TRUE)` instead — `set_preset(NULL)` is the same shape as `set_preset()` and falls through to factory defaults rather than clearing the session.

Cascade with `preset()`. A per-spec `preset()` always wins over the session default. The session default fills in only when the spec carries no preset of its own.

Value

The previous session `preset_spec` *(invisible).* Returns `NULL` when no session preset was attached prior to the call. Capture it to round-trip a temporary override: `old <- set_preset(...); set_preset(old)`. Mirrors `ggplot2::theme_set()` and `base::options()` — the canonical tidyverse save/restore primitive.

See Also

Per-spec partner: `preset()` — overrides the session default on one chain.

Inspect: `get_preset()`.

Entry / terminal verbs: `tabular()`, `emit()`, `as_grid()`.

Examples

```
# ---- Example 1: Sticky session default for an analysis script ----
#
# The submission's safety tables all use portrait letter, 9pt
# Times New Roman with 1-inch margins. Set once at the top of the
# analysis script and every `tabular()` chain inherits it — no
# per-table `preset()` call needed unless one table deviates.
set_preset(
  font_size   = 9,
  font_family = "Times New Roman",
  orientation = "portrait",
  paper_size  = "letter",
  margins     = 1
)

# Subsequent tabular() chains pick up the session preset at render.
demo_n <- stats::setNames(cdisc_saf_n$n, cdisc_saf_n$arm_short)
tabular(
  cdisc_saf_ae,
  titles = c(
    "Table 14.3.1",
    "Overall Summary of Adverse Events",
    "Safety Population"
  ),
  footnotes = "Subjects counted once per category."
) |>
  cols(
    stat_label = col_spec(label = "Category"),
    placebo    = col_spec(label = "Placebo\nN={demo_n['placebo']}"),
    drug_50    = col_spec(label = "Drug 50\nN={demo_n['drug_50']}"),
    drug_100   = col_spec(label = "Drug 100\nN={demo_n['drug_100']}"),
    Total      = col_spec(label = "Total\nN={demo_n['Total']}")
  )

# ---- Example 2: Reset the session default mid-script ----
#
# The first half of the script produces safety tables at 9pt; the
# second half produces efficacy tables at 10pt on landscape A4. A
# single `set_preset(.reset = TRUE, ...)` resets the cascade before
# the second batch starts.
set_preset(font_size = 9, paper_size = "letter")
get_preset()@font_size  # 9

set_preset(
  .reset      = TRUE,
  font_size   = 10,
  orientation = "landscape",
  paper_size  = "a4"
)
get_preset()@orientation  # "landscape"

# Reset the session default so subsequent examples / R sessions
```

```
# are not affected.
set_preset(.reset = TRUE)

# ---- Example 3: Save and restore around a renegade table ----
#
# Most of the submission renders portrait letter at 9pt. One
# renegade efficacy table needs landscape A4 at 10pt. Capture
# the prior session preset, render the renegade, then restore.
set_preset(font_size = 9, paper_size = "letter")

old <- set_preset(
  font_size   = 10,
  paper_size  = "a4",
  orientation = "landscape"
)
# ... one renegade render ...
if (is.null(old)) {
  set_preset(.reset = TRUE)   # was no prior — clear
} else {
  set_preset(old)              # round-trip via the positional `new` arg
}
get_preset()@paper_size  # "letter" — restored

# ---- Example 4: Snapshot current preset, mutate, restore ----
#
# Capture whatever the session preset is right now (may be NULL),
# let a downstream helper mutate it, then put it back when done.
set_preset(font_size = 9, paper_size = "letter")
snapshot <- get_preset()

# Simulate downstream code mutating session state.
set_preset(font_size = 11, orientation = "landscape")

# Restore. The wholesale-install path of `set_preset(new)`
# accepts any `preset_spec` returned by `get_preset()` /
# `set_preset()`.
if (is.null(snapshot)) {
  set_preset(.reset = TRUE)
} else {
  set_preset(snapshot)
}
get_preset()@font_size    # 9 — restored

# Reset for subsequent examples / R sessions.
set_preset(.reset = TRUE)
```

`sort_rows` *Sort the display rows*

Description

Attach a `sort_spec` to a `tabular_spec`. The engine applies the sort before pagination, so by may reference any column in `spec@data` whether or not the column is declared in `cols()`.

Usage

```
sort_rows(.spec, by = character(), descending = FALSE)
```

Arguments

`.spec`	*The* `tabular_spec` *to attach the sort to.* `<tabular_spec>: required`.

by	*Ordered column names to sort by, in precedence order.* `<character>: default character()`. Length 0 is accepted (no-op sort). May reference columns not declared in `cols()` — sort-only helper columns ride along through the engine.
	Restriction: Every entry must be a column in `spec@data`. Cannot reference arm columns produced by `pivot_across()`; pivot upstream of the sort instead. Arm cells hold rendered stat strings (e.g. `"75.2 (8.3)"`) that do not order meaningfully.
	`# Two-key hierarchical sort: SOC clusters by descending count,`
	`# each PT nested under its SOC.`
	`sort_rows(by = c("soc_n", "n_total"), descending = c(TRUE, TRUE))`

descending	*Per-key sort direction.* `<logical(1) | logical(length(by))>: default FALSE`. `TRUE` sorts the corresponding key descending; length 1 recycles to every key. **Restriction:** No NAs. Length must be 1 or `length(by)`. **Tip:** For mixed-direction multi-key sorts, pass `length(by)` values; the engine inverts the `xtfrm` rank of each descending key and calls `order()` once on all keys.

Details

Replace, not stack. A second `sort_rows()` call REPLACES the prior sort — sort is a single spec, not a stackable list. Call with no arguments to clear.

NA last, regardless of direction. NA values in a sort key are placed at the end whether the key is ascending or descending (matching `order(..., na.last = TRUE)`).

Factor levels drive the order. Factor columns sort by factor levels, not by the character label. The CDISC BOR ordering (`CR < PR < SD < NON-CR/NON-PD < PD < NE < MISSING`) survives a tabular pipeline without an explicit `mutate()` — coerce `stat_label` to a factor with the levels in clinical order upstream, then `sort_rows(by = "stat_label")` does the rest.

Value

The updated `tabular_spec`. Continue chaining with `style()`, `paginate()`, `preset()`, then render via `emit()` (or resolve without I/O via `as_grid()`).

See Also

Sibling build verbs: `cols()` / `col_spec()`, `headers()`, `style()`, `paginate()`, `preset()`.

Entry / terminal verbs: `tabular()`, `emit()`, `as_grid()`.

Examples

```
# ---- Example 1: AE table clustered by SOC, PTs nested by count ----
#
# AE-by-SOC/PT table sorted so each SOC is followed immediately by
# its own preferred terms, SOC clusters in descending subject-count
# order. The sort runs on the bundled numeric helpers `soc_n` and
# `n_total`, not the formatted `Total` text, which would sort
# lexically ("14" < "171" < "29").
n <- stats::setNames(cdisc_saf_n$n, cdisc_saf_n$arm_short)

tabular(
  cdisc_saf_aesocpt,
  titles = c(
    "Table 14.3.1",
    "Adverse Events by System Organ Class and Preferred Term",
    "Safety Population"
  ),
  footnotes = "Subjects are counted once per SOC and once per PT."
) |>
  cols(
    label    = col_spec(label = "SOC / PT", indent = "indent_level"),
    soc      = col_spec(visible = FALSE),
    row_type = col_spec(visible = FALSE),
    soc_n    = col_spec(visible = FALSE),
    n_total  = col_spec(visible = FALSE),
    placebo  = col_spec(label = "Placebo\nN={n['placebo']}"),
    drug_50  = col_spec(label = "Drug 50\nN={n['drug_50']}"),
    drug_100 = col_spec(label = "Drug 100\nN={n['drug_100']}"),
    Total    = col_spec(label = "Total\nN={n['Total']}")
  ) |>
  sort_rows(by = c("soc_n", "n_total"), descending = c(TRUE, TRUE))

# ---- Example 2: BOR table in CDISC factor order ----
#
# Efficacy BOR table that must appear in CDISC clinical order
# (CR < PR < SD < NON-CR/NON-PD < PD < NE < MISSING), then the
# derived ORR / CBR / DCR rate rows ordered by `groupid`,
# not alphabetical. `cdisc_eff_resp$stat_label` arrives as character, so
# coerce to a factor with the canonical levels upstream and
# `sort_rows()` uses those levels directly.
bor_levels <- c(
  "CR", "PR", "SD", "NON-CR/NON-PD", "PD", "NE", "MISSING",
  "ORR (CR + PR)", "CBR (CR + PR + SD)",
  "DCR (CR + PR + SD + NON-CR/NON-PD)", "95% CI (Clopper-Pearson)"
)
eff <- cdisc_eff_resp
eff$stat_label <- factor(eff$stat_label, levels = bor_levels)
ne <- stats::setNames(cdisc_eff_n$n, cdisc_eff_n$arm_short)

tabular(
  eff,
  titles = c(
```

```
    "Table 14.2.1",
    "Best Overall Response and Response Rates",
    "Efficacy Evaluable Population"
  ),
  footnotes = "Response per RECIST 1.1, investigator assessment."
) |>
  cols(
    stat_label  = col_spec(label = "Response"),
    row_type    = col_spec(visible = FALSE),
    groupid     = col_spec(visible = FALSE),
    group_label = col_spec(visible = FALSE),
    placebo    = col_spec(label = "Placebo\nN={ne['placebo']}"),
    drug_50    = col_spec(label = "Drug 50\nN={ne['drug_50']}"),
    drug_100   = col_spec(label = "Drug 100\nN={ne['drug_100']}")
  ) |>
  sort_rows(by = c("groupid", "stat_label"))

# ---- Example 3: Mixed-direction multi-key sort with hidden helper ----
#
# Demographics-style table sorted by `variable` ascending and a
# hidden numeric key descending. The `descending` argument takes
# one value per `by` entry so each key can flip direction
# independently. The helper column rides in `spec@data` for the
# sort but never renders (visible = FALSE on its col_spec).
demo <- cdisc_saf_demo
demo$display_order <- match(demo$variable, unique(demo$variable))

tabular(demo, titles = "Demographics, ranked within section") |>
  cols(
    variable      = col_spec(usage = "group", label = "Characteristic"),
    stat_label    = col_spec(label = "Statistic"),
    display_order = col_spec(visible = FALSE),
    placebo       = col_spec(label = "Placebo",  align = "decimal"),
    drug_50       = col_spec(label = "Drug 50",  align = "decimal"),
    drug_100      = col_spec(label = "Drug 100", align = "decimal"),
    Total         = col_spec(label = "Total",    align = "decimal")
  ) |>
  sort_rows(
    by         = c("display_order", "stat_label"),
    descending = c(FALSE, TRUE)
  )
```

`style` *Attach a style layer to a* `tabular_spec` *or* `style_template`

Description

One verb, one cascade. Each `style()` call appends a single `style_layer` (location + style attributes) to the spec or template. Layers accumulate in declaration order; the engine merges them at render time so later layers win per attribute, NA-valued fields leave the prior layer intact.

Usage

```
style(.spec, ..., .at = cells_body())
```

Arguments

`.spec`	*A* `tabular_spec` *OR a* `tabular_style_template`. `<tabular_spec | tabular_style_template>: re` Dot-prefixed so R's partial argument matching cannot accidentally bind a short attribute name in `...` to the spec slot. When piping through `style_template() |> style(...)` layers accumulate onto the template instead of a spec.
`...`	*Named style attributes.* At least one required. See the *Style attributes* section for the recognised names.
`.at`	*Location object selecting which surface the layer targets.* `<tabular_location>: default cells_body(` Build with one of the `cells_*()` constructors; see `cells_body()` and siblings. Dot-prefixed (tidyverse convention) because it comes AFTER `...` — that way a user-passed style attribute can never collide with this arg's name.

Value

The updated `tabular_spec` (or `tabular_style_template`, when called against one).

Locations

The `.at` argument selects which surface the layer targets. Every region of the rendered page has a `cells_*()` constructor:

- `cells_body()` — body cells (default)
- `cells_headers()` — column header band
- `cells_group_headers()` — synthetic group-header rows
- `cells_title()` — title block
- `cells_subgroup_labels()` — subgroup banner row
- `cells_footnotes()` — footnote block
- `cells_pagehead()` — page-header band
- `cells_pagefoot()` — page-footer band
- `cells_table()` — table-wide regions (outer borders, body-row separators)

Body filters live on `cells_body()`: `i = 1:3` for integer-index rows, `j = "Total"` for column-name targeting, `where = <expr>` for a quosure-captured predicate evaluated against `spec@data`.

Style attributes

Each layer carries a `style_node` built from `....` Recognised attribute names:

- Text — `bold`, `italic`, `underline`, `color`, `background`, `font_family`, `font_size`
- Alignment — `halign` (`"left"` / `"center"` / `"right"`), `valign` (`"top"` / `"middle"` / `"bottom"`)
- Borders — `border` (umbrella), `border_top`, `border_bottom`, `border_left`, `border_right` (each takes a `brdr()` value or the literal `"none"`); per-side scalars `border_<side>_{style,width,color}` for finer control

- Padding — `padding` (a scalar applies to all four sides; a named vector `c(top = , right = , bottom = , left = )` sets each side); or the per-side scalars `padding_<side>` directly
- Spacing — `blank_above`, `blank_below` (integer blank lines above / below the block — for `cells_title()` / `cells_footnotes()` / `cells_subgroup_labels()`)
- Inline — `pretext`, `posttext` (literal text prepended / appended around the cell value)

Unknown attribute names emit a `cli::cli_warn` and drop from the constructed node; the engine never sees a foreign property.

See Also

Companion verbs: `cols()`, `headers()`, `preset()`, `set_preset()`.

Location constructors: `cells_body()`, `cells_headers()`, `cells_group_headers()`, `cells_title()`, `cells_subgroup_labels()`, `cells_footnotes()`, `cells_pagehead()`, `cells_pagefoot()`, `cells_table()`.

Style values: `brdr()`, `style_template()`.

Examples

```
# ---- AE table by SOC and PT with per-row indent + styled hierarchy ----
# `cdisc_saf_aesocpt` ships with `indent_level` (0 on overall/SOC rows,
# 1 on PT rows); `col_spec(indent = "indent_level")` drives the
# PT indent on the `label` column.
tabular(cdisc_saf_aesocpt, titles = "Adverse Events by SOC / PT",
        footnotes = "") |>
  cols(
    label    = col_spec(label = "Category", align = "left",
                        indent = "indent_level"),
    soc      = col_spec(visible = FALSE),
    row_type = col_spec(visible = FALSE),
    soc_n    = col_spec(visible = FALSE),
    n_total  = col_spec(visible = FALSE),
    placebo  = col_spec(label = "Placebo",  align = "decimal"),
    drug_50  = col_spec(label = "Drug 50",  align = "decimal"),
    drug_100 = col_spec(label = "Drug 100", align = "decimal"),
    Total    = col_spec(label = "Total",    align = "decimal")
  ) |>
  # SOC summary rows bolded (depth 0 — flush)
  style(bold = TRUE,
        .at = cells_body(where = row_type == "soc")) |>
  # Overall row gets a light background
  style(background = "#f0f0f0",
        .at = cells_body(where = row_type == "overall"))

# ---- Chrome styling ----
# Each layer changes the surface VISIBLY from its default: a coloured
# rule under the header band, a dark-blue header text, a left-aligned
# title (default is centred), and a blank line above + below the title.
tabular(cdisc_saf_demo, titles = "Demographic Characteristics") |>
  style(color = "#1a5276", .at = cells_headers()) |>
  style(border_bottom = brdr("thick", "double", "#1a5276"),
        .at = cells_headers()) |>
```

```
  style(halign = "left", .at = cells_title()) |>
  style(blank_above = 1, blank_below = 1,
        .at = cells_title())

# ---- Table-wide borders ----
tabular(cdisc_saf_demo) |>
  style(border = brdr("medium"),
        .at = cells_table(side = "outer")) |>
  style(border_top = brdr("hairline", "dotted"),
        .at = cells_table(side = "rows"))

# ---- House style via style_template() ----
house <- style_template() |>
  style(color = "#1F3B5C", background = "#DBE4F0", .at = cells_headers()) |>
  style(border_top = brdr("thick"), .at = cells_headers()) |>
  style(border_bottom = brdr("thick"), .at = cells_headers()) |>
  style(border_bottom = brdr("medium"),
        .at = cells_table(side = "outer_bottom"))
# Attach once via set_preset(); every tabular() chain then inherits it.
set_preset(.style = house, font_size = 9)
set_preset(.reset = TRUE) # restore the default for later examples
```

`style_template` *Reusable style template (for house-style presets)*

Description

Build a reusable, composable style template by chaining `style()` calls against a `tabular_style_template`. The template carries an ordered list of `style_layer` records and can be attached to `preset()` / `set_preset()` as a `style =` argument — every downstream `tabular()` chain then inherits the template's layers via the engine cascade.

Usage

```
style_template()

is_style_template(x)
```

Arguments

`x`	*Any R object.* The predicate inspects the class via `inherits()`; no other introspection is performed.

Details

One verb, two surfaces. The same `style(.spec_or_template, ..., .at = ...)` call that attaches a layer to a per-table spec also accumulates layers onto a template. Symmetric API — no need to learn a second function for the multi-table use case.

Submission workflow. A submission typically renders 100–200 tables with one visual identity. Build the template once at the top of the submission script, pass it to `set_preset(style = template)`, and every subsequent `tabular()` produces output that inherits the same column-header rules, group-header bolding, title spacing, and outer-frame borders without a single per-table `style()` call.

Cascade order. Engines apply layers low-to-high priority: backend defaults → session preset's `@style` → spec preset's `@style` → per-spec `style()` layers. Later layers override prior ones per attribute; NA fields leave the prior layer's value in place.

Value

A `tabular_style_template` — a small S3 list with a `layers` slot. Pipe through `style()` to add layers.

See Also

Style verb: `style()` — the same verb chains onto a spec or a template.

Locations: `cells_body` — locations that name the *where* half of every layer.

Examples

```
# ---- Sponsor "house style" composed once ----
#
# The result becomes the default look for every table rendered
# against this preset. No per-table style() boilerplate.
house <- style_template() |>
  style(background = "#DBE4F0", .at = cells_headers(level = -1)) |>
  style(color = "#1F3B5C", .at = cells_group_headers()) |>
  style(
    border_top    = brdr("thick", "double"),
    border_bottom = brdr("thick", "double"),
    .at = cells_headers()
  ) |>
  style(blank_above = 1, blank_below = 1, .at = cells_title())

length(house$layers)

# ---- Verify class ----
is_style_template(house)
```

`subgroup` *Partition the report by a variable*

Description

Attach a subgroup_spec to a tabular_spec. At render time the engine partitions spec@data by the unique values of by, runs the full resolve pipeline per group, and concatenates the results. **A hard page break is inserted between groups** — every subgroup value starts on its own page. A centred banner line appears above the column-header rule on every page of the group (including continuation pages), matching the canonical submission page-layout convention.

Usage

```
subgroup(.spec, by, label = NULL, big_n = NULL, big_n_fmt = "\n(N={n})")
```

Arguments

.spec	*The* tabular_spec *to partition.* <tabular_spec>: required.
by	*Column name(s) to partition by.* <character>: required. Must reference a column in spec@data. Length-0 (or character(0)) clears the partition. Matches the by = arg convention of sort_rows(). **Multi-variable.** Pass c("var1", "var2") to cross on every combination present in the data. Multi-var partitions require an explicit label template (the single-var auto-default does not generalise).
label	*Banner template.* <character(1) | NULL>: default NULL. Glue-style template with {column_name} placeholders. NULL derives a default from the partition variable's attr(data[[by]], "label") (falling back to the column name). **Tip:** reference auxiliary columns to inline the BigN or any qualifier that is constant within group — e.g. "Cohort: {cohort} (N = {n})". **Restriction:** Every {col} reference must be a column in spec@data. Unknown columns raise tabular_error_subgroup_template_unknown_col.
big_n	*Per-page BigN denominators.* <data.frame> | NULL: default NULL. A table giving the (N=x) denominator each arm's header should show on each subgroup page. Each arm is named as it appears in the header — either a data column (the N rides that column's leaf label) **or** a headers() band label (the N rides that spanner band). Ns are non-negative whole numbers; provide one per by combination present in the data. Accepts **either** shape: • **Wide** — the by column(s) plus one numeric column per arm (cells are the Ns). • **Long** — the by column(s) plus one arm-name column and one numeric N column, i.e. dplyr::count() / summarise() output used directly with no reshaping.

```
# Wide: one column per arm.
wide <- tibble::tribble(
  ~sex, ~placebo, ~drug_50, ~Total,
  "F",       24L,       9L,    42L,
  "M",       18L,      15L,    47L
)
# Long: count()-style, pivoted internally. Equivalent to `wide`.
long <- tibble::tribble(
```

```
  ~sex, ~arm,      ~n,
  "F",  "placebo", 24L,
  "F",  "drug_50",  9L,
  "F",  "Total",   42L,
  "M",  "placebo", 18L,
  "M",  "drug_50", 15L,
  "M",  "Total",   47L
)
spec |> subgroup(by = "sex", big_n = long)
```

Requirement: band keying needs `headers()` **before** `subgroup()` in the pipeline; each arm name must resolve to exactly one leaf XOR one band. Every missing per-page N is a call-time error, never a silently wrong denominator.

Note: the per-arm N renders in every backend. The paged backends (RTF, PDF / LaTeX, DOCX) carry it on the column header that repeats on every page of the subgroup. HTML and Markdown are continuous (one stacked table, one header), so they instead emit a per-arm N row directly under each subgroup banner, the `(N=x)` aligned beneath its arm column.

`big_n_fmt` *Per-page BigN template.* `<character(1)>: default "\n(N={n})"`. Appended to each arm's header label, with `{n}` substituted by that page/column's integer N. Only the `{n}` token is allowed; the default puts the N on its own line under the arm name.

Details

Label is a glue-style template. When `label` carries `{col}` placeholders, the engine substitutes each placeholder against the FIRST ROW of the group's filtered data — so any column whose value is constant within group (BigN, cohort descriptor, qualifier text) can ride into the banner. Columns that vary within group also resolve, but always to the first row's value; pre-compute aggregates upstream.

Default label (when `label = NULL`, single var): the engine generates `"<attr(data[[by]], 'label') %||% by>: {<by>}"`, so `subgroup(by = "cohort")` renders banners like `"Cohort: A"` and `"Cohort: B"` without further configuration.

Replace, not stack. A second `subgroup()` call REPLACES the prior partition — subgroup is a single spec, not a stackable list. Passing `by = character(0)` clears the slot, though typical clinical pipelines set the partition once up front.

Display-side only. `subgroup()` partitions a pre-summarised wide data frame; it does not aggregate, filter, or weight. The user supplies one summary row per displayed row per group; tabular's job is solely to lay them out with the per-group banner and page break.

Multi-variable crossing. `by = c("SEX", "AGEGR1")` partitions on every combination present in the data (first variable varies slowest, matching `expand.grid()` convention). An explicit `label` template is required for multi-var partitions since the single-var default `"<var>: {<var>}"` does not generalise; raise `tabular_error_subgroup_label_required` otherwise.

Auto-hide of partition + template columns. Every column named in `by`, plus every column referenced via a `{col}` placeholder in `label`, automatically flips to `visible = FALSE` at engine time. Users do not restate `col_spec(visible = FALSE)` inside `cols()` for these columns — mirroring the `col_spec(indent = ...)` auto-hide ergonomic.

Value

The updated `tabular_spec`. Continue chaining or resolve via `as_grid()` / `emit()`.

See Also

Pipeline siblings: `sort_rows()`, `paginate()`.

Resolve / render: `as_grid()`, `emit()`.

Examples

```
# ---- Example 1: Vital signs split into one page set per sex ----
#
# The simplest partition: a single clinical variable. Each `sex`
# value gets its own page set with a centred `Sex: <value>` banner
# above the column-header rule on every page, separated by hard page
# breaks. With no `label` template the banner uses the variable's
# `label` attribute when present (set here), falling back to the
# column name. Within each page, parameter nests visit nests the
# statistic rows.
vs <- cdisc_saf_subgroup
attr(vs$sex, "label") <- "Sex"

tabular(
  vs,
  titles = c(
    "Table 14.2.1",
    "Vital Signs by Visit",
    "Safety Population"
  ),
  footnotes = "Descriptive statistics by treatment arm."
) |>
  cols(
    sex_n      = col_spec(visible = FALSE),
    paramcd    = col_spec(visible = FALSE),
    param      = col_spec(usage = "group", label = "Parameter"),
    visit      = col_spec(usage = "group", label = "Visit"),
    stat_label = col_spec(label = "Statistic"),
    placebo    = col_spec(label = "Placebo",  align = "decimal"),
    drug_50    = col_spec(label = "Drug 50",  align = "decimal"),
    drug_100   = col_spec(label = "Drug 100", align = "decimal"),
    Total      = col_spec(label = "Total",    align = "decimal")
  ) |>
  subgroup(by = "sex")

# ---- Example 2: Partition by Sex with inline BigN via template ----
#
# `label` is a glue-style template; any column whose value is
# constant within group can ride into the banner. `cdisc_saf_subgroup`
# ships a partition-constant `sex_n` BigN column alongside the value
# cells, so each banner reads `"Sex: F (N = 143)"`, etc. `sex` and
# `sex_n` auto-hide from the body (partition `by` and template-
# referenced columns).
```

```
tabular(cdisc_saf_subgroup, titles = "Vital Signs by Visit") |>
  cols(
    paramcd    = col_spec(visible = FALSE),
    param      = col_spec(usage = "group", label = "Parameter"),
    visit      = col_spec(usage = "group", label = "Visit"),
    stat_label = col_spec(label = "Statistic"),
    placebo    = col_spec(label = "Placebo",  align = "decimal"),
    drug_50    = col_spec(label = "Drug 50",  align = "decimal"),
    drug_100   = col_spec(label = "Drug 100", align = "decimal"),
    Total      = col_spec(label = "Total",    align = "decimal")
  ) |>
  subgroup(by = "sex", label = "Sex: {sex} (N = {sex_n})")

# ---- Example 3: Multi-variable crossing (Sex x Visit) ----
#
# Pass two columns to partition on every combination present in the
# data. The label template MUST reference each variable explicitly
# because the single-var auto-default does not generalise. The cross
# varies the first column (sex) slowest and the second (visit)
# fastest, giving page sequence F/Baseline, F/Week 8, ..., M/Baseline,
# ... Parameter nests the statistic rows within each page.
tabular(cdisc_saf_subgroup, titles = "Vital Signs by Sex and Visit") |>
  cols(
    sex_n      = col_spec(visible = FALSE),
    paramcd    = col_spec(visible = FALSE),
    param      = col_spec(usage = "group", label = "Parameter"),
    stat_label = col_spec(label = "Statistic"),
    placebo    = col_spec(label = "Placebo",  align = "decimal"),
    drug_50    = col_spec(label = "Drug 50",  align = "decimal"),
    drug_100   = col_spec(label = "Drug 100", align = "decimal"),
    Total      = col_spec(label = "Total",    align = "decimal")
  ) |>
  subgroup(
    by    = c("sex", "visit"),
    label = "Sex: {sex} / Visit: {visit}"
  )

# ---- Example 4: Per-page BigN — different (N=) per sex page ----
#
# Each sex page has a different per-arm population, so the `(N=x)`
# in the arm headers must vary by page. `big_n` is a wide table:
# the `by` column plus one column per arm (named as the data
# column), cells are the page-specific Ns. Each arm header then
# reads e.g. `Placebo` over `(N=53)` on the Female page and
# `(N=33)` on the Male page. RTF / PDF / DOCX carry the N on the
# repeating header; HTML and Markdown add a per-arm N row under each
# banner.
big_n <- tibble::tribble(
  ~sex, ~placebo, ~drug_50, ~drug_100, ~Total,
  "F",       53L,      55L,       35L,    143L,
  "M",       33L,      41L,       37L,    111L
)
tabular(cdisc_saf_subgroup, titles = "Vital Signs by Visit") |>
```

```
  cols(
    sex_n      = col_spec(visible = FALSE),
    paramcd    = col_spec(visible = FALSE),
    param      = col_spec(usage = "group", label = "Parameter"),
    visit      = col_spec(usage = "group", label = "Visit"),
    stat_label = col_spec(label = "Statistic"),
    placebo    = col_spec(label = "Placebo",  align = "decimal"),
    drug_50    = col_spec(label = "Drug 50",  align = "decimal"),
    drug_100   = col_spec(label = "Drug 100", align = "decimal"),
    Total      = col_spec(label = "Total",    align = "decimal")
  ) |>
  subgroup(by = "sex", label = "Sex: {sex}", big_n = big_n)

# ---- Example 5: Clear a partition with subgroup(character()) ----
#
# `subgroup(by = character())` (or `subgroup(by = NULL)`) explicitly
# clears any prior partition — useful in programmatically-built
# pipelines where a downstream branch decides not to paginate by
# group after all. Give `sex` a `usage = "group"` role up front:
# while the sex partition is active it overrides that role (sex
# becomes the per-page banner); once cleared, sex falls back to a
# group level, so the pooled single-page render nests sex, parameter,
# and visit rather than leaving a stray partition column behind.
tabular(cdisc_saf_subgroup, titles = "Pooled (no sex partition)") |>
  cols(
    sex_n      = col_spec(visible = FALSE),
    paramcd    = col_spec(visible = FALSE),
    sex        = col_spec(usage = "group", label = "Sex"),
    param      = col_spec(usage = "group", label = "Parameter"),
    visit      = col_spec(usage = "group", label = "Visit"),
    stat_label = col_spec(label = "Statistic"),
    placebo    = col_spec(label = "Placebo",  align = "decimal"),
    drug_50    = col_spec(label = "Drug 50",  align = "decimal"),
    drug_100   = col_spec(label = "Drug 100", align = "decimal"),
    Total      = col_spec(label = "Total",    align = "decimal")
  ) |>
  subgroup("sex", label = "Sex: {sex}") |>
  # Decide later that the sex split was the wrong default —
  # clear it before rendering.
  subgroup(character())
```

`tabular` *Start a tabular display*

Description

Wrap a pre-summarised data frame into a `tabular_spec` ready for the verb chain. `tabular()` is the entry verb — it owns the `data`, `titles`, and `footnotes` slots; every downstream verb (`cols()`, `headers()`, `sort_rows()`, `style()`, `paginate()`, `preset()`) returns an updated spec for further chaining, terminating in `emit()` (write to file) or `as_grid()` (resolve without writing).

Usage

```
tabular(data, titles = NULL, footnotes = NULL)
```

Arguments

data	*The display rows.* <data.frame>: required. Pre-summarised wide-format data; tibbles, data.tables, and arrow tables are coerced via as.data.frame(). Factor columns are preserved (their levels drive sort_rows()). **Restriction:** At least one column; column names must be unique. Zero rows is accepted (engine renders a "No data" stub). **Interaction:** The cards-format counterparts (cdisc_saf_demo_ard, cdisc_saf_aesocpt_ard) are NOT accepted directly; pipe through pivot_across() first.

titles	*Page-title block, one element per row.* <character> | NULL: default NULL. Each element renders on its own centred line; embedded \n wraps within that row. The backend collapses unused rows so the column-header band sits flush against the lowest used title.
	Restriction: No NAs.
	Each element supports glue-style {expr} interpolation: braces are evaluated as R code in the calling environment at build time, e.g. "N total = {sum(n)}". Double a brace ({{ or }}) for a literal one. An md() / html() element is passed through without interpolation.
	`# Canonical 3-line title block with BigN-qualified population.`
	`n <- stats::setNames(cdisc_saf_n$n, cdisc_saf_n$arm_short)`
	`titles = c(`
	`  "Table 14.3.1",`
	`  "Adverse Events by System Organ Class and Preferred Term",`
	`  "Safety Population"`
	`)`

footnotes	*Page-footnote block, one element per row.* <character> | NULL: default NULL. User-supplied prose rows only; the backend appends its own program-path / program-name / timestamp band below them at render time.
	Restriction: No NAs.
	Each element supports glue-style {expr} interpolation (see titles).
	`# Canonical 3-line footnote block.`
	`footnotes = c(`
	`  "Subjects are counted once per SOC and once per PT.",`
	`  "Percentages based on N per treatment group.",`
	`  "TEAE = treatment-emergent adverse event."`
	`)`

Details

Pre-summarised input contract. data is one row per displayed row of the final table. tabular() does not aggregate, filter, weight, or generate subtotal rows — those happen upstream in cards, dplyr, or SAS. If the upstream is a long cards::ard_stack() ARD, pipe through pivot_across() first to land in the wide shape tabular() accepts.

Multi-line titles and footnotes by contract. Clinical tables routinely carry 2-4 title rows and 1-4 user footnote rows. Pass each row as one element of the character vector; the backend renders each element on its own line, collapsing unused rows so the column-header band sits flush against the lowest used title.

Value

A `tabular_spec` *S7 object.* Pipe it into `cols()`, `headers()`, `sort_rows()`, `style()`, `paginate()`, and `preset()` to build the display, then into `emit()` to render or `as_grid()` to resolve without writing.

See Also

Downstream build verbs: `cols()` / `col_spec()`, `headers()`, `sort_rows()`, `style()`, `paginate()`, `preset()`.

Terminal verbs: `emit()` (write), `as_grid()` (resolve without I/O).

Input helper: `pivot_across()` (cards ARD -> wide).

Demo data: `cdisc_saf_demo`, `cdisc_saf_aesocpt`, `cdisc_eff_resp`, `cdisc_saf_n`, `cdisc_eff_n`.

Examples

```
# ---- Example 1: Adverse-event table by SOC and Preferred Term ----
#
# The regulatory work-horse layout: AE-by-SOC/PT with the
# canonical 3-line title block (table number, description,
# population qualifier with BigN drawn inline from `cdisc_saf_n`) and a
# two-line footnote block explaining the denominator. The
# downstream pipeline hides the hierarchy markers (`row_type`,
# `soc_n`, `n_total`) but keeps them in the data so `sort_rows()`
# can arrange SOCs and PTs in descending order of subject count.
# The dataset already ships `n_total` and `soc_n`; here we slice to
# the overall row plus the two highest-incidence SOCs to keep the
# preview compact.
ae <- cdisc_saf_aesocpt
keep_soc <- head(unique(ae$soc[ae$row_type == "soc"]), 2L)
ae <- ae[ae$row_type == "overall" | ae$soc %in% keep_soc, ]
n <- stats::setNames(cdisc_saf_n$n, cdisc_saf_n$arm_short)

tabular(
  ae,
  titles = c(
    "Table 14.3.1",
    "Adverse Events by System Organ Class and Preferred Term",
    "Safety Population"
  ),
  footnotes = c(
    "Subjects are counted once per SOC and once per PT.",
    "Percentages based on N per treatment group."
  )
) |>
  cols(
```

```
    label    = col_spec(label = "SOC / PT", indent = "indent_level"),
    soc      = col_spec(visible = FALSE),
    soc_n    = col_spec(visible = FALSE),
    row_type = col_spec(visible = FALSE),
    n_total  = col_spec(visible = FALSE),
    placebo  = col_spec(label = "Placebo\nN={n['placebo']}"),
    drug_50  = col_spec(label = "Drug 50\nN={n['drug_50']}"),
    drug_100 = col_spec(label = "Drug 100\nN={n['drug_100']}"),
    Total    = col_spec(label = "Total\nN={n['Total']}")
  ) |>
  sort_rows(by = c("soc_n", "n_total"), descending = c(TRUE, TRUE))

# ---- Example 2: Best overall response with CDISC factor ordering ----
#
# Efficacy table where response categories must appear in CDISC
# clinical order (CR < PR < SD < NON-CR/NON-PD < PD < NE <
# MISSING), then the derived ORR / CBR / DCR rate rows, not
# alphabetical. `groupid` keeps the four sections ordered while the
# `stat_label` factor orders the response block; `sort_rows()` does
# both in one pass. `groupid` / `group_label` ride along hidden.
bor_levels <- c(
  "CR", "PR", "SD", "NON-CR/NON-PD", "PD", "NE", "MISSING",
  "ORR (CR + PR)", "CBR (CR + PR + SD)",
  "DCR (CR + PR + SD + NON-CR/NON-PD)", "95% CI (Clopper-Pearson)"
)
eff <- cdisc_eff_resp
eff$stat_label <- factor(eff$stat_label, levels = bor_levels)
ne <- stats::setNames(cdisc_eff_n$n, cdisc_eff_n$arm_short)

tabular(
  eff,
  titles = c(
    "Table 14.2.1",
    "Best Overall Response and Response Rates",
    "Efficacy Evaluable Population"
  ),
  footnotes = "Response per RECIST 1.1, investigator assessment."
) |>
  cols(
    stat_label  = col_spec(label = "Response"),
    row_type    = col_spec(visible = FALSE),
    groupid     = col_spec(visible = FALSE),
    group_label = col_spec(visible = FALSE),
    placebo     = col_spec(label = "Placebo\nN={ne['placebo']}"),
    drug_50     = col_spec(label = "Drug 50\nN={ne['drug_50']}"),
    drug_100    = col_spec(label = "Drug 100\nN={ne['drug_100']}")
  ) |>
  sort_rows(by = c("groupid", "stat_label"))

# ---- Example 3: Minimal three-line BigN table from cdisc_saf_n ----
#
# The smallest viable `tabular()` call: the bundled `cdisc_saf_n` 4-row
# BigN table, a single-line title, no footnotes. The default
```

```
# `col_spec` per column kicks in, giving sensible labels (the
# data frame's column names) and left-aligned text. Useful when
# teaching the core API shape without the clinical-context
# surface noise.
tabular(cdisc_saf_n, titles = "Safety-population BigN per arm")

# ---- Example 4: Nested vital-signs panel — two group levels ----
#
# The canonical by-visit vitals shape: each `param` nests its
# `visit` blocks, and each visit nests the statistic rows. Two
# columns carry `usage = "group"` (`param` then `visit`), so the
# engine renders two levels of nested section headers above the
# `stat_label` stub. The CDISC `paramcd` rides along as the natural
# sort key but hides at render via `col_spec(visible = FALSE)`.
# Sliced to the two blood-pressure parameters for a compact preview;
# the full 4-parameter frame nests the same way.
n <- stats::setNames(cdisc_saf_n$n, cdisc_saf_n$arm_short)
vs <- cdisc_saf_vital[cdisc_saf_vital$paramcd %in% c("DIABP", "SYSBP"), ]
tabular(
  vs,
  titles = c(
    "Table 14.4.1",
    "Summary of Vital Signs",
    "Safety Population"
  ),
  footnotes = "Statistics computed on observed cases."
) |>
  cols(
    paramcd    = col_spec(visible = FALSE),
    param      = col_spec(usage = "group", label = "Parameter"),
    visit      = col_spec(usage = "group", label = "Visit"),
    stat_label = col_spec(label = "Statistic"),
    placebo    = col_spec(
      label = "Placebo\nN={n['placebo']}",
      align = "decimal"
    ),
    drug_50    = col_spec(
      label = "Drug 50\nN={n['drug_50']}",
      align = "decimal"
    ),
    drug_100   = col_spec(
      label = "Drug 100\nN={n['drug_100']}",
      align = "decimal"
    )
  )
```

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