

# Amazing Document

Amazing Location

Filippo Gambarota

2024-07-04

## Table of contents

1	Quarto	1
1.1	General Markup . . . . .	1
1.2	Math . . . . .	1
1.3	Citations . . . . .	3
1.4	Code chunks - Plots . . . . .	3
1.5	Code chunks - Tables . . . . .	5
1.6	Code chunks - Tables . . . . .	6
1.7	Inline code chunks . . . . .	6
1.8	References . . . . .	7

## 1 Quarto

### 1.1 General Markup

You can write standard markdown code. Using **bold**, *italic* or underlined text. You can include an external figure and also using cross reference with `@fig-quarto` that produce Figure [1](#)

### 1.2 Math

You can write math using Latex code:

```
$$
y = \beta_0 + \beta_1 + \epsilon
$$
```



Figure 1: My beautiful caption

$$y = \beta_0 + \beta_1 + \epsilon$$

And also inline math using `\alpha` that produce  $\alpha$

### 1.3 Citations

You can cite references from a `.bib` file using the syntax `[@Chen2021-jb]` that produce (Chen et al. 2021). We can also cite multiple authors `[@Morey2011-zc; @Lakens2018-ri]` (Morey and Rouder 2011; Lakens, Scheel, and Isager 2018) or suppress the author name `[-@Valentine2011-yq]` (2011).

A reference section will be automatically created at the end of the document (see Section 1.8).

This is the result:

```
dat <- iris
summary(iris)
```

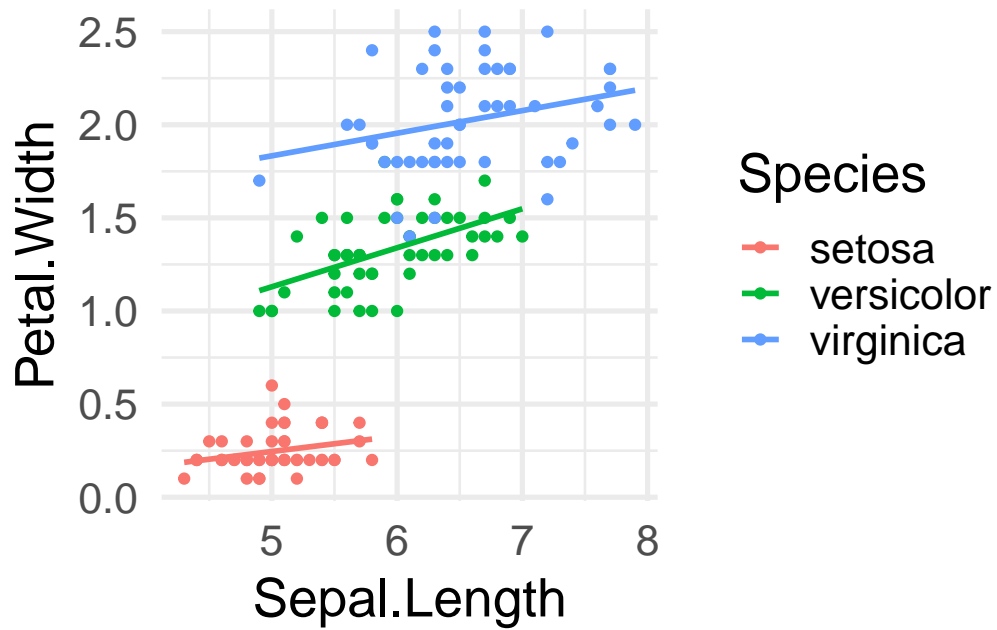
Sepal.Length	Sepal.Width	Petal.Length	Petal.Width
Min. :4.300	Min. :2.000	Min. :1.000	Min. :0.100
1st Qu.:5.100	1st Qu.:2.800	1st Qu.:1.600	1st Qu.:0.300
Median :5.800	Median :3.000	Median :4.350	Median :1.300
Mean :5.843	Mean :3.057	Mean :3.758	Mean :1.199
3rd Qu.:6.400	3rd Qu.:3.300	3rd Qu.:5.100	3rd Qu.:1.800
Max. :7.900	Max. :4.400	Max. :6.900	Max. :2.500
Species			
setosa :50			
versicolor:50			
virginica :50			

### 1.4 Code chunks - Plots

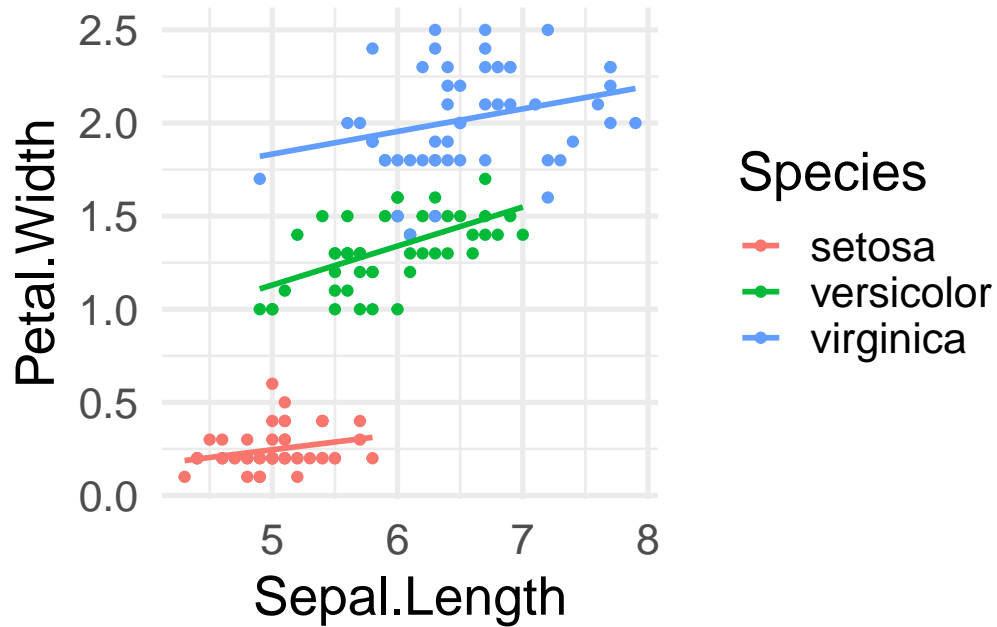
```
library(ggplot2)
dat |>
  ggplot(aes(x = Sepal.Length, y = Petal.Width, color = Species)) +
  geom_point() +
```

```
geom_smooth(method = "lm", se = FALSE) +  
theme_minimal(20)
```

`geom\_smooth()` using formula = 'y ~ x'



`geom\_smooth()` using formula = 'y ~ x'



## 1.5 Code chunks - Tables

You can also create already formatted tables with the statistics. Let's fit a simple linear model:

```
fit <- lm(Petal.Width ~ Sepal.Length * Species, data = dat)
summary(fit)
```

Call:

```
lm(formula = Petal.Width ~ Sepal.Length * Species, data = dat)
```

Residuals:

Min	1Q	Median	3Q	Max
-0.56675	-0.10596	-0.02419	0.09624	0.50897

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	-0.17022	0.38833	-0.438	0.66180
Sepal.Length	0.08314	0.07739	1.074	0.28444
Speciesversicolor	0.25348	0.49994	0.507	0.61292
Speciesvirginica	1.39633	0.48104	2.903	0.00428 **

```

Sepal.Length:Speciesversicolor  0.12621    0.09371    1.347  0.18014
Sepal.Length:Speciesvirginica   0.03827    0.08848    0.433  0.66599
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.1909 on 144 degrees of freedom
Multiple R-squared:  0.9394,    Adjusted R-squared:  0.9372 
F-statistic: 446.1 on 5 and 144 DF,  p-value: < 2.2e-16

```

## 1.6 Code chunks - Tables

Let's produce the table with the `broom` and `kableExtra` packages:

```

library(flextable)
library(broom)

fit |>
  broom::tidy() |>
  flextable() |>
  autofit() |>
  theme_booktabs()

```

Table 1: My caption

term	estimate	std.error	statistic	p.value
(Intercept)	-0.17022108	0.38833483	-0.4383359	0.6617
Sepal.Length	0.08314444	0.07738610	1.0744106	0.2844
Speciesversicolor	0.25347680	0.49993857	0.5070159	0.6129
Speciesvirginica	1.39632946	0.48104236	2.9027162	0.0042
Sepal.Length:Speciesversicolor	0.12621275	0.09370888	1.3468601	0.1801
Sepal.Length:Speciesvirginica	0.03827201	0.08848065	0.4325467	0.6659

## 1.7 Inline code chunks

If you want to use R code within the text to report statistics you can use the syntax ``r r code``. For example:

- the average `Sepal.Length` for the `Setosa` group is ``r mean(iris$Sepal.Length[iris$Species == 'setosa'])``

Become

- the average `Sepal.Length` for the `Setosa` group is 5.006

## 1.8 References

Go back to Section [1.3](#)

- Chen, Gang, Daniel S Pine, Melissa A Brotman, Ashley R Smith, Robert W Cox, and Simone P Haller. 2021. “Trial and Error: A Hierarchical Modeling Approach to Test-Retest Reliability.” *NeuroImage* 245 (December): 118647. <https://doi.org/10.1016/j.neuroimage.2021.118647>.
- Lakens, Daniël, Anne M Scheel, and Peder M Isager. 2018. “Equivalence Testing for Psychological Research: A Tutorial.” *Adv. Methods Pract. Psychol. Sci.* 1 (2): 259–69. <https://doi.org/10.1177/2515245918770963>.
- Morey, Richard D, and Jeffrey N Rouder. 2011. “Bayes Factor Approaches for Testing Interval Null Hypotheses.” *Psychol. Methods* 16 (4): 406–19. <https://doi.org/10.1037/a0024377>.
- Valentine, Jeffrey C, Anthony Biglan, Robert F Boruch, Felipe González Castro, Linda M Collins, Brian R Flay, Sheppard Kellam, Eve K Mościcki, and Steven P Schinke. 2011. “Replication in Prevention Science.” *Prev. Sci.* 12 (2): 103–17. <https://doi.org/10.1007/s11121-011-0217-6>.