# 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+LaTeXworld, 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!

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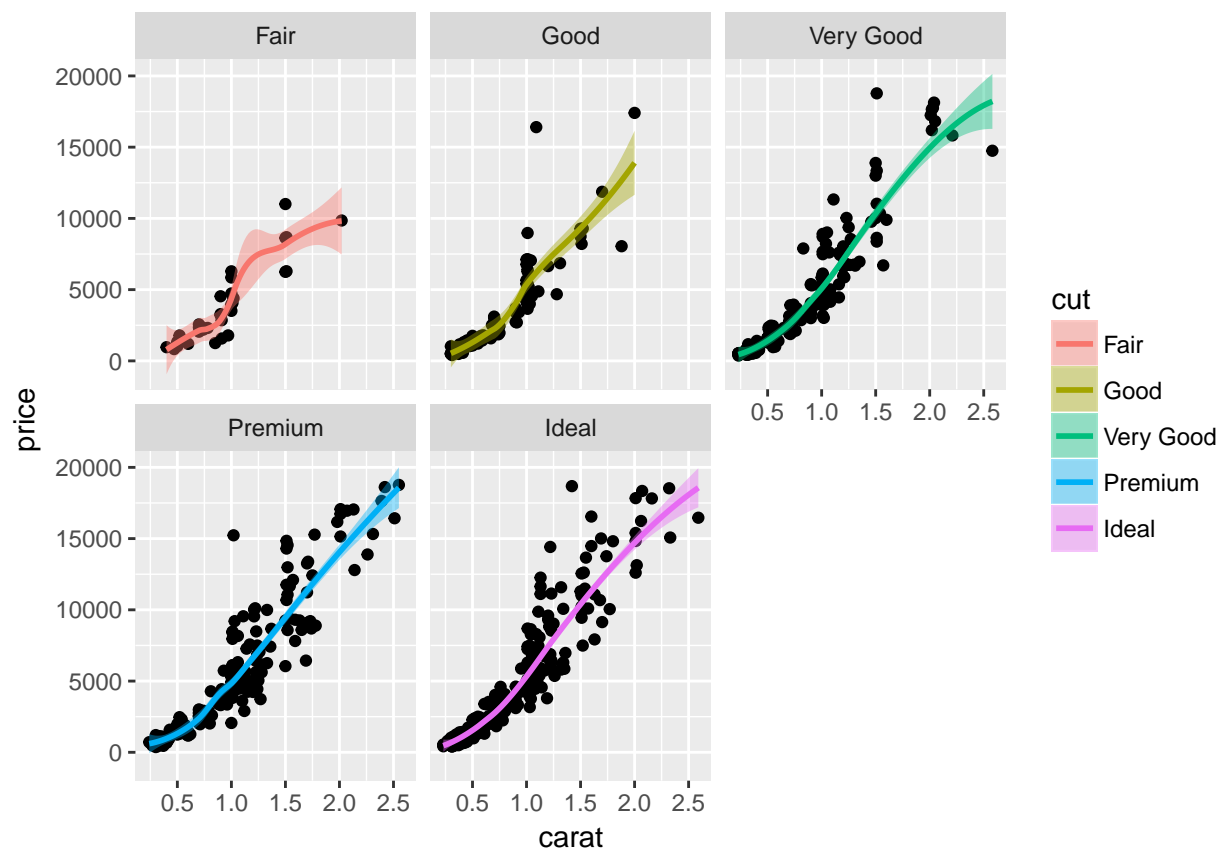
```
## Warning: Ignoring unknown aesthetics: text
```

```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
# 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
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
```

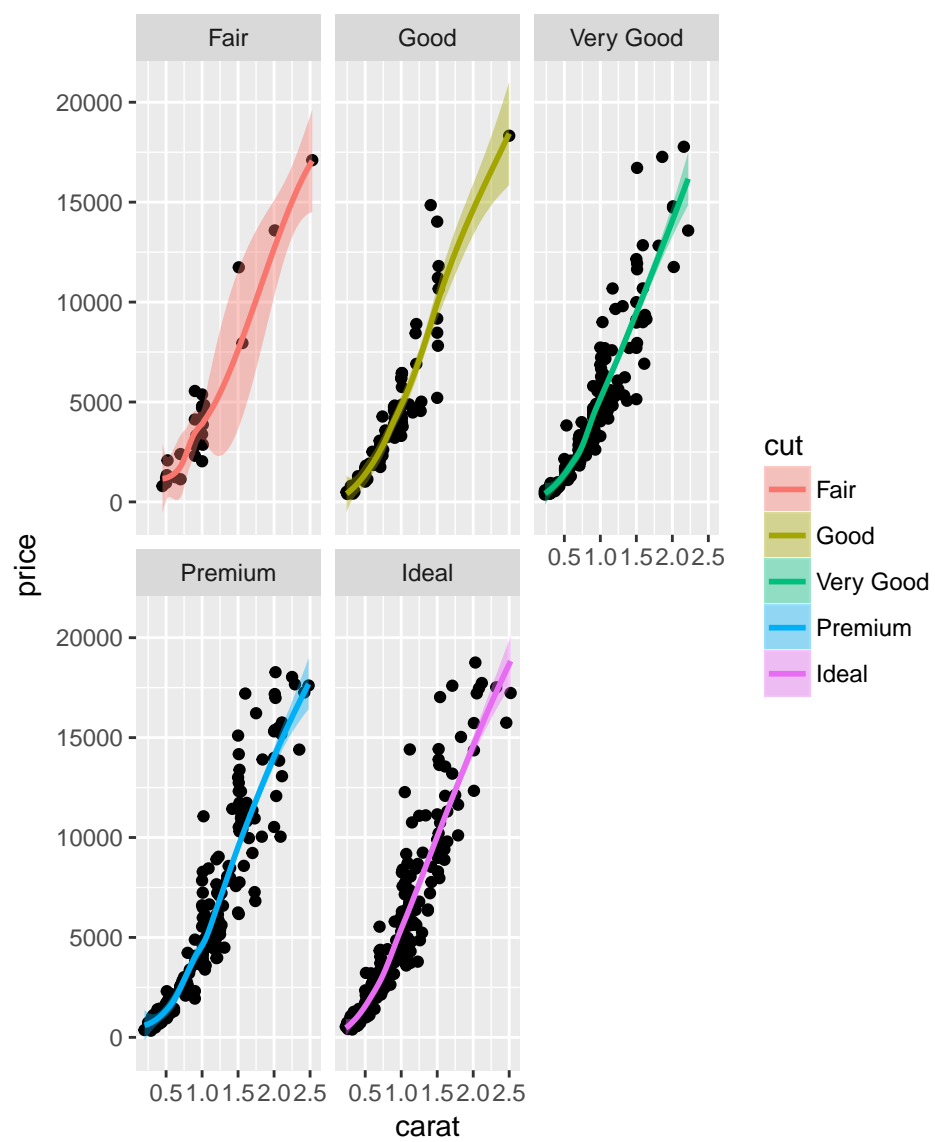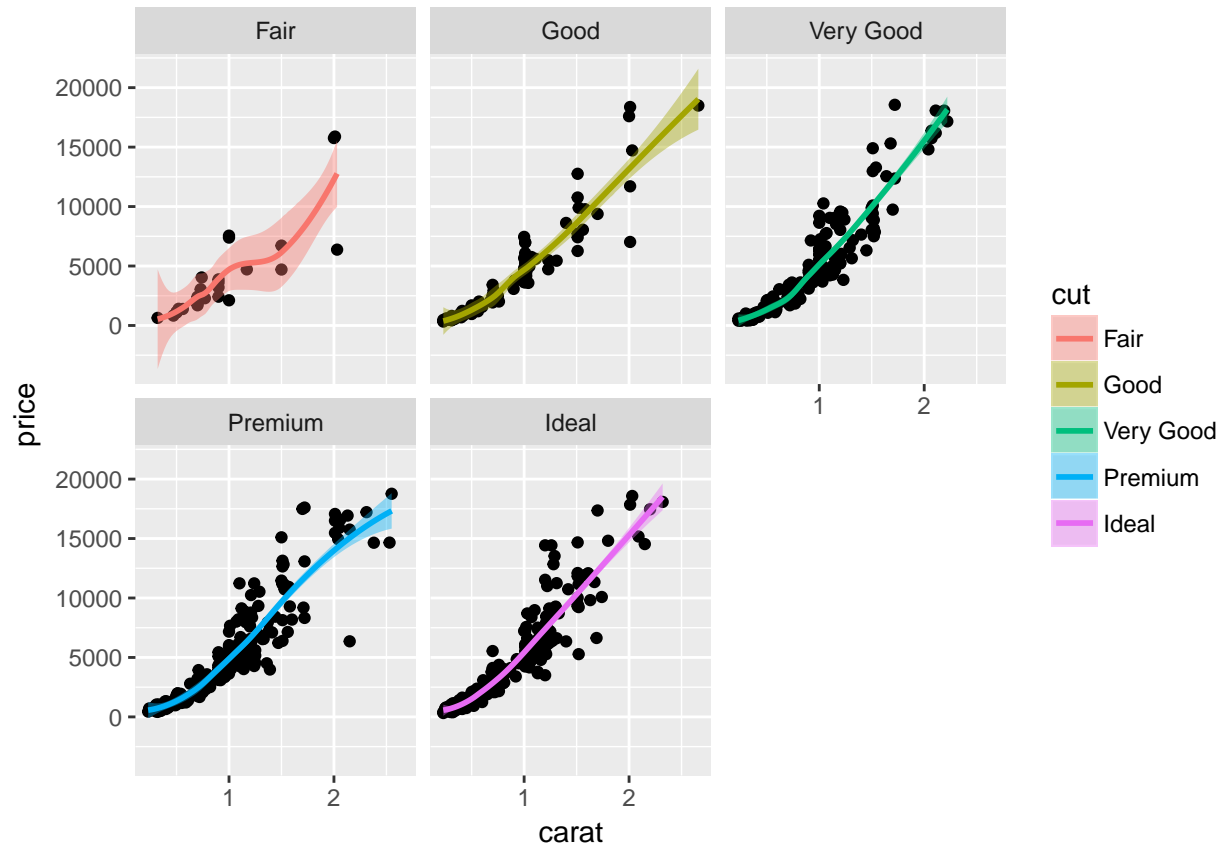**or the other way, run code but don't show it**

Figure 3: here's some text

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:

## Including python code with syntax highlighting

Use the following syntax to include `python` code with proper syntax hihglighting:

````
```python
f = open("/path/to/file")
lines = f.readlines()
```
````

````
```bash
````

```
wget <>
for VAR in file.txt; do ...
```

## 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

Cooney, C.R., Bright, J.A., Capp, E.J.R., Chira, A.M., Hughes, E.C., Moody, C.J.A., Nouri, L.O., Varley, Z.K. & Thomas, G.H. (2017). Mega-evolutionary dynamics of the adaptive radiation of birds. *Nature*, **542**, 344–347.

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