

# Package ‘mellio’

July 6, 2026

**Title** Polished, Editable Tables and Statistical Results

**Version** 1.0.1

**Description** Sends supported 'R' objects to the 'Mellio' web app and creates polished, editable statistical tables in 'R'. The 'mellio\_open' interface handles common hypothesis tests, model objects, model comparisons, descriptive summaries, tabular data, plots, and image files. The 'melliotab' interface formats data frames, model summaries, correlation matrices, and side-by-side comparison tables with APA-style numeric formatting, confidence intervals, table notes, and optional significance markers. Manual table helpers can copy or save 'melliotab' output as 'HTML', 'LaTeX', or 'Markdown' when file-based handoff is needed. Payloads include package-version metadata to support reproducible reporting and software citation.

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**URL** <https://www.mellioapp.com>, <https://github.com/NicoMel1907/mellio-r>

**BugReports** <https://github.com/NicoMel1907/mellio-r/issues>

**Depends** R (>= 4.1.0)

**Imports** gt (>= 0.10.0), jsonlite, methods, broom (>= 1.0.0), rlang (>= 1.0.0), cli (>= 3.6.0)

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## Description

mellio provides two main workflows:

## Details

- `mellio_open()` sends supported R objects to the Mellio web app. Statistical results open as Result Cards, tabular data opens in the Tables workspace, and supported plots or image files open in Figures.
- `melliotab()` creates polished, editable tables directly in R for data frames, model summaries, correlation matrices, and model comparisons.

## Common `mellio_open()` inputs

`mellio_open()` supports common `htest` objects such as `t.test()`, `cor.test()`, and `chisq.test()`; model objects such as `lm`, `glm`, `aov`, `lme4` mixed models, `lavaan` fits, survival models, ordinal models, and selected optional-package result classes; data frames, matrices, and base table objects; `ggplot2`, `lattice`, `htmlwidget`, recorded plot, and image-file inputs.

## Common `melliotab()` workflow

Use `melliotab(x)` to create a table, then apply table modifiers such as `mt_title()`, `mt_note()`, `mt_decimals()`, `mt_format_ci()`, `mt_sig_stars()`, `mt_spanner()`, `mt_section_title()`, and `mt_simplify_headers()`. Pass two or more model objects to `melliotab(m1, m2, ...)` to create a side-by-side model comparison table. For file-based handoff, use `mt_copy()` or `mt_save()` to copy or save a finished table as HTML, LaTeX, or Markdown.

## Quick reference

Function or option	What it does	Common values
<code>melliotab()</code>	Creates a formatted table in R	<code>style = "apa7"</code> or <code>"ieee"</code>
<code>mellio_open()</code>	Opens supported objects in Mellio	Models, tests, tables, data, plots
<code>style / mt_set_style()</code>	Sets or changes table style	<code>"apa7"</code> , <code>"ieee"</code>
<code>title / mt_title()</code>	Sets the table title	Text
<code>number / mt_number()</code>	Sets the table number	Number or text
<code>note / mt_note()</code>	Adds a table note	Text
<code>source / mt_source()</code>	Adds source text	Text
<code>decimals, p_decimals / mt_decimals()</code>	Controls rounding	<code>decimals = 2</code> , <code>p_decimals = 3</code>
<code>mt_sig_stars()</code>	Adds significance stars to an existing table	<code>remove_p = TRUE</code> or <code>FALSE</code>
<code>mt_remove_leading_zeros()</code>	Controls leading zeros	<code>TRUE</code> , <code>FALSE</code>
<code>mt_diagonal()</code>	Formats correlation matrices	<code>mode = "dash"</code> ; <code>triangle = "lower"</code>
<code>mt_spanner()</code>	Adds a spanning column header	Label text and columns
<code>mt_section_title()</code>	Adds a section-title row	<code>before =</code> or <code>after =</code> a row number

mt_indent()	Indents selected rows	rows =; level = 1, 2, or 3
mt_copy() / mt_save()	Copies or saves a table	Clipboard, .html, .tex, .md

### Privacy and provenance

By default, Mellio payloads include R/package-version metadata and data fingerprints where available. Local machine details such as user name, host name, working directory, git state, and script path are not included unless you opt in with `options(mellio.provenance = "full")`. Set `options(mellio.provenance = FALSE)` to omit provenance metadata.

### Citation

Use `citation("mellio")` to get the package citation.

### Author(s)

**Maintainer:** Melih Sahin <nicomelpro@pm.me>

### See Also

[mellio\\_open\(\)](#), [melliotab\(\)](#), [mt\\_save\(\)](#), [mt\\_copy\(\)](#)

---

knit\_print.melliotab *Knit print method for R Markdown / Quarto*

---

### Description

Automatically detects the output format and uses the appropriate backend.

### Usage

```
knit_print.melliotab(x, ...)
```

### Arguments

x	A melliotab object
...	Additional arguments

### Value

knitr output

---

melliotab.mediate	<i>Create a formatted statistical table</i>
-------------------	---

---

### Description

The main entry point for melliotab. Accepts data frames, model objects, or correlation matrices and formats them according to the specified citation style. Passing two or more model objects creates a side-by-side model comparison table.

### Usage

```
## S3 method for class 'mediate'
melliotab(
  x,
  style = "apa7",
  title = NULL,
  number = NULL,
  note = NULL,
  source = NULL,
  decimals = 2L,
  p_decimals = 3L,
  ...
)

## S3 method for class 'summary.mediate'
melliotab(
  x,
  style = "apa7",
  title = NULL,
  number = NULL,
  note = NULL,
  source = NULL,
  decimals = 2L,
  p_decimals = 3L,
  ...
)

## S3 method for class 'medSummary'
melliotab(x, ..., section = NULL)

## S3 method for class 'medSummary2'
melliotab(x, ..., section = NULL)

## S3 method for class 'modmedSummary'
melliotab(x, ..., section = NULL)

## S3 method for class 'modmedSummary2'
```

```
melliotab(x, ..., section = NULL)

melliotab(x, ...)

## Default S3 method:
melliotab(x, ..., section = NULL)

## S3 method for class '`NULL`'
melliotab(x, ...)

## S3 method for class 'character'
melliotab(
  x,
  style = "apa7",
  title = NULL,
  number = NULL,
  note = NULL,
  source = NULL,
  decimals = 2L,
  p_decimals = 3L,
  ...
)

## S3 method for class 'summaryDefault'
melliotab(
  x,
  style = "apa7",
  title = NULL,
  number = NULL,
  note = NULL,
  source = NULL,
  decimals = 2L,
  p_decimals = 3L,
  ...
)

## S3 method for class 'table'
melliotab(
  x,
  style = "apa7",
  title = NULL,
  number = NULL,
  note = NULL,
  source = NULL,
  decimals = 2L,
  p_decimals = 3L,
  ...
)
```

```
## S3 method for class 'data.frame'
melliotab(
  x,
  style = "apa7",
  title = NULL,
  number = NULL,
  note = NULL,
  source = NULL,
  decimals = 2L,
  p_decimals = 3L,
  ...
)
```

```
## S3 method for class 'lm'
melliotab(
  x,
  style = "apa7",
  title = NULL,
  number = NULL,
  note = NULL,
  source = NULL,
  conf.int = TRUE,
  conf.level = 0.95,
  decimals = 2L,
  p_decimals = 3L,
  ...
)
```

```
## S3 method for class 'glm'
melliotab(
  x,
  style = "apa7",
  title = NULL,
  number = NULL,
  note = NULL,
  source = NULL,
  conf.int = TRUE,
  exponentiate = FALSE,
  decimals = 2L,
  p_decimals = 3L,
  ...
)
```

```
## S3 method for class 'aov'
melliotab(
  x,
  style = "apa7",
```

```
    title = NULL,
    number = NULL,
    note = NULL,
    source = NULL,
    decimals = 2L,
    p_decimals = 3L,
    effect_size = TRUE,
    ...
)

## S3 method for class 'htest'
melliotab(
  x,
  style = "apa7",
  title = NULL,
  number = NULL,
  note = NULL,
  source = NULL,
  decimals = 2L,
  p_decimals = 3L,
  ...
)

## S3 method for class 'matrix'
melliotab(
  x,
  style = "apa7",
  title = NULL,
  number = NULL,
  note = NULL,
  source = NULL,
  decimals = 2L,
  p_decimals = 3L,
  diagonal = "dash",
  triangle = "all",
  ...
)

## S3 method for class 'lavaan'
melliotab(
  x,
  style = "apa7",
  title = NULL,
  number = NULL,
  note = NULL,
  source = NULL,
  what = NULL,
  section = NULL,
```

```

    standardized = TRUE,
    decimals = 2L,
    p_decimals = 3L,
    ...
)

## S3 method for class 'FitDiff'
melliotab(
  x,
  style = "apa7",
  title = NULL,
  number = NULL,
  note = NULL,
  source = NULL,
  section = NULL,
  what = NULL,
  decimals = 2L,
  p_decimals = 3L,
  ...
)

## S3 method for class 'fa'
melliotab(
  x,
  style = "apa7",
  title = NULL,
  number = NULL,
  note = NULL,
  source = NULL,
  section = NULL,
  what = NULL,
  cut = 0,
  sort = FALSE,
  decimals = 2L,
  p_decimals = 3L,
  ...
)

```

### Arguments

x	A data.frame, model object (lm, glm, aov, htest), or correlation matrix
style	Citation style: "apa7" or "ieec"
title	Table title
number	Table number (integer or character)
note	Table note text
source	Table source text
decimals	Decimal places for estimates/statistics (1-4)

p_decimals	Decimal places for p-values (2-4)
...	Additional arguments passed to methods
section	Optional section selector for multi-section tables. Examples include "fit", "loadings", "paths", "covariances", "defined", "reliability", or "modification_indices" for structural model payloads; "loadings", "variance", or "fit" for EFA; and "comparison", "fit", or "diff" for FitDiff objects.
conf.int	Include confidence intervals (default TRUE)
conf.level	Confidence level (default 0.95)
exponentiate	Show exponentiated coefficients (odds ratios for logistic)
effect_size	Include effect size (eta-squared) for ANOVA
diagonal	Diagonal display: "dash" (em-dash), "one" (keep 1.00), "blank"
triangle	Which triangle to show: "all", "lower", "upper"
what	Backward-compatible alias for section in methods that previously used what. Prefer section.
standardized	Include standardized estimates (default TRUE)
cut	Minimum absolute loading to display (default 0, show all). Loadings below this threshold are shown as blank cells.
sort	Sort items by their primary loading (default FALSE)

### Value

A melliotab object

### Supported inputs

melliotab() is intended for table output inside R. It supports plain data frames, matrices, base table objects, correlation matrices, common model objects, hypothesis-test objects, and payloads created by mellio\_payload(). For objects that can produce several tables, call melliotab(x) once to see the available section choices, then request one explicitly, for example melliotab(fit, section = "loadings").

### Common modifiers

The mt\_\*() helpers are optional table modifiers. They follow the same pattern as many R table packages: create a table once, then add formatting only where needed. Common helpers include mt\_title(), mt\_note(), mt\_decimals(), mt\_format\_ci(), mt\_remove\_leading\_zeros(), mt\_sig\_stars(), mt\_spanner(), mt\_indent(), and mt\_section\_title().

Significance stars are never added by default. Use mt\_sig\_stars() only when that convention is appropriate for your manuscript, course, or journal.

### Examples

```
# From a data frame
df <- data.frame(
  Variable = c("Age", "Gender"),
  B = c(0.45, -1.23),
```

```
    SE = c(0.12, 0.34),
    t = c(3.75, -3.62),
    p = c(0.0003, 0.0004)
  )
melliotab(df, style = "apa7", title = "Regression Results")

# From a linear model
model <- lm(Ozone ~ Temp + Wind, data = airquality)
melliotab(model, style = "apa7", title = "Predictors of ozone concentration")

# Compare multiple models side by side
m1 <- lm(Ozone ~ Temp, data = airquality)
m2 <- lm(Ozone ~ Temp + Wind, data = airquality)
m3 <- lm(Ozone ~ Temp + Wind + Solar.R, data = airquality)
melliotab(
  m1, m2, m3,
  labels = c("Step 1", "Step 2", "Step 3"),
  dep.var.labels = "Ozone concentration"
)
```

---

`mellio_addin_send`*RStudio addin — Send the selected R expression to Mellio*

---

## Description

Reads the active selection in the RStudio editor, evaluates it in the global environment, and opens the result as a Result Card in the Mellio web app. The selected text is preserved as the displayed call so the saved card still says e.g. "t.test(score ~ group, data = df)" rather than the evaluated variable.

## Usage

```
mellio_addin_send()
```

## Details

Registered via `inst/rstudio/addins.dcf`. Appears in RStudio's **Addins** menu once the package is loaded.

## Value

Invisibly NULL. Side effect: opens the browser at Mellio.

## See Also

Other R bridge: [mellio\\_capture\(\)](#), [mellio\\_compare\(\)](#), [mellio\\_open\(\)](#), [mellio\\_payload\(\)](#), [mellio\\_to\\_json\(\)](#), [print.mellio\\_payload\(\)](#)

**Examples**

```

if (interactive() &&
    requireNamespace("rstudioapi", quietly = TRUE) &&
    rstudioapi::isAvailable()) {
  # Highlight t.test(extra ~ group, data = sleep) in RStudio
  # Addins menu -> Send to Mellio
  mellio_addin_send()
}

```

---

mellio\_anova\_pairwise *Recompute one-way ANOVA pairwise contrasts under a different correction*

---

**Description**

Lets the Lab switch the multiple-comparison adjustment without refitting the model: it reuses an aov object already held in the (WebR) session and runs the contrasts straight through `mellio_payload()`'s `emmGrid` method.

**Usage**

```
mellio_anova_pairwise(fit, by = NULL, adjust = "tukey")
```

**Arguments**

<code>fit</code>	A fitted one-way aov/lm object.
<code>by</code>	Optional grouping factor name; inferred from the model when NULL.
<code>adjust</code>	Multiple-comparison adjustment passed to <code>emmeans::contrast()</code> (e.g. "tukey", "bonferroni", "holm", "sidak", "fdr", "none").

**Value**

A pairwise-comparisons payload (table fields + `pairwise_forest`).

---

mellio\_capture *Capture the current graphics device and open it in Mellio*

---

**Description**

Convenience wrapper for base R plots. Call after producing a base plot with `plot()`, `hist()`, `barplot()`, or another graphics function.

**Usage**

```
mellio_capture(...)
```

**Arguments**

... Arguments passed to [mellio\\_open\(\)](#), such as `title`, `number`, `note`, and `browse`.

**Value**

Invisibly, the Mellio URL string.

**See Also**

Other R bridge: [mellio\\_addin\\_send\(\)](#), [mellio\\_compare\(\)](#), [mellio\\_open\(\)](#), [mellio\\_payload\(\)](#), [mellio\\_to\\_json\(\)](#), [print.mellio\\_payload\(\)](#)

**Examples**

```
if (interactive()) {
  plot(mtcars$wt, mtcars$mpg)
  mellio_capture(
    title = "Fuel efficiency by weight",
    number = 1,
    browse = FALSE
  )
}
```

---

mellio\_compare

*Compare nested regression models as a Mellio Stats card*


---

**Description**

Builds a hierarchical-regression comparison payload from two or more nested model objects. Unlike `mellio_payload(anova(m1, m2))`, this keeps the original models available so Mellio can report model  $R^2$ , adjusted  $R^2$ ,  $\Delta R^2$ , and the nested-model F-change.

**Usage**

```
mellio_compare(..., labels = NULL, .call = NULL)
```

**Arguments**

... Nested model objects, usually `lm` objects ordered from the baseline model to the final model.

labels Optional model labels. Defaults to "Model 1", "Model 2", and so on.

.call Optional call string for provenance / display.

**Value**

A `mellio_payload` object.

**See Also**

Other R bridge: [mellio\\_addin\\_send\(\)](#), [mellio\\_capture\(\)](#), [mellio\\_open\(\)](#), [mellio\\_payload\(\)](#), [mellio\\_to\\_json\(\)](#), [print.mellio\\_payload\(\)](#)

**Examples**

```
m1 <- lm(mpg ~ wt + hp, data = mtcars)
m2 <- lm(mpg ~ wt + hp + cyl, data = mtcars)
p <- mellio_compare(m1, m2)
p$type
```

---

mellio\_open

*Open a table, statistical result, or plot in Mellio*


---

**Description**

Unified entry point for sending R objects to the Mellio web app. Statistical results and tables open as Stats Result Cards; plots open in the web app's Figures editor.

**Usage**

```
mellio_open(x, ..., browse = TRUE, .call = NULL)
```

**Arguments**

x	An R object supported by Mellio.
...	Additional arguments forwarded to the relevant Mellio constructor or payload method.
browse	Open the browser? TRUE by default. Set FALSE to return the URL without launching anything.
.call	Internal captured user call for provenance.

**Value**

Invisibly, the URL string.

**Supported inputs**

mellio\_open() routes objects by class:

- Statistical results such as `htest`, `lm`, `glm`, `aov`, `lavaan`, `mixed-model`, `survival`, `ordinal`, `mediation`, and selected optional-package result classes open as structured Result Cards.
- Data frames, matrices, base table objects, and non-statistical `melliotab` objects open in the Tables workspace.
- `ggplot2`, `lattice`, `htmlwidget`, recorded plot, and supported image-file inputs open in Figures.

Optional model and figure integrations use packages listed in `Suggests`. If an optional package is not installed, the corresponding object class is skipped or reported with an informative message.

### Privacy and destination

`mellio_open()` opens `https://www.mellioapp.com` by default. Advanced users can set `options(mellio.editor_url = "https://...")`, but should only use a trusted Mellio deployment. The R payload is encoded in the URL fragment. URL fragments are not sent as HTTP requests to the server, but the full URL can still be visible to the browser, the opened web app, browser history, extensions, and anyone the URL is shared with.

By default, Mellio payloads include R/package-version metadata and data fingerprints where available. Local machine details are opt-in: `options(mellio.provenance = "full")`. To omit provenance metadata, use `options(mellio.provenance = FALSE)`.

### Plot size limits

Plots are transported through the URL hash. Very large images may exceed browser URL limits; reduce width, height, or dpi, or save the image and upload it manually in Mellio.

### See Also

Other R bridge: [mellio\\_addin\\_send\(\)](#), [mellio\\_capture\(\)](#), [mellio\\_compare\(\)](#), [mellio\\_payload\(\)](#), [mellio\\_to\\_json\(\)](#), [print.mellio\\_payload\(\)](#)

### Examples

```
if (interactive()) {
  mellio_open(t.test(extra ~ group, data = sleep))

  m1 <- lm(Ozone ~ Temp, data = airquality)
  m2 <- lm(Ozone ~ Temp + Wind, data = airquality)
  m3 <- lm(Ozone ~ Temp + Wind + Solar.R, data = airquality)
  mellio_open(
    m1, m2, m3,
    labels = c("Step 1", "Step 2", "Step 3"),
    dep.var.labels = "Ozone concentration"
  )
}
```

---

`mellio_payload`*Build a Mellio Result Card payload from an R object*

---

### Description

Converts a supported R model or test object into a structured JSON payload (a "Result Card") that Mellio renders in the Stats section. Pure and offline — no network calls. Use [mellio\\_open\(\)](#) to additionally open the payload in the Mellio web app.

**Usage**

```
## S3 method for class 'aov'
mellio_payload(x, focal = NULL, controls = NULL, ..., .call = NULL)

## S3 method for class 'summary.aov'
mellio_payload(
  x,
  focal = NULL,
  controls = NULL,
  ...,
  .call = NULL,
  .env = parent.frame()
)

## S3 method for class 'aovlist'
mellio_payload(x, ..., .call = NULL)

## S3 method for class 'afex_aov'
mellio_payload(x, ..., .call = NULL)

## S3 method for class 'anova'
mellio_payload(x, focal = NULL, controls = NULL, ..., .call = NULL)

## S3 method for class 'brmsfit'
mellio_payload(x, ..., .call = NULL)

## S3 method for class 'stanreg'
mellio_payload(x, ..., .call = NULL)

## S3 method for class 'glm'
mellio_payload(
  x,
  ...,
  .call = NULL,
  focal = NULL,
  controls = NULL,
  exponentiate = FALSE,
  conf.int = TRUE,
  conf.level = 0.95
)

## S3 method for class 'rlm'
mellio_payload(x, ..., .call = NULL)

## S3 method for class 'gam'
mellio_payload(x, ..., .call = NULL)

## S3 method for class 'lme'
```

```
mellio_payload(x, ..., .call = NULL)

## S3 method for class 'glmTMB'
mellio_payload(x, ..., .call = NULL)

## S3 method for class 'kmeans'
mellio_payload(x, ..., .call = NULL)

## S3 method for class 'hclust'
mellio_payload(x, ..., .call = NULL)

## S3 method for class 'randomForest'
mellio_payload(x, ..., .call = NULL)

## S3 method for class 'coxph'
mellio_payload(x, ..., .call = NULL)

## S3 method for class 'numeric'
mellio_payload(x, name = NULL, ..., .call = NULL)

## S3 method for class 'summaryDefault'
mellio_payload(x, ..., .call = NULL)

## S3 method for class 'fa'
mellio_payload(x, ..., .call = NULL)

## S3 method for class 'principal'
mellio_payload(x, ..., .call = NULL)

## S3 method for class 'factanal'
mellio_payload(x, ..., .call = NULL)

## S3 method for class 'prcomp'
mellio_payload(x, ..., .call = NULL)

## S3 method for class 'effectsize_table'
mellio_payload(x, ..., .call = NULL)

## S3 method for class 'effectsize_difference'
mellio_payload(x, ..., .call = NULL)

## S3 method for class 'effectsize_anova'
mellio_payload(x, ..., .call = NULL)

## S3 method for class 'see_effectsize_table'
mellio_payload(x, ..., .call = NULL)

## S3 method for class 'FitDiff'
```

```
mellio_payload(x, what = NULL, ..., .call = NULL)

## S3 method for class 'geeglm'
mellio_payload(x, ..., .call = NULL)

## S3 method for class 'glmerMod'
mellio_payload(
  x,
  ...,
  .call = NULL,
  exponentiate = FALSE,
  conf.int = TRUE,
  conf.level = 0.95
)

## S3 method for class 'htest'
mellio_payload(x, .data = NULL, ..., .call = NULL, .env = parent.frame())

## S3 method for class 'lavaan'
mellio_payload(
  x,
  focal = NULL,
  diagram_omit = NULL,
  standardized = TRUE,
  ...,
  .call = NULL
)

## S3 method for class 'lm'
mellio_payload(x, focal = NULL, controls = NULL, ..., .call = NULL)

## S3 method for class 'lmerMod'
mellio_payload(x, ..., .call = NULL)

## S3 method for class 'manova'
mellio_payload(
  x,
  tests = c("Pillai", "Wilks", "Hotelling-Lawley", "Roy"),
  ...,
  .call = NULL
)

## S3 method for class 'summary.manova'
mellio_payload(x, ..., .call = NULL)

## S3 method for class 'mediate'
mellio_payload(x, ..., .call = NULL)
```

```
## S3 method for class 'summary.mediate'  
mellio_payload(x, ..., .call = NULL)  
  
## S3 method for class 'multinom'  
mellio_payload(x, ..., .call = NULL)  
  
## S3 method for class 'polr'  
mellio_payload(x, ..., .call = NULL, conf.int = TRUE, conf.level = 0.95)  
  
## S3 method for class 'clm'  
mellio_payload(x, ..., .call = NULL, conf.int = TRUE, conf.level = 0.95)  
  
## S3 method for class 'TukeyHSD'  
mellio_payload(x, ..., .call = NULL)  
  
## S3 method for class 'pairwise.htest'  
mellio_payload(x, ..., .call = NULL, .env = parent.frame())  
  
## S3 method for class 'dunn_test'  
mellio_payload(x, ..., .call = NULL)  
  
## S3 method for class 'wilcox_test'  
mellio_payload(x, ..., .call = NULL)  
  
## S3 method for class 't_test'  
mellio_payload(x, ..., .call = NULL)  
  
## S3 method for class 'dunnTest'  
mellio_payload(x, ..., .call = NULL)  
  
## S3 method for class 'dunn.test'  
mellio_payload(x, ..., .call = NULL)  
  
## S3 method for class 'emmGrid'  
mellio_payload(x, ..., .call = NULL)  
  
## S3 method for class 'emm_list'  
mellio_payload(x, ..., .call = NULL)  
  
## S3 method for class 'glht'  
mellio_payload(x, ..., .call = NULL)  
  
## S3 method for class 'summary.glht'  
mellio_payload(x, ..., .call = NULL)  
  
## S3 method for class 'medSummary'  
mellio_payload(x, ..., .call = NULL)
```

```
## S3 method for class 'medSummary2'
mellio_payload(x, ..., .call = NULL)

## S3 method for class 'modmedSummary'
mellio_payload(x, ..., .call = NULL)

## S3 method for class 'modmedSummary2'
mellio_payload(x, ..., .call = NULL)

## S3 method for class 'alpha'
mellio_payload(x, ..., .call = NULL)

## S3 method for class 'corr.test'
mellio_payload(x, ..., .call = NULL)

## S3 method for class 'character'
mellio_payload(x, title = NULL, ..., .call = NULL)

## S3 method for class 'data.frame'
mellio_payload(x, title = NULL, ..., .call = NULL)

## S3 method for class 'survfit'
mellio_payload(x, ..., .call = NULL, .env = parent.frame())

## S3 method for class 'Arima'
mellio_payload(x, ..., .call = NULL)

## S3 method for class 'forecast_ARIMA'
mellio_payload(x, ..., .call = NULL)

## S3 method for class 'ARIMA'
mellio_payload(x, ..., .call = NULL)

## S3 method for class 'ets'
mellio_payload(x, ..., .call = NULL)

## S3 method for class 'forecast'
mellio_payload(x, ..., .call = NULL)

mellio_payload(x, ...)

## S3 method for class 'mellio_payload'
mellio_payload(x, ..., .call = NULL)

## Default S3 method:
mellio_payload(x, ..., .call = NULL)

## S3 method for class '`NULL`'
```

```

mellio_payload(x, ..., .call = NULL)

## S3 method for class 'table'
mellio_payload(x, ..., .call = NULL)

## S3 method for class 'matrix'
mellio_payload(x, ..., .call = NULL)

## S3 method for class 'melliotab'
mellio_payload(x, ..., .call = NULL)

```

### Arguments

<code>x</code>	A supported R object.
<code>focal</code>	Optional character vector of model terms to mark as the focal predictor(s). Recognised by <code>lm/aov/anova</code> methods.
<code>controls</code>	Optional character vector of model terms to mark as controls (vs focal predictors) — recognised by <code>lm/aov/anova</code> methods.
<code>...</code>	Additional arguments passed to the dispatched method.
<code>.call</code>	Internal — captured user call, used to attribute provenance to the calling script rather than this dispatch.
<code>.env</code>	Optional environment used when recovering source variables for supported test objects.
<code>exponentiate</code>	Logical. For GLM-style models, exponentiate coefficient estimates (for example, odds ratios in logistic models).
<code>conf.int</code>	Logical. Include coefficient confidence intervals when supported by the broom method.
<code>conf.level</code>	Confidence level for coefficient intervals.
<code>name</code>	Optional name to attach to the payload (used by the numeric/vector descriptive method).
<code>what</code>	Optional <code>FitDiff</code> table to extract: "comparison", "fit", or "diff". Defaults to the first available table.
<code>.data</code>	Optional <code>data.frame</code> to enrich supported <code>htest</code> results with observed descriptives, effect sizes, and figure data. When omitted, Mellio tries to recover simple source variables from the calling environment before falling back to test-only output.
<code>diagram_omit</code>	Optional character vector of parameter keys or variable names to omit from the generated SEM path diagram while retaining them in diagram metadata. Use exact path keys like "y ~ ideology" or a variable name like "ideology" for hidden covariate-style paths.
<code>standardized</code>	Include standardized estimates and standardized-solution metadata when available.
<code>tests</code>	Multivariate test statistics to extract (manova method). Defaults to all four classical tests.
<code>title</code>	Optional title override ( <code>psych/character/data.frame</code> methods).

**Details**

Supported in v0: objects of class `htest` (`t.test`, `cor.test`, `wilcox.test`, `chisq.test`, `fisher.test`).

Schema: see `docs/STATS-R-BRIDGE-SCHEMA.md` in the repo. The payload is value-only: numeric statistics, p-values, and CIs go through unformatted; the Mellio web app applies citation-style rules (decimals, italics, leading zeros).

**Value**

A list with class `mellio_payload`, structured according to the v0.1 schema.

**See Also**

[mellio\\_open\(\)](#) to open the result in Mellio. [mellio\\_to\\_json\(\)](#) to serialise the payload offline.

Other R bridge: [mellio\\_addin\\_send\(\)](#), [mellio\\_capture\(\)](#), [mellio\\_compare\(\)](#), [mellio\\_open\(\)](#), [mellio\\_to\\_json\(\)](#), [print.mellio\\_payload\(\)](#)

**Examples**

```
tt <- t.test(extra ~ group, data = sleep)
p <- mellio_payload(tt)
p$type
p$fields$statistic
```

---

mellio\_to\_json

*Serialise a Mellio payload to JSON*


---

**Description**

Serialise a Mellio payload to JSON

**Usage**

```
mellio_to_json(payload, pretty = FALSE)
```

**Arguments**

payload	A <code>mellio_payload</code> object from <a href="#">mellio_payload()</a> .
pretty	Pretty-print with line breaks (default FALSE).

**Value**

A length-1 character vector containing the JSON.

**See Also**

[mellio\\_payload\(\)](#) to build the payload, [mellio\\_open\(\)](#) to send it directly to the Mellio web app.

Other R bridge: [mellio\\_addin\\_send\(\)](#), [mellio\\_capture\(\)](#), [mellio\\_compare\(\)](#), [mellio\\_open\(\)](#), [mellio\\_payload\(\)](#), [print.mellio\\_payload\(\)](#)

**Examples**

```
p <- mellio_payload(t.test(extra ~ group, data = sleep))
cat(mellio_to_json(p, pretty = TRUE))
```

---

mt_as_gt	<i>Convert a melliotab object to a gt table</i>
----------	---

---

**Description**

Convert a melliotab object to a gt table

**Usage**

```
mt_as_gt(x)
```

**Arguments**

x                    A melliotab object

**Value**

A gt table object

---

mt_as_html	<i>Get HTML string from a melliotab object</i>
------------	--

---

**Description**

Produces a standalone HTML fragment with the title rendered above the table (outside the gt borders), matching the viewer layout.

**Usage**

```
mt_as_html(x)
```

**Arguments**

x                    A melliotab object

**Value**

Character string of HTML

---

mt_as_latex	<i>Convert a melliotab object to LaTeX</i>
-------------	--

---

**Description**

Convert a melliotab object to LaTeX

**Usage**

```
mt_as_latex(x)
```

**Arguments**

x                    A melliotab object

**Value**

Character string of LaTeX code

---

mt_as_markdown	<i>Convert a melliotab object to Markdown</i>
----------------	---

---

**Description**

Convert a melliotab object to Markdown

**Usage**

```
mt_as_markdown(x)
```

**Arguments**

x                    A melliotab object

**Value**

Character string of Markdown table

---

mt_copy	<i>Copy a melliotab table to the system clipboard</i>
---------	---

---

**Description**

Copies the formatted table to the clipboard as rich HTML so it can be pasted into Word with formatting preserved.

**Usage**

```
mt_copy(x)
```

**Arguments**

x                    A melliotab object

**Value**

Invisible melliotab object (for piping)

**Examples**

```
if (interactive()) {  
  model <- lm(mpg ~ wt + hp, data = mtcars)  
  tab <- melliotab(model, title = "Regression Results")  
  mt_copy(tab)  
  # Now paste into Word  
}
```

---

mt_decimals	<i>Set decimal places</i>
-------------	---------------------------

---

**Description**

Set decimal places

**Usage**

```
mt_decimals(x, decimals = 2L, p_decimals = 3L)
```

**Arguments**

x                    A melliotab object  
decimals            Decimal places for estimates/statistics  
p\_decimals          Decimal places for p-values

**Value**

Modified melliottab object

---

mt_diagonal	<i>Set correlation matrix display options</i>
-------------	---

---

**Description**

Set correlation matrix display options

**Usage**

```
mt_diagonal(
  x,
  mode = c("dash", "one", "blank"),
  triangle = c("all", "lower", "upper")
)
```

**Arguments**

x	A melliottab object
mode	Diagonal display: "dash", "one", "blank"
triangle	Triangle to show: "all", "lower", "upper"

**Value**

Modified melliottab object

---

mt_format_ci	<i>Format confidence intervals</i>
--------------	------------------------------------

---

**Description**

Format confidence intervals

**Usage**

```
mt_format_ci(x, decimals = NULL, bracket = TRUE)
```

**Arguments**

x	A melliottab object
decimals	Decimal places for CI values (NULL uses table default)
bracket	Whether to use bracket notation

**Value**

Modified melliottab object

---

mt_indent	<i>Indent row labels</i>
-----------	--------------------------

---

**Description**

Indent row labels

**Usage**

```
mt_indent(x, rows, level = 1L)
```

**Arguments**

x	A melliottab object
rows	Row indices to indent
level	Indentation level (1-3)

**Value**

Modified melliottab object

---

mt_note	<i>Set table note</i>
---------	-----------------------

---

**Description**

Set table note

**Usage**

```
mt_note(x, note)
```

**Arguments**

x	A melliottab object
note	Note text

**Value**

Modified melliottab object

mt\_number                    *Set table number*

---

**Description**

Set table number

**Usage**

```
mt_number(x, number)
```

**Arguments**

x	A melliotab object
number	Table number

**Value**

Modified melliotab object

---

mt\_remove\_leading\_zeros  
*Control leading zero removal*

---

**Description**

Control leading zero removal

**Usage**

```
mt_remove_leading_zeros(x, enabled = TRUE)
```

**Arguments**

x	A melliotab object
enabled	Whether to remove leading zeros

**Value**

Modified melliotab object

---

mt_save	<i>Save a melliotab table to file</i>
---------	---------------------------------------

---

**Description**

Auto-detects the format from the file extension.

**Usage**

```
mt_save(x, filename, ...)
```

**Arguments**

x	A melliotab object
filename	Output file path. Supported extensions: .html, .tex, .md
...	Additional arguments passed to format-specific functions

**Value**

Invisible file path

**Examples**

```
model <- lm(mpg ~ wt + hp, data = mtcars)
tbl <- melliotab(model, style = "apa7", title = "Results")

html_file <- tempfile(fileext = ".html")
tex_file <- tempfile(fileext = ".tex")
md_file <- tempfile(fileext = ".md")

mt_save(tbl, html_file)
mt_save(tbl, tex_file)
mt_save(tbl, md_file)
```

---

mt_section_title	<i>Add a section title row</i>
------------------	--------------------------------

---

**Description**

Add a section title row

**Usage**

```
mt_section_title(x, label, before = NULL, after = NULL)
```

**Arguments**

x	A melliottab object
label	Section title text
before	Row index to insert before
after	Row index to insert after

**Value**

Modified melliottab object

---

mt_set_style	<i>Change the citation style</i>
--------------	----------------------------------

---

**Description**

Change the citation style

**Usage**

```
mt_set_style(x, style = c("apa7", "ieee"))
```

**Arguments**

x	A melliottab object
style	Style name: "apa7" or "ieee"

**Value**

Modified melliottab object

---

mt_sig_stars	<i>Add significance stars</i>
--------------	-------------------------------

---

**Description**

Add significance stars

**Usage**

```
mt_sig_stars(
  x,
  target = "auto",
  remove_p = TRUE,
  levels = c(`*` = 0.05, `**` = 0.01, `***` = 0.001)
)
```

**Arguments**

x	A melliottab object
target	Column to add stars to ("auto" to detect)
remove_p	Whether to remove the p-value column
levels	Named vector of significance thresholds

**Value**

Modified melliottab object

---

mt\_simplify\_headers     *Simplify SPSS verbose headers*

---

**Description**

Simplify SPSS verbose headers

**Usage**

mt\_simplify\_headers(x)

**Arguments**

x	A melliottab object
---	---------------------

**Value**

Modified melliottab object

---

mt\_source                 *Set table source*

---

**Description**

Set table source

**Usage**

mt\_source(x, source)

**Arguments**

x	A melliottab object
source	Source text

**Value**

Modified melliottab object

---

mt_spanner	<i>Add a spanning column header</i>
------------	-------------------------------------

---

**Description**

Add a spanning column header

**Usage**

```
mt_spanner(x, label, columns, level = 1L)
```

**Arguments**

x	A melliottab object
label	Spanner label text
columns	Column indices or names covered by the spanner
level	Spanner level (1 = closest to data)

**Value**

Modified melliottab object

---

mt_title	<i>Set table title</i>
----------	------------------------

---

**Description**

Set table title

**Usage**

```
mt_title(x, title)
```

**Arguments**

x	A melliottab object
title	Title text

**Value**

Modified melliottab object

---

print.melliotab      *Print a melliotab object*

---

**Description**

Renders the table in the RStudio Viewer pane (or browser).

**Usage**

```
## S3 method for class 'melliotab'  
print(x, ...)
```

**Arguments**

x	A melliotab object
...	Ignored

**Value**

Invisible melliotab object

---

print.mellio\_payload      *Print method for Mellio payloads*

---

**Description**

Compact summary of a mellio\_payload object. Use [mellio\\_to\\_json\(\)](#) to see the full structure or [str\(\)](#) to inspect the field tree.

**Usage**

```
## S3 method for class 'mellio_payload'  
print(x, ...)
```

**Arguments**

x	A mellio_payload object.
...	Unused.

**Value**

Invisibly returns x.

**See Also**

Other R bridge: [mellio\\_addin\\_send\(\)](#), [mellio\\_capture\(\)](#), [mellio\\_compare\(\)](#), [mellio\\_open\(\)](#), [mellio\\_payload\(\)](#), [mellio\\_to\\_json\(\)](#)

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