

Project One

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Usage Notes

- System setup
 - Install `quarto` executable from <https://quarto.org>
- To compile report:
 - From the command line: `quarto render reportTemplate.qmd --to html`
 - To only render `html` use `quarto render reportTemplate.qmd`
 - Inside RStudio: press **Render** from a recent RStudio
- Commenting/annotation/highlighting
 - If you have a free account with `hypothes.is`, will be placing the report on a permanent location on a web server, and want to enable highlighting, comments, and annotations by readers of the report, set `hypothesis: true` See <https://quarto.org/docs/output-formats/html-basics.html#commenting>
- Note on markdown tables
 - To keep markdown tables from devoting more space to a column than needed, make the second line of the table look like `-|-|`

- Use `require(qreport)` to get the `kabl` function which makes it easy to combine multiple tables into one block

Thanks to Max Rohde for starting this template.

```
require(Hmisc)
# Make base graphics look better:
spar <- function(bot=0, left=0, top=0, rt=0)
  par(mar=c(3.25 + bot, 5 + left, 0.5 + top, 0.5 * rt),
      lwd=1.75, mgp=c(2.0, 0.475, 0), tcl=-0.4, xpd=FALSE, ps=14,
      cex.lab=1.15, cex.axis=0.8)
# Set abbreviations for chunk option names
knitr::set_alias(w = 'fig.width', h = 'fig.height')

options(prType='html') # for certain Hmisc and rms functions
# Get dataset from Dept of Biostatistics dataset repository
getHdata(pbc)
pbc[1:20, 1:8]
```

	bili	albumin	stage	protime	sex	fu.days	age	spiders
1	14.5	2.60	4	12.2	female	400	58.76523	present
2	1.1	4.14	3	10.6	female	4500	56.44627	present
3	1.4	3.48	4	12.0	male	1012	70.07255	absent
4	1.8	2.54	4	10.3	female	1925	54.74059	present
5	3.4	3.53	3	10.9	female	1504	38.10541	present
6	0.8	3.98	3	11.0	female	2503	66.25873	absent
7	1.0	4.09	3	9.7	female	1832	55.53457	absent
8	0.3	4.00	3	11.0	female	2466	53.05681	absent
9	3.2	3.08	2	11.0	female	2400	42.50787	present
10	12.6	2.74	4	11.5	female	51	70.55989	present
11	1.4	4.16	4	12.0	female	3762	53.71389	present
12	3.6	3.52	4	13.6	female	304	59.13758	present
13	0.7	3.85	3	10.6	female	3577	45.68925	absent
14	0.8	2.27	4	11.0	male	1217	56.22177	absent
15	0.8	3.87	3	11.0	female	3584	64.64613	absent
16	0.7	3.66	3	10.8	female	3672	40.44353	absent
17	2.7	3.15	4	10.5	female	769	52.18344	absent
18	11.4	2.80	4	12.4	female	131	53.93018	present
19	0.7	3.56	3	11.0	female	4232	49.56057	absent

Table 1: Two parts of 'pbc' data frame

bili	albumin	stage		bili	albumin	stage	protime
14.5	2.60	4	21	0.6	3.83	4	11.4
1.1	4.14	3	22	3.4	3.63	4	11.6
1.4	3.48	4	23	17.4	2.94	4	11.7
1.8	2.54	4	24	2.1	4.00	2	9.9
3.4	3.53	3	25	0.7	4.10	2	11.3
0.8	3.98	3	26	5.2	3.68	3	9.9
1.0	4.09	3	27	21.6	3.31	4	12.0
0.3	4.00	3	28	17.2	3.23	4	13.0
3.2	3.08	2	29	0.7	3.78	2	10.6
12.6	2.74	4	30	3.6	2.54	4	11.0
1.4	4.16	4	31	4.7	3.44	2	10.3
3.6	3.52	4	32	1.8	3.34	4	10.6
0.7	3.85	3	33	0.8	3.19	3	12.0
0.8	2.27	4	34	0.8	3.70	2	10.5
0.8	3.87	3	35	1.2	3.20	3	10.6
0.7	3.66	3	36	0.3	3.39	2	10.6
2.7	3.15	4	37	7.1	3.01	4	12.0
11.4	2.80	4	38	3.3	3.53	4	11.0
0.7	3.56	3	39	0.7	3.00	4	10.6
5.1	3.51	4	40	1.3	3.34	4	11.0

```
20 5.1 3.51 4 13.0 female 1356 59.95346 absent
```

```
# Take two tables and produce one html section
require(qreport) # makes kables easy to use and provides various Quarto helpers
kabl(pbc[1:20, 1:3], pbc[21:40, 1:4], caption='Two parts of `pbc` data frame')
```

1 Descriptive Statistics

```
describe(pbc)
```

A marginal note goes here. It can be as long as you want and can include raw R output.

```
spar(top=1) # allow for title (title produced by default by hist)
with(pbc, hist(albumin, nclass=30))
```

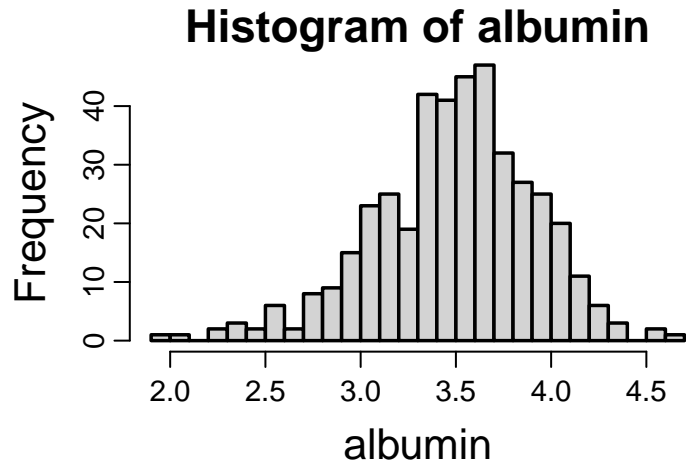


Figure 1: Histogram of serum albumin

```
# To just use the caption in the margin, use spar() and hist(..., main='')
```

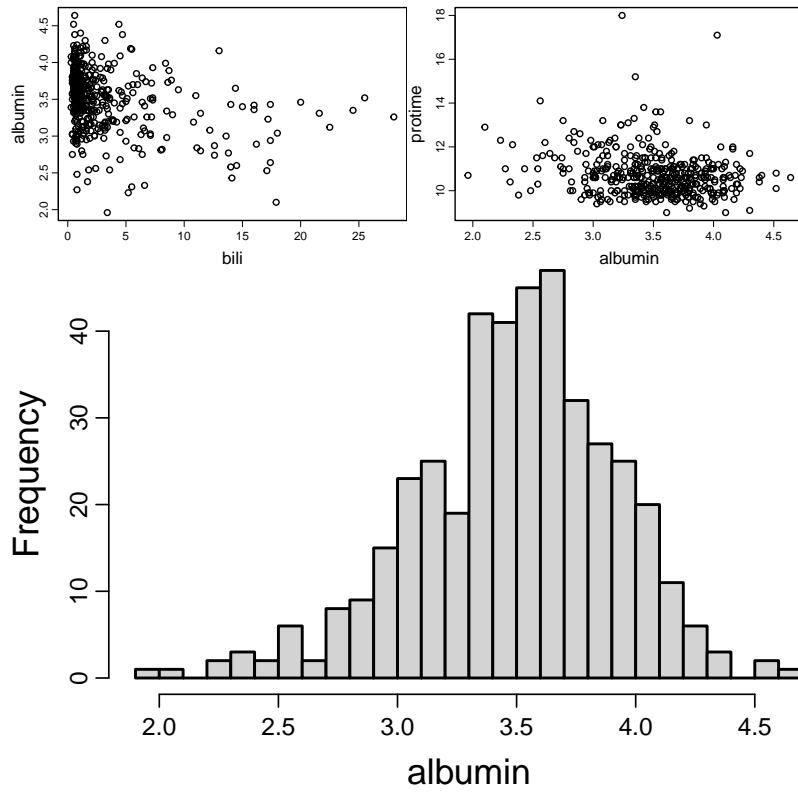
Quarto has a nice way of letting you lay out plots. In the following example layout: `[[1,1], [1]]` in the chunk header¹ specifies that there are two rows of plots, with the first row containing two plots and the second only one, with the one made wider to fill the whole space.

```
with(pbc, {
  spar()
  plot(bili, albumin)
  plot(albumin, protime)
  hist(albumin, nclass=25, main='') } )
```

2 Running quarto

The `yaml` header in this template will cause both `html` and `pdf` files (through `LaTeX`) to be produced. To only produce one

¹See [this](#) for more information



output format, run e.g. `quarto render my.qmd --to html`.

To make your script dual-purpose you can't always reliably use marginal notes in LaTeX using this `quarto` syntax:

So automatically sense which output format is being created and create a character string that will work for both `html` and `LaTeX`. For `LaTeX`, a boxed note in the body of the document will appear.

some text ... some text ...

```
ishtml <- knitr::is_html_output()
mNote <- if(ishtml) '.column-margin' else '.callout-note appearance="minimal"'
```

Then use

```
# Make a temporary mNote string for illustration
mNote <- '.callout-note appearance="minimal"'
```

some text ... some text ...

3 Computing Environment

```
# ggplot2 was not actually used, only imported by qreport
grateful::cite_packages(pkgs='Session', output='paragraph', out.dir='.',
  cite.tidyverse=FALSE, omit=c('grateful', 'ggplot2'))
```

We used R version 4.4.0 (R Core Team 2024) and the following R packages: `data.table` v. 1.15.4 (Barrett et al. 2024), `Hmisc` v. 5.1.3 (Harrell Jr 2024), `qreport` v. 1.0.1 (Harrell 2024).

The code was run on macOS Sonoma 14.4.1.

Barrett, Tyson, Matt Dowle, Arun Srinivasan, Jan Gorecki, Michael Chirico, and Toby Hocking. 2024. *data.table: Extension of “data.frame”*. <https://CRAN.R-project.org/package=data.table>.

- Harrell, Frank. 2024. *qreport: Statistical Reporting with “Quarto”*. <https://hbiostat.org/R/qreport/>.
- Harrell Jr, Frank E. 2024. *Hmisc: Harrell Miscellaneous*. <https://hbiostat.org/R/Hmisc/>.
- R Core Team. 2024. *R: A Language and Environment for Statistical Computing*. Vienna, Austria: R Foundation for Statistical Computing. <https://www.R-project.org/>.