

# Learn Tables

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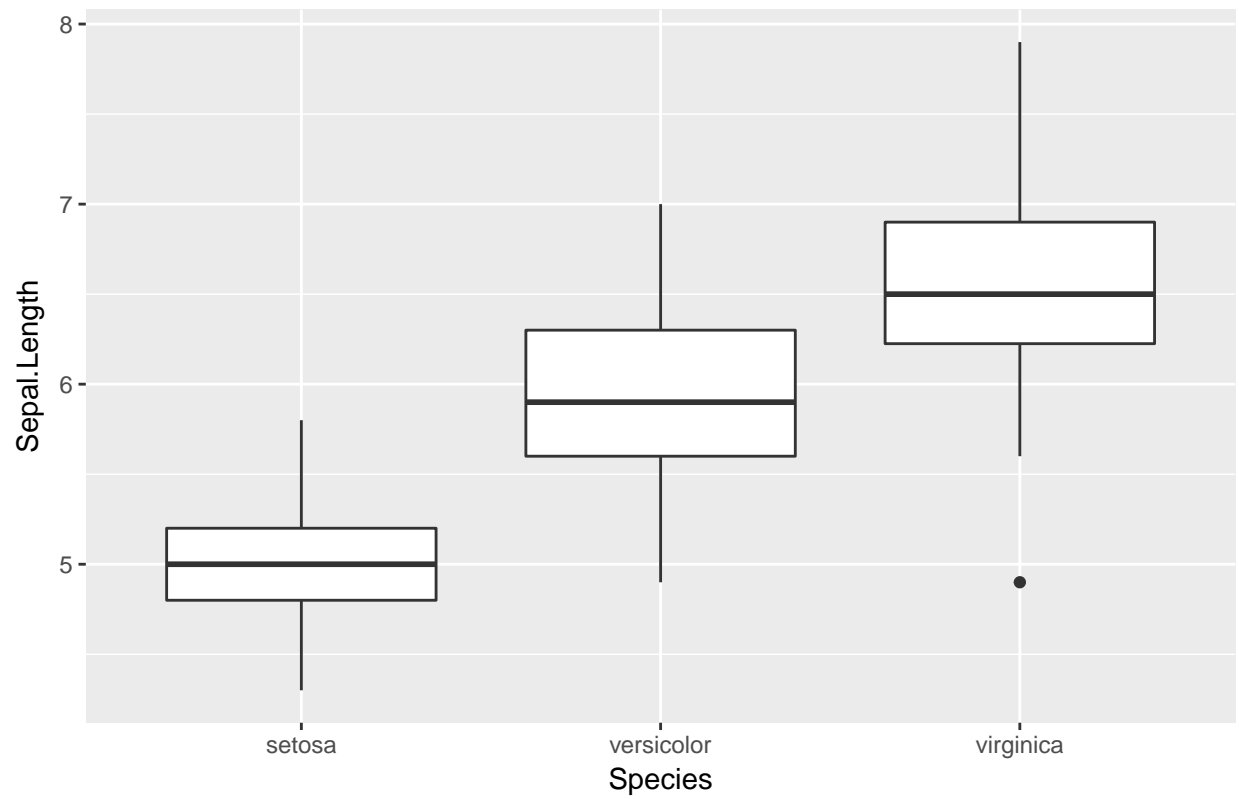
## Introduction

This report uses the Iris data to learn about tables in R Markdown.

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
<b>1</b>	5.1	3.5	1.4	0.2	setosa
<b>2</b>	4.9	3	1.4	0.2	setosa
<b>3</b>	4.7	3.2	1.3	0.2	setosa
<b>4</b>	4.6	3.1	1.5	0.2	setosa
<b>5</b>	5	3.6	1.4	0.2	setosa
<b>6</b>	5.4	3.9	1.7	0.4	setosa
<b>...</b>	...	...	...	...	NA
<b>145</b>	6.7	3.3	5.7	2.5	virginica
<b>146</b>	6.7	3	5.2	2.3	virginica
<b>147</b>	6.3	2.5	5	1.9	virginica
<b>148</b>	6.5	3	5.2	2	virginica
<b>149</b>	6.2	3.4	5.4	2.3	virginica
<b>150</b>	5.9	3	5.1	1.8	virginica

```
ggplot(iris, aes(x = Species, y = Sepal.Length)) + geom_boxplot() +  
  ggtitle("Boxplot of Cool Variables")
```

Boxplot of Cool Variables



```
pander(describe(iris[, -5], fast = T), caption = "Numeric Variables")
```

Table 2: Numeric Variables

	vars	n	mean	sd	min	max	range	se
<b>Sepal.Length</b>	1	150	5.843	0.8281	4.3	7.9	3.6	0.06761
<b>Sepal.Width</b>	2	150	3.057	0.4359	2	4.4	2.4	0.03559
<b>Petal.Length</b>	3	150	3.758	1.765	1	6.9	5.9	0.1441
<b>Petal.Width</b>	4	150	1.199	0.7622	0.1	2.5	2.4	0.06224

```
pander(table(iris$Species), caption = "Categorical Variable")
```

Table 3: Categorical Variable

setosa	versicolor	virginica
50	50	50

```
ztable(headTail(iris, 6, 6))
```

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
1	5.1	3.5	1.4	0.2	setosa
2	4.9	3	1.4	0.2	setosa
3	4.7	3.2	1.3	0.2	setosa
4	4.6	3.1	1.5	0.2	setosa
5	5	3.6	1.4	0.2	setosa
6	5.4	3.9	1.7	0.4	setosa
...	...	...	...	...	NA
145	6.7	3.3	5.7	2.5	virginica
146	6.7	3	5.2	2.3	virginica
147	6.3	2.5	5	1.9	virginica
148	6.5	3	5.2	2	virginica
149	6.2	3.4	5.4	2.3	virginica
150	5.9	3	5.1	1.8	virginica

```
ztable(describe(iris, fast = T))
```

	vars	n	mean	sd	min	max	range	se
Sepal.Length	1	150.00	5.84	0.83	4.30	7.90	3.60	0.07
Sepal.Width	2	150.00	3.06	0.44	2.00	4.40	2.40	0.04
Petal.Length	3	150.00	3.76	1.77	1.00	6.90	5.90	0.14
Petal.Width	4	150.00	1.20	0.76	0.10	2.50	2.40	0.06
Species*	5	150.00			Inf	-Inf	-Inf	

```
mod <- lm(Sepal.Length ~ Species, iris)
mod1 <- update(mod, . ~ . + Sepal.Width)
texreg(list(mod, mod1), float.pos = 'h')
```

```
pander(mod)
```

	Model 1	Model 2
(Intercept)	5.01*** (0.07)	2.25*** (0.37)
Speciesversicolor	0.93*** (0.10)	1.46*** (0.11)
Speciesvirginica	1.58*** (0.10)	1.95*** (0.10)
Sepal.Width		0.80*** (0.11)
R <sup>2</sup>	0.62	0.73
Adj. R <sup>2</sup>	0.61	0.72
Num. obs.	150	150
RMSE	0.51	0.44

\*\*\* $p < 0.001$ , \*\* $p < 0.01$ , \* $p < 0.05$

Table 4: Statistical models

Table 5: Fitting linear model: Sepal.Length ~ Species

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	5.006	0.0728	68.76	1.134e-113
<b>Speciesversicolor</b>	0.93	0.103	9.033	8.77e-16
<b>Speciesvirginica</b>	1.582	0.103	15.37	2.215e-32