Combining LaTeX and markdown for reports

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Here is a Markdown subheading (Level 2)

We can use markdown syntax to *italicize* or **bold** or ~~strikethrough~~ text. Since Markdown doesn't include small-caps functionality, we can still use LaTeXfunctionality to WRITE IN SMALL CAPS.

We can use markdown syntax to include images:

Figure 1: Here is a forest in Papua New Guinea

However, there are some limits to markdown- for example, we can't resize the figure to make it larger. We can always turn to LaTeXcode to specify options for the image:

Figure 2: Tropical forest!

Here is another Markdown subheading

Let's add some equations

Here is LATEXcode to write the likelihood equation that PyRate uses to estimate rates of speciation and extinction[1] (incedently, look! a footnote!). We can write the equation as an in-line equation...

$P(X|s,e,q) = \prod_{i=1}^{n} P_{NHPP}(t_1^i, \ldots t_{k_i}^i | s_i, e_i, q)$

or as a numbered equation in the `equation` environment:

$$P(X|s,e,q) = \prod_{i=1}^{n} P_{NHPP}(t_1^i, \ldots t_{k_i}^i | s_i, e_i, q) \tag{1}$$

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[1]https://academic.oup.com/sysbio/article/63/3/349/1650079/Bayesian-Estimation-of-Speciation-and-Extinction

Citing documents

In this RMarkdown+LaTeX world, citing documents becomes super easy. We have included the following lines in the `YAML` header:

```
bibliography: biblio.bib
csl: ecology-letters.csl
```

The first line here tells the software that knits our document that the bibiolography for the document is stored in `biblio.bib`; the second line tells the software that a style-guide that describes exactly how we want our references formatted is saved at `ecology-letters.csl`. **Note**: You can download the style sheet for your journal of choice from this repository of style sheets[2].

Let's quickly inspect the contents of the files `biblio.bib`, which contains the BibTeX formatted citations for the Cooney et al. paper that we have used as a source for beak morphology data and for PyRate. **NOTE** also that we are using the `system()` function in `R` to execute shell commands from `R`- you may find this handy later on!

```r
system("cat biblio.bib", intern = T)
```

```
##  [1] "@article{Cooney_2017,"
##  [2] "\tdoi = {10.1038/nature21074},"
##  [3] "\turl = {https://doi.org/10.1038%2Fnature21074},"
##  [4] "\tyear = 2017,"
##  [5] "\tmonth = {feb},"
##  [6] "\tpublisher = {Springer Nature},"
##  [7] "\tvolume = {542},"
##  [8] "\tnumber = {7641},"
##  [9] "\tpages = {344--347},"
## [10] "\tauthor = {Christopher R. Cooney and Jen A. Bright and Elliot J. R. Capp and A
## [11] "\ttitle = {Mega-evolutionary dynamics of the adaptive radiation of birds},"
## [12] "\tjournal = {Nature}"
## [13] "}"
## [14] "@article{Silvestro_2014,"
## [15] "\tdoi = {10.1111/2041-210x.12263},"
## [16] "\turl = {https://doi.org/10.1111%2F2041-210x.12263},"
## [17] "\tyear = 2014,"
## [18] "\tmonth = {sep},"
## [19] "\tpublisher = {Wiley-Blackwell},"
## [20] "\tvolume = {5},"
## [21] "\tnumber = {10},"
## [22] "\tpages = {1126--1131},"
## [23] "\tauthor = {Daniele Silvestro and Nicolas Salamin and Jan Schnitzler},"
## [24] "\teditor = {Liam Revell},"
```

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[2]https://www.zotero.org/styles

```
## [25] "\ttitle = {{PyRate}: a new program to estimate speciation and extinction rates
## [26] "\tjournal = {Methods in Ecology and Evolution}"
## [27] "}"
## [28] ""
```

Given that we have those two entries in the `biblio.bib` file, we can cite them in the document using the syntax `Here's a sentence that cites both papers [@Cooney_2017; @Silvestro_2014]`. Here's a sentence that cites both papers (Silvestro *et al.* 2014; Cooney *et al.* 2017).

A chunk of R code

Just like any Rmd document, we can add R code chunks to this document:

```r
# make a plot using ggplot2
library(ggplot2)

# I sample from the diamonds dataset
data(diamonds)
d <- diamonds[sample(nrow(diamonds), 1000), ]

# build the plot, of Price of Diamond v. Carat
# Facet by the quality of the cut
p <- ggplot(data = d, aes(x = carat, y = price)) +
  geom_point(aes(text = paste("Clarity:", clarity))) +
  geom_smooth(aes(colour = cut, fill = cut)) + facet_wrap(~ cut)
```
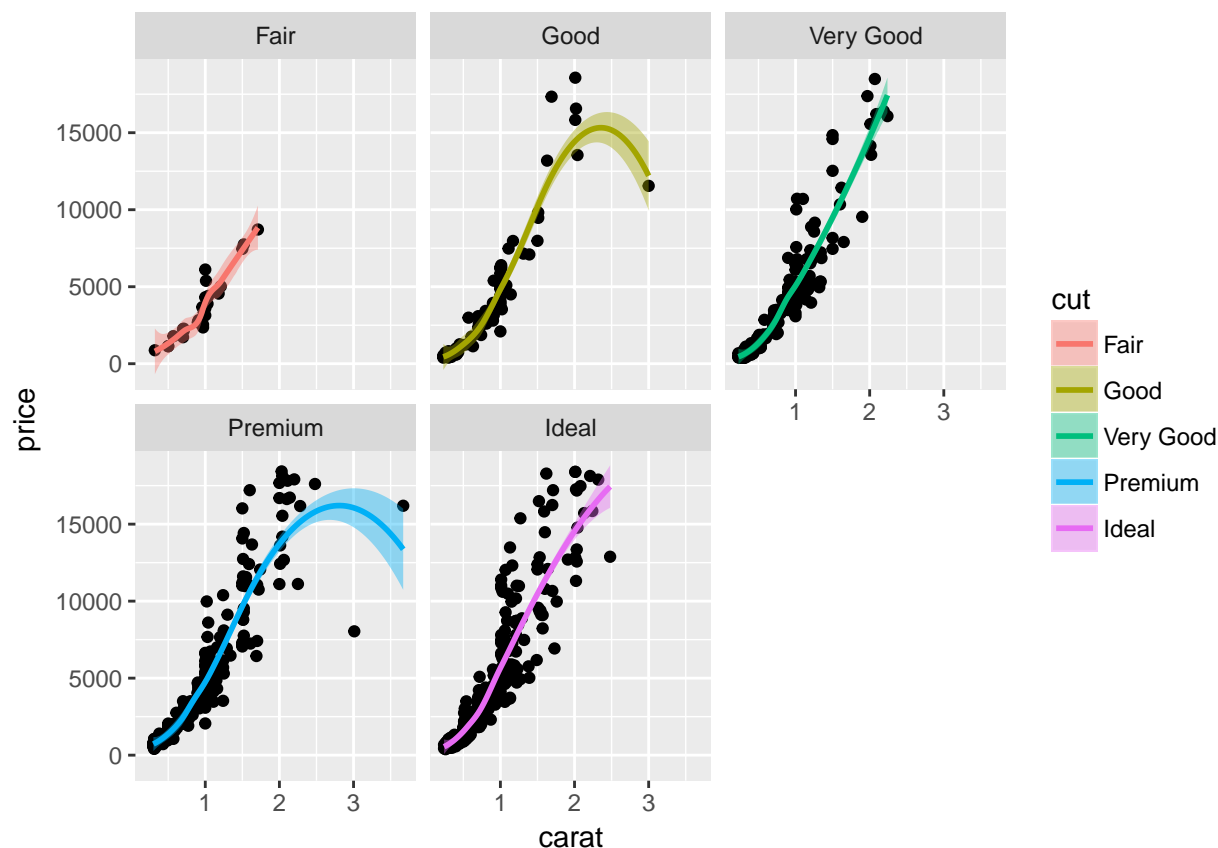
```
## Warning: Ignoring unknown aesthetics: text
```

```r
p
```

```
## `geom_smooth()` using method = 'loess'
```

Controlling plot size

We can control the size of the plot by adding the `fig.height` and `fig.width` arguments to the definition of the R chunk:
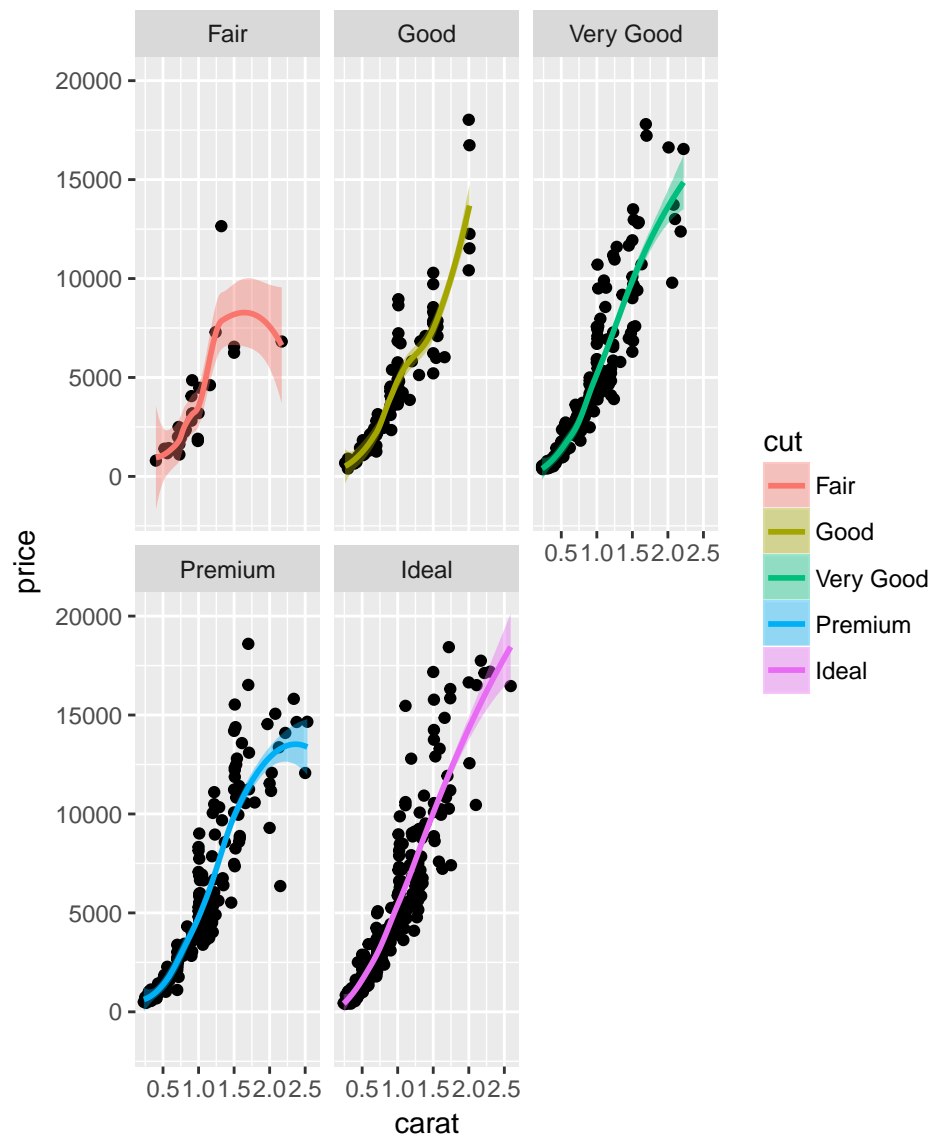
```r
# make a plot using ggplot2
library(ggplot2)

# I sample from the diamonds dataset
data(diamonds)
d <- diamonds[sample(nrow(diamonds), 1000), ]

# build the plot, of Price of Diamond v. Carat
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p <- ggplot(data = d, aes(x = carat, y = price)) +
  geom_point(aes(text = paste("Clarity:", clarity))) +
  geom_smooth(aes(colour = cut, fill = cut)) + facet_wrap(~ cut)
```

```
## Warning: Ignoring unknown aesthetics: text
```

```r
p
```

```
## `geom_smooth()` using method = 'loess'
```

Controlling code display, show code but don't run it

We might want to show code that we don't actually run in the document. We can use the `eval = F` argument in the definiton of the R code chunk

```r
# make a plot using ggplot2
library(ggplot2)

# I sample from the diamonds dataset
data(diamonds)
d <- diamonds[sample(nrow(diamonds), 1000), ]

# build the plot, of Price of Diamond v. Carat
# Facet by the quality of the cut
```

```
p <- ggplot(data = d, aes(x = carat, y = price)) +
  geom_point(aes(text = paste("Clarity:", clarity))) +
  geom_smooth(aes(colour = cut, fill = cut)) + facet_wrap(~ cut)


p
```
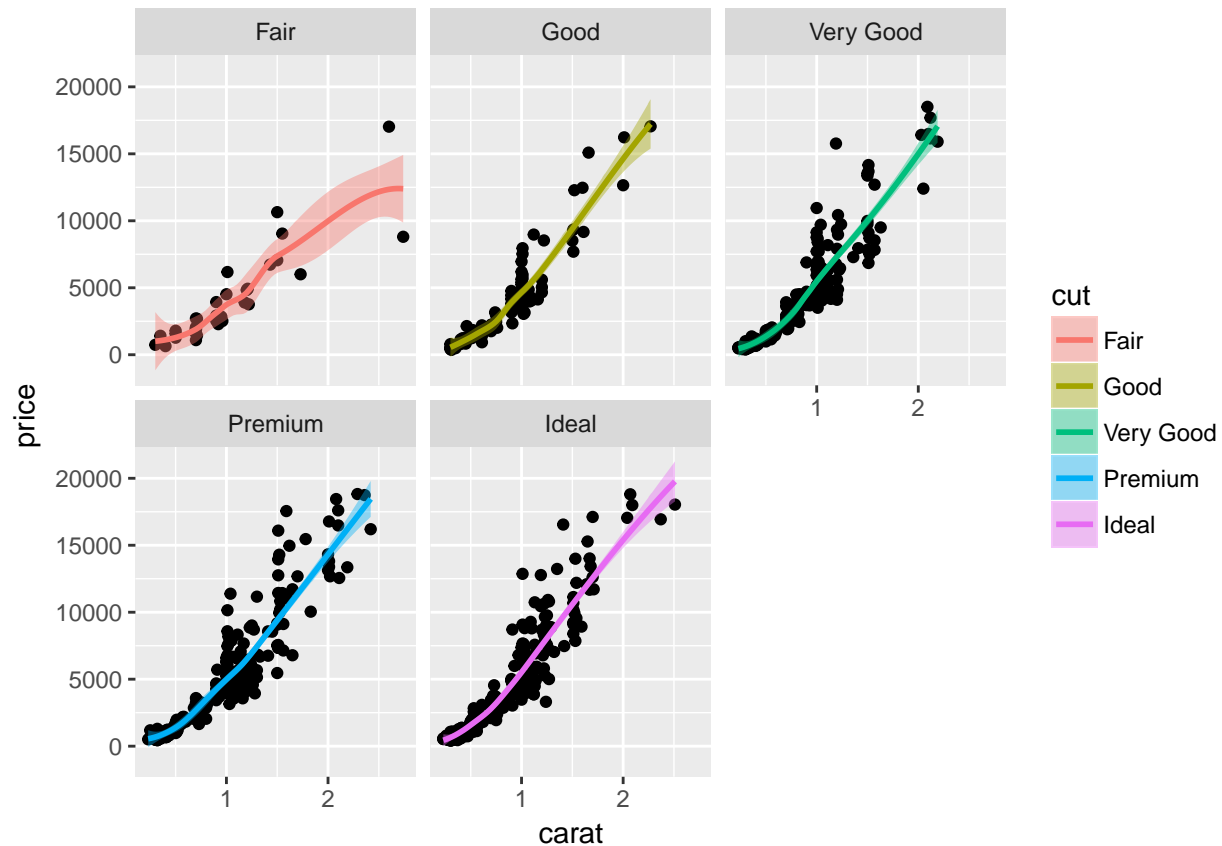
or the other way, run code but don't show it

Alternatively, we might want to run some code and show the output, but not actually show the code. We can do this with the argument `echo = F`

```
## Warning: Ignoring unknown aesthetics: text
```

```
## `geom_smooth()` using method = 'loess'
```


Other sources of help

There's a lot of great places to get help on RMarkdown documents online:

- RStudio's guide to Rmarkdown: link

- WriteLatex's guide to Latex : link

- Yihui Xie's book on Knitr: link

Finally, importing in the references

In the current setup, RStudio's Rmd to PDF conversion adds a bibiolography to the end of the paper on a new page. Recall that the citations are being formatted according to `ecology-letters.csl`. So, we add a subheading for the references section at the end of our document:

References

```python
#some python code
f = open("/path/to/file")
lines= f.readline()
```

1.Cooney, C.R., Bright, J.A., Capp, E.J.R., Chira, A.M., Hughes, E.C. & Moody, C.J.A. *et al.* (2017). Mega-evolutionary dynamics of the adaptive radiation of birds. *Nature*, 542, 344–347.

2.Silvestro, D., Salamin, N. & Schnitzler, J. (2014). PyRate: A new program to estimate speciation and extinction rates from incomplete fossil data. *Methods in Ecology and Evolution*, 5, 1126–1131.