Advanced Features: zztab2fig

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zztab2fig v0.2.0 introduced substantial enhancements for publication-quality table formatting. This vignette demonstrates the advanced capabilities that distinguish zztab2fig from simpler table packages:

- **Table footnotes** with multiple notation types (general, numbered, alphabetic, symbol)
- **Spanning headers** for grouped column layouts common in clinical tables
- **Multi-row cells** for hierarchical data presentation
- **Decimal alignment** via siunitx integration
- **LaTeX figure placement helpers** for precise document integration

These features address requirements frequently encountered in medical, scientific, and social science publications.

Setup

```
library(zztab2fig)
```

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1. Table Footnotes

Professional tables often require footnotes to explain abbreviations, provide context, or indicate significance levels. zztab2fig provides full footnote support via the `t2f_footnote()` function.

Basic Footnotes

```
results <- data.frame(
  Variable = c("Age", "BMI", "Systolic BP", "HbA1c"),
  Treatment = c("52.3 (8.2)", "28.1 (4.3)", "142.5 (18.3)", "7.2 (1.1)"),
  Control = c("51.8 (7.9)", "27.9 (4.1)", "140.2 (17.1)", "7.4 (1.2)"),
  `P-value` = c("0.542", "0.631", "0.048", "0.089"),
  check.names = FALSE
)

fn <- t2f_footnote(
  general = c(
    "Values are mean (SD) unless otherwise noted.",
    "BMI = body mass index; BP = blood pressure; HbA1c = hemoglobin A1c."
  )
)

t2f(results,
    filename = "baseline_characteristics",
    sub_dir = output_dir,
    caption = "Baseline Characteristics by Treatment Group",
```

```
    footnote = fn,
    theme = "nejm")
```

Table 1: Baseline Characteristics by Treatment Group

Variable	Treatment	Control	P_value
Age	52.3 (8.2)	51.8 (7.9)	0.542
BMI	28.1 (4.3)	27.9 (4.1)	0.631
Systolic BP	142.5 (18.3)	140.2 (17.1)	0.048
HbA1c	7.2 (1.1)	7.4 (1.2)	0.089

Note:
Values are mean (SD) unless otherwise noted.
BMI = body mass index; BP = blood pressure;
HbA1c = hemoglobin A1c.

Multiple Footnote Types (APA Style)

APA format requires specific footnote organization: general notes, then specific notes, then probability notes.

```
anova_results <- data.frame(
  Source = c("Treatment", "Time", "Treatment x Time", "Error"),
  SS = c(245.32, 189.45, 52.18, 1024.56),
  df = c(2, 3, 6, 108),
  MS = c(122.66, 63.15, 8.70, 9.49),
  F = c(12.93, 6.66, 0.92, NA),
  p = c("<0.001", "0.002", "0.485", NA)
)

anova_results$F[1] <- t2f_mark("12.93", 1, "symbol")
anova_results$F[2] <- t2f_mark("6.66", 2, "symbol")

fn_apa <- t2f_footnote(
  general = "SS = sum of squares; MS = mean square.",
  symbol = c("p < .001", "p < .01"),
  title_general = "Note.",
  title_symbol = NULL,
  footnote_as_chunk = TRUE
)

t2f(anova_results,
    filename = "anova_table",
    sub_dir = output_dir,
    caption = "Analysis of Variance Results",
    footnote = fn_apa,
    theme = "apa")
```

Table 1: Analysis of Variance Results

Source	SS	df	MS	F	p
Treatment	245.32	2	122.66	12.93*	<0.001
Time	189.45	3	63.15	6.66†	0.002
Treatment x Time	52.18	6	8.70	0.92	0.485
Error	1024.56	108	9.49	NA	NA

Note. SS = sum of squares; MS = mean square. * p ¡ .001 † p ¡ .01

Numbered Footnotes for Specific Cells

```
endpoints <- data.frame(
  Endpoint = c("Primary: ADAS-Cog14", "Secondary: CDR-SB",
               "Secondary: ADCS-ADL", "Exploratory: Brain Volume"),
  Difference = c("-0.45", "-0.21", "0.18", "-2.1%"),
  CI = c("(-0.82, -0.08)", "(-0.39, -0.03)", "(-0.15, 0.51)",
         "(-3.8%, -0.4%)"),
  P = c("0.018", "0.024", "0.285", "0.016")
)

endpoints$Endpoint[1] <- t2f_mark(endpoints$Endpoint[1], 1, "number")
endpoints$Difference[4] <- t2f_mark(endpoints$Difference[4], 2, "number")

fn_numbered <- t2f_footnote(
  number = c(
    "Co-primary endpoint with CDR-SB.",
    "Percentage change from baseline in whole brain volume."
  )
)

t2f(endpoints,
    filename = "endpoints_table",
    sub_dir = output_dir,
    caption = "Efficacy Endpoints at Week 78",
    footnote = fn_numbered,
    theme = "nejm")
```

Table 1: Efficacy Endpoints at Week 78

Endpoint	Difference	CI	P
Primary: ADAS-Cog14[1]	-0.45	(-0.82, -0.08)	0.018
Secondary: CDR-SB	-0.21	(-0.39, -0.03)	0.024
Secondary: ADCS-ADL	0.18	(-0.15, 0.51)	0.285
Exploratory: Brain Volume	-2.1%[2]	(-3.8%, -0.4%)	0.016

[1] Co-primary endpoint with CDR-SB.
[2] Percentage change from baseline in whole brain volume.

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2. Spanning Headers (Grouped Columns)

Spanning headers group related columns under a common label, essential for complex tables comparing multiple conditions or timepoints.

Basic Spanning Header

```
comparison <- data.frame(
  Measure = c("Score A", "Score B", "Score C"),
  T_Mean = c(23.4, 18.7, 42.1),
  T_SD = c(5.2, 3.8, 8.9),
  C_Mean = c(21.2, 19.1, 38.5),
  C_SD = c(4.9, 4.1, 9.2)
)
names(comparison) <- c("Measure", "Mean", "SD", "Mean", "SD")

hdr <- t2f_header_above(
  " " = 1,
  "Treatment" = 2,

  "Control" = 2
)

t2f(comparison,
    filename = "treatment_comparison",
    sub_dir = output_dir,
    caption = "Treatment vs Control Outcomes",
    header_above = hdr)
```

Table 1: Treatment vs Control Outcomes

	Treatment		Control	
Measure	**Mean**	**SD**	**Mean**	**SD**
Score A	23.4	5.2	21.2	4.9
Score B	18.7	3.8	19.1	4.1
Score C	42.1	8.9	38.5	9.2

Multiple Header Rows

```
longitudinal <- data.frame(
  Variable = c("Cognitive", "Functional", "Behavioral"),
  W12_T = c(-1.2, -0.8, -0.3),
  W12_C = c(-0.9, -0.6, -0.2),
  W24_T = c(-2.1, -1.5, -0.5),
  W24_C = c(-1.4, -1.0, -0.3),
  W52_T = c(-3.8, -2.8, -0.9),
  W52_C = c(-2.2, -1.8, -0.5)
)
names(longitudinal) <- c("Domain", "Trt", "Ctrl", "Trt", "Ctrl", "Trt", "Ctrl")

headers <- list(
  t2f_header_above(
    " " = 1,
    "Week 12" = 2,
    "Week 24" = 2,
    "Week 52" = 2
  ),
  t2f_header_above(
    " " = 1,
    "Change from Baseline" = 6,
    line = FALSE
  )
)

t2f(longitudinal,
    filename = "longitudinal_outcomes",
    sub_dir = output_dir,
    caption = "Change from Baseline by Timepoint",
    header_above = headers,
    theme = "nature")
```

Table 1: Change from Baseline by Timepoint

	Change from Baseline					
	Week 12		Week 24		Week 52	
Domain	Trt	Ctrl	Trt	Ctrl	Trt	Ctrl
Cognitive	-1.2	-0.9	-2.1	-1.4	-3.8	-2.2
Functional	-0.8	-0.6	-1.5	-1.0	-2.8	-1.8
Behavioral	-0.3	-0.2	-0.5	-0.3	-0.9	-0.5

---

3. Multi-Row Cells (Collapsed Rows)

When data has hierarchical structure, collapsing repeated values into multi-row cells improves readability.

Basic Row Collapsing

```
subgroup <- data.frame(
  Category = c("Age", "Age", "Sex", "Sex", "Race", "Race", "Race"),
  Subgroup = c("<65", ">=65", "Male", "Female", "White", "Black", "Asian"),
  N = c(245, 189, 218, 216, 312, 67, 55),
  Effect = c(0.42, 0.38, 0.41, 0.39, 0.40, 0.44, 0.36),
  CI = c("(0.28, 0.56)", "(0.22, 0.54)", "(0.27, 0.55)", "(0.24, 0.54)",
         "(0.28, 0.52)", "(0.24, 0.64)", "(0.14, 0.58)")
)

t2f(subgroup,
    filename = "subgroup_analysis",
    sub_dir = output_dir,
    caption = "Subgroup Analysis of Treatment Effect",
    collapse_rows = t2f_collapse_rows(
      columns = 1,
      valign = "top",
      latex_hline = "major"
    ))
```

Table 1: Subgroup Analysis of Treatment Effect

Category	Subgroup	N	Effect	CI
Age	<65	245	0.42	(0.28, 0.56)
Age	>=65	189	0.38	(0.22, 0.54)
Sex	Male	218	0.41	(0.27, 0.55)
Sex	Female	216	0.39	(0.24, 0.54)
Race	White	312	0.40	(0.28, 0.52)
Race	Black	67	0.44	(0.24, 0.64)
Race	Asian	55	0.36	(0.14, 0.58)

Multiple Column Collapse

```
adverse_events <- data.frame(
  System = c(rep("Nervous System", 3), rep("Gastrointestinal", 3),
             rep("General", 2)),
  Category = c("Headache", "Dizziness", "Somnolence",
               "Nausea", "Diarrhea", "Vomiting",
               "Fatigue", "Pyrexia"),
  Treatment = c(45, 32, 18, 28, 22, 15, 38, 12),
  Placebo = c(41, 28, 14, 25, 19, 12, 35, 10)
)

t2f(adverse_events,
    filename = "adverse_events",
    sub_dir = output_dir,
    caption = "Adverse Events by System Organ Class",
    collapse_rows = t2f_collapse_rows(
      columns = 1,
      valign = "middle",
      latex_hline = "major"
    ),
    theme = "nejm")
```

Table 1: Adverse Events by System Organ Class

System	Category	Treatment	Placebo
Nervous System	Headache	45	41
Nervous System	Dizziness	32	28
Nervous System	Somnolence	18	14
Gastrointestinal	Nausea	28	25
Gastrointestinal	Diarrhea	22	19
Gastrointestinal	Vomiting	15	12
General	Fatigue	38	35
General	Pyrexia	12	10

---

4. Decimal Alignment

Proper decimal alignment makes numeric tables easier to read and compare. zztab2fig provides siunitx integration for precise alignment.

Basic Decimal Alignment

```
stats <- data.frame(
  Parameter = c("Mean", "Median", "SD", "Min", "Max"),
  Treatment = c(127.45, 125.00, 18.234, 89.1, 178.92),
  Control = c(124.82, 123.50, 17.891, 91.3, 172.45)
)

t2f(stats,
    filename = "summary_stats",
    sub_dir = output_dir,
    caption = "Summary Statistics by Group",
    align = list(
      "l",
      t2f_decimal(3, 2),
      t2f_decimal(3, 2)
    ))
```

Table 1: Summary Statistics by Group

Parameter	Treatment	Control
Mean	127.450	124.820
Median	125.000	123.500
SD	18.234	17.891
Min	89.100	91.300
Max	178.920	172.450

Mixed Alignment with Custom Formats

```
coefs <- data.frame(
  Term = c("(Intercept)", "Age", "Sex (Male)", "BMI", "Smoking"),
  Estimate = c(2.345, 0.082, -0.451, 0.123, 0.892),
  SE = c(0.234, 0.015, 0.198, 0.028, 0.245),
  t = c(10.02, 5.47, -2.28, 4.39, 3.64),
  p = c("<0.001", "<0.001", "0.024", "<0.001", "<0.001")
)

t2f(coefs,
    filename = "regression_coefs",
    sub_dir = output_dir,
    caption = "Regression Coefficients",
    align = list(
      "l",
      t2f_siunitx(table_format = "1.3"),
      t2f_siunitx(table_format = "1.3"),
      t2f_siunitx(table_format = "2.2"),
      "r"
    ))
```

Table 1: Regression Coefficients

Term	Estimate	SE	t	p
(Intercept)	2.345	0.234	10.02	<0.001
Age	0.082	0.015	5.47	<0.001
Sex (Male)	-0.451	0.198	-2.28	0.024
BMI	0.123	0.028	4.39	<0.001
Smoking	0.892	0.245	3.64	<0.001

5. Short Captions

For documents with a List of Tables, short captions provide concise entries while the full caption remains with the table.

```
detailed_results <- data.frame(
  Outcome = c("Primary", "Secondary 1", "Secondary 2"),
  Estimate = c(0.45, 0.32, 0.28),
  CI = c("(0.22, 0.68)", "(0.15, 0.49)", "(0.08, 0.48)"),
  P = c("0.001", "0.012", "0.042")
)

t2f(detailed_results,
    filename = "efficacy_results",
    sub_dir = output_dir,
    caption = paste(
      "Efficacy Results from the Phase 3 Randomized Controlled Trial",
      "of Drug X versus Placebo in Patients with Moderate-to-Severe",
      "Condition Y (Modified Intention-to-Treat Population)"
    ),
    caption_short = "Efficacy Results from Phase 3 Trial",
    label = "tab:efficacy")
```

Table 1: Efficacy Results from the Phase 3 Randomized Controlled Trial of Drug X versus Placebo in Patients with Moderate-to-Severe Condition Y (Modified Intention-to-Treat Population)

Outcome	Estimate	CI	P
Primary	0.45	(0.22, 0.68)	0.001
Secondary 1	0.32	(0.15, 0.49)	0.012
Secondary 2	0.28	(0.08, 0.48)	0.042

---

6. Combining Advanced Features

Real-world tables often require multiple advanced features simultaneously.

Publication-Ready Clinical Table

```
clinical <- data.frame(
  Endpoint = c("ADAS-Cog14", "ADAS-Cog14", "CDR-SB", "CDR-SB"),
  Timepoint = c("Week 52", "Week 78", "Week 52", "Week 78"),
  N_T = c(423, 398, 423, 398),
  N_C = c(421, 395, 421, 395),
  Diff = c(-0.31, -0.45, -0.15, -0.21),
  CI_Low = c(-0.58, -0.82, -0.28, -0.39),
  CI_High = c(-0.04, -0.08, -0.02, -0.03),
  P = c("0.024", "0.018", "0.025", "0.024")
)

clinical$Diff <- sapply(seq_len(nrow(clinical)), function(i) {
  if (as.numeric(clinical$P[i]) < 0.05) {
    t2f_mark(as.character(clinical$Diff[i]), 1, "symbol")
  } else {
```

```
    as.character(clinical$Diff[i])
  }
})

hdr <- t2f_header_above(
  " " = 2,
  "N" = 2,
  "Treatment Effect" = 4
)

fn <- t2f_footnote(
  general = "Difference is treatment minus placebo (negative favors treatment).",
  symbol = "p < 0.05 vs placebo.",
  title_general = "Note:"
)

t2f(clinical,
    filename = "clinical_efficacy",
    sub_dir = output_dir,
    caption = "Efficacy Outcomes in the Modified ITT Population",
    caption_short = "Efficacy Outcomes",
    label = "tab:efficacy",
    header_above = hdr,
    footnote = fn,
    collapse_rows = t2f_collapse_rows(columns = 1, valign = "top"),
    theme = "nejm")
```

Table 1: Efficacy Outcomes in the Modified ITT Population

		N		Treatment Effect			
Endpoint	**Timepoint**	**N_T**	**N_C**	**Diff**	**CI_Low**	**CI_High**	**P**
ADAS-Cog14	Week 52	423	421	-0.31*	-0.58	-0.04	0.024
ADAS-Cog14	Week 78	398	395	-0.45*	-0.82	-0.08	0.018
CDR-SB	Week 52	423	421	-0.15*	-0.28	-0.02	0.025
CDR-SB	Week 78	398	395	-0.21*	-0.39	-0.03	0.024

Note:
Difference is treatment minus placebo (negative favors treatment).
* p ¡ 0.05 vs placebo.

---

7. LaTeX Figure Placement Helpers

After generating tables, use these helpers to include them in LaTeX documents with precise placement control. These functions output raw LaTeX code for use in `.Rnw` or `.tex` documents.

Standard Figure Float

The `t2f_include()` function wraps the PDF in a figure environment:

```
t2f(mtcars[1:5, 1:4], filename = "demo_table", sub_dir = "tables")

t2f_include("tables/demo_table",
            caption = "Motor Trend Car Data (First 5 Rows)",
            label = "fig:mtcars",
            position = "htbp")
```

Generated LaTeX:

```
\begin{figure}[htbp]
\centering
\includegraphics{tables/demo_table_cropped.pdf}
\caption{Motor Trend Car Data (First 5 Rows)}
\label{fig:mtcars}
\end{figure}
```

Exact Placement (No Floating)

For precise placement without LaTeX float behavior:

```
t2f_include_inline("tables/demo_table",
                   width = "0.8\\textwidth",
                   vspace = "1em")
```

Side-by-Side Tables

```
t2f(mtcars[1:5, 1:3], filename = "table_a", sub_dir = "tables")
t2f(mtcars[1:5, 4:6], filename = "table_b", sub_dir = "tables")

t2f_include_sidebyside(
  "tables/table_a", "tables/table_b",
  caption1 = "(a) Performance",
  caption2 = "(b) Design",
  main_caption = "Motor Trend Car Data by Category",
  main_label = "fig:mtcars_combined"
)
```

Margin Placement

For documents with wide margins (Tufte style, etc.):

```
t2f_include_margin("tables/demo_table",
                   caption = "Summary",
                   method = "sidenotes")
```

Text Wrapping

```
t2f_include_wrap("tables/demo_table",
                 placement = "r",
                 wrap_width = "0.45\\textwidth",
                 caption = "Car data summary")
```

8. Cross-References

Generate LaTeX cross-reference commands from R:

```
cat("As shown in ")
t2f_ref("fig:mtcars")
cat(", the fuel efficiency varies considerably.")

ref_text <- sprintf("Results are presented in %s.",
                    t2f_ref("tab:efficacy", cat = FALSE))
cat(ref_text)
```

Summary

zztab2fig v0.2.0 provides comprehensive support for publication-quality tables:

- **Footnotes**: General, numbered, alphabetic, and symbol notation
- **Spanning headers**: Single or multiple levels of grouped columns
- **Multi-row cells**: Automatic collapsing of hierarchical data
- **Decimal alignment**: siunitx integration for precise number formatting
- **Short captions**: For List of Tables entries
- **Figure placement**: Float, inline, margin, wrap, and side-by-side options

These features can be combined to create tables meeting the most demanding journal requirements while maintaining a clean R-based workflow.