

Creating Clinical Tables in R with rtables Package

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Agenda

01

Overview

02

Basics of rtables

03

Examples

04

Using tern

Agenda

01

Overview

02

Basics of rtables

03

Examples

04

Using tern

Clinical reporting packages listed on pharmaverse website

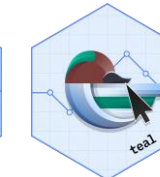
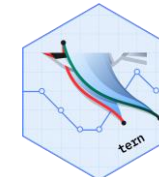
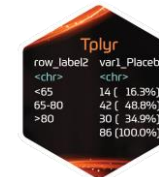
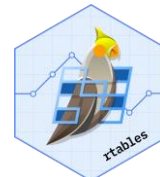
CRF

SDTM

ADaM

TLGs

eSub



Clinical reporting packages listed on pharmaverse website

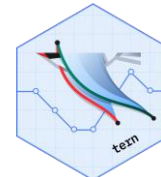
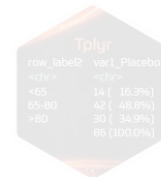
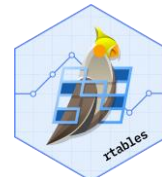
CRF

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eSub



rtables

- R package developed by Roche.
- Open source (Apache License, Version 2.0)
- Provides a framework to create, tabulate and output tables in R.
- table rendering (ASCII, HTML, etc.) is separate from the data model.
- Always has access to the non-rounded/non-formatted numbers.



Agenda

01

Overview

02

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03

Examples

04

Using tern

Program structure

```
library(rtables)
```

Table layout

```
lyt <- basic_table(title = "Title", main_footer = "Footnotes.") %>%  
  split_cols_by("ARM") %>%  
  split_rows_by("SEX") %>%  
  analyze("AGE", afun = a_summary)
```

```
tbl <- build_table(lyt, adsl)
```

Building table object

```
export_as_txt(tbl, "table.txt", page_type = "a4")
```

Export

Layout

```
lyt <- basic_table(title = "Title", main_footer = "Footnotes.") %>%
  split_cols_by("ARM") %>%
  split_rows_by("SEX") %>%
  analyze("AGE", afun = a_summary)
```

Title

	A: Drug X	B: Placebo	C: Combination

F			
n	79	77	66
Mean (SD)	32.8 (6.1)	34.1 (7.1)	35.2 (7.4)
Median	32.0	32.0	35.0
Min - Max	21.0 - 47.0	23.0 - 58.0	21.0 - 64.0
M			
n	51	55	60
Mean (SD)	35.6 (7.1)	37.4 (8.7)	35.4 (8.2)
Median	37.0	37.0	33.5
Min - Max	23.0 - 50.0	21.0 - 62.0	20.0 - 69.0

Footnotes.

Layout

```
lyt <- basic_table(title = "Title", main_footer = "Footnotes.") %>%
  split_cols_by("ARM") %>%
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Title			
	A: Drug X	B: Placebo	C: Combination
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Min - Max	23.0 - 50.0	21.0 - 62.0	20.0 - 69.0
Footnotes.			

Layout

```
lyt <- basic_table(title = "Title", main_footer = "Footnotes.") %>%
  split_cols_by("ARM") %>%
  split_rows_by("SEX") %>%
  analyze("AGE", afun = a_summary)
```

Title			
	A: Drug X	B: Placebo	C: Combination
F			
n	79	77	66
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Footnotes.

Layout

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lyt <- basic_table(title = "Title", main_footer = "Footnotes.") %>%
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Title

	A: Drug X	B: Placebo	C: Combination
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Title

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Footnotes.

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lyt <- basic_table(title = "Title", main_footer = "Footnotes.") %>%
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```

Analysis function

Title

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Footnotes.

Analysis function

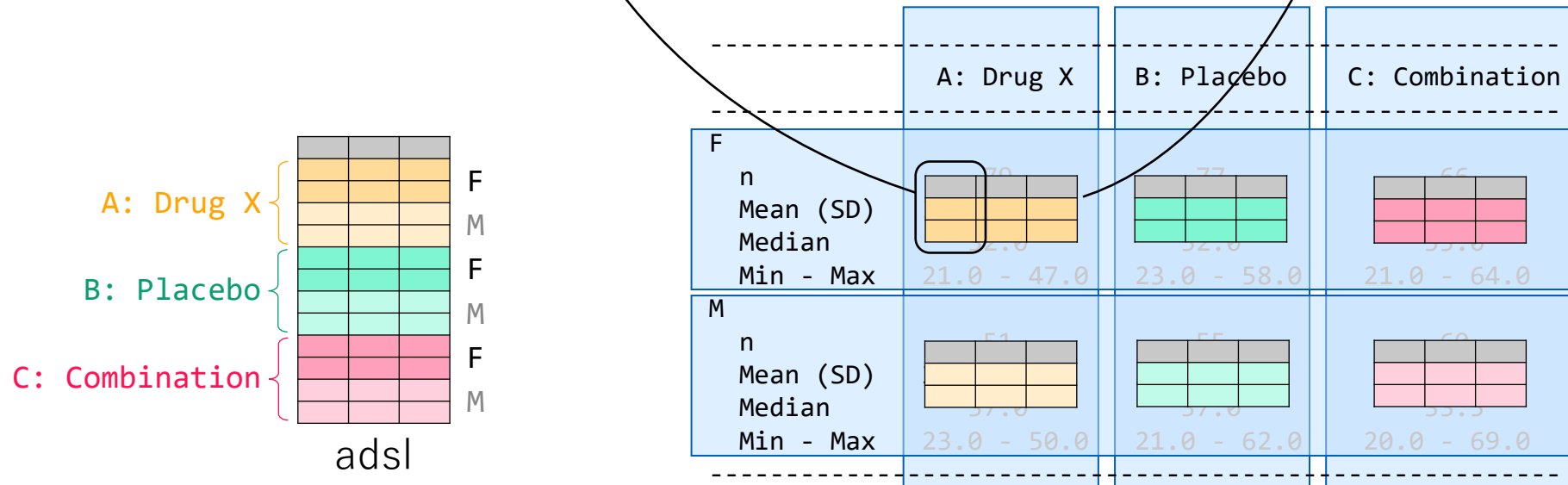
```
a_summary <- function(x) {
  ...
}
```

or

```
a_summary <- function(df) {
  ...
}
```

receive a column (variable)

receive a data frame



Analysis function

```

a_summary <- function(x) {
  in_rows(
    n = rcell(
      sum(!is.na(x)), format = "xx"
    ),
    mean_sd = rcell(
      c(mean(x), sd(x)), format = "xx.x (xx.x)"
    ),
    median = rcell(
      median(x), format = "xx.x"
    ),
    min_max = rcell(
      range(x), format = "xx.x - xx.x"
    ),
    .labels = c("n", "Mean (SD)", "Median", "Min - Max")
  )
}

```

```

lyt <- basic_table() %>%
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  split_rows_by("SEX") %>%
  analyze("AGE", afun = a_summary)

```

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    ),
    min_max = rcell(
      range(x), format = "xx.x - xx.x"
    ),
    .labels = c("n", "Mean (SD)", "Median", "Min - Max")
  )
}

```

```

lyt <- basic_table() %>%
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```

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Analysis function

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      median(x), format = "xx.x"
    ),
    min_max = rcell(
      range(x), format = "xx.x - xx.x"
    ),
    .labels = c("n", "Mean (SD)", "Median", "Min - Max")
  )
}

```

```

lyt <- basic_table() %>%
  split_cols_by("ARM") %>%
  split_rows_by("SEX") %>%
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```

	A: Drug X	B: Placebo	C: Combination
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Export

rtable object

`build_table(lyt, adsl)`



`export_as_txt()`

`export_as_rtf()`
via r2rtf package

`export_as_pdf()`

`as_html()`
for Shiny app, etc.

Title

	A: Drug X	B: Placebo	C: Combination
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Footnotes.

Title

	A: Drug X	B: Placebo	C: Combination
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n	79	77	66
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Footnotes.

docx, pptx via flextable package

Agenda

01

Overview

02

Basics of rtables

03

Examples

04

Using tern

Examples

- Demographics
- Laboratory Results
- Adverse Events

Demographics

```
a_summary_num <- function(x) {
  in_rows(
    n = rcell(sum(!is.na(x)), format = "xx"),
    mean_sd = rcell(c(mean(x), sd(x)), format = "xx.x (xx.x)"),
    median = rcell(median(x), format = "xx.x"),
    min_max = rcell(range(x), format = "xx.x - xx.x"),
    .labels = c("n", "Mean (SD)", "Median", "Min - Max")
  )
}
```

[1]

```
a_summary_fct <- function(x, .N_col) {
  in_rows(
    n = rcell(sum(!is.na(x)), format = "xx"),
    .list = as.list(table(x)) %>%
      lapply(function(n) {
        rcell(c(n, n / .N_col), format = "xx (xx.x%)")
      })
  )
}
```

[2]

```
lyt <- basic_table(title = "Demographics", main_footer = " ") %>%
  split_cols_by("ARMCD") %>%
  add_colcounts() %>%
  analyze("AGE", afun = a_summary_num, var_labels = "Age (year)") %>%
  analyze("AGEGR1", afun = a_summary_fct, var_labels = "Age (year)")
```

[3]

```
build_table(lyt, adsl)
```

Demographics

	ARM A (N=134)	ARM B (N=134)
Age (year)		
n	134	134
Mean (SD)	33.8 (6.6)	35.4 (7.9)
Median	33.0	35.0
Min - Max	21.0 - 50.0	21.0 - 62.0
Age (year)		
n	134	134
< 65	134 (100.0%)	134 (100.0%)
>= 65	0 (0.0%)	0 (0.0%)

Demographics

```

a_summary_num <- function(x) {
  in_rows(
    n = rcell(
      sum(!is.na(x)), format = "xx"
    ),
    mean_sd = rcell(
      c(mean(x), sd(x)), format = "xx.x (xx.x)"
    ),
    median = rcell(
      median(x), format = "xx.x"
    ),
    min_max = rcell(
      range(x), format = "xx.x - xx.x"
    ),
    .labels = c(
      "n", "Mean (SD)", "Median", "Min - Max"
    )
  )
}

```

[1]

Same as described in previous slide

Demographics

	ARM A (N=134)	ARM B (N=134)
Age (year)		
n	134	134
Mean (SD)	33.8 (6.6)	35.4 (7.9)
Median	33.0	35.0
Min - Max	21.0 - 50.0	21.0 - 62.0
Age (year)		
n	134	134
< 65	134 (100.0%)	134 (100.0%)
>= 65	0 (0.0%)	0 (0.0%)

Demographics

```

a_summary_fct <- function(x, .N_col) {
  in_rows(
    n = rcell(sum(!is.na(x)), format = "xx"),
    .list = as.list(table(x)) %>%
      lapply(function(n) { Counts the number of subjects
        rcell(
          c(n, n / .N_col), format = "xx (xx.x%)"
        )
      })
  )
}

```

[2]

Demographics

	ARM A (N=134)	ARM B (N=134)
Age (year)		
n	134	134
Mean (SD)	33.8 (6.6)	35.4 (7.9)
Median	33.0	35.0
Min - Max	21.0 - 50.0	21.0 - 62.0
Age (year)		
n	134	134
< 65	134 (100.0%)	134 (100.0%)
>= 65	0 (0.0%)	0 (0.0%)

Demographics

```
lyt <- basic_table(
  title = "Demographics",
  main_footer = " "
) %>%
  split_cols_by("ARMCD") %>%
  add_colcounts() %>%
  analyze(
    "AGE",
    afun = a_summary_num,
    var_labels = "Age (year)"
  ) %>%
  analyze(
    "AGEGR1",
    afun = a_summary_fct,
    var_labels = "Age (year)"
  )
```

```
build_table(lyt, adsl)
```

[3]

Demographics

	ARM A (N=134)	ARM B (N=134)
Age (year)		
n	134	134
Mean (SD)	33.8 (6.6)	35.4 (7.9)
Median	33.0	35.0
Min - Max	21.0 - 50.0	21.0 - 62.0
Age (year)		
n	134	134
< 65	134 (100.0%)	134 (100.0%)
>= 65	0 (0.0%)	0 (0.0%)

Laboratory Results

```

a_summary_num <- function(x) {
  in_rows(
    n = rcell(sum(!is.na(x)), format = "xx"),
    mean_sd = rcell(c(mean(x), sd(x)), format = "xx.x (xx.x)"),
    median = rcell(median(x), format = "xx.x"),
    min_max = rcell(range(x), format = "xx.x - xx.x"),
    .labels = c("n", "Mean (SD)", "Median", "Min - Max")
  )
}

lyt <- basic_table(title = "Lab Results", main_footer = " ") %>%
  split_cols_by("ARMCD") %>%
  add_colcounts() %>%
  split_rows_by(
    "PARAM", split_fun = drop_split_levels,
    split_label = "Parameter", label_pos = "topleft",
    section_div = ""
  ) %>%
  split_rows_by(
    "AVISIT", split_fun = drop_split_levels,
    split_label = "Visit", label_pos = "topleft",
    section_div = ""
  ) %>%
  analyze("AVAL", afun = a_summary_num)

build_table(lyt, adlb, alt_counts_df = adsl) %>%
  prune_table()

```

Lab Results

Parameter	ARM A (N=134)	ARM B (N=134)

Visit		

Alanine Aminotransferase (U/L)		
BASELINE		
n	134	134
Mean (SD)	49.6 (8.3)	50.3 (8.3)
Median	49.6	50.2
Min - Max	24.0 - 70.9	26.2 - 79.1
WEEK 1 DAY 8		
n	134	134
Mean (SD)	48.6 (8.0)	50.4 (7.9)
Median	48.4	50.2
Min - Max	27.7 - 64.6	21.7 - 67.5
WEEK 2 DAY 15		
n	134	134
Mean (SD)	49.4 (8.5)	50.2 (8.5)
Median	48.3	50.0
Min - Max	24.3 - 71.1	24.4 - 71.1

Laboratory Results

```

a_summary_num <- function(x) {
  in_rows(
    n = rcell(
      sum(!is.na(x)), format = "xx"
    ),
    mean_sd = rcell(
      c(mean(x), sd(x)), format = "xx.x (xx.x)"
    ),
    median = rcell(
      median(x), format = "xx.x"
    ),
    min_max = rcell(
      range(x), format = "xx.x - xx.x"
    ),
    .labels = c(
      "n", "Mean (SD)", "Median", "Min - Max"
    )
  )
}

```

[1]

Same as described in previous slide

Lab Results

Parameter	ARM A	ARM B
Visit	(N=134)	(N=134)

Alanine Aminotransferase (U/L)

BASELINE

n	134	134
Mean (SD)	49.6 (8.3)	50.3 (8.3)
Median	49.6	50.2
Min - Max	24.0 - 70.9	26.2 - 79.1

WEEK 1 DAY 8

n	134	134
Mean (SD)	48.6 (8.0)	50.4 (7.9)
Median	48.4	50.2
Min - Max	27.7 - 64.6	21.7 - 67.5

WEEK 2 DAY 15

n	134	134
Mean (SD)	49.4 (8.5)	50.2 (8.5)
Median	48.3	50.0
Min - Max	24.3 - 71.1	24.4 - 71.1

Laboratory Results

```

lyt <- basic_table(
  title = "Lab Results",
  main_footer = " "
) %>%
split_cols_by("ARMCD") %>%
add_colcounts() %>%
split_rows_by(
  "PARAM", split_fun = drop_split_levels,
  split_label = "Parameter", label_pos = "topleft",
  section_div = ""
) %>%
split_rows_by(
  "AVISIT", split_fun = drop_split_levels,
  split_label = "Visit", label_pos = "topleft",
  section_div = ""
) %>%
analyze("AVAL", afun = a_summary_num)

```

[2]

Lab Results

Parameter	ARM A (N=134)	ARM B (N=134)
Visit		
Alanine Aminotransferase (U/L)		
BASELINE		
n	134	134
Mean (SD)	49.6 (8.3)	50.3 (8.3)
Median	49.6	50.2
Min - Max	24.0 - 70.9	26.2 - 79.1
WEEK 1 DAY 8		
n	134	134
Mean (SD)	48.6 (8.0)	50.4 (7.9)
Median	48.4	50.2
Min - Max	27.7 - 64.6	21.7 - 67.5
WEEK 2 DAY 15		
n	134	134
Mean (SD)	49.4 (8.5)	50.2 (8.5)
Median	48.3	50.0
Min - Max	24.3 - 71.1	24.4 - 71.1

Laboratory Results

```
build_table(
  lyt,
  adlb, Uses adsl for column count
  alt_counts_df = adsl
) %>% prune_table()
Removes if the subset is empty
```

[3]

Lab Results

Parameter	ARM A	ARM B
Visit	(N=134)	(N=134)
Alanine Aminotransferase (U/L)		
BASELINE		
n	134	134
Mean (SD)	49.6 (8.3)	50.3 (8.3)
Median	49.6	50.2
Min - Max	24.0 - 70.9	26.2 - 79.1
WEEK 1 DAY 8		
n	134	134
Mean (SD)	48.6 (8.0)	50.4 (7.9)
Median	48.4	50.2
Min - Max	27.7 - 64.6	21.7 - 67.5
WEEK 2 DAY 15		
n	134	134
Mean (SD)	49.4 (8.5)	50.2 (8.5)
Median	48.3	50.0
Min - Max	24.3 - 71.1	24.4 - 71.1

Adverse Events

```

a_num_patients <- function(x, labelstr, .N_col) {
  n <- length(unique(x))
  in_rows(
    unique = rcell(c(n, n / .N_col), format = "xx (xx.x%)"),
    nonunique = rcell(length(x), format = "xx"),
    .labels = c(
      unique = "Total number of pts with at least one AE",
      nonunique = "Total number of events"
    )
  )
}

a_count_occ <- function(df, .var, .N_col) {
  counts <- table(unique(df[, c(.var, "USUBJID")])[[.var]])
  in_rows(
    .list = as.list(counts) %>%
      lapply(function(n) {
        rcell(c(n, n / .N_col), format = "xx (xx.x%)")
      })
  )
}

lyt <- basic_table(
  title = "Adverse events",
  main_footer = "MedDRA version xx.x"
) %>%
  split_cols_by("ARMCD") %>%
  add_colcounts() %>%
  analyze("USUBJID", afun = a_num_patients) %>%
  split_rows_by(
    "AEBODSYS",
    split_label = "System Organ Class",
    label_pos = "topleft",
    child_labels = "visible"
  ) %>%
  summarize_row_groups("USUBJID", cfun = a_num_patients) %>%
  analyze("AEDECOD", afun = a_count_occ, indent_mod = -1) %>%
  append_topleft(" Preferred Term")

build_table(lyt, adae, alt_counts_df = ads1) %>%
  prune_table()

```

[1]

[2]

[3]

Adverse events

System Organ Class Preferred Term	ARM A (N=134)	ARM B (N=134)
Total number of pts with at least one AE	102 (76.1%)	99 (73.9%)
Total number of events	261	268
c1 A.1		
Total number of pts with at least one AE	78 (58.2%)	75 (56.0%)
Total number of events	132	130
dcd A.1.1.1.1	50 (37.3%)	45 (33.6%)
dcd A.1.1.1.2	48 (35.8%)	48 (35.8%)
c1 B.2		
Total number of pts with at least one AE	79 (59.0%)	74 (55.2%)
Total number of events	129	138
dcd B.2.1.2.1	49 (36.6%)	44 (32.8%)
dcd B.2.2.3.1	48 (35.8%)	54 (40.3%)

MedDRA version xx.x

Adverse Events

```

lyt <- basic_table(
  title = "Adverse events",
  main_footer = "MedDRA version xx.x"
) %>%
  split_cols_by("ARMCD") %>%
  add_colcounts() %>%
  analyze("USUBJID", afun = a_num_patients) %>%
  split_rows_by(
    "AEBODSYS",
    split_label = "System Organ Class",
    label_pos = "topleft",
    child_labels = "visible"
  ) %>%
  summarize_row_groups("USUBJID", cfun = a_num_patients) %>%
  analyze(
    "AEDECOD",
    afun = a_count_occ,
    indent_mod = -1
  ) %>%
  append_topleft(" Preferred Term")

build_table(lyt, adae, alt_counts_df = adsl) %>%
  prune_table()

```

[3]

Adverse events

System Organ Class Preferred Term	ARM A (N=134)	ARM B (N=134)
Total number of pts with at least one AE	102 (76.1%)	99 (73.9%)
Total number of events	261	268
c1 A.1		
Total number of pts with at least one AE	78 (58.2%)	75 (56.0%)
Total number of events	132	130
dcd A.1.1.1.1	50 (37.3%)	45 (33.6%)
dcd A.1.1.1.2	48 (35.8%)	48 (35.8%)
c1 B.2		
Total number of pts with at least one AE	79 (59.0%)	74 (55.2%)
Total number of events	129	138
dcd B.2.1.2.1	49 (36.6%)	44 (32.8%)
dcd B.2.2.3.1	48 (35.8%)	54 (40.3%)

MedDRA version xx.x

Adverse Events

```
a_num_patients <- function(x, labelstr, .N_col) {
  n <- length(unique(x))
  in_rows(
    unique = rcell(
      c(n, n / .N_col),
      format = "xx (xx.x%)"
    ),
    nonunique = rcell(
      length(x),
      format = "xx"
    ),
    .labels = c(
      unique = "Total number of pts with at least one AE",
      nonunique = "Total number of events"
    )
  )
}
```

[1]

Adverse events

System Organ Class Preferred Term	ARM A (N=134)	ARM B (N=134)
Total number of pts with at least one AE	102 (76.1%)	99 (73.9%)
Total number of events	261	268
c1 A.1		
Total number of pts with at least one AE	78 (58.2%)	75 (56.0%)
Total number of events	132	130
dcd A.1.1.1.1	50 (37.3%)	45 (33.6%)
dcd A.1.1.1.2	48 (35.8%)	48 (35.8%)
c1 B.2		
Total number of pts with at least one AE	79 (59.0%)	74 (55.2%)
Total number of events	129	138
dcd B.2.1.2.1	49 (36.6%)	44 (32.8%)
dcd B.2.2.3.1	48 (35.8%)	54 (40.3%)

MedDRA version xx.x

Adverse Events

```

a_count_occ <- function(df, .var, .N_col) {
  counts <- table(unique(df[, c(.var, "USUBJID")])[[.var]])
  in_rows(
    .list = as.list(counts) %>%
      lapply(function(n) {
        rcell(c(n, n / .N_col), format = "xx (xx.x%)")
      })
  )
}

```

Adverse events

System Organ Class Preferred Term	ARM A (N=134)	ARM B (N=134)
Total number of pts with at least one AE	102 (76.1%)	99 (73.9%)
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MedDRA version xx.x

Agenda

01

Overview

02

Basics of rtables

03

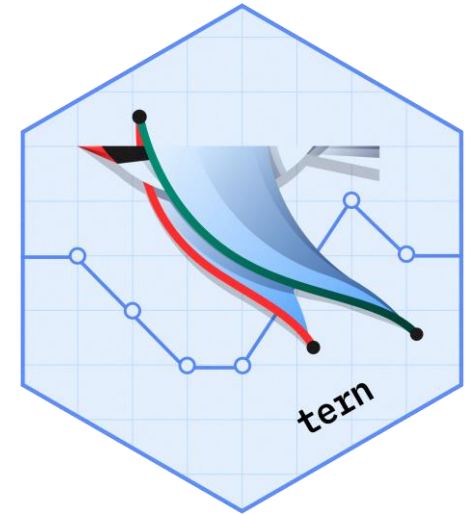
Examples

04

Using tern

tern

- R package contains analysis functions to create tables and graphs used for clinical trial reporting.
- Built on top of rtables package.
- Complicated rtables codes are represented more simple and easy to understand using tern.
- Open source (Apache License, Version 2.0)



Demographics using tern

```
lyt <- basic_table(
  title = "Demographics",
  main_footer = " "
) %>%
  split_cols_by("ARMCD") %>%
  add_colcounts() %>%
  analyze_vars(
    "AGE",
    var_labels = "Age (year)",
    .stats = c("n", "mean_sd", "median", "range")
  ) %>%
  analyze_vars(
    "AGEGR1",
    var_labels = "Age (year)",
    .stats = c("n", "count_fraction")
  )
build_table(lyt, adsl)
```

tern function

tern function

Demographics

	ARM A (N=134)	ARM B (N=134)
Age (year)		
n	134	134
Mean (SD)	33.8 (6.6)	35.4 (7.9)
Median	33.0	35.0
Min - Max	21.0 - 50.0	21.0 - 62.0
Age (year)		
n	134	134
< 65	134 (100.0%)	134 (100.0%)
>= 65	0 (0.0%)	0 (0.0%)

Adverse Events using tern

```
lyt <- basic_table(
  title = "Adverse events",
  main_footer = "MedDRA version xx.x"
) %>%
  split_cols_by("ARMCD") %>%
  add_colcounts() %>%
  analyze_num_patients(
    "USUBJID",
    .stats = c("unique", "nonunique"),
    .labels = c(
      unique = "Total number of pts with at least one AE",
      nonunique = "Total number of events"
    )
  ) %>%
  split_rows_by(
    "AEBODSYS",
    split_label = "System Organ Class",
    label_pos = "topleft",
    child_labels = "visible"
  ) %>%
  summarize_num_patients(
    "USUBJID",
    .stats = c("unique", "nonunique"),
    .labels = c(
      unique = "Total number of pts with at least one AE",
      nonunique = "Total number of events"
    )
  ) %>%
  count_occurrences("AEDECOD", .indent_mods = -1L) %>%
  append_topleft(" Preferred Term")
  tern function

build_table(lyt, adae, alt_counts_df = ads1) %>%
  prune_table()
```

Adverse events

System Organ Class Preferred Term	ARM A (N=134)	ARM B (N=134)
Total number of pts with at least one AE	102 (76.1%)	99 (73.9%)
Total number of events	261	268
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MedDRA version xx.x

TLG Catalog

TLG Catalog - Stable
Stable

DMT01

Demographics and Baseline Characteristics

<>

Data Setup

Table with an Additional Study-Specific Continuous Variable

Table with an Additional Study-Specific Categorical Variable

Table with Subgrouping for Some Analyses

Table with Additional Vital Signs Baseline Values

Table with Additional Values from ADSUB

tea1 App

Reproducibility

▼ Code

```

1 vars <- c("AGE", "AGEGR1", "SEX", "ETHNIC", "RACE", "BMRKR1")
2 var_labels <- c(
3   "Age (yr)",
4   "Age Group",
5   "Sex",
6   "Ethnicity",
7   "Race",
8   "Continuous Level Biomarker 1"
9 )
10
11 result <- basic_table(show_colcounts = TRUE) %>%
12   split_cols_by(var = "ACTARM") %>%
13   add_overall_col("All Patients") %>%
14   analyze_vars(
15     vars = vars,
16     var_labels = var_labels
17   ) %>%
18   build_table(ads1)
19
20 result
                
```

	A: Drug X (N=134)	B: Placebo (N=134)	C: Combination (N=132)	All Patients (N=400)
Age (yr)				
n	134	134	132	400
Mean (SD)	33.8 (6.6)	35.4 (7.9)	35.4 (7.7)	34.9 (7.4)
Median	33.0	35.0	35.0	34.0
Min - Max	21.0 - 50.0	21.0 - 62.0	20.0 - 69.0	20.0 - 69.0
Age Group				
n	134	134	132	400
18-40	113 (84.3%)	103 (76.9%)	106 (80.3%)	322 (80.5%)
41-64	21 (15.7%)	31 (23.1%)	25 (18.9%)	77 (19.2%)
>=65	0	0	1 (0.8%)	1 (0.2%)
Sex				
n	134	134	132	400
Female	79 (59%)	82 (61.2%)	70 (53%)	231 (57.8%)
Male	55 (41%)	52 (38.8%)	62 (47%)	169 (42.2%)
Ethnicity				
n	134	134	132	400
NOT REPORTED	6 (4.5%)	10 (7.5%)	11 (8.3%)	27 (6.8%)
HISPANIC OR LATINO	15 (11.2%)	18 (13.4%)	15 (11.4%)	48 (12%)
NOT HISPANIC OR LATINO	104 (77.6%)	103 (76.9%)	101 (76.5%)	308 (77%)



- Introduction
- Tables
 - ADA
 - Adverse Events
 - Concomitant Medications
 - Deaths
 - Demography
 - DMT01
 - Disclosures
 - Disposition
 - ECG
 - Efficacy
 - Exposure
 - Lab Results
 - Medical History
 - Pharmacokinetic
 - Risk Management Plan
 - Safety
 - Vital Signs
- Listings
- Graphs
- Appendix
- Index

Impression

- **Easy to design table layouts**
 - Basically, defined as column splits and row splits
- **Easy to define analysis functions.**
 - Receives subset data
 - Separated from table layout
- **Difficult to make tables that deviates from the pattern composed by column and row splits.**
- **Analysis functions tend to be complicated**
 - Use tern package

INNOVATION BEYOND IMAGINATION