Package: clerkR (via r-universe)

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Title Publication-Ready Tables for Biomedical Research

Version 0.1.2

Description Transforms standard R data frames into publication-ready tables across a handful of common archetypes found in biomedical and neuroscience manuscripts: descriptive/Table 1 with group comparisons, heritability and variance components, correlation and partial correlation, regression coefficients, and simple descriptive summaries. Provides a unified rendering pipeline targeting 'gt' (Word/PDF), 'reactable' (HTML), and LaTeX outputs, with consistent theming, domain/section grouping, footnote handling for transformed variables, and FDR annotation.

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Contents

`clerk_colour` *Access a single clerkR colour by name*

Description

Convenience accessor for a single named colour from the clerkR palette.

Usage

```
clerk_colour(name)
```

Arguments

`name`	Character string. One of the named entries in `clerk_palette()`.

Value

A single hex colour string.

Examples

```
clerk_colour("navy")
clerk_colour("header_bg")
```

---

clerk_cor_example *Synthetic partial correlation results for clerkR examples*

Description

A synthetic dataset of partial correlation results (age + sex controlled) between eight predictor variables and two cognitive outcomes, designed to illustrate `tbl_correlation()`. All values are simulated and bear no relation to any real study.

Usage

```
clerk_cor_example
```

Format

A data frame with 16 rows and 5 variables:

variable Predictor variable name (character).

outcome Outcome variable name: `"tmt_time"` or `"verbal_fluency"` (character).

n Sample size for each correlation (integer).

r Partial correlation coefficient (numeric).

p Two-tailed p-value (numeric).

Source

Simulated data generated in `data-raw/clerk_cor_example.R`.

---

clerk_diverging *Build a clerkR diverging colour scale*

Description

Returns a vector of `n` hex colours interpolated along the clerkR diverging scale: dusty terracotta (`#D4907E`) — neutral off-white (`#F0EEEC`) — navy (`#293681`). Suitable for use with `gt::data_color()` or `scales::col_numeric()`.

Usage

```
clerk_diverging(n = 9, reverse = FALSE)
```

Arguments

`n`	Integer. Number of colour steps (default `9`). Use an odd number to include the neutral midpoint.
`reverse`	Logical. Reverse the scale direction (default `FALSE`, terracotta = low, navy = high).

Value

A character vector of `n` hex colour codes.

Examples

```
clerk_diverging()
clerk_diverging(n = 5)
clerk_diverging(n = 11, reverse = TRUE)
```

`clerk_example` *Synthetic example dataset for clerkR*

Description

A synthetic dataset of 300 participants with demographic, metabolic, anthropometric, cognitive, and mental health variables, designed to illustrate `tbl_descriptive()` and other `clerkR` table constructors. All values are simulated and bear no relation to any real study.

Usage

```
clerk_example
```

Format

A data frame with 300 rows and 12 variables:

sex Factor: `"Female"` / `"Male"`.

age Age in years (numeric).

hdl HDL cholesterol in mmol/L (numeric).

glucose Fasting glucose in mmol/L (numeric).

bmi Body mass index in kg/m² (numeric).

waist Waist circumference in cm (numeric).

systolic_bp Systolic blood pressure in mmHg (numeric).

tmt_time Trail Making Test completion time in seconds, log-scale analysis recommended (numeric).

verbal_fluency Verbal fluency score — number of words in 60 s (numeric).

bdi Beck Depression Inventory total score (numeric).

panas_neg PANAS negative affect subscale score (numeric).

life_satisfaction Life Satisfaction Scale total score (numeric).

Source

Simulated data generated in `data-raw/clerk_example.R`.

`clerk_h2_example` *Synthetic heritability estimates for clerkR examples*

Description

A synthetic data frame of narrow-sense heritability (h^2) estimates for three cortical shape metrics across four covariate models, designed to illustrate `tbl_heritability()`. Column names match the output of `R-itable::herit_batch()` for direct compatibility. All values are simulated.

Usage

```
clerk_h2_example
```

Format

A data frame with 12 rows and 7 variables:

trait Phenotype name (character).

covariates Covariate model label (character).

h2 Narrow-sense heritability point estimate (numeric).

ci_lo Lower 95% profile-likelihood CI bound (numeric).

ci_hi Upper 95% profile-likelihood CI bound (numeric).

pval One-sided LRT p-value (numeric).

sigma2_a Additive genetic variance component (numeric).

sigma2_e Residual variance component (numeric).

Source

Simulated data generated in `data-raw/clerk_h2_example.R`.

`clerk_options` *clerkR session options*

Description

`clerk_options()` gets or sets session-level formatting defaults used by all `tbl_*` constructors. Defaults are loaded automatically when the package is attached and follow biomed/APA conventions.

Call with no arguments to inspect current settings. Call with named arguments to change one or more. Call with `reset = TRUE` to restore factory defaults.

Usage

```
clerk_options(
  digits = NULL,
  r_digits = NULL,
  p_digits = NULL,
  p_threshold = NULL,
  p_style = NULL,
  stars = NULL,
  star_thresholds = NULL,
  fdr_ns = NULL,
  fdr_alpha = NULL,
  fdr_ns_label = NULL,
  domain_other = NULL,
  reset = FALSE
)
```

Arguments

`digits`	Integer. Decimal places for continuous summary statistics (default `2`).
`r_digits`	Integer. Decimal places for correlation coefficients and h^2 estimates (default `3`).
`p_digits`	Integer. Decimal places for p-values (default `3`).
`p_threshold`	Numeric. Raw p-values below this are shown as `"< {threshold}"` (default `0.001`). Display only, not a significance threshold.
`p_style`	Character string controlling p-value display style:
	`"apa"` APA format: `= 0.032`, `< 0.001` (default).
	`"plain"` Plain decimal: `0.032`, `< 0.001`.
	`"stars"` Significance stars only, no numeric p.
	`"stars_p"` Stars alongside numeric p.
`stars`	Logical. Append significance stars (default `FALSE`).
`star_thresholds`	Numeric vector of length 3. Cutoffs for `*`, `**`, `***` (default `c(0.05, 0.01, 0.001)`).

`fdr_ns`	Logical. Replace the FDR p-value cell with `fdr_ns_label` when `p(FDR) >= fdr_alpha` (default `TRUE`).
`fdr_alpha`	Numeric. Alpha applied to the BH-adjusted p-value. Cells where `p(FDR) >= fdr_alpha` show `fdr_ns_label` (default `0.05`).
`fdr_ns_label`	Character string for non-surviving FDR cells (default `"ns"`).
`domain_other`	Character string used as the domain label for variables not assigned to any domain, and for all variables when no domains are specified. Default `""` (blank — no section header shown). Set to e.g. `"Other"` to collect unassigned variables under a named section.
`reset`	Logical. Restore factory defaults (default `FALSE`).

Value

A named list of current option values, returned invisibly.

Examples

```
clerk_options()
clerk_options(p_style = "apa", stars = TRUE)
clerk_options(fdr_alpha = 0.01)
clerk_options(domain_other = "Other")
clerk_options(reset = TRUE)
```

`clerk_palette` *clerkR colour palette*

Description

Returns the named clerkR colour palette as a character vector of hex codes. Individual colours can be accessed by name via `clerk_colour()`.

The palette pairs a formal cool-blue range (navy → light teal → near-white) with a dusty terracotta warm pole for diverging scales.

Usage

```
clerk_palette()
```

Value

A named character vector of hex codes.

Examples

```
clerk_palette()
clerk_palette()[["header_bg"]]
```

clerk_reg_example *Synthetic regression results for clerkR examples*

Description

A synthetic data frame of linear regression results (outcome: log TMT completion time) designed to illustrate `tbl_regression()`. Mimics the output of `broom::tidy(lm(...), conf.int = TRUE)`. All values are simulated.

Usage

```
clerk_reg_example
```

Format

A data frame with 7 rows and 6 variables:

term Model term / predictor name (character).

estimate Regression coefficient (numeric).

std.error Standard error of the estimate (numeric).

conf.low Lower 95% confidence interval bound (numeric).

conf.high Upper 95% confidence interval bound (numeric).

p.value Two-tailed p-value (numeric).

Source

Simulated data generated in `data-raw/clerk_reg_example.R`.

clerk_render *Render a clerk_tbl to its target output format*

Description

Dispatches to the correct renderer based on the `output` slot set at construction time (`tbl_descriptive(..., output = "gt"|"html"|"latex")`). All render arguments (`title`, `subtitle`, `footnote`) can be supplied here and are forwarded to the underlying renderer.

Usage

```
clerk_render(
  x,
  title = NULL,
  subtitle = NULL,
  footnote = NULL,
  fdr_footnote = TRUE,
  ...
)
```

Arguments

x	A clerk_tbl object.
title	Optional character string for the table title.
subtitle	Optional character string for the table subtitle.
footnote	Optional additional footnote text. Appended after any automatic footnotes (log-transform, FDR).
fdr_footnote	Logical. Automatically add a source note explaining the FDR correction when a p_fdr column is present (default TRUE).
...	Passed to the underlying render_gt(), render_reactable(), or render_latex().

Value

A gt_tbl, htmltools::tagList, or knit_asis object depending on the output slot of x.

Examples

```
tbl_descriptive(clerk_example, group = sex, output = "gt", fdr = TRUE) |>
  clerk_render(title = "Table 1")

tbl_descriptive(clerk_example, group = sex, output = "html") |>
  clerk_render(title = "Sample characteristics")
```

---

clerk_sequential *Build a clerkR sequential colour scale*

Description

Returns a vector of n hex colours interpolated along the clerkR sequential scale: near-white (#D0E7E6) → navy (#293681). Suitable for shading columns by magnitude (e.g. heritability h^2, correlation r).

Usage

```
clerk_sequential(n = 7, reverse = FALSE)
```

Arguments

n	Integer. Number of colour steps (default 7).
reverse	Logical. Reverse the scale direction (default FALSE, light = low, dark = high).

Value

A character vector of n hex colour codes.

Examples

```
clerk_sequential()
clerk_sequential(n = 5, reverse = TRUE)
```

---

clerk_theme *Apply the clerkR gt theme to a gt table*

Description

Applies the clerkR visual style to an existing `gt_tbl` object: light teal column headers with navy text, near-white row group bars, clean borders, and consistent typography. Can be applied after any `gt` pipeline.

This function is called automatically by `render_gt()` and `render_latex()`; you only need it directly if you are building a `gt` table outside of the `tbl_*` constructors.

Usage

```
clerk_theme(gt_tbl)
```

Arguments

`gt_tbl`	A `gt_tbl` object.

Value

A `gt_tbl` object with clerkR styling applied.

Examples

```
## Not run:
gt::gt(mtcars) |> clerk_theme()

## End(Not run)
```

---

render_gt *Render a clerk_tbl as a gt table (Word / PDF)*

Description

Renders a `clerk_tbl` as a `gt` table with clerkR styling applied via `clerk_theme()`. Domain groupings become row-group labels; log-transformed variables receive an automatic footnote; FDR-corrected tables receive an automatic source note. Typically called indirectly via `clerk_render()`.

Usage

```
render_gt(
  x,
  title = NULL,
  subtitle = NULL,
  footnote = NULL,
  fdr_footnote = TRUE,
  ...
)
```

Arguments

x	A clerk_tbl object.
title	Optional table title.
subtitle	Optional table subtitle.
footnote	Optional additional footnote.
fdr_footnote	Logical. Add an automatic FDR source note when a p_fdr column is present (default TRUE).
...	Reserved for future use.

Value

A gt_tbl object.

Examples

```
tbl_descriptive(clerk_example, group = sex) |>
  render_gt(title = "Table 1")
```

---

render_latex *Render a clerk_tbl as a LaTeX table*

Description

Renders a clerk_tbl as a LaTeX table via gt::as_latex(). Typically called indirectly via clerk_render().

Usage

```
render_latex(
  x,
  title = NULL,
  subtitle = NULL,
  footnote = NULL,
  fdr_footnote = TRUE,
  ...
)
```

Arguments

x	A clerk_tbl object.
title	Optional table title (used as the \caption{}).
subtitle	Optional subtitle appended to the caption.
footnote	Optional additional footnote.
fdr_footnote	Logical. Add an automatic FDR source note (default TRUE).
...	Reserved for future use.

Value

A knit_asis character object containing the LaTeX table source.

Examples

```
tbl_descriptive(clerk_example, group = sex, output = "latex") |>
  clerk_render(title = "Sample characteristics by sex")
```

---

render_reactable *Render a clerk_tbl as an interactive HTML table*

Description

Renders a clerk_tbl as a reactable interactive HTML table with optional title and subtitle rendered above the widget. Typically called indirectly via clerk_render().

Usage

```
render_reactable(x, title = NULL, subtitle = NULL, footnote = NULL, ...)
```

Arguments

x	A clerk_tbl object.
title	Optional character string displayed as a heading above the table.
subtitle	Optional character string displayed as a subheading.
footnote	Optional character string displayed as a note below the table.
...	Passed to reactable::reactable().

Value

An htmltools::tagList containing the title, reactable widget, and optional footnote, or a bare reactable if no title/subtitle/footnote are provided.

Examples

```
tbl_correlation(clerk_cor_example, output = "html") |>
  clerk_render(title = "Partial correlations", subtitle = "age + sex controlled")
```

`tbl_correlation` *Correlation / partial correlation table*

Description

Formats a tidy data frame of (partial) correlation results into a publication-ready table. Column-name arguments accept character strings. Defaults match a typical correlation results frame with columns named `variable`, `outcome`, `r`, and `p`.

Formatting defaults are inherited from `clerk_options()` and can be overridden per call.

Usage

```
tbl_correlation(
  data,
  predictor = "variable",
  outcome = "outcome",
  r = "r",
  p = "p",
  n = NULL,
  extra_cols = NULL,
  domains = list(),
  fdr = FALSE,
  fdr_within = NULL,
  r_digits = NULL,
  p_digits = NULL,
  p_threshold = NULL,
  p_style = NULL,
  stars = NULL,
  fdr_ns = NULL,
  fdr_alpha = NULL,
  domain_other = NULL,
  pivot = FALSE,
  output = c("gt", "html", "latex")
)
```

Arguments

`data`	A tidy data frame of correlation results.
`predictor`	Character string. Predictor column name. Default `"variable"`.
`outcome`	Character string. Outcome column name. Default `"outcome"`.
`r`	Character string. Correlation coefficient column. Default `"r"`.
`p`	Character string. P-value column. Default `"p"`.
`n`	Character string or `NULL`. Sample size column. Default `NULL`.
`extra_cols`	Character vector of additional columns to carry through.
`domains`	A named list mapping predictor names to domain/section labels.

fdr	Logical. Apply BH FDR correction (default FALSE).
fdr_within	Character string or NULL. Column to group FDR within.
r_digits	Integer. Decimal places for r.
p_digits	Integer. Decimal places for p-values.
p_threshold	Numeric. P-values below this are shown as "< {threshold}". Inherits from clerk_options()$p_threshold if NULL.
p_style	Character. P-value style.
stars	Logical. Append significance stars.
fdr_ns	Logical. Replace non-surviving FDR p-values with "ns".
fdr_alpha	Numeric. Alpha level for FDR survival (BH-adjusted p).
domain_other	Character string. Label for variables not assigned to any domain. Default "" (blank). Inherits from clerk_options()$domain_other.
pivot	Logical. Pivot to wide format (default FALSE).
output	Character string. One of "gt" (default), "html", or "latex".

Value

A clerk_tbl object with type "correlation".

Examples

```
tbl_correlation(
  clerk_cor_example,
  domains = list(
    "Metabolic"      = c("hdl", "glucose", "bmi"),
    "Anthropometric" = c("waist", "systolic_bp"),
    "Mental health"  = c("bdi", "panas_neg")
  ),
  fdr    = TRUE,
  output = "gt"
) |> clerk_render(title = "Partial correlations (age + sex controlled)")
```

---

tbl_descriptive *Descriptive summary table with group comparisons (Table 1)*

Description

Produces a descriptive/Table 1-style summary of a data frame, with optional group comparisons. Formatting defaults are inherited from clerk_options().

Usage

```
tbl_descriptive(
  data,
  group = NULL,
  vars = NULL,
  domains = list(),
  log_vars = character(0),
  digits = NULL,
  p_digits = NULL,
  p_threshold = NULL,
  p_style = NULL,
  stars = NULL,
  fdr = FALSE,
  fdr_ns = NULL,
  fdr_alpha = NULL,
  domain_other = NULL,
  overall = TRUE,
  output = c("gt", "html", "latex")
)
```

Arguments

`data`	A data frame.
`group`	<tidy-select> Grouping variable.
`vars`	<tidy-select> Variables to include. Defaults to all columns except `group`.
`domains`	A named list mapping variable names to domain/section labels.
`log_vars`	Character vector of log-transformed variable names.
`digits`	Integer. Decimal places for continuous variables.
`p_digits`	Integer. Decimal places for p-values.
`p_threshold`	Numeric. P-values below this are shown as `"< {threshold}"`. Inherits from `clerk_options()$p_threshold` if `NULL`.
`p_style`	Character. P-value style (`"apa"`, `"plain"`, `"stars"`, `"stars_p"`).
`stars`	Logical. Append significance stars.
`fdr`	Logical. Apply BH FDR correction (default `FALSE`).
`fdr_ns`	Logical. Replace non-surviving FDR p-values with `"ns"`.
`fdr_alpha`	Numeric. Alpha level for FDR survival (BH-adjusted p).
`domain_other`	Character string. Label for variables not assigned to any domain. Default `""` (blank). Inherits from `clerk_options()$domain_other`.
`overall`	Logical. Include an overall column (default `TRUE`).
`output`	Character string. One of `"gt"`, `"html"`, or `"latex"`.

Value

A `clerk_tbl` object with type `"descriptive"`.

Examples

```
tbl_descriptive(
  clerk_example,
  group   = sex,
  domains = list(
    "Metabolic"    = c("hdl", "glucose", "bmi"),
    "Cognitive"    = c("tmt_time", "verbal_fluency"),
    "Mental health"= c("bdi", "panas_neg")
  ),
  log_vars = "tmt_time",
  output   = "gt"
) |> clerk_render(title = "Table 1. Sample characteristics by sex")
```

---

tbl_heritability *Heritability and variance components table*

Description

Formats a tidy data frame of narrow-sense heritability estimates (h2) into a publication-ready table. Column-name defaults match `R-itable::herit_batch()` output directly. Formatting defaults inherited from `clerk_options()`.

Usage

```
tbl_heritability(
  data,
  metric = "trait",
  h2 = "h2",
  ci_low = "ci_lo",
  ci_high = "ci_hi",
  p = "pval",
  sigma2_a = NULL,
  sigma2_e = NULL,
  model = NULL,
  domains = list(),
  fdr = FALSE,
  fdr_within = NULL,
  r_digits = NULL,
  p_digits = NULL,
  p_threshold = NULL,
  p_style = NULL,
  stars = NULL,
  fdr_ns = NULL,
  fdr_alpha = NULL,
  domain_other = NULL,
  output = c("gt", "html", "latex")
)
```

Arguments

`data`	A tidy data frame with one row per trait x covariate model.
`metric`	Character string. Trait column name. Default `"trait"`.
`h2`	Character string. h2 estimate column. Default `"h2"`.
`ci_low`	Character string. Lower CI column. Default `"ci_lo"`.
`ci_high`	Character string. Upper CI column. Default `"ci_hi"`.
`p`	Character string. P-value column. Default `"pval"`.
`sigma2_a`	Character string or `NULL`. Additive genetic variance column.
`sigma2_e`	Character string or `NULL`. Residual variance column.
`model`	Character string or `NULL`. Covariate model column. Pass `"covariates"` for `herit_batch()` output.
`domains`	A named list mapping trait names to domain/section labels.
`fdr`	Logical. Apply BH FDR correction (default `FALSE`).
`fdr_within`	Character string or `NULL`. Column to group FDR within.
`r_digits`	Integer. Decimal places for h2 and variance components.
`p_digits`	Integer. Decimal places for p-values.
`p_threshold`	Numeric. P-values below this are shown as `"< {threshold}"`. Inherits from `clerk_options()$p_threshold` if `NULL`.
`p_style`	Character. P-value style.
`stars`	Logical. Append significance stars.
`fdr_ns`	Logical. Replace non-surviving FDR p-values with `"ns"`.
`fdr_alpha`	Numeric. Alpha level for FDR survival (BH-adjusted p).
`domain_other`	Character string. Label for variables not assigned to any domain. Default `""` (blank). Inherits from `clerk_options()$domain_other`.
`output`	Character string. One of `"gt"`, `"html"`, or `"latex"`.

Value

A `clerk_tbl` object with type `"heritability"`.

Examples

```
tbl_heritability(
  clerk_h2_example,
  model    = "covariates",
  sigma2_a = "sigma2_a",
  sigma2_e = "sigma2_e",
  fdr      = TRUE,
  output   = "gt"
) |> clerk_render(title = "Heritability estimates")
```

`tbl_regression` *Regression coefficients table*

Description

Formats a tidy data frame of regression results into a publication-ready table. Accepts `broom::tidy()` output directly. Formatting defaults inherited from `clerk_options()`.

Usage

```
tbl_regression(
  data,
  term = "term",
  estimate = "estimate",
  std_error = "std.error",
  conf_low = "conf.low",
  conf_high = "conf.high",
  p = "p.value",
  model = NULL,
  domains = list(),
  exponentiate = FALSE,
  fdr = FALSE,
  fdr_within = NULL,
  ci_sep = ", ",
  digits = NULL,
  p_digits = NULL,
  p_threshold = NULL,
  p_style = NULL,
  stars = NULL,
  fdr_ns = NULL,
  fdr_alpha = NULL,
  domain_other = NULL,
  output = c("gt", "html", "latex")
)
```

Arguments

`data`	A tidy data frame of regression results.
`term`	Character string. Model term column. Default `"term"`.
`estimate`	Character string. Coefficient column. Default `"estimate"`.
`std_error`	Character string. SE column. Default `"std.error"`.
`conf_low`	Character string. Lower CI column. Default `"conf.low"`.
`conf_high`	Character string. Upper CI column. Default `"conf.high"`.
`p`	Character string. P-value column. Default `"p.value"`.
`model`	Character string or `NULL`. Multiple-model column.

`domains`	A named list mapping term names to domain/section labels.
`exponentiate`	Logical. Exponentiate estimates and CIs (default `FALSE`).
`fdr`	Logical. Apply BH FDR correction (default `FALSE`).
`fdr_within`	Character string or `NULL`. Column to group FDR within.
`ci_sep`	Character string separating CI bounds (default `", "`).
`digits`	Integer. Decimal places for estimates.
`p_digits`	Integer. Decimal places for p-values.
`p_threshold`	Numeric. P-values below this are shown as `"< {threshold}"`. Inherits from `clerk_options()$p_threshold` if `NULL`.
`p_style`	Character. P-value style.
`stars`	Logical. Append significance stars.
`fdr_ns`	Logical. Replace non-surviving FDR p-values with `"ns"`.
`fdr_alpha`	Numeric. Alpha level for FDR survival (BH-adjusted p).
`domain_other`	Character string. Label for variables not assigned to any domain. Default `""` (blank). Inherits from `clerk_options()$domain_other`.
`output`	Character string. One of `"gt"`, `"html"`, or `"latex"`.

Value

A `clerk_tbl` object with type `"regression"`.

Examples

```
tbl_regression(
  clerk_reg_example,
  domains = list(
    "Cardiometabolic" = c("bmi", "waist", "systolic_bp"),
    "Mental health"   = c("bdi", "panas_neg")
  ),
  fdr    = TRUE,
  output = "gt"
) |> clerk_render(title = "Linear regression: TMT completion time")
```

`tbl_simple` *Simple descriptive summary table (no inferential tests)*

Description

Produces a concise descriptive summary — mean ± SD for continuous variables and n (%) for categorical variables — with no group comparisons or statistical tests. Formatting defaults inherited from `clerk_options()`.

Usage

```
tbl_simple(
  data,
  vars = NULL,
  domains = list(),
  log_vars = character(0),
  digits = NULL,
  domain_other = NULL,
  output = c("gt", "html", "latex")
)
```

Arguments

`data`	A data frame.
`vars`	<tidy-select> Variables to include. Defaults to all columns.
`domains`	A named list mapping variable names to domain/section labels.
`log_vars`	Character vector of log-transformed variable names.
`digits`	Integer. Decimal places for continuous variables.
`domain_other`	Character string. Label for variables not assigned to any domain. Default `""` (blank). Inherits from `clerk_options()$domain_other`.
`output`	Character string. One of `"gt"` (default), `"html"`, or `"latex"`.

Value

A `clerk_tbl` object with type `"simple"`.

Examples

```
tbl_simple(
  clerk_example,
  domains  = list(
    "Metabolic"    = c("hdl", "glucose", "bmi"),
    "Mental health"= c("bdi", "panas_neg")
  ),
  log_vars = "tmt_time",
  output   = "gt"
) |> clerk_render(title = "Descriptive statistics")
```

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