Dynamic documents in R

Making tables in R Markdown

2021-10-23

Working with descriptive tables

```r
descriptives <- diabetes %>%
  filter(!is.na(glyhb)) %>%
  mutate(
    diabetic = case_when(
      glyhb >= 6.5 ~ "Diabetic",
      glyhb < 6.5 ~ "Healthy",
      NA ~ NA_character_
    ),
    bmi = (weight / height^2) * 703
  ) %>%
  group_by(diabetic) %>%
  summarise(n = n(), across(c(glyhb, bmi, age), mean, na.rm = TRUE))
```

Descriptive statistics table

Standard tibble **display**

```
descriptives
```

```
## # A tibble: 2 × 5
##   diabetic      n glyhb   bmi   age
##   <chr>     <int> <dbl> <dbl> <dbl>
## 1 Diabetic     65  9.89  30.8  58.4
## 2 Healthy     325  4.73  28.4  44.4
```

Descriptive statistics table

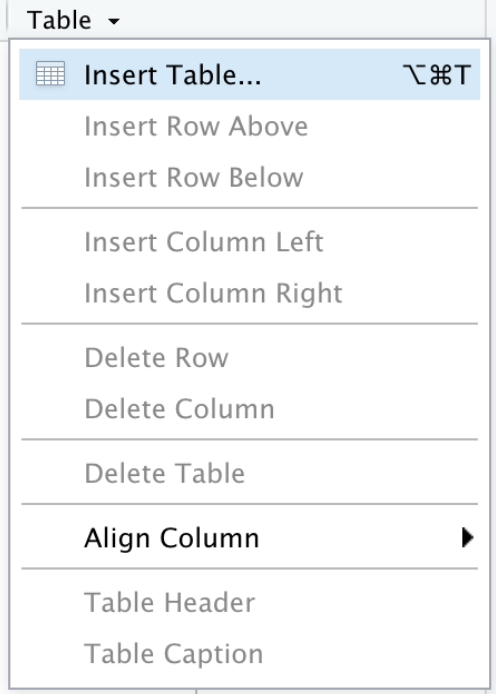
Standard tibble display

```
descriptives
```

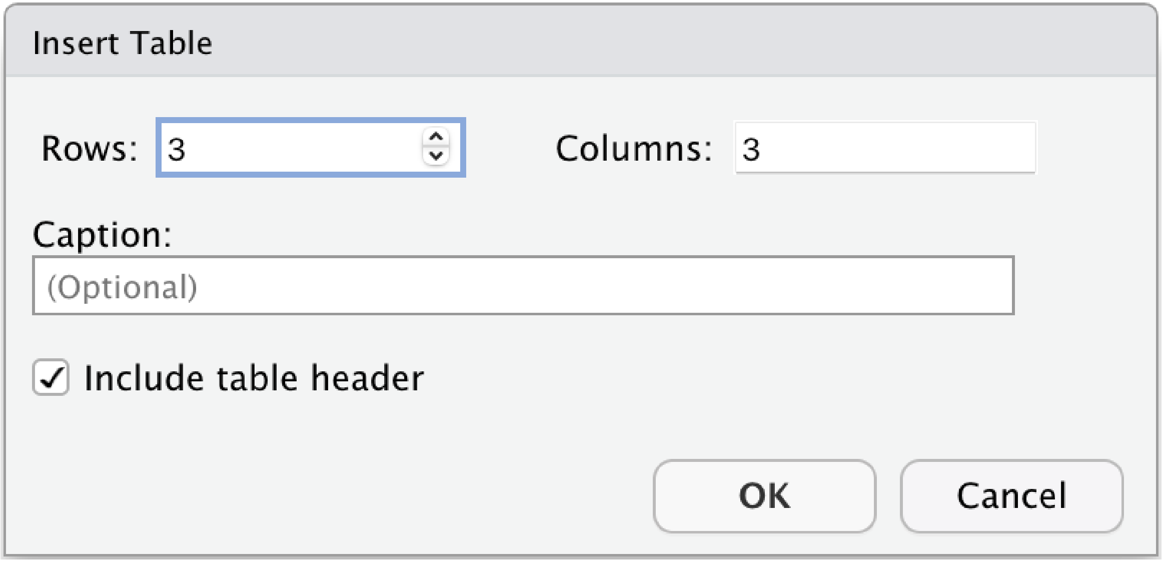
```
## # A tibble: 2 × 5
##   diabetic     n glyhb   bmi   age
##   <chr>    <int> <dbl> <dbl> <dbl>
## 1 Diabetic    65  9.89  30.8  58.4
## 2 Healthy    325  4.73  28.4  44.4
```

Useful in console, but less so for reports or presentation

Visual R Markdown tables



Visual R Markdown tables



Insert Table

Rows: 3

Columns: 3

Caption:

(Optional)

☑ Include table header

Your turn 1

Using Visual R Markdown, create a markdown table that represents these data:

The Physicians' Health Study enrolled over 22,000 male physicians to study the effect of low-dose aspirin on myocardial infarctions (heart attacks). Of those who took aspirin, 129 had heart attacks, while 10,898 did not. Of those who took the placebo, 239 had heart attacks and 10,795 did not.

knitr::kable()

kable() **creates formatted tables from rectangular objects (data.frames, matrices, and tibbles)**

```
kable(descriptives)
```

diabetic	n	glyhb	bmi	age
Diabetic	65	9.886615	30.80235	58.43077
Healthy	325	4.730400	28.38114	44.44308

Formats include pipe **('|'), HTML (**html**), LaTeX (**latex**), and reStructuredText (**rst**)**

kable(): underlying structure

Simple and pipe work in most output document formats

```
knitr::kable(x = descriptives, format = "simple")
diabetic      n      glyhb        bmi        age
---------  ----  ---------  ---------  ---------
Diabetic     65   9.886615   30.80235   58.43077
Healthy     325   4.730400   28.38114   44.44308
```

```
knitr::kable(x = descriptives, format = "pipe")
|diabetic |   n|    glyhb|      bmi|      age|
|:--------|---:|--------:|--------:|--------:|
|Diabetic |  65| 9.886615| 30.80235| 58.43077|
|Healthy  | 325| 4.730400| 28.38114| 44.44308|
```

kable() **options: column names**

Supply a vector of new names with col.names argument

```r
kable(descriptives,
  col.names = c("Diabetes Status", "N", "A1c", "BMI", "Age")
)
```

Diabetes Status	N	A1c	BMI	Age
Diabetic	65	9.886615	30.80235	58.43077
Healthy	325	4.730400	28.38114	44.44308

kable() options: number format

Use digits for decimal place

```
kable(descriptives,
  digits = 1
)
```

diabetic	n	glyhb	bmi	age
Diabetic	65	9.9	30.8	58.4
Healthy	325	4.7	28.4	44.4

kable() options: add caption

Add caption with caption argument

```r
kable(descriptives,
  caption = "Descriptive statistics"
)
```

Table: Descriptive statistics

diabetic	n	glyhb	bmi	age
Diabetic	65	9.886615	30.80235	58.43077
Healthy	325	4.730400	28.38114	44.44308

Your turn 2

Using the tidy() **function from** broom**, turn** response_model **and** marker_model **into dataframes, binding them together with** bind_rows()

Turn the resulting dataframe into a table using kable()

Set the eval **chunk option to** TRUE

Knit

```
response_model <- glm(response ~ age + stage, data = trial,
                      family = binomial)
marker_model <- lm(marker ~ trt + stage + age, data = trial)
```

Your turn 2

```
models <- bind_rows(tidy(response_model), tidy(marker_model))
kable(models)
```

term	estimate	std.error	statistic	p.value
(Intercept)	-1.4862242	0.6202284	-2.3962530	0.0165637
age	0.0193911	0.0114681	1.6908683	0.0908620
stageT2	-0.5414264	0.4400027	-1.2305071	0.2185073
stageT3	-0.0595348	0.4504203	-0.1321761	0.8948450
stageT4	-0.2310863	0.4482284	-0.5155549	0.6061653
(Intercept)	0.8336800	0.2497219	3.3384338	0.0010317
trtDrug B	-0.2009397	0.1290364	-1.5572330	0.1212427
stageT2	0.3841096	0.1734658	2.2143255	0.0281131
stageT3	0.2838452	0.1895362	1.4975777	0.1360653
stageT4	0.1987877	0.1818389	1.0932073	0.2758227
age	-0.0004592	0.0044877	-0.1023233	0.9186185

gtsummary

Create publication-ready analytic and summary tables

Good support for wide variety of output formats

Built on the larger gt package

tbl_cross()

Creates a cross-tabulation of two categorical variables

```r
library(gtsummary)
tbl_cross(
  data,
  row = x,
  col = y
)
```

tbl_cross()

```r
table_data <- diabetes %>%
  mutate(
    # create diabetic category based on A1c and calculate bmi
    diabetic = case_when(
      glyhb >= 6.5 ~ "Diabetic",
      glyhb < 6.5 ~ "Healthy",
      NA ~ NA_character_
    ), bmi = (weight / height^2) * 703
  ) %>%
  select(diabetic, age, gender, bmi)
```

tbl_cross()

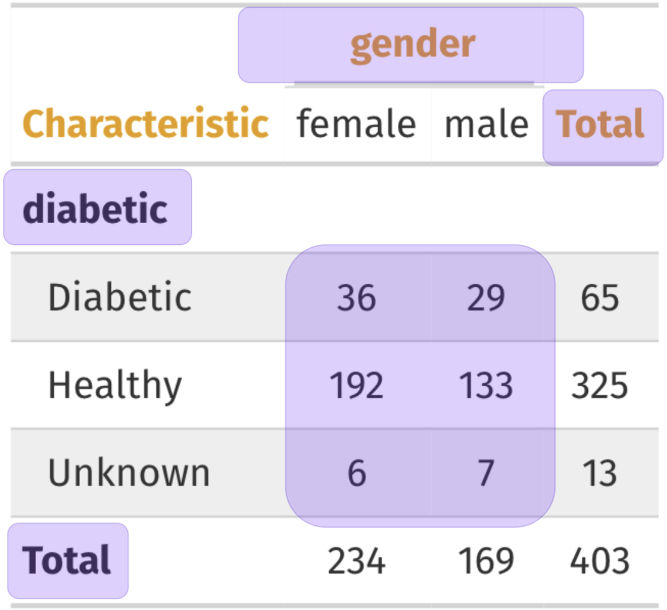
```
tbl_cross(table_data, row = diabetic, col = gender)
```

tbl_cross()

```
tbl_cross(table_data, row = diabetic, col = gender)
```

	gender		
Characteristic	female	male	**Total**
diabetic			
Diabetic	36	29	65
Healthy	192	133	325
Unknown	6	7	13
Total	234	169	403

tbl_cross() output



	gender		
Characteristic	female	male	**Total**
diabetic			
Diabetic	36	29	65
Healthy	192	133	325
Unknown	6	7	13
Total	234	169	403

tbl_cross(): **variable names**

gtsummary **uses the** labelled **package to create labels**

```
library(labelled)
var_label(table_data$diabetic) <- "Diabetes Status"
var_label(table_data$diabetic)
```

tbl_cross(): **variable names**

gtsummary **uses the** labelled **package to create labels**

```r
library(labelled)
var_label(table_data$diabetic) <- "Diabetes Status"
var_label(table_data$diabetic)
```

```
## [1] "Diabetes Status"
```

tbl_cross(): **variable names**

Set multiple variable lables with list()

```
var_label(table_data) <- list(
  gender = "Gender",
  diabetic = "Diabetes Status"
)
```

tbl_cross(): **variable names**

```
tbl_cross(table_data, diabetic, gender)
```

	Gender		
Characteristic	female	male	**Total**
Diabetes Status			
Diabetic	36	29	65
Healthy	192	133	325
Unknown	6	7	13
Total	234	169	403

Your turn 3

Create a contingency table of `trial` **(a dataset from gtsummary) using** `tbl_cross()`**: set** `trt` **to the rows and** `response` **to the columns.**

Add a p-value with `add_p()`

Knit

Your turn 3

```
trial %>%
  tbl_cross(row = trt, col = response) %>%
  add_p()
```

	Tumor Response				
Characteristic	0	1	Unknown	**Total**	**p-value**[1]
Chemotherapy Treatment					0.7
Drug A	67	28	3	98	
Drug B	65	33	4	102	
Total	132	61	7	200	

[1] Fisher's exact test

tbl_summary()

Calculates descriptive statistics

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Calculates descriptive statistics

Can split calculations by groups (i.e. categorical or dichotomous variables)

tbl_summary()

Calculates descriptive statistics

Can split calculations by groups (i.e. categorical or dichotomous variables)

Sensible defaults; easily customized

tbl_summary(): basic use

```
var_label(table_data) <- list(
  gender = "Gender",
  diabetic = "Diabetes Status",
  age = "Age",
  bmi = "BMI"
)

tbl_summary(table_data)
```

tbl_summary(): **basic use**

Characteristic	**N = 403**[1]
Diabetes Status	
Diabetic	65 (17%)
Healthy	325 (83%)
Unknown	13
Age	45 (34, 60)
Gender	
female	234 (58%)
male	169 (42%)
BMI	28 (24, 32)
Unknown	6

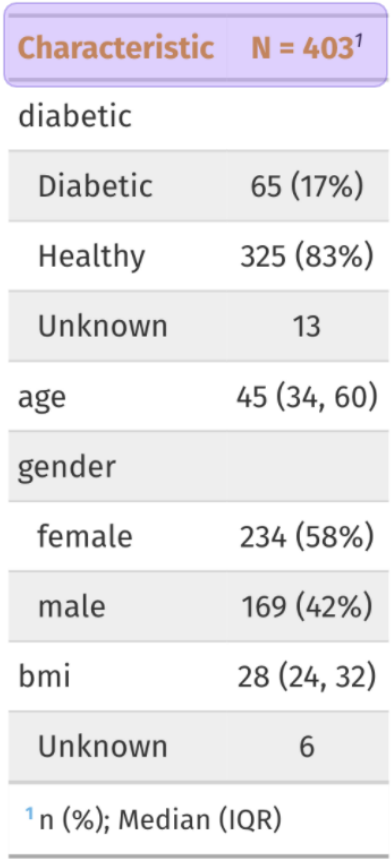
[1] n (%); Median (IQR)

tbl_summary(): basic use

Automatically adds header:

- Characteristic = variable

- N = nrow(diabetes)

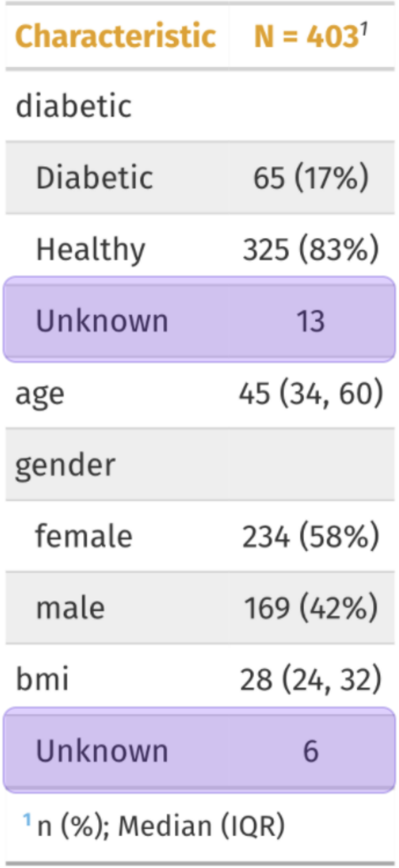


Characteristic	N = 403[1]
diabetic	
Diabetic	65 (17%)
Healthy	325 (83%)
Unknown	13
age	45 (34, 60)
gender	
female	234 (58%)
male	169 (42%)
bmi	28 (24, 32)
Unknown	6

[1] n (%); Median (IQR)

tbl_summary(): basic use

Missing = Unknown



Characteristic	N = 403[1]
diabetic	
Diabetic	65 (17%)
Healthy	325 (83%)
Unknown	13
age	45 (34, 60)
gender	
female	234 (58%)
male	169 (42%)
bmi	28 (24, 32)
Unknown	6

[1] n (%); Median (IQR)

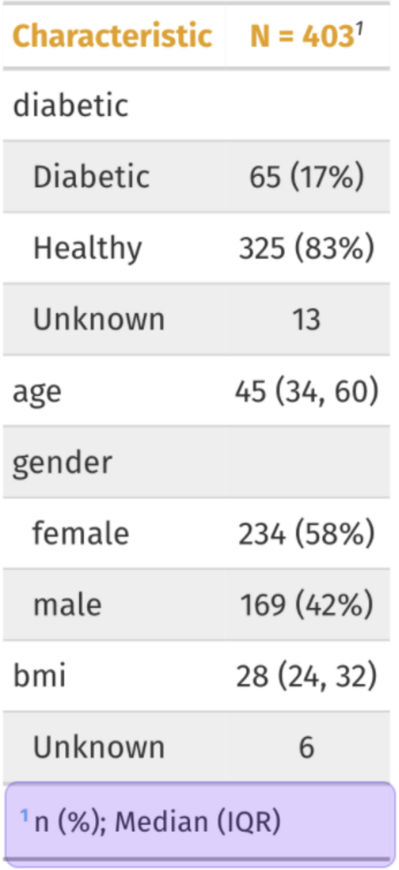
tbl_summary(): **basic use**

Source note lists summary statistics:

- **n(%)** = !is.na(var)**/403**

- **Median** = median(var)

- **IQR** = IQR(var)



Characteristic	N = 403[1]
diabetic	
Diabetic	65 (17%)
Healthy	325 (83%)
Unknown	13
age	45 (34, 60)
gender	
female	234 (58%)
male	169 (42%)
bmi	28 (24, 32)
Unknown	6

[1] n (%); Median (IQR)

tbl_summary(): variable levels

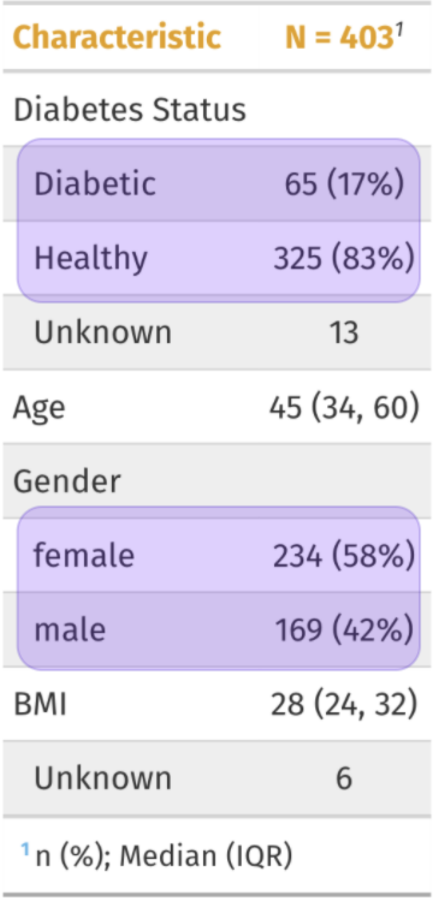
Variable levels are indented

```r
table(table_data$diabetic)
```

```
##
## Diabetic  Healthy
##       65      325
```

```r
table(table_data$gender)
```

```
##
## female   male
##    234    169
```



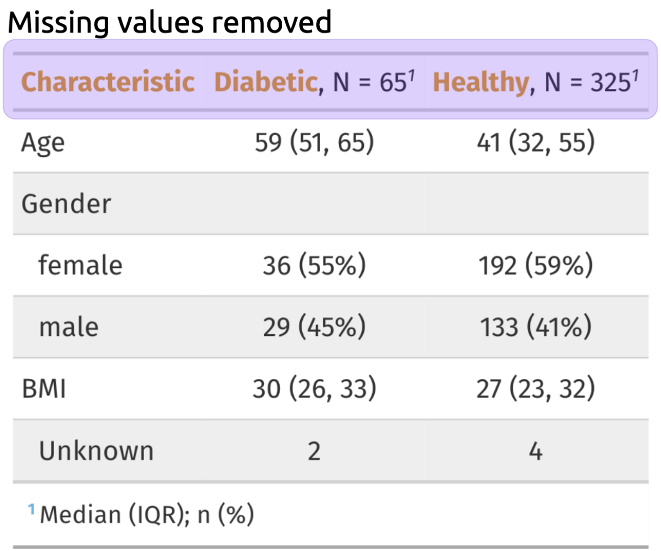
Characteristic	N = 403[1]
Diabetes Status	
Diabetic	65 (17%)
Healthy	325 (83%)
Unknown	13
Age	45 (34, 60)
Gender	
female	234 (58%)
male	169 (42%)
BMI	28 (24, 32)
Unknown	6

[1] n (%); Median (IQR)

tbl_summary(): split by groups

Split the summary table by a grouping variable

```
table_data %>%
  select(diabetic, age, gender, bmi) %>%
  tbl_summary(by = diabetic)
```



Missing values removed

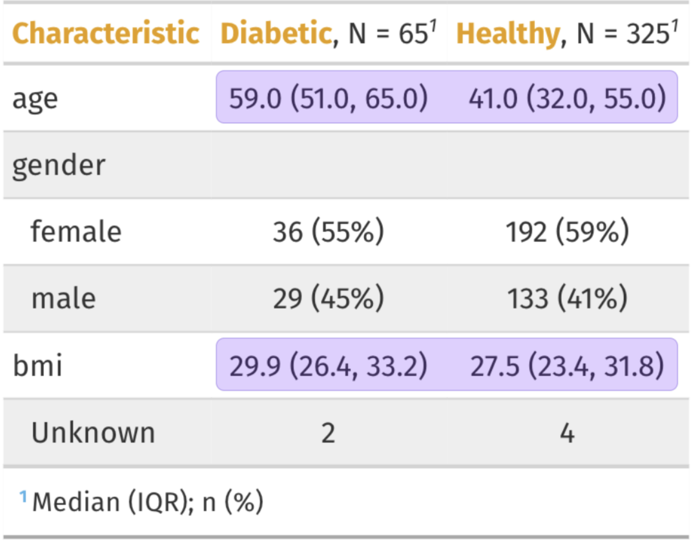
Characteristic	**Diabetic**, N = 65[1]	**Healthy**, N = 325[1]
Age	59 (51, 65)	41 (32, 55)
Gender		
female	36 (55%)	192 (59%)
male	29 (45%)	133 (41%)
BMI	30 (26, 33)	27 (23, 32)
Unknown	2	4

[1] Median (IQR); n (%)

tbl_summary(): **digits**

Change number formats with digits

```
table_data %>%
  select(diabetic, age, gender, bmi) %>%
  tbl_summary(
    by = diabetic,
    digits = all_continuous() ~ 1
  )
```



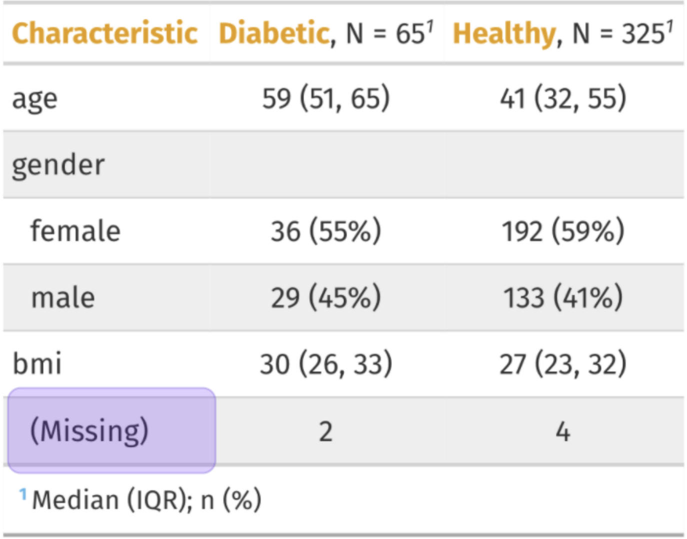
Characteristic	Diabetic, N = 65[1]	Healthy, N = 325[1]
age	59.0 (51.0, 65.0)	41.0 (32.0, 55.0)
gender		
female	36 (55%)	192 (59%)
male	29 (45%)	133 (41%)
bmi	29.9 (26.4, 33.2)	27.5 (23.4, 31.8)
Unknown	2	4

[1] Median (IQR); n (%)

tbl_summary(): **missing_text**

Rename missing value label with missing_text

```
table_data %>%
  select(diabetic, age, gender, bmi) %>%
  tbl_summary(
    by = diabetic,
    missing_text = "(Missing)"
  )
```



Characteristic	**Diabetic**, N = 65[1]	**Healthy**, N = 325[1]
age	59 (51, 65)	41 (32, 55)
gender		
female	36 (55%)	192 (59%)
male	29 (45%)	133 (41%)
bmi	30 (26, 33)	27 (23, 32)
(Missing)	2	4

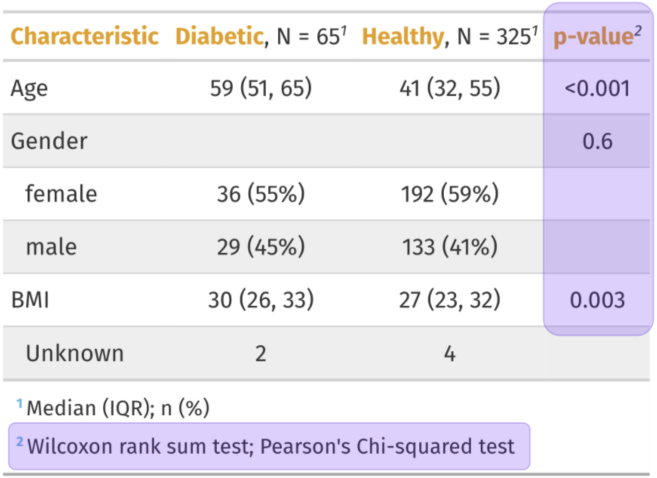
[1] Median (IQR); n (%)

tbl_summary(): tests & p-values

Add tests and p-values (with one function!)

```
table_data %>%
  select(diabetic, age, gender, bmi) %>%
  tbl_summary(by = diabetic) %>%
  add_p()
```

p-value column added



Characteristic	Diabetic, N = 65[1]	Healthy, N = 325[1]	p-value[2]
Age	59 (51, 65)	41 (32, 55)	<0.001
Gender			0.6
female	36 (55%)	192 (59%)	
male	29 (45%)	133 (41%)	
BMI	30 (26, 33)	27 (23, 32)	0.003
Unknown	2	4	

[1] Median (IQR); n (%)

[2] Wilcoxon rank sum test; Pearson's Chi-squared test

tests included in footnote

tbl_summary(): statistic

```
tbl_summary(
  table_data,
  statistic = list(all_continuous() ~ "{mean} ({sd})")
)
```

Supply statistic arguments in list() (separate with ~)

tbl_summary(): **statistic**

```
tbl_summary(
  table_data,
  statistic = list(all_continuous() ~ "{mean} ({sd})")
)
```

Access variables by name or type (all_continuous(), all_categorical(), all_dichotomous(), etc.)

tbl_summary(): statistic

```
tbl_summary(
  table_data,
  statistic = list(all_continuous() ~ "{mean} ({sd})")
)
```

Access statistic with curly brackets (i.e. {mean}, {sd}, etc.). See ?tbl_summary for options

tbl_summary(): **statistic**

Characteristic	**N = 403**[1]
Diabetes Status	
Diabetic	65 (17%)
Healthy	325 (83%)
Unknown	13
Age	47 (16)
Gender	
female	234 (58%)
male	169 (42%)
BMI	29 (7)
Unknown	6

[1] n (%); Mean (SD)

Add other elements to table

Function	Description
add_p()	add p-values to the output comparing values across groups
add_overall()	add a column with overall summary statistics
add_n()	add a column with N (or N missing) for each variable
add_difference()	add column for difference between two group, confidence interval, and p-value
add_stat_label()	add label for the summary statistics shown in each row
add_stat()	generic function to add a column with user-defined values
add_q()	add a column of q values to control for multiple comparisons

gtsummary functions to format table

Function	Description
modify_header()	update column headers
modify_footnote()	update column footnote
modify_spanning_header()	update spanning headers
modify_caption()	update table caption/title
bold_labels()	bold variable labels
bold_levels()	bold variable levels
italicize_labels()	italicize variable labels
italicize_levels()	italicize variable levels
bold_p()	bold significant p-values

Your Turn 4

Create a summary table of trial **by the** trt **variable.**

Modify the label for grade **to say "Tumor Grade"**

Add an overall column and a p-value

Modify the table to use Mean (SD) and n (%) via the statistic **argument:** list(all_continuous() ~ "{mean} ({sd})", all_categorical() ~ "{n} ({p}%)")

Bold the labels

Modify the header with modify_spanning_header(c("stat_1", "stat_2") ~ "**Treatment Received**")

Your Turn 4

```r
trial %>%
  tbl_summary(
    by = trt,
    label = grade ~ "Tumor Grade",
    statistic = list(
      all_continuous() ~ "{mean} ({sd})",
      all_categorical() ~ "{n} ({p}%)"
    )
  ) %>%
  bold_labels() %>%
  modify_spanning_header(
    c("stat_1", "stat_2") ~ "**Treatment Received**"
  ) %>%
  add_overall() %>%
  add_p()
```

Your Turn 4

		Treatment Received		
Characteristic	**Overall**, N = 200[1]	**Drug A**, N = 98[1]	**Drug B**, N = 102[1]	**p-value**[2]
Age	47 (14)	47 (15)	47 (14)	0.7
Unknown	11	7	4	
Marker Level (ng/mL)	0.92 (0.86)	1.02 (0.89)	0.82 (0.83)	0.085
Unknown	10	6	4	
T Stage				0.9
T1	53 (26%)	28 (29%)	25 (25%)	
T2	54 (27%)	25 (26%)	29 (28%)	
T3	43 (22%)	22 (22%)	21 (21%)	
T4	50 (25%)	23 (23%)	27 (26%)	
Tumor Grade				0.9
I	68 (34%)	35 (36%)	33 (32%)	
II	68 (34%)	32 (33%)	36 (35%)	
III	64 (32%)	31 (32%)	33 (32%)	
Tumor Response	61 (32%)	28 (29%)	33 (34%)	0.5
Unknown	7	3	4	
Patient Died	112 (56%)	52 (53%)	60 (59%)	0.4
Months to Death/Censor	19.6 (5.3)	20.2 (5.0)	19.0 (5.5)	0.14

[1] Mean (SD); n (%)

[2] Wilcoxon rank sum test; Pearson's Chi-squared test

Other tbl_summary() arguments

See the other options with ?tbl_summary()

Argument	Description
label	specify the variable labels printed in table
type	specify the variable type (e.g. continuous, categorical, etc.)
statistic	change the summary statistics presented
digits	number of digits the summary statistics will be rounded to
missing	whether to display a row with the number of missing observations
missing_text	text label for the missing number row
sort	change the sorting of categorical levels by frequency
percent	print column, row, or cell percentages
include	list of variables to include in summary table

tbl_regression()

```r
model_data <- diabetes %>% mutate(bmi = (weight / height^2) * 703)
glyhb_model <- lm(glyhb ~ bmi + age, data = model_data)
tbl_regression(glyhb_model)
```

tbl_regression()

```r
model_data <- diabetes %>% mutate(bmi = (weight / height^2) * 703)
glyhb_model <- lm(glyhb ~ bmi + age, data = model_data)
tbl_regression(glyhb_model)
```

Characteristic	Beta	95% CI[1]	p-value
bmi	0.04	0.01, 0.08	0.006
age	0.05	0.03, 0.06	<0.001

[1] CI = Confidence Interval

tbl_regression(): **variable labels**

Add labels just like tbl_summary()

```r
var_label(model_data) <- list(
  bmi = "BMI",
  glyhb = "A1c",
  age = "Age"
)
glyhb_model <- lm(glyhb ~ bmi + age, data = model_data)
tbl_regression(glyhb_model)
```

tbl_regression(): **variable labels**

Add labels just like tbl_summary()

```
var_label(model_data) <- list(
  bmi = "BMI",
  glyhb = "A1c",
  age = "Age"
)
glyhb_model <- lm(glyhb ~ bmi + age, data = model_data)
tbl_regression(glyhb_model)
```

Characteristic	Beta	95% CI[1]	p-value
BMI	0.04	0.01, 0.08	0.006
Age	0.05	0.03, 0.06	<0.001

[1] CI = Confidence Interval

tbl_regression(): **other options**

Argument	Description
label	modify variable labels in table
exponentiate	exponentiate model coefficients
include	names of variables to include in output. Default is all variables
show_single_row	By default, categorical variables are printed on multiple rows. If a variable is dichotomous and you wish to print the regression coefficient on a single row, include the variable name(s) here.
conf.level	confidence level of confidence interval
intercept	indicates whether to include the intercept
estimate_fun	function to round and format coefficient estimates
pvalue_fun	function to round and format p-values
tidy_fun	function to specify/customize tidier function

tbl_regression(): **Model statistics**

Add model statistics from broom::glance()

```
tbl_regression(glyhb_model) %>%
  add_glance_source_note()
```

tbl_regression(): **Model statistics**

Add model statistics from broom::glance()

```
tbl_regression(glyhb_model) %>%
  add_glance_source_note()
```

Characteristic	Beta	95% CI[1]	p-value
BMI	0.04	0.01, 0.08	0.006
Age	0.05	0.03, 0.06	<0.001

[1] CI = Confidence Interval

R^2 = 0.132; Adjusted R^2 = 0.127; Sigma = 2.06; Statistic = 28.9; p-value = <0.001; df = 2; Log-likelihood = -821; AIC = 1,650; BIC = 1,666; Deviance = 1,617; Residual df = 381; No. Obs. = 384

tbl_regression(): **other add options**

Function	Description
add_global_p()	adds the global p-value for a categorical variables
add_glance_source_note()	adds statistics from glance() as source note
add_vif()	adds column of the variance inflation factors (VIF)
add_q()	add a column of q values to control for multiple comparisons

tbl_regression(): **format options**

```r
tbl_regression(glyhb_model) %>%
  add_glance_source_note() %>%
  bold_p() %>%
  bold_labels()
```

tbl_regression(): format options

```
tbl_regression(glyhb_model) %>%
  add_glance_source_note() %>%
  bold_p() %>%
  bold_labels()
```

Characteristic	Beta	95% CI[1]	p-value
BMI	0.04	0.01, 0.08	**0.006**
Age	0.05	0.03, 0.06	**<0.001**

[1] CI = Confidence Interval

R^2 = 0.132; Adjusted R^2 = 0.127; Sigma = 2.06; Statistic = 28.9; p-value = <0.001; df = 2; Log-likelihood = -821; AIC = 1,650; BIC = 1,666; Deviance = 1,617; Residual df = 381; No. Obs. = 384

tbl_regression(): **modify caption**

```r
tbl_regression(glyhb_model) %>%
  add_glance_source_note() %>%
  bold_p() %>%
  bold_labels() %>%
  modify_caption("**Association of BMI and A1c adjusted for age**")
```

tbl_regression(): modify caption

```
tbl_regression(glyhb_model) %>%
  add_glance_source_note() %>%
  bold_p() %>%
  bold_labels() %>%
  modify_caption("**Association of BMI and A1c adjusted for age**")
```

Association of BMI and A1c adjusted for age

Characteristic	**Beta**	**95% CI**[1]	**p-value**
BMI	0.04	0.01, 0.08	**0.006**
Age	0.05	0.03, 0.06	**<0.001**

[1] CI = Confidence Interval

R^2 = 0.132; Adjusted R^2 = 0.127; Sigma = 2.06; Statistic = 28.9; p-value = <0.001; df = 2; Log-likelihood = -821; AIC = 1,650; BIC = 1,666; Deviance = 1,617; Residual df = 381; No. Obs. = 384

Your turn 5

Create a regression table for response model; **exponentiate the output with** exponentiate = TRUE

Add a global P-value

Add the model statistics via add_glance_source_note()

Italicize the variable levels

Merge the table you just made with marker_table **using** tbl_merge()

Your turn 5

```
response_table <- response_model %>%
  tbl_regression(
    exponentiate = TRUE
  ) %>%
  add_global_p() %>%
  add_glance_source_note() %>%
  italicize_levels()

marker_table <- marker_model %>%
  tbl_regression() %>%
  add_global_p()

both_tables <- list(response_table, marker_table)
tbl_merge(both_tables)
```

Your turn 5

	Table 1			Table 2		
Characteristic	**OR**[1]	**95% CI**[1]	**p-value**	**Beta**	**95% CI**[1]	**p-value**
Age	1.02	1.00, 1.04	0.087	0.00	-0.01, 0.01	>0.9
T Stage			0.6			0.2
T1	—	—		—	—	
T2	0.58	0.24, 1.37		0.38	0.04, 0.73	
T3	0.94	0.39, 2.28		0.28	-0.09, 0.66	
T4	0.79	0.33, 1.90		0.20	-0.16, 0.56	
Chemotherapy Treatment						0.12
Drug A				—	—	
Drug B				-0.20	-0.46, 0.05	

[1] OR = Odds Ratio, CI = Confidence Interval

Null deviance = 229; Null df = 182; Log-likelihood = -112; AIC = 234; BIC = 250; Deviance = 224; Residual df = 178; No. Obs. = 183

Cross-referencing tables

A bookdown output format, e.g.

bookdown::html_document2

Cross-referencing tables

A bookdown output format, e.g. bookdown::html_document2

A table caption (caption = "Table title", modify_caption())

Cross-referencing tables

A bookdown output format, e.g. bookdown::html_document2

A table caption (caption = "Table title", modify_caption()**)**

A named code chunk ({r chunk-name}**)**

Cross-referencing tables

A bookdown output format, e.g. bookdown::html_document2

A table caption (caption = "Table title", modify_caption()**)**

A named code chunk ({r chunk-name}**)**

Reference with \@ref(tab:chunk-name)

Your Turn 6

Modify the YAML header to use bookdown::html_document2 **as the output**

Add a caption to the merged table above using modify_caption()

Reference that table below using this format: \@ref(tab:name-of-chunk)

Your turn 6

```r
tbl_merge(both_tables) %>%
  modify_caption(
    "Regression models of participant markets and response"
  )
```

Your turn 6

Regression models of participant markets and response

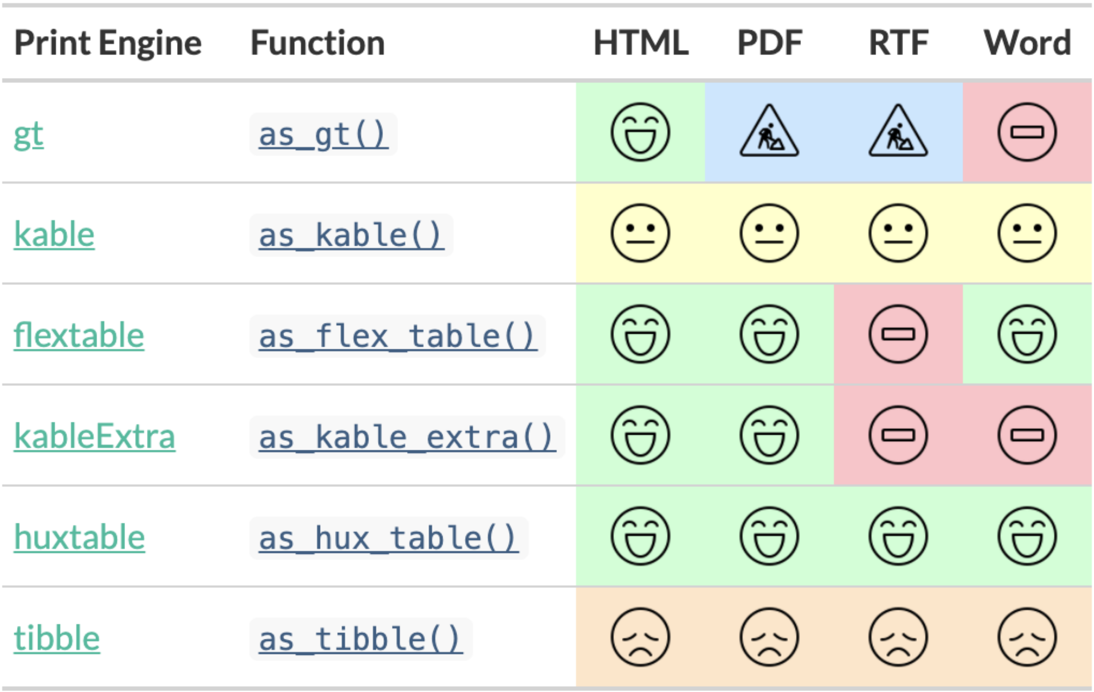
	Table 1			Table 2		
Characteristic	**OR**[1]	**95% CI**[1]	**p-value**	**Beta**	**95% CI**[1]	**p-value**
Age	1.02	1.00, 1.04	0.087	0.00	-0.01, 0.01	>0.9
T Stage			0.6			0.2
T1	—	—		—	—	
T2	0.58	0.24, 1.37		0.38	0.04, 0.73	
T3	0.94	0.39, 2.28		0.28	-0.09, 0.66	
T4	0.79	0.33, 1.90		0.20	-0.16, 0.56	
Chemotherapy Treatment						0.12
Drug A				—	—	
Drug B				-0.20	-0.46, 0.05	

[1] OR = Odds Ratio, CI = Confidence Interval

Null deviance = 229; Null df = 182; Log-likelihood = -112; AIC = 234; BIC = 250; Deviance = 224; Residual df = 178; No. Obs. = 183

> In Table 1, we show two regression models: a linear model of participant markets and a logistic regression model of participant response.

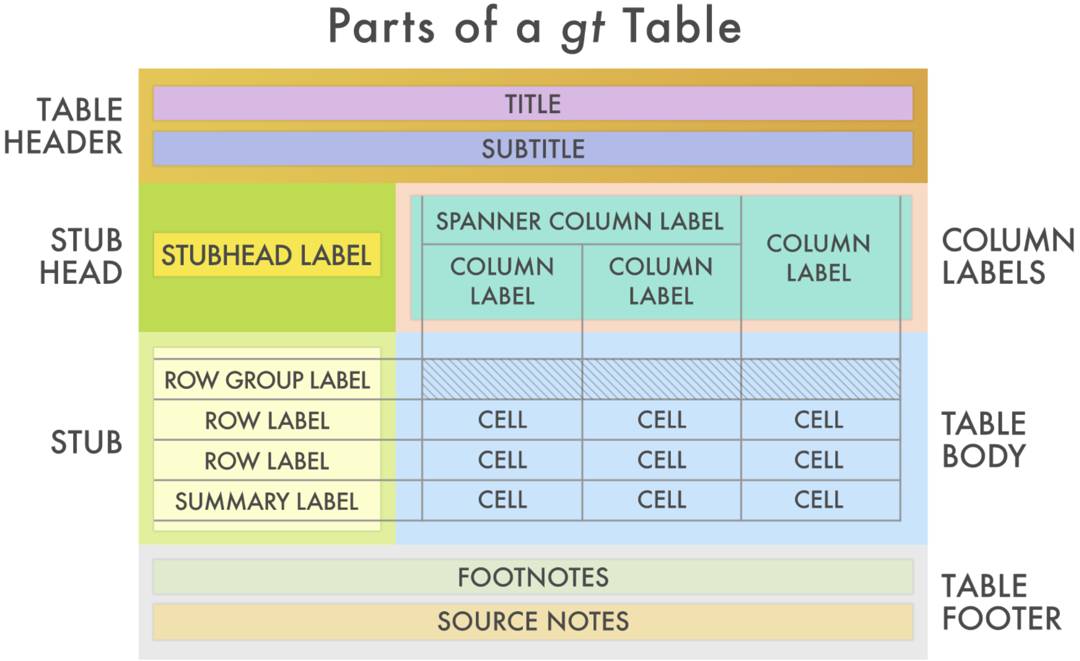
gtsummary: Output formats



Print Engine	Function	HTML	PDF	RTF	Word
gt	`as_gt()`	😆	🚧	🚧	⛔
kable	`as_kable()`	😐	😐	😐	😐
flextable	`as_flex_table()`	😆	😆	⛔	😆
kableExtra	`as_kable_extra()`	😆	😆	⛔	⛔
huxtable	`as_hux_table()`	😆	😆	😆	😆
tibble	`as_tibble()`	😞	😞	😞	😞

Also check out the gt package!

"construct a wide variety of useful tables with a cohesive set of table parts"



Resources

R Markdown Cookbook: Tables: A series of recipes using `kable()` and friends

gtsummary Website: Many vignettes to learn more about gtsummary

gt Website: Vignettes and a short course on learning gt