Carnet R

Cacher

```r
library(gitcreds)
gitcreds_set()
```

Cacher

```
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
```

```
-> Adding new credentials...
-> Removing credentials from cache...
-> Done.
```

Cacher

```
git config --global user.email " celiaok44@gmail.com"
git config --global user.name "herroug celia"
```

Cacher

```r
library(dada2); packageVersion("dada2")
```

```
[1] '1.28.0'
```

Cacher

```
library(dplyr)

iris %>%
  filter(Sepal.Length > 6) %>% # filtered using size of Sepal Length
  filter(Species == "versicolor") # and the species
```

Sépale.Longueur	Sépale.Largeur	Pétale.Longueur	Pétale.Largeur	Espèces
<double>	<double>	<double>	<double>	<fctr>
7.0	3.2	4.7	1.4	versicolor
6.4	3.2	4.5	1,5	versicolor
6.9	3.1	4.9	1,5	versicolor
6.5	2.8	4.6	1,5	versicolor
6.3	3.3	4.7	1.6	versicolor
6.6	2.9	4.6	1.3	versicolor
6.1	2.9	4.7	1.4	versicolor
6.7	3.1	4.4	1.4	versicolor
6.2	2.2	4.5	1,5	versicolor
6.1	2.8	4.0	1.3	versicolor

1 à 10 sur 20 rangées   Précédent **1** 2 Suivant

Cacher

NA

Cacher

```
iris %>%
  select(Sepal.Length, Species) %>%
  mutate(Sepal.Length2 = Sepal.Length * 2) %>%
  mutate(Sepal.Length2_squared = Sepal.Length2 * Sepal.Length2)
```
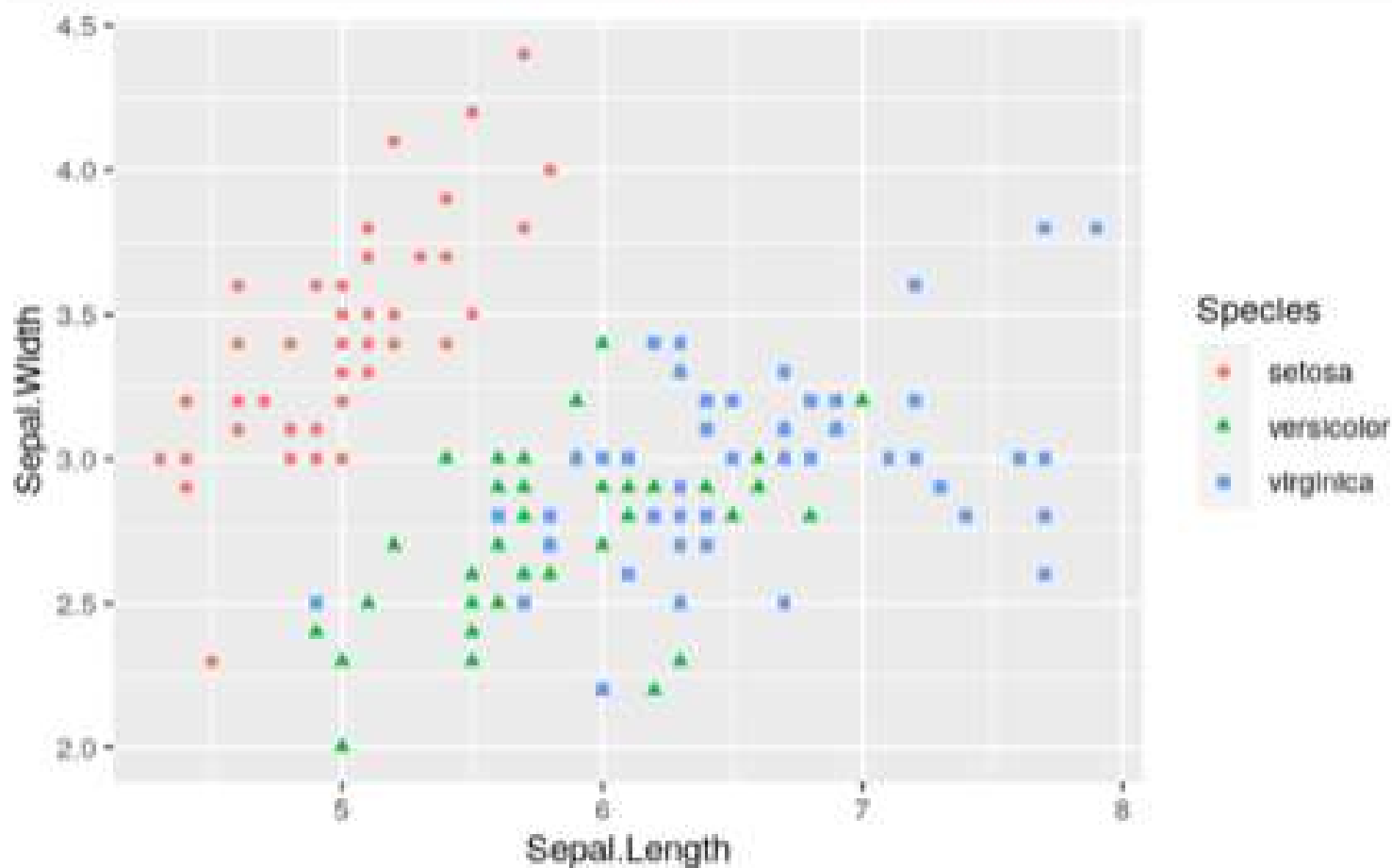
Sépale.Longueur	Espèces	Sépale.Longueur2	Sépale.Length2_squared
<double>	<fctr>	<double>	<double>
5.1	sétosa	10.2	104.04
4.9	sétosa	9.8	96.04
4.7	sétosa	9.4	88.36
4.6	sétosa	9.2	84,64
5.0	sétosa	10,0	100,00

```
iris %>%
  select(Sepal.Length, Species) %>%
  mutate(Sepal.Length2 = Sepal.Length * 2) %>%
  mutate(Sepal.Length2_squared = Sepal.Length2 * Sepal.Length2)
```

Sépale.Longueur	Espèces	Sépale.Longueur2	Sépale.Length2_squared
<double>	<fctr>	<double>	<double>
5.1	sétosa	10.2	104.04
4.9	sétosa	9.8	96.04
4.7	sétosa	9.4	88.36
4.6	sétosa	9.2	84,64
5.0	sétosa	10,0	100,00
5.4	sétosa	10.8	116,64
4.6	sétosa	9.2	84,64
5.0	sétosa	10,0	100,00
4.4	sétosa	8.8	77.44
4.9	sétosa	9.8	96.04

1 à 10 sur 150 lignes   Précédent **1** 2 3 4 5 6 _ 15 Suivant

Cacher

```
# we can calorize and give a shape by month
# scatter plot
ggplot(data = iris, aes(Sepal.Length, Sepal.Width)) +
  geom_point(aes(color = Species, shape = Species)) # shape is the same thing with classical plot on R
```
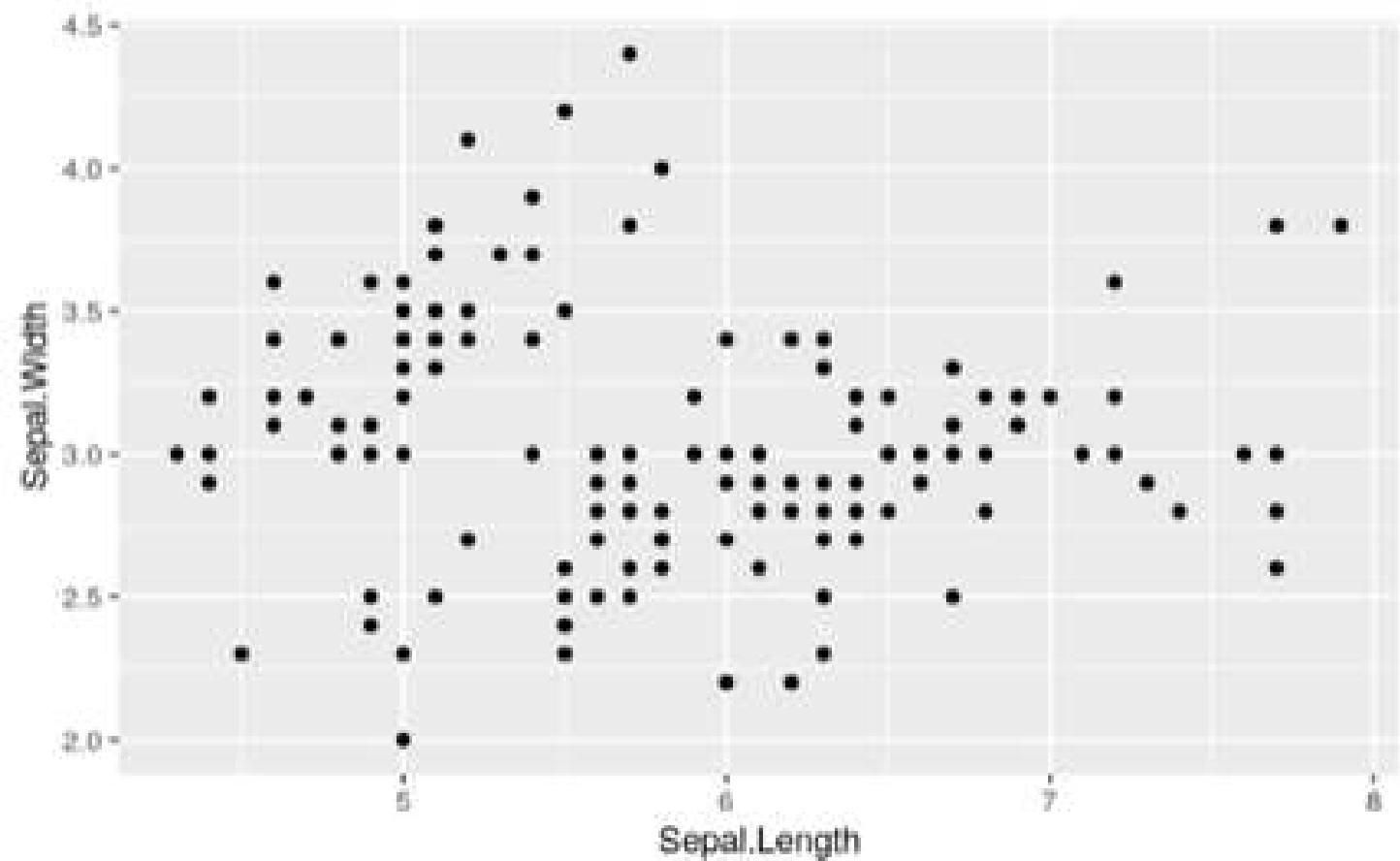
```
# we can calorize and give a shape by month
# scatter plot
ggplot(data = iris, aes(Sepal.Length, Sepal.Width)) +
  geom_point(aes(color = Species, shape = Species)) # shape is the same thing with classical plot on R
```
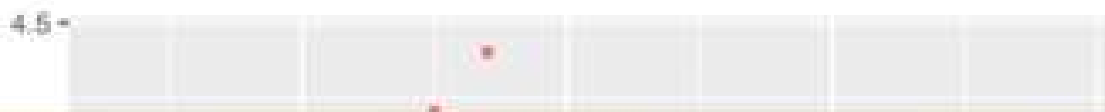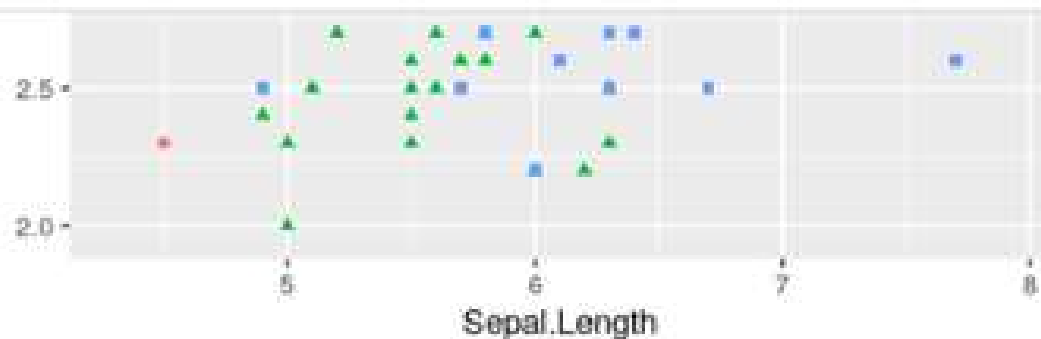
Cacher

```r
library(ggplot2)
# scatter plot
ggplot(data = iris, aes(Sepal.Length, Sepal.Width)) + #  what I want to represent
  geom_point() # how I represent it
```


Cacher

```r
# we can colorize and give a shape by month
# scatter plot
ggplot(data = iris, aes(Sepal.Length, Sepal.Width)) +
  geom_point(aes(color = Species, shape = Species)) # shape is the same thing with classical plot on #
```

```
#Boxplot
ggplot(data = iris, aes(Species, Sepal.Length)) + #  what I want to represent
  geom_boxplot(aes(color = Species, fill = Species), alpha=0.4) + # how I represent it. Here I changed geometry using boxplo
t.
  labs(x ="Species", y = "Sepal.Length (mm)") +
  theme_minimal()
```