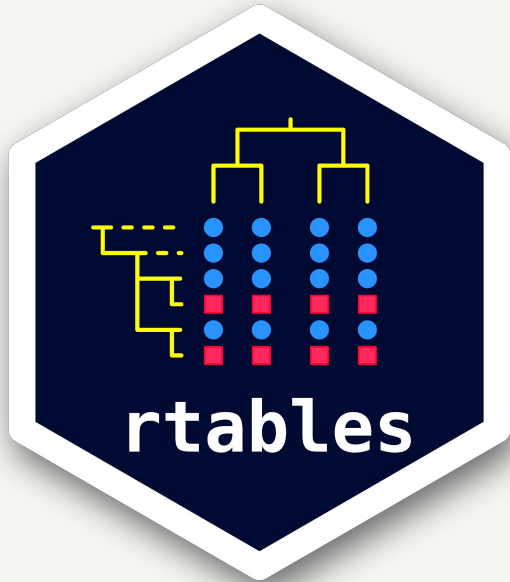


rtables: existing, fit for purpose, production ready

Gabriel Becker, presented by Liming Li



rtables

existing, fit for purpose, production ready

Gabriel Becker, Architect
Liming Li, senior data scientist

Who We Are

Gabriel Becker

- Architect, primary author of `rtables` and related packages
- Frequent collaborator with R-core on improvements to R itself

Liming Li

- Technical Lead - chevron team, NEST Project
- Author of ``mrmr``, ``sasr`` packages

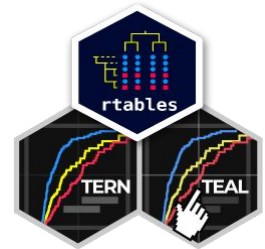
Production Ready - The Proof Is In The Pudding

TLG-catalog

Fully reproducible, open-source code to generate hundreds of clinical trial analysis and reporting tables

- 6 Table Categories
- 88 Top-level Catalog Entries
- ~225 Table Variants
- All entries use `rtables` as their core underlying table engine

<https://insightengineering.github.io/tlg-catalog/>

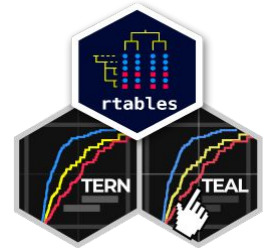


TLG-catalog - Table Variant Counts By Category*

- Adverse event - 68
- Safety(Concomitant Medication, ECG, Vital Sign, etc) - 49
- Efficacy - 39
- Lab Results - 38
- Pharmacokinetic - 12
- Other - 26

* These categories are organizational within the tlg-catalog and do not have a broader meaning

<https://insightengineering.github.io/tlg-catalog/>



Chevron - package supporting regulatory reporting

- Built on top of rtables, tern
- Covering a big amount of standard templates
- One-line to generate tables
- Moderate flexibility of customization
- Highly scalable
- To be open-sourced soon!



Adoption Within Roche

- Roche has adopted `rtables` in production for table generation
- `chevron` is built on `rtables` to provide user with standard tables
- `tern` provide analyze functionality for customized analysis
- Submission of first Roche clinical trial analyzed via R (`rtables/chevron/tern`) in preparation
- All new trials expected to follow suit moving forward

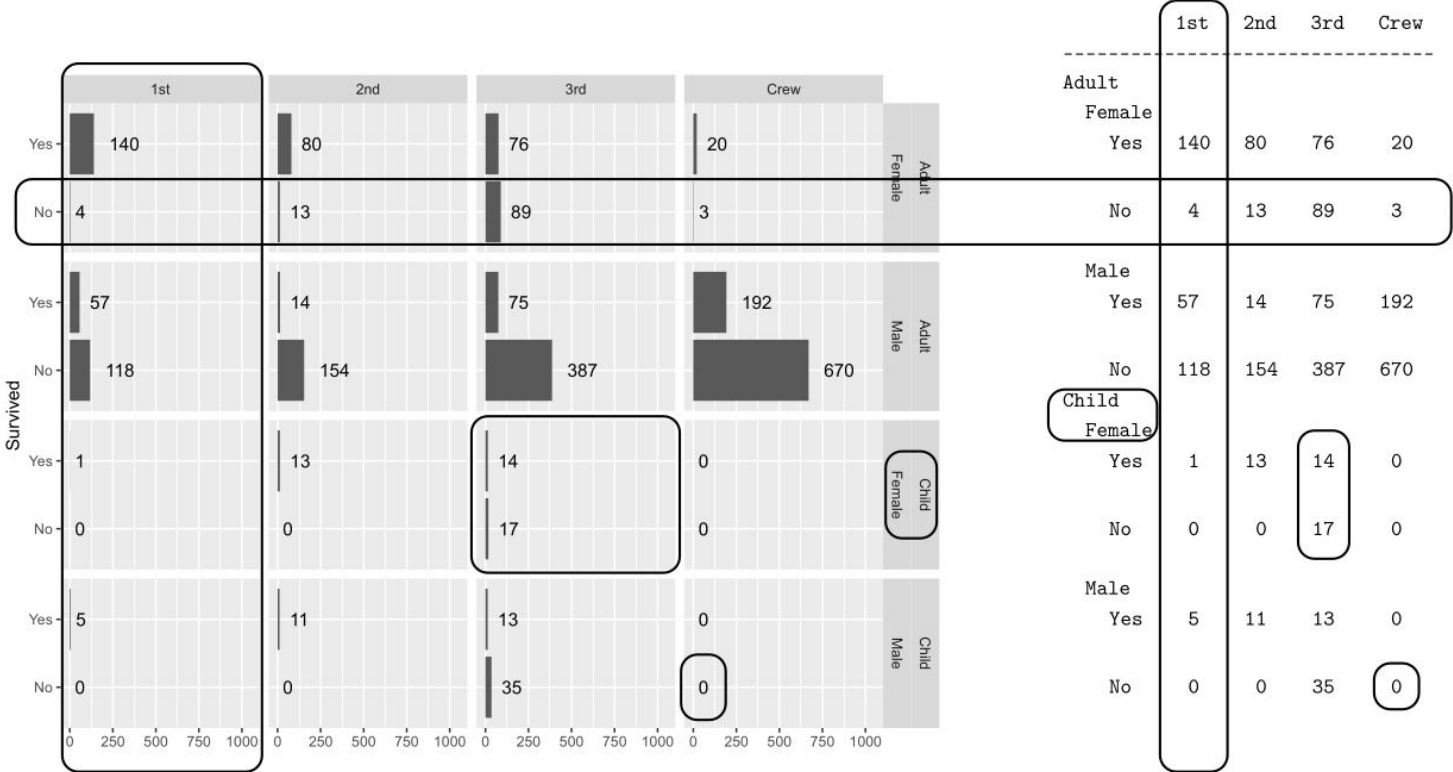
Paradigm Shift - The `rtables` Conceptual Model

The First Step In Creating a Table

Calculating cell values, right?



Reporting Tables Are Faceted Data Visualizations



Imagine Manually Subsetting Facet Data When Using `ggplot2` (or `lattice`)



Subsetting data and calculating facet statistics

Humans



Computers



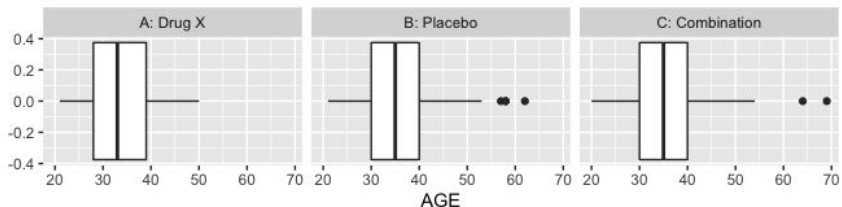
Tables As Faceted Data Visualizations

Declaring Facets

- `split_rows_by()` (and `siblings`) add row faceting structure
- `split_cols_by()` (and `siblings`) add column faceting structure
- Column and row facet structure declared independently
 - As in `facet_grid(rows = , cols =)`

Column Faceting - ggplot2 and rtables

```
ggplot(ex_adsl, mapping = aes(x = AGE)) +
  geom_boxplot() +
  facet_grid(cols = vars(ARM))
```



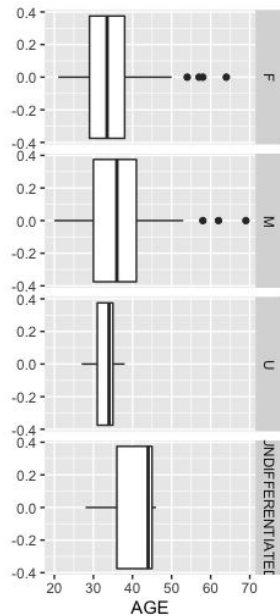
```
lyt <- basic_table() |>
  split_cols_by("ARM") |>
  analyze("AGE", range, format = "xx.xx - xx.xx")

build_table(lyt, ex_adsl)
```

	A: Drug X	B: Placebo	C: Combination
range	21.00 - 50.00	21.00 - 62.00	20.00 - 69.00

Row Faceting - ggplot2 and rtables

```
ggplot(ex_adsl, mapping = aes(x = AGE)) +
  geom_boxplot() +
  facet_grid(rows = vars(SEX))
```



```
lyt2 <- basic_table() |>
  split_rows_by("SEX") |>
  analyze("AGE", range,
    format = "xx.xx - xx.xx")
```

```
build_table(lyt2, ex_adsl)
```

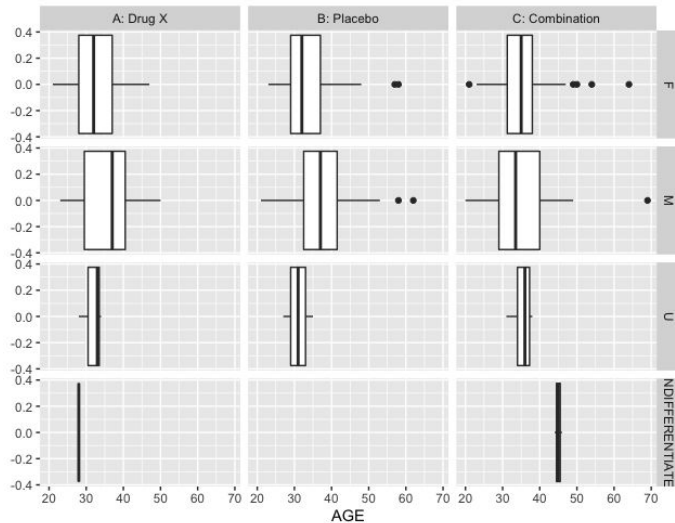
	all obs
F	
range	21.00 - 64.00
M	
range	20.00 - 69.00
U	
range	27.00 - 38.00
UNDIFFERENTIATED	
range	28.00 - 46.00

Grid Faceting - ggplot2 and rtables

```
ggplot(ex_adsl, mapping = aes(x = AGE)) +
  geom_boxplot() +
  facet_grid(rows = vars(SEX),
            cols = vars(ARM))
```

```
lyt3 <- basic_table() |>
  split_cols_by("ARM") |>
  split_rows_by("SEX") |>
  analyze("AGE", range, format = "xx.xx - xx.xx")
```

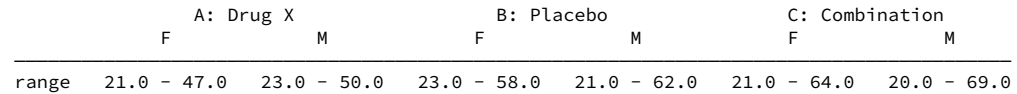
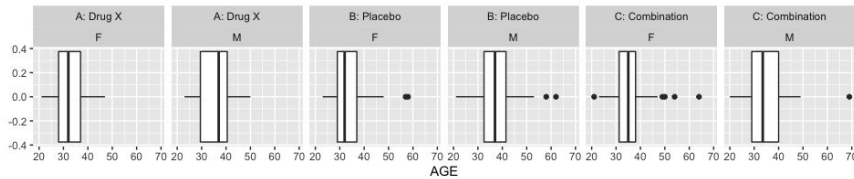
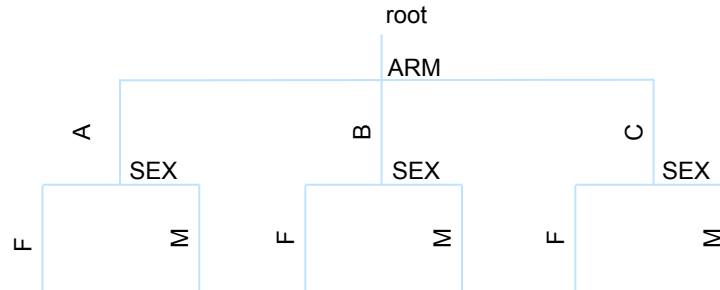
```
build_table(lyt3, ex_adsl)
```



	A: Drug X	B: Placebo	C: Combination
F			
range	21.00 - 47.00	23.00 - 58.00	21.00 - 64.00
M			
range	23.00 - 50.00	21.00 - 62.00	20.00 - 69.00
U			
range	28.00 - 34.00	27.00 - 35.00	31.00 - 38.00
UNDIFFERENTIATED			
range	28.00 - 28.00	Inf - -Inf	44.00 - 46.00

Nested Faceting Structure

Consecutive splits give nested facet structure, same as giving multiple variables in one dim to `facet_grid()`



Pooling of Groups

```
library(tibble)
combodf <- tribble(
  ~valname, ~label, ~levelcombo, ~exargs,
  "A_B", "Arms A+B", c("A: Drug X", "B: Placebo"), list(),
  "A_C", "Arms A+C", c("A: Drug X", "C: Combination"), list())

lyt <- basic_table(show_colcounts = TRUE) %>%
  split_cols_by("ARM", split_fun = add_combo_levels(combodf)) %>%
  analyze("AGE")

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

	A: Drug X (N=121)	B: Placebo (N=106)	C: Combination (N=129)	Arms A+B (N=227)	Arms A+C (N=250)
Mean	34.91	33.02	34.57	34.03	34.73

That's it. That's all it takes.

Faceting is *fully* customizable

- Restrict to allowed level combinations when splitting on logically nested concepts
 - E.g., AEBODSYS -> AEDECOD
 - `trim_levels_to_map`, `trim_levels_in_group`
- Require, restrict, reorder, drop facets
- Combine existing facets into new virtual facets
 - all/total facet simply a special case of this
- Facet based on quartiles/bins of non-categorical variable
- Literally anything else you can possibly think of
 - `make_split_fun`

Group summaries

```
ex_adsl3 <- ex_adsl |>
  mutate(B1HL = factor(ifelse(BMRKR1 > mean(BMRKR1), "H", "L"),
                        levels = c("L", "H")))
```

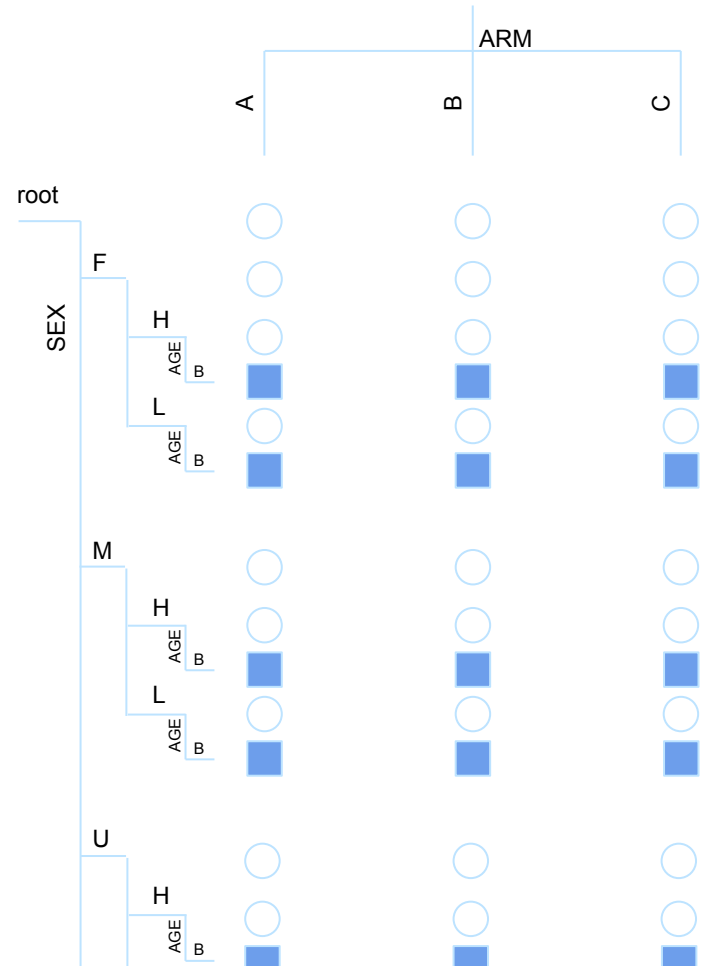
```
lyt <- basic_table() |>
  split_cols_by("ARM") |>
  split_rows_by("SEX") |>
  split_rows_by("B1HL") |>
  analyze("AGE", \(x) list(B = "a"))
```

```
build_table(lyt, ex_adsl3)
```

Group summaries

```
lyt <- basic_table() |>
  split_cols_by("ARM") |>
  split_rows_by("SEX") |>
  split_rows_by("B1HL") |>
  analyze("AGE", \(x) list(B = "a"))
```

```
build_table(lyt, ex_adsl3)
```

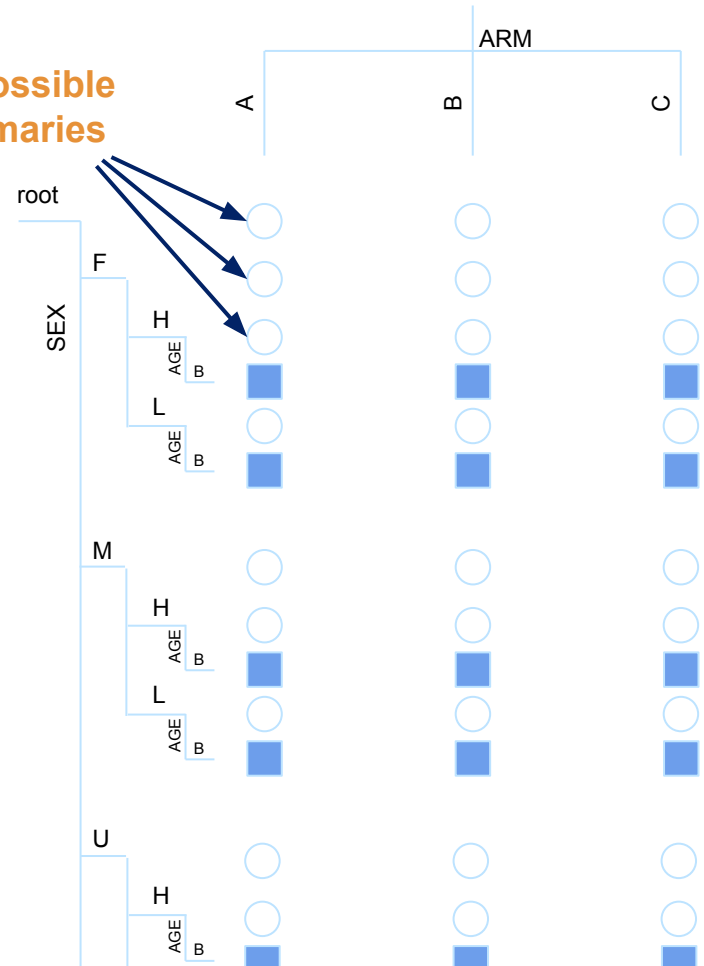


Group summaries

```
lyt <- basic_table() |>
  split_cols_by("ARM") |>
  split_rows_by("SEX") |>
  split_rows_by("B1HL") |>
  analyze("AGE", \(x) list(B = "a"))
```

```
build_table(lyt, ex_adsl3)
```

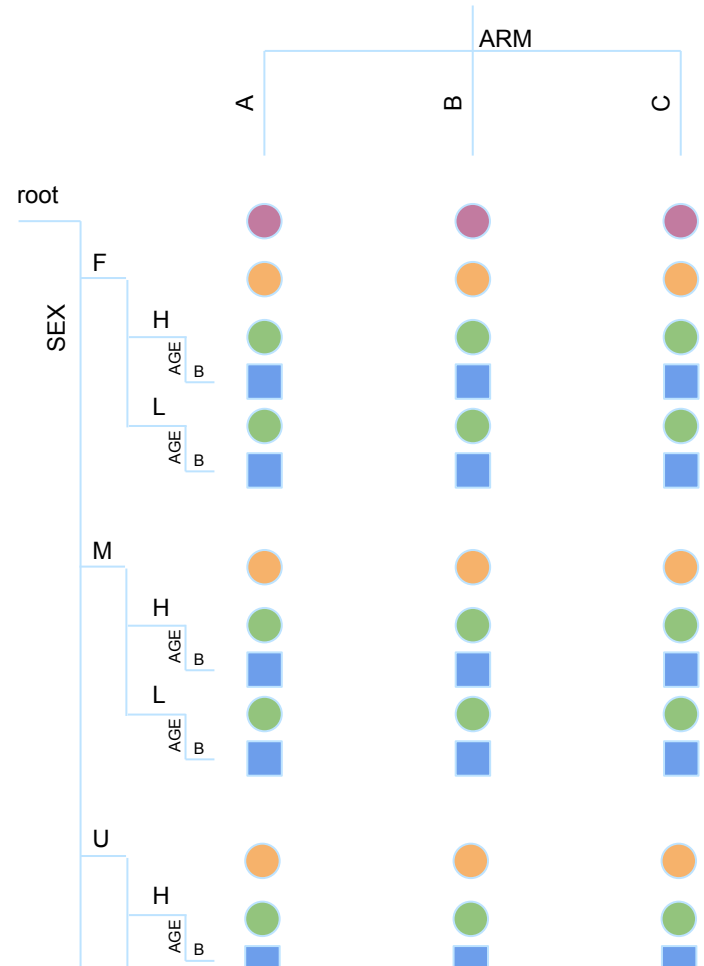
3 levels of possible group summaries



Group summaries

```
lyt <- basic_table() |>
  split_cols_by("ARM") |>
  summarize_row_groups() |>
  split_rows_by("SEX") |>
  summarize_row_groups() |>
  split_rows_by("B1HL") |>
  summarize_row_groups() |>
  analyze("AGE", afun = \(x) list(B = "a"))
```

```
build_table(lyt, ex_adsl3)
```



Viewing Complex Multi-Section Tables through the `rtables` lense

Effect/Covariate Included in the Model	n	Treatment Effect Adjusted for Covariate			
		Hazard Ratio	95% CI	p-value	Interaction p-value
Treatment:					
A: Drug X vs control (B: Placebo)	247	0.70	(0.51, 0.96)	0.0293	
Covariate:					
Age	247				0.8626
34		0.70	(0.51, 0.97)		
RACE	247				0.9197
ASIAN		0.75	(0.48, 1.16)		
BLACK OR AFRICAN AMERICAN		0.66	(0.34, 1.28)		
WHITE		0.65	(0.33, 1.27)		

Effect/Covariate Included in the Model	Treatment Effect Adjusted for Covariate				
	n	Hazard Ratio	95% CI	p-value	Interaction p-value
Treatment:					
A: Drug X vs control (B: Placebo)	247	0.70	(0.51, 0.96)	0.0293	
Covariate:					
Age	247				0.8626
34		0.70	(0.51, 0.97)		
RACE	247				0.9197
ASIAN		0.75	(0.48, 1.16)		
BLACK OR AFRICAN AMERICAN		0.66	(0.34, 1.28)		
WHITE		0.65	(0.33, 1.27)		

Two distinct top-level sections

Effect/Covariate Included in the Model	Treatment Effect Adjusted for Covariate				
	n	Hazard Ratio	95% CI	p-value	Interaction p-value
Treatment:					
A: Drug X vs control (B: Placebo)	247	0.70	(0.51, 0.96)	0.0293	
Covariate:					
Age	247				0.8626
34		0.70	(0.51, 0.97)		
RACE	247				0.9197
ASIAN		0.75	(0.48, 1.16)		
BLACK OR AFRICAN AMERICAN		0.66	(0.34, 1.28)		
WHITE		0.65	(0.33, 1.27)		

Two subsections
in "Covariate"
table
(one per variable)

Effect/Covariate Included in the Model	Treatment Effect Adjusted for Covariate				
	n	Hazard Ratio	95% CI	p-value	Interaction p-value
Treatment:					
A: Drug X vs control (B: Placebo)	247	0.70	(0.51, 0.96)	0.0293	
Covariate:					
Age	247			0.8626	
34		0.70	(0.51, 0.97)		
RACE	247			0.9197	
ASIAN		0.75	(0.48, 1.16)		
BLACK OR AFRICAN AMERICAN		0.66	(0.34, 1.28)		
WHITE		0.65	(0.33, 1.27)		

Values for
"Covariate as a
Whole"
(content rows)

Effect/Covariate Included in the Model	Treatment Effect Adjusted for Covariate				
	n	Hazard Ratio	95% CI	p-value	Interaction p-value
Treatment:					
A: Drug X vs control (B: Placebo)	247	0.70	(0.51, 0.96)	0.0293	
Covariate:					
Age	247				0.8626
34		0.70	(0.51, 0.97)		
RACE	247				0.9197
ASIAN		0.75	(0.48, 1.16)		
BLACK OR AFRICAN AMERICAN		0.66	(0.34, 1.28)		
WHITE		0.65	(0.33, 1.27)		

Values for each level within each Covariate (analysis rows)

Columns Reflect
different elements
of the same
model fit

Effect/Covariate Included in the Model

n Hazard Ratio 95% CI p-value Interaction p-value

Treatment:

A: Drug X vs control (B: Placebo)

247 0.70 (0.51, 0.96) 0.0293

Covariate:

Age	247			0.8626
34		0.70	(0.51, 0.97)	
RACE	247			0.9197
ASIAN		0.75	(0.48, 1.16)	
BLACK OR AFRICAN AMERICAN		0.66	(0.34, 1.28)	
WHITE		0.65	(0.33, 1.27)	

Now suppose we have `cox_model_main_el_direct`

- Caches cox models based on the row facet it is in
- Extracts a particular aspect of the model based on
 - Which one depends on 'variable' associated with table column
 - Whether it is generating a covariate summary or individual effect row

Full reproducible code available in the advanced rtables training section here:

https://insightengineering.github.io/adv_rtables_training/training2.html#30

Then the code for our table looks something like

```

myvars <- list("n", "hr", c("lcl", "ucl"), "pval", "pval_inter")
myvarlabs <- c("n", "Hazard Ratio", "95% CI", "p-value (eff)", "p-value (inter)")
formats <- c(n = "xx", hr = "xx.xx", lcl = "(xx.xx, xx.xx)", pval = "xx.xxxx", pval_inter = "xx.xxxx")
env <- new.env()
env_lst <- replicate(length(myvars), list(env))

lyt <- basic_table() %>%
  split_cols_by_multivar(rep("STUDYID", length = length(myvars)),
                        varlabels = myvarlabs,
                        extra_args = list(model_el = myvars,
                                          cache_env = env_lst)) %>%
  summarize_row_groups(cfun = cox_model_main_el_direct) %>%
  split_rows_by_multivar(c("AGE", "RACE"),
                        varlabels = c("Age", "Ethnicity"),
                        split_label = "Covariate:",
                        indent_mod = -1) %>%
  summarize_row_groups(cfun = cox_model_el_direct,
                        extra_args = list(cov_main = TRUE)) %>%
  analyze_colvars(afun = cox_model_el_direct)

```

Columns For Different Aspects Of The Model

```

lyt <- basic_table() %>%
  split_cols_by_multivar(rep("STUDYID", length = length(myvars)),
    varlabels = myvarlabs,
    extra_args = list(model_el = myvars,
      cache_env = env_lst) %>%
  summarize_row_groups(cfun = cox_model_main_el_direct) %>%
  split_rows_by_multivar(c("AGE", "RACE"),
    varlabels = c("Age", "Ethnicity"),
    split_label = "Covariate:",
    indent_mod = -1) %>%
  summarize_row_groups(cfun = cox_model_el_direct,
    extra_args = list(cov_main = TRUE)) %>%
  analyze_colvars(afun = cox_model_el_direct)
  
```

Columns Reflect different elements of the same model fit

Effect/Covariate Included in the Model	n	Hazard Ratio	95% CI	Treatment Effect Adjusted for Covariate p-value	Interaction p-value
Treatment: A: Drug X vs control (B: Placebo)	247	0.70	(0.51, 0.96)	0.0293	
Covariate: Age	247	0.70	(0.51, 0.97)		0.8626
34					
RACE	247				0.9197
ASIAN		0.75	(0.48, 1.16)		
BLACK OR AFRICAN AMERICAN		0.66	(0.34, 1.28)		
WHITE		0.65	(0.33, 1.27)		

Summary Of Overall Model

```

lyt <- basic_table() %>%
  split_cols_by_multivar(rep("STUDYID", length = length(myvars)),
    varlabels = myvarlabs,
    extra_args = list(model_el = myvars,
      cache_env = env_lst)) %>%
  summarize_row_groups(cfun = cox_model_main_el_direct) %>%
  split_rows_by_multivar(c("AGE", "RACE"),
    varlabels = c("Age", "Ethnicity"),
    split_label = "Covariate:",
    indent_mod = -1) %>%
  summarize_row_groups(cfun = cox_model_el_direct,
    extra_args = list(cov_main = TRUE)) %>%
  analyze_colvars(afun = cox_model_el_direct)

```

Effect/Covariate Included in the Model	n	Treatment Effect Adjusted for Covariate			
		Hazard Ratio	95% CI	p-value	Interaction p-value
Treatment:					
A: Drug X vs control (B: Placebo)	247	0.70	(0.51, 0.96)	0.0293	
Covariate:					
Age	247				0.8626
RACE	247	0.70	(0.51, 0.97)		0.9197
ASIAN		0.75	(0.48, 1.16)		
BLACK OR AFRICAN AMERICAN		0.66	(0.34, 1.28)		
WHITE		0.65	(0.33, 1.27)		

Two distinct top-level sections

Facet By Covariate

```
lyt <- basic_table() %>%
  split_cols_by_multivar(rep("STUDYID", length = length(myvars)),
    varlabels = myvarlabs,
    extra_args = list(model_el = myvars,
      cache_env = env_lst)) %>%
  summarize_row_groups(cfun = cox_model_main_el_direct) %>%
  split_rows_by_multivar(c("AGE", "RACE"),
    varlabels = c("Age", "Ethnicity"),
    split_label = "Covariate:",
    indent_mod = -1) %>%
  summarize_row_groups(cfun = cox_model_el_direct,
    extra_args = list(cov_main = TRUE)) %>%
  analyze_colvars(afun = cox_model_el_direct)
```

Effect/Covariate Included in the Model	Treatment Effect Adjusted for Covariate			
	n	Hazard Ratio	95% CI	p-value
Treatment:				
A: Drug X vs control (B: Placebo)	247	0.70	(0.51, 0.96)	0.0293
Covariate:				
Age	247	0.70	(0.51, 0.97)	0.8626
RACE	247			0.9197
ASIAN		0.75	(0.48, 1.16)	
BLACK OR AFRICAN AMERICAN		0.66	(0.34, 1.28)	
WHITE		0.65	(0.33, 1.27)	

Two subsections
in "Covariate"
table
(one per variable)

Covariate Model Summaries

```

lyt <- basic_table() %>%
  split_cols_by_multivar(rep("STUDYID", length = length(myvars)),
    varlabels = myvarlabs,
    extra_args = list(model_el = myvars,
      cache_env = env_lst)) %>%
  summarize_row_groups(cfun = cox_model_main_el_direct) %>%
  split_rows_by_multivar(c("AGE", "RACE"),
    varlabels = c("Age", "Ethnicity"),
    split_label = "Covariate:",
    indent_mod = -1) %>%
  summarize_row_groups(cfun = cox_model_el_direct,
    extra_args = list(cov_main = TRUE)) %>%
  analyze_colvars(afun = cox_model_el_direct)

```

Effect/Covariate Included in the Model	n	Treatment Effect Adjusted for Covariate			
		Hazard Ratio	95% CI	p-value	Interaction p-value
Treatment:					
A: Drug X vs control (B: Placebo)	247	0.70	(0.51, 0.96)	0.0293	
Covariate:					
Age	247	0.70	(0.51, 0.97)	0.8626	
RACE	247				0.9197
ASIAN		0.75	(0.48, 1.16)		
BLACK OR AFRICAN AMERICAN		0.66	(0.34, 1.28)		
WHITE		0.65	(0.33, 1.27)		

Values for "Covariate as a Whole" (content rows)

Covariate Model Individual Terms

```
lyt <- basic_table() %>%
  split_cols_by_multivar(rep("STUDYID", length = length(myvars)),
    varlabels = myvarlabs,
    extra_args = list(model_el = myvars,
      cache_env = env_lst)) %>%
  summarize_row_groups(cfun = cox_model_main_el_direct) %>%
  split_rows_by_multivar(c("AGE", "RACE"),
    varlabels = c("Age", "Ethnicity"),
    split_label = "Covariate:",
    indent_mod = -1) %>%
  summarize_row_groups(cfun = cox_model_el_direct,
    extra_args = list(cov_main = TRUE)) %>%
  analyze_colvars(afun = cox_model_el_direct)
```

Effect/Covariate Included in the Model	Treatment Effect Adjusted for Covariate				
	n	Hazard Ratio	95% CI	p-value	Interaction p-value
Treatment:					
A: Drug X vs control (B: Placebo)	247	0.70	(0.51, 0.96)	0.0293	
Covariate:					
AGE	247				0.8626
34		0.70	(0.51, 0.97)		
RACE	247				0.9197
ASIAN		0.75	(0.48, 1.16)		
BLACK OR AFRICAN AMERICAN		0.66	(0.34, 1.28)		
WHITE		0.65	(0.33, 1.27)		

Values for each level within each Covariate (analysis rows)

But Wait - There's More!

A Ton More We Don't Have Time To Show You

- Context-preserving horizontal and vertical pagination
 - Group summaries repeated after vertical pagebreaks
 - “Page-by” splitting where values of a splitting variable are rendered as sections of pages with page titles
 - Specify page size/font etc (monospace only)
- Full Control of how values are rendered
 - Multi-valued cells
 - Convenient format declaration
 - Full control via functions
 - Decimal alignment within columns supported
- Title/Footer materials
- Referential Footnotes on columns, rows and cells
 - Including repeated symbols (same footnote on multiple cells)
- Listings support via separate `rlistings` package with simplified interface
- Tables modeled as objects
 - Interact with table after creation
 - Modify formats, etc
 - Query values programmatically
- Specified column widths and word-wrapping
 - Row labels
 - Cell values
- `qtable` - easy start akin to `qplot` from `ggplot2`

Q & A

Doing now what patients need next



Presentation title

Presentation subtitle

Name, position

DATE | confidentiality level

Presentation title

Presentation subtitle

Name, position

Table of contents

Chapter divider title

Slide title

Subtitle goes here but is not mandatory

Table design - copy/paste to reuse

	Column A	Column B	Column C	Column D
Row 1				
Row 2				
Row 3				

“Use this slide to insert a longer quote into your presentation. The quote can be multiple lines of text or even more than one paragraph.”

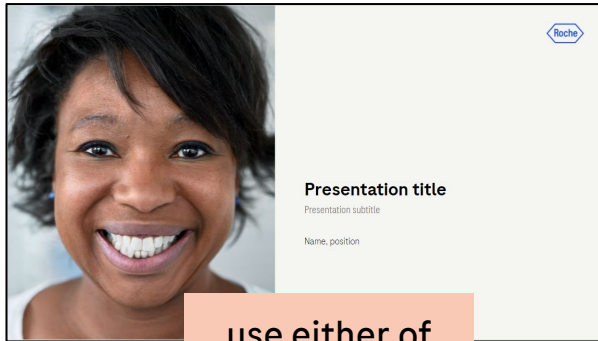
- John Doe

“Use this slide to insert a shorter quote into your presentation. Use the placeholder on the left to insert an image.”

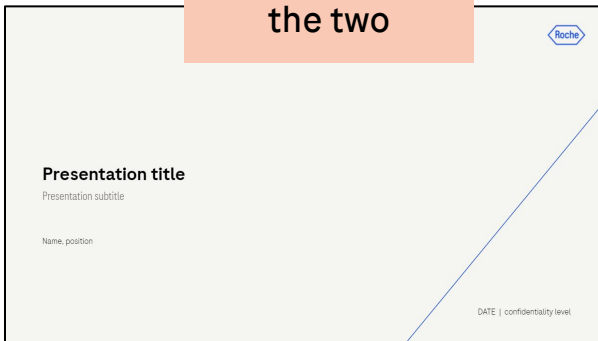
- Jane Doe

Doing now what patients need next

How to use the cover slide layouts



use either of
the two



Default cover

- If you want to exchange the image, click the image and hit “replace image”, then select the picture from your computer
- Fill in title, subtitle, presenter information, date & confidentiality level (public use, for internal use only, confidential, secret)
- Delete the alternative cover layout

Alternative cover

- Used when a longer title is required (e.g. scientific context) or when the use of an image would be inappropriate
- Fill in title, subtitle, presenter information, date & confidentiality level (public use, for internal use only, confidential, secret)
- Delete the default cover layout

Footnotes

If you need to include footnotes or references in your presentation, you must do so manually by using the pre-styled content elements found here. Just copy and paste the footnotes below in the exact same position and change the text.

For referencing to the footnotes within the text, use these numbers: ¹ ² ³ ⁴ ⁵ ⁶ ⁷ ⁸ ⁹ ¹⁰







¹ Ornare donec felis nascetur class

² Sed do eiusmod tempor incididunt

³ Labore et dolore magna aliquat





Colour palette





Primary colours / Roche Blue





Dark Blue		#022366
Roche Blue		#0b41cd
Light Blue		#1482FA
Extra Light Blue		#BDE3FF

Colour palette

Accent colours





Extra Dark Orange		#B22B0D
Dark Orange		#ED4A0D
Orange		#FF7D29
Light Orange		#FFBD69






Extra Dark Red		#8C0000
Dark Red		#C40000
Red		#FF1F26
Light Red		#FF8782

Extra Dark Purple		#7D0096
Dark Purple		#BC36F0
Purple		#E085FC
Light Purple		#F2D4FF

Colour palette




Base colours: neutrals and greys

Neutral 1		#FAC9B5
Neutral 2		#FAD6C7
Neutral 3		#FFE8DE
Neutral 4		#FFF7F5

Grey 1		#544F4F
Grey 2		#706B69
Grey 3		#C2BAB5
Grey 4		#DBD6D1
Grey 5		#F5F5F2

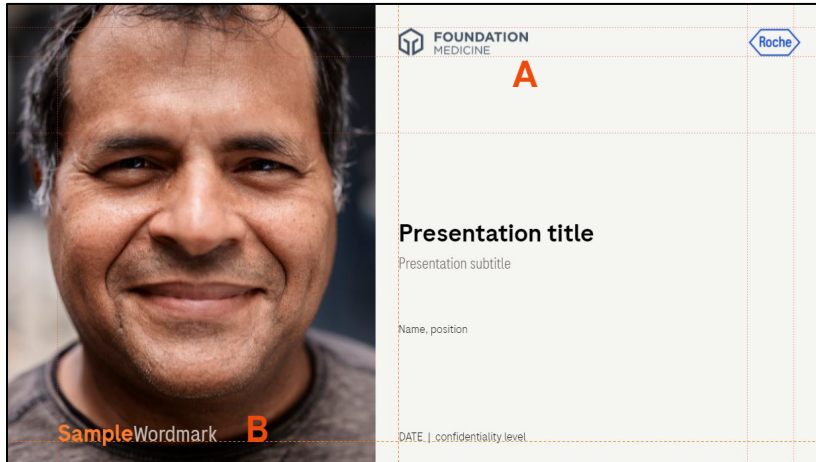
Colour palette

Status colours: used for traffic light charts, project reporting or in financial context

Red		#FF1F26
Yellow		#FFD60C
Green		#00B458

Wordmarks and partner logos

Default cover



Use View/Guides/Show Guides to help you position the logo or word mark

A: partner logos

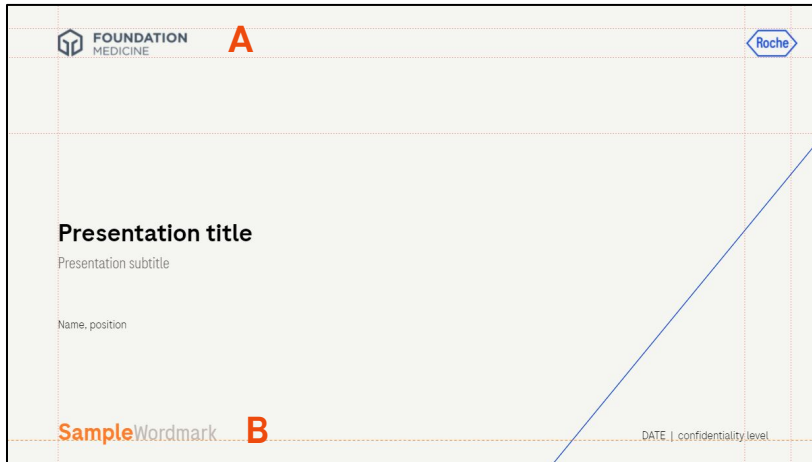
- e.g. in co-branding situations, joint ventures etc.
- Left-align the logo with the title/subtitle
- The logo height should be the same as the Roche hexagon height

B: word marks

- e.g. for internal projects, org units etc.
- The baseline of the word mark is aligned with the baseline of the date and confidentiality level
- Left-align the word mark with the guideline showing you the left margin

Wordmarks and partner logos

Alternative cover



Use View/Guides/Show Guides to help you position the logo or word mark

A: partner logos

- e.g. in co-branding situations, joint ventures etc.
- Left-align the logo with the guideline showing you the left margin
- The logo height should be the same as the Roche hexagon height

B: word marks

- e.g. for internal projects, org units etc.
- The baseline of the word mark is aligned with the baseline of the date and confidentiality level
- Left-align the word mark with the guideline showing you the left margin