Journal Club Bioinfo

The Tidyverse: A collection of R packages designed for data science.

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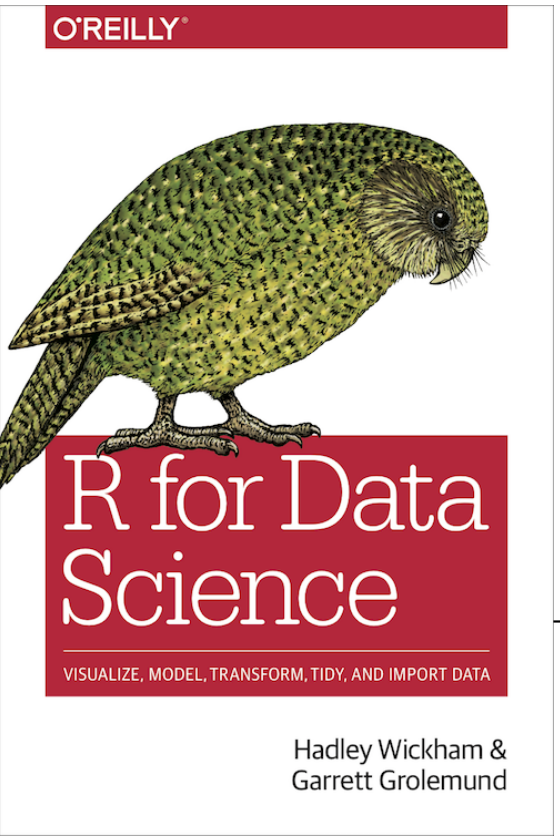
R for data science

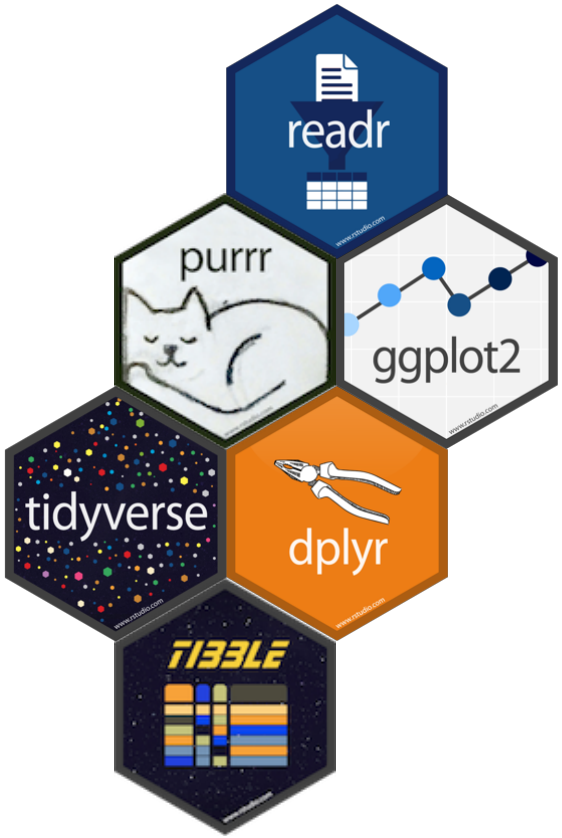


- **R for data science** : The best place to start learning the tidyverse by Hadley Wickham and Garrett Grolemund [a].
- **ggplot2 : elegant graphics for data science** by Hadley Wickham. Goes into greater depth into the ggplot2 visualisation system.

a. available online : https://r4ds.had.co.nz.

Tidyverse & tidy data

Tidyverse



R packages for data science

The tidyverse is an opinionated collection of R packages designed for data science. All packages share an underlying design philosophy, grammar, and data structures.
https://www.tidyverse.org/

```
install.packages("tidyverse")
```

Tidyverse

```
require(tidyverse)
```

```
## Loading required package: tidyverse
```

```
## -- Attaching packages ----------------------------------------- tidyverse 1.2.1 --
```

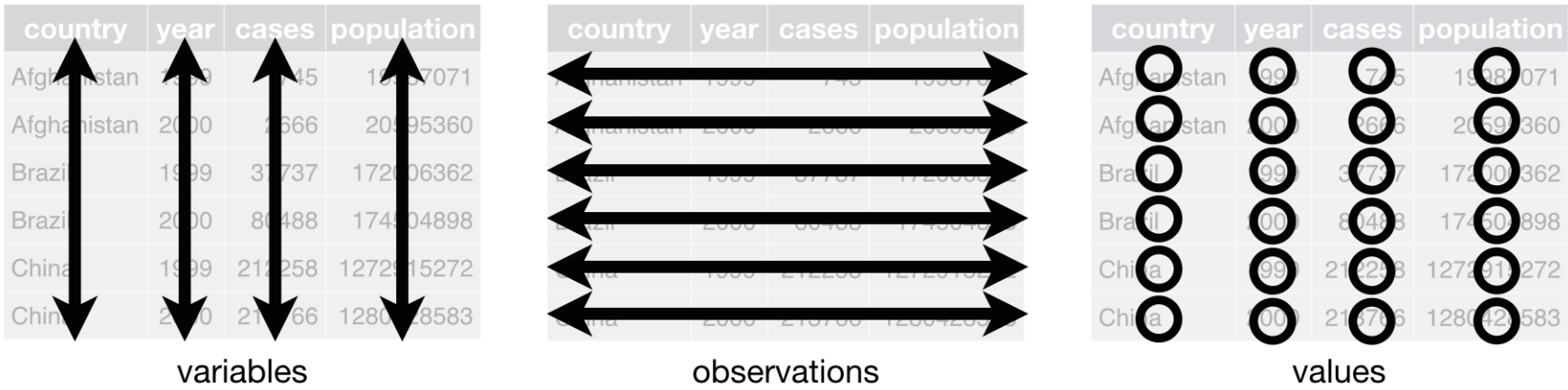
```
## v ggplot2 3.1.0     v purrr   0.2.5
## v tibble  2.0.1     v dplyr   0.7.8
## v tidyr   0.8.2     v stringr 1.4.0
## v readr   1.3.1     v forcats 0.3.0
```

```
## -- Conflicts -------------------------------------------- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

Tidy data

Tidying : *structuring datasets to facilitate analysis.*

A tidy dataset :

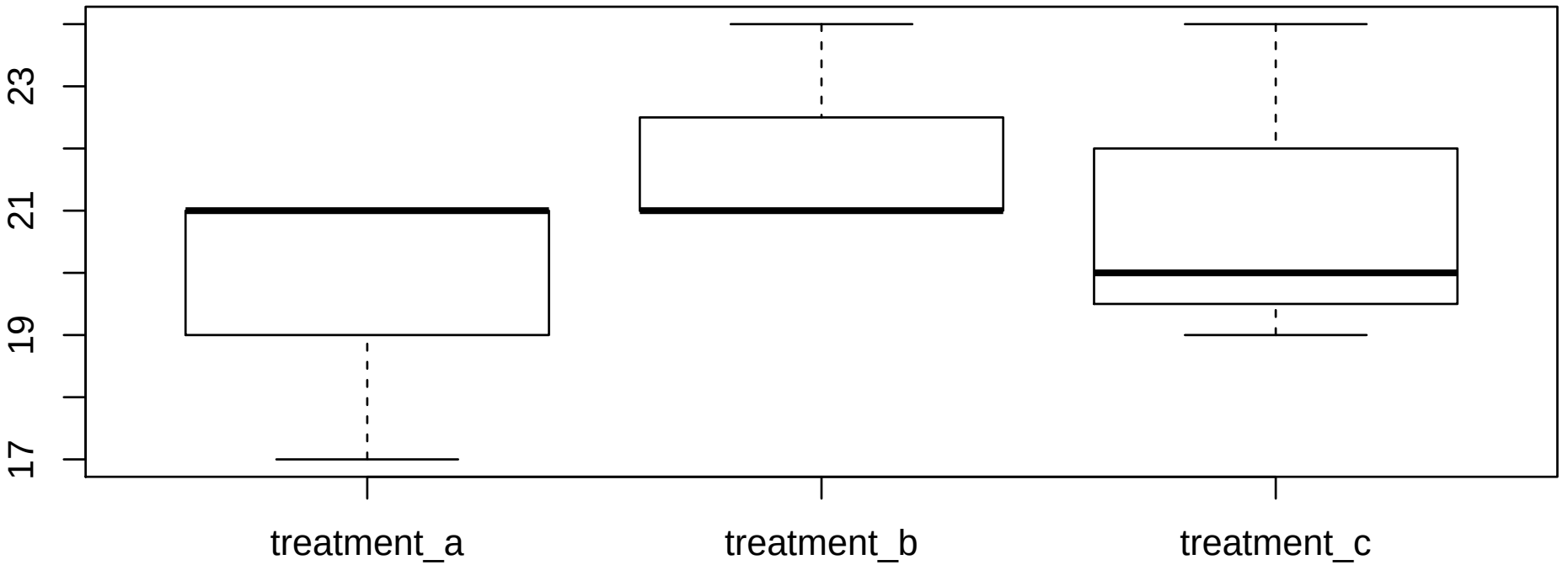


Why tidying a dataset ?

TABLE 1 – Typical presentation dataset

	treatment_a	treatment_b	treatment_c
John Smith	17	21	24
Jane Doe	21	24	19
Mary Johnson	21	21	20

```
boxplot(treatments)
```



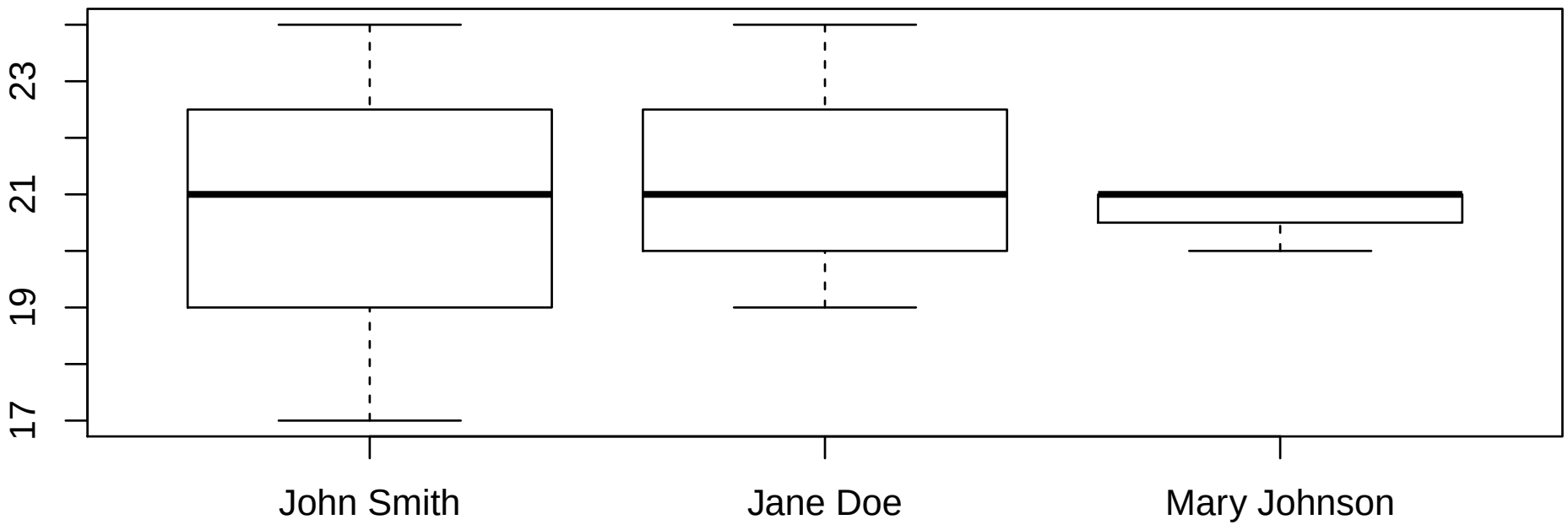
Why tidying a dataset ?

```
treatments.2 <- t(treatments)
```

TABLE 2 – The same data but structured differently

	John Smith	Jane Doe	Mary Johnson
treatment_a	17	21	21
treatment_b	21	24	21
treatment_c	24	19	20

```
boxplot(treatments.2)
```

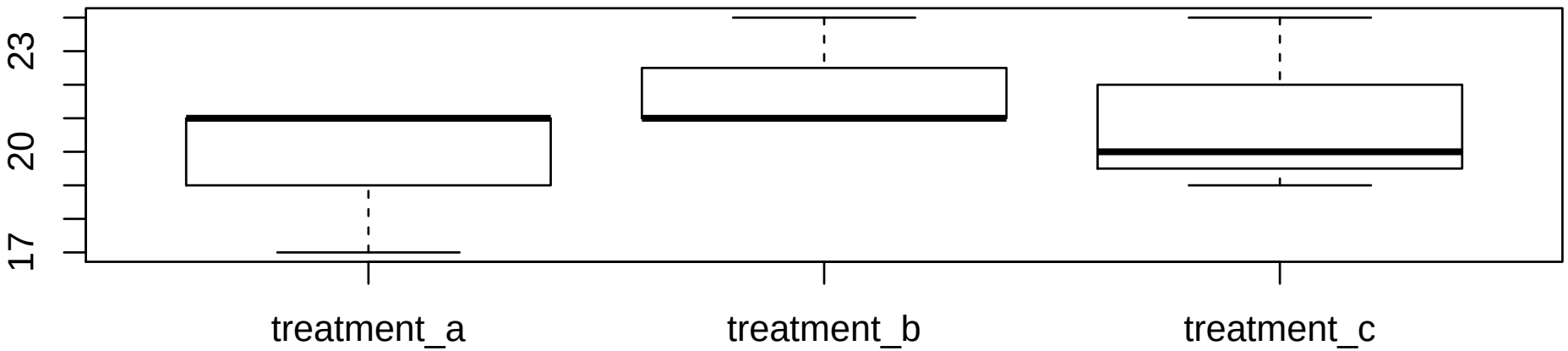


Why tidying a dataset ?

TABLE 3 – An exemple of a tidy dataset

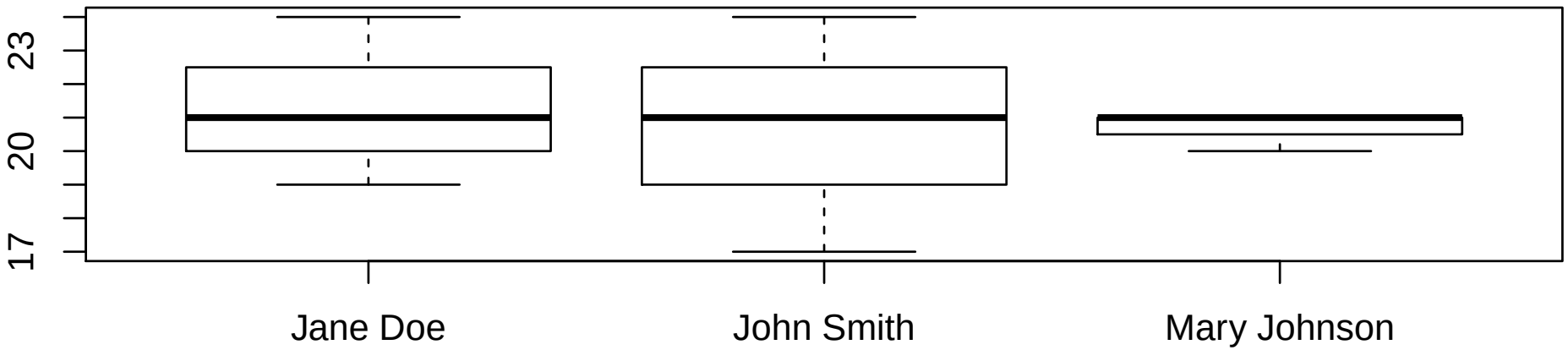
person	treatment	result
John Smith	treatment_a	17
Jane Doe	treatment_a	21
Mary Johnson	treatment_a	21
John Smith	treatment_b	21
Jane Doe	treatment_b	24
Mary Johnson	treatment_b	21
John Smith	treatment_c	24
Jane Doe	treatment_c	19
Mary Johnson	treatment_c	20

```
boxplot(result~treatment,data=treatments.3)
```

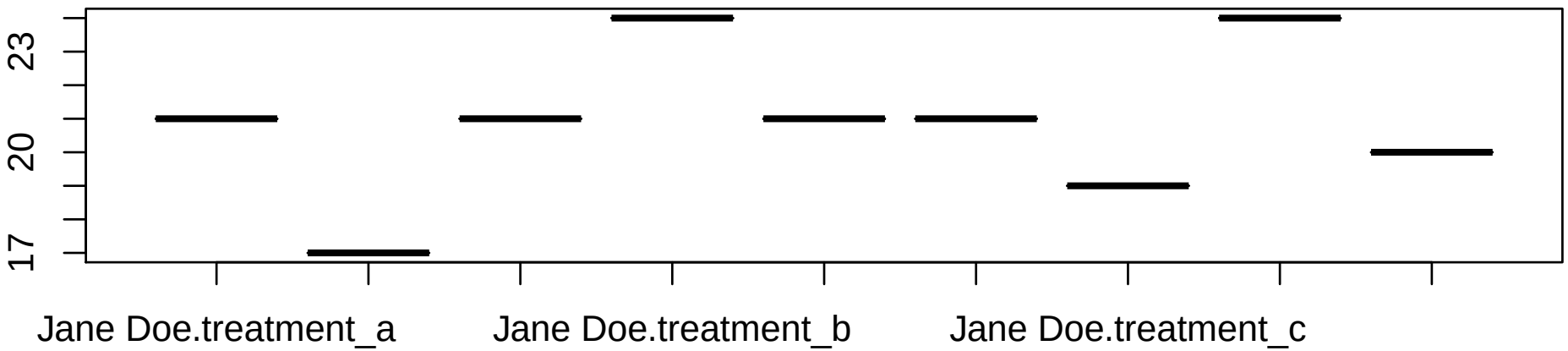


Why tidying a dataset ?

```
boxplot(result~person,data=treatments.3)
```




```
boxplot(result~person+treatment,data=treatments.3)
```



Pipe and tibble

Pipes

The pipe %>% :

- Come from the **magrittr** package by Stefan Milton Bache.
- Automatically loaded in tidyverse.
- Equivalent to | in bash

```
cat iris.tsv | cut -f5 | sed 's/^./\U&/' | head
```

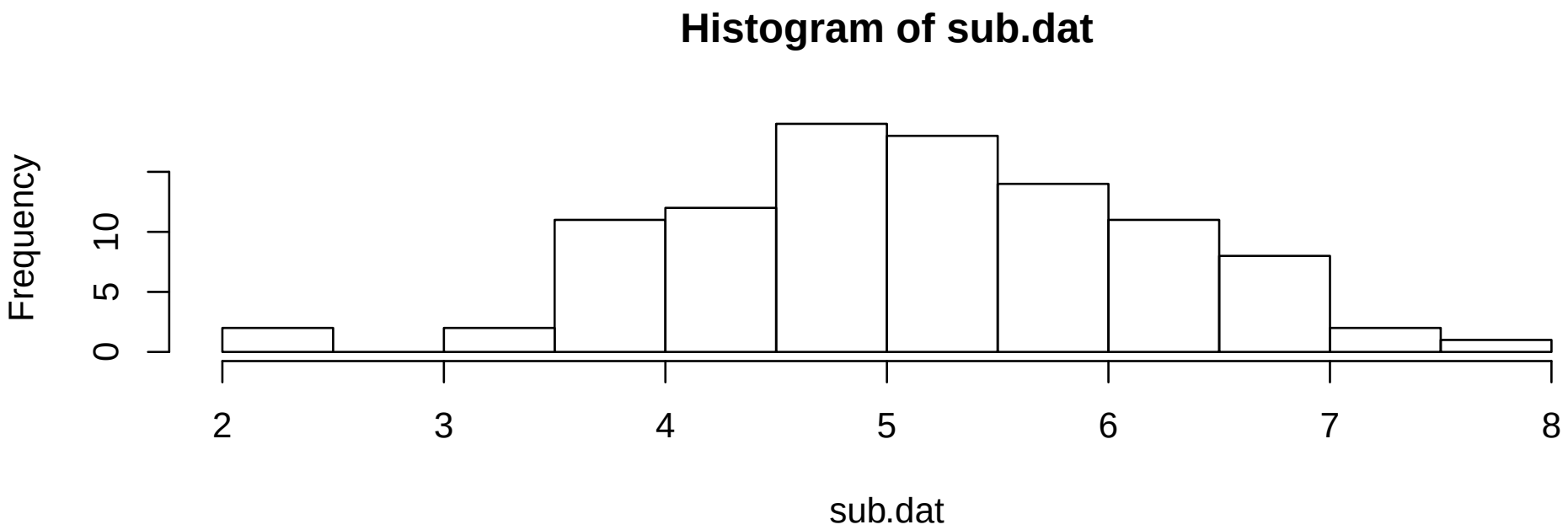
```
## Species
## Setosa
## Setosa
## Setosa
## Setosa
## Setosa
## Setosa
## Setosa
## Setosa
## Setosa
```

```
read_tsv("iris.tsv",col_names = F) %>% pull(5) %>% str_to_title() %>% head
```

```
## [1] "Species" "Setosa"  "Setosa"  "Setosa"  "Setosa"  "Setosa"
```

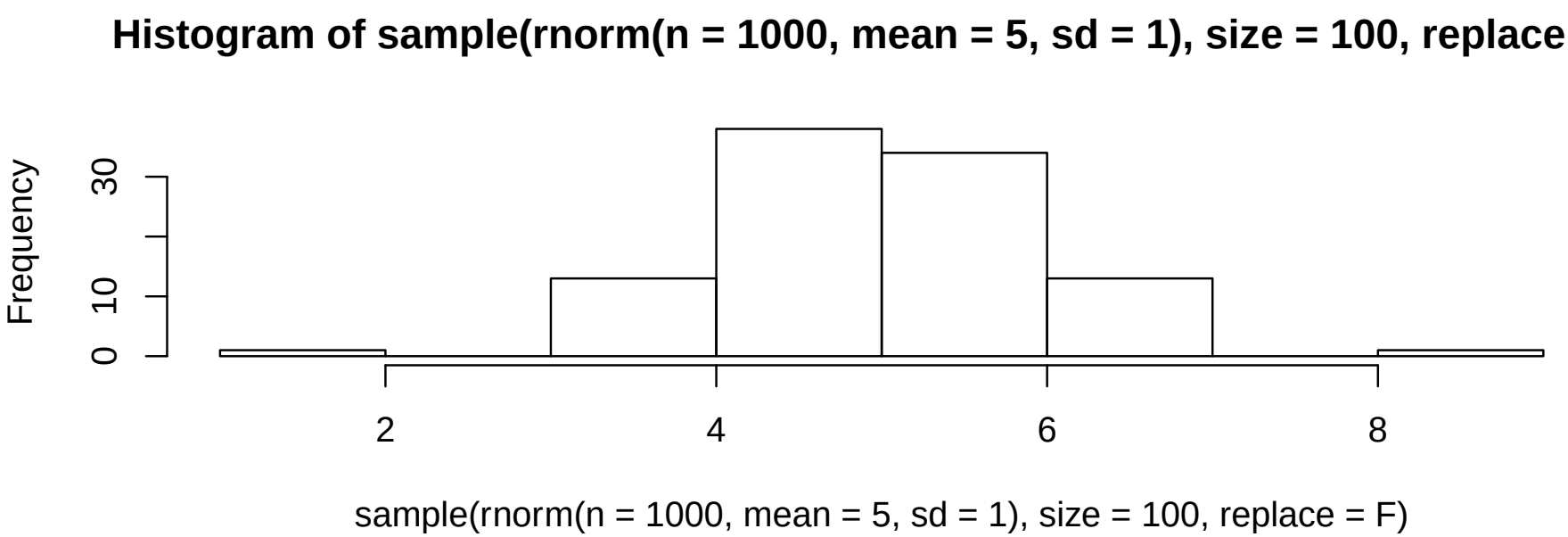
Pipes vs no pipes : without pipe

```
ex.dat <- rnorm(n = 1000,mean = 5,sd=1)
sub.dat <- sample(ex.dat,size = 100,replace=F)
hist(sub.dat)
```



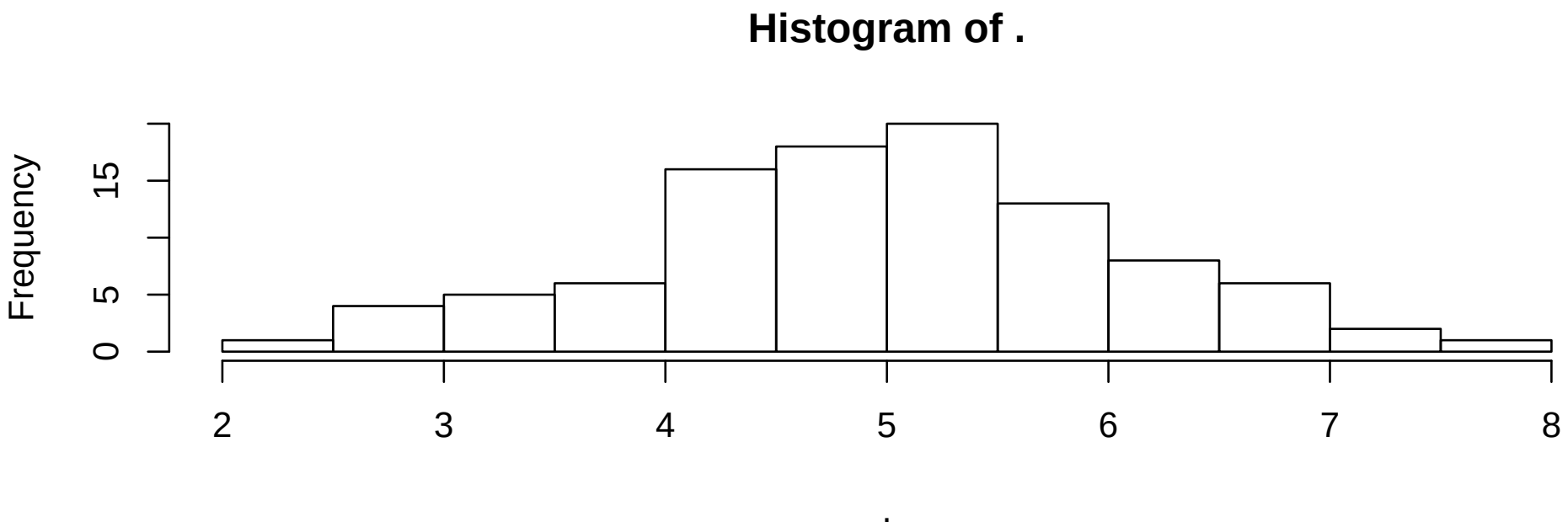
Pipes vs no pipes : without pipe

```
hist(sample(rnorm(n = 1000,mean = 5,sd=1),size = 100,replace=F))
```



Pipes vs no pipes : with pipe

```
rnorm(n = 1000,mean = 5,sd=1) %>%
    sample(size = 100,replace=F) %>%
    hist()
```



Tibbles : tibble::tibble

```
my.tibble <- tibble(
    person = c("John Smith","Jane Doe","Mary Johnson"),
    treatment_a = sample(10:25,size = 3,replace = T),
    treatment_b = sample(10:25,size = 3,replace = T),
    treatment_c = sample(10:25,size = 3,replace = T)
)
```

```
## # A tibble: 3 x 4
##   person       treatment_a treatment_b treatment_c
##   <chr>              <int>       <int>       <int>
## 1 John Smith            18          12          15
## 2 Jane Doe              17          15          17
## 3 Mary Johnson          14          14          15
```

Tibbles : tibble::tibble()

Pros :

- Cells can contain list and data.frame.
- It never changes an input's type (i.e., no more `stringsAsFactors = FALSE`!).
- Can use not valid R variable names (`:)`) as column names.
- Refined print method that shows only the first 10 rows.

Cons :

- It never uses `row.names()`.
  - use `tibble::rownames_to_column()`.

```
treatments %>% tibble::rownames_to_column("person") %>%
    as_tibble() %>%
    rename(`:)` = person)
```

```
## # A tibble: 3 x 4
##   `:)`          treatment_a treatment_b treatment_c
##   <chr>               <int>       <int>       <int>
## 1 John Smith             17          21          24
## 2 Jane Doe               21          24          19
## 3 Mary Johnson           21          21          20
```

Split a dataset into multiples dataset using tidyr::nest()

```
my.tibble.split <- my.tibble %>% group_by(person) %>% nest(.key = Data)
my.tibble.split
```

```
## # A tibble: 3 x 2
##   person       Data
##   <chr>        <list>
## 1 John Smith   <tibble [1 x 3]>
## 2 Jane Doe     <tibble [1 x 3]>
## 3 Mary Johnson <tibble [1 x 3]>
```

```
my.tibble.split[["Data"]][[1]]
```

```
## # A tibble: 1 x 3
##   treatment_a treatment_b treatment_c
##         <int>       <int>       <int>
## 1          18          12          15
```

Read/write tibbles : readr::read_* / readr::write_*

Read/write tibbles : :

- `readr::read_*` :
  - `read_csv` : comma delimited files.
  - `read_csv2` : semi-colon delimited files.
  - `read_tsv` : tab delimited files.
  - `read_delim` : any delimiter.
- `readr::write_*` :
  - `write_csv` : comma delimited files.
  - `write_csv2` : semi-colon delimited files.
  - `write_tsv` : tab delimited files.
  - `write_delim` : any delimiter.

Read/write tibbles : readr::read_* / readr::write_*

```
read_tsv("iris.tsv",
         col_types = cols(
            Sepal.Length = col_double(),Sepal.Width = col_double(),
            Petal.Length = col_double(),Petal.Width = col_double(),
            Species = col_character()
         )
    )
```

```
## # A tibble: 150 x 5
##    Sepal.Length Sepal.Width Petal.Length Petal.Width Species
##           <dbl>       <dbl>        <dbl>       <dbl> <chr>
##  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
##  7          4.6         3.4          1.4         0.3 setosa
##  8          5           3.4          1.5         0.2 setosa
##  9          4.4         2.9          1.4         0.2 setosa
## 10          4.9         3.1          1.5         0.1 setosa
## # ... with 140 more rows
```

Tidying dataset

Using tidyr to reshape data

Use tidyr::gather() and tidyr::spread() to reorganize the value.

```
treatments %>% tibble::rownames_to_column("person") %>%
    tidyr::gather(key="treatment",value = "result",-person)
```

```
##          person   treatment result
## 1    John Smith treatment_a     17
## 2      Jane Doe treatment_a     21
## 3 Mary Johnson treatment_a     21
## 4    John Smith treatment_b     21
## 5      Jane Doe treatment_b     24
## 6 Mary Johnson treatment_b     21
## 7    John Smith treatment_c     24
## 8      Jane Doe treatment_c     19
## 9 Mary Johnson treatment_c     20
```

```
treatment.3 %>% spread(key = "treatment",value = "result")
```

```
##          person treatment_a treatment_b treatment_c
## 1      Jane Doe          21          24          19
## 2    John Smith          17          21          24
## 3 Mary Johnson          21          21          20
```

Using tidyr to reshape data

```
treatment.3 %>% separate(person,into = c("First Name","Last Name"),sep=" ")
```

```
##   First Name Last Name   treatment result
## 1       John     Smith treatment_a     17
## 2       Jane       Doe treatment_a     21
## 3       Mary   Johnson treatment_a     21
## 4       John     Smith treatment_b     21
## 5       Jane       Doe treatment_b     24
## 6       Mary   Johnson treatment_b     21
## 7       John     Smith treatment_c     24
## 8       Jane       Doe treatment_c     19
## 9       Mary   Johnson treatment_c     20
```

Manipulate a dataset using dplyr

dplyr

`dplyr` :

- Manipulate variables.
- Manipulate observations.
- Group / summarise observations.

TABLE 4 – iris dataset

Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
5.1	3.5	1.4	0.2	setosa
4.9	3.0	1.4	0.2	setosa
4.7	3.2	1.3	0.2	setosa
4.6	3.1	1.5	0.2	setosa
5.0	3.6	1.4	0.2	setosa
5.4	3.9	1.7	0.4	setosa

iris dataset

The famous (Fisher's or Anderson's) iris data set gives the measurements in centimeters of the variables sepal length and width and petal length and width, respectively, for 50 flowers from each of 3 species of iris. The species are Iris setosa, versicolor, and virginica. (from ?iris)

Manipulate **variables** using dplyr::select()

```
iris.tbl %>% select(1:3)
iris.tbl %>% select(Sepal.Length,Sepal.Width,Petal.Length)
iris.tbl %>% select(Sepal.Length:Petal.Length)
iris.tbl %>% select(-Petal.Width,-Species)
```

```
## # A tibble: 150 x 3
##    Sepal.Length Sepal.Width Petal.Length
##           <dbl>       <dbl>        <dbl>
##  1          5.1         3.5          1.4
##  2          4.9         3            1.4
##  3          4.7         3.2          1.3
##  4          4.6         3.1          1.5
##  5          5           3.6          1.4
##  6          5.4         3.9          1.7
##  7          4.6         3.4          1.4
##  8          5           3.4          1.5
##  9          4.4         2.9          1.4
## 10          4.9         3.1          1.5
## # ... with 140 more rows
```

Manipulate **variables** using dplyr::select()

```
iris.tbl %>% select(starts_with("Petal"))
```

```
## # A tibble: 150 x 2
##    Petal.Length Petal.Width
##           <dbl>       <dbl>
##  1          1.4         0.2
##  2          1.4         0.2
##  3          1.3         0.2
##  4          1.5         0.2
##  5          1.4         0.2
##  6          1.7         0.4
##  7          1.4         0.3
##  8          1.5         0.2
##  9          1.4         0.2
## 10          1.5         0.1
## # ... with 140 more rows
```

Manipulate **variables** using dplyr::pull()

```
iris.tbl %>% select(Sepal.Length)
```

```
## # A tibble: 150 x 1
##    Sepal.Length
##           <dbl>
## 1           5.1
## 2           4.9
## 3           4.7
## 4           4.6
## 5           5
## # ... with 145 more rows
```

```
iris.tbl %>% pull(Sepal.Length)
```

```
## [1] 5.1 4.9 4.7 4.6 5.0
```

Modify **variables** using dplyr::mutate()

```
iris.tbl %>%
    mutate(Petal.Length =
               scales::percent(Petal.Length/max(Petal.Length))
           )
```

```
## # A tibble: 150 x 5
##    Sepal.Length Sepal.Width Petal.Length Petal.Width Species
##           <dbl>       <dbl> <chr>               <dbl> <fct>
##  1          5.1         3.5 20.3%                 0.2 setosa
##  2          4.9         3   20.3%                 0.2 setosa
##  3          4.7         3.2 18.8%                 0.2 setosa
##  4          4.6         3.1 21.7%                 0.2 setosa
##  5          5           3.6 20.3%                 0.2 setosa
##  6          5.4         3.9 24.6%                 0.4 setosa
##  7          4.6         3.4 20.3%                 0.3 setosa
##  8          5           3.4 21.7%                 0.2 setosa
##  9          4.4         2.9 20.3%                 0.2 setosa
## 10          4.9         3.1 21.7%                 0.1 setosa
## # ... with 140 more rows
```

Create **variables** using dplyr::mutate()

```
iris.tbl %>%
    #Case 1
    mutate(Size = dplyr::case_when(
            Petal.Length >= 4 & Petal.Width >= 1.3 ~ "Big",
            Petal.Length < 4 & Petal.Width < 1.3 ~ "Small"
        )
    ) %>%
    #Case 2
    mutate(Ratio_Petal_Sepal_width = Petal.Width/Sepal.Width)
```

```
## # A tibble: 3 x 7
##   Ratio_Petal_Sep~ Size  Sepal.Length Sepal.Width Petal.Length Petal.Width
##              <dbl> <chr>        <dbl>       <dbl>        <dbl>       <dbl>
## 1           0.0571 Small          5.1         3.5          1.4         0.2
## 2           0.0667 Small          4.9         3            1.4         0.2
## 3           0.0625 Small          4.7         3.2          1.3         0.2
## # ... with 1 more variable: Species <fct>
```

other functions :

- dplyr::mutate_all() : Apply a function to every columns.
- dplyr::mutate_at() : Apply a function to specific column.

Mutating joins using dplyr::*_join()

```
iris.meta <- tibble(
    Species = factor(c("setosa","versicolor","virginica")),
    Colony = c("A","A","B") ,
    Ploidy = c("diploid","hexaploid","tetraploid"),
    `Common name` = c("Beachhead iris","Harlequin blueflag","Virginia iris")
)
```

TABLE 5 – Metadata for iris dataset

Species	Colony	Ploidy	Common name
setosa	A	diploid	Beachhead iris
versicolor	A	hexaploid	Harlequin blueflag
virginica	B	tetraploid	Virginia iris

Arrange dataset using dplyr::arrange()

```
iris.tbl %>% arrange(Petal.Length) %>% slice(1:5)
```

```
## # A tibble: 5 x 5
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
##          <dbl>       <dbl>        <dbl>       <dbl> <fct>
## 1          4.6         3.6            1         0.2 setosa
## 2          4.3         3              1.1       0.1 setosa
## 3          5.8         4              1.2       0.2 setosa
## 4          5           3.2            1.2       0.2 setosa
## 5          4.7         3.2            1.3       0.2 setosa
```

```
iris.tbl %>% filter(min_rank(Petal.Length) <= 5)
iris.tbl %>% top_n(-5,Petal.Length)
```

Use `desc()` to order by high to low.

Manipulate **observations** using dplyr::filter()

```
iris.tbl %>% filter(Sepal.Length < 7) %>% slice(1:5)
```

```
## # A tibble: 5 x 5
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
##          <dbl>       <dbl>        <dbl>       <dbl> <fct>
## 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
```

```
iris.tbl %>% filter(Species ==  "setosa") %>% slice(1:5)
```

```
## # A tibble: 5 x 5
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
##          <dbl>       <dbl>        <dbl>       <dbl> <fct>
## 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
```

Manipulate **observations** using dplyr::filter()

```
iris.tbl %>%
    filter(Sepal.Length < 7) %>%
    filter(Species ==  "setosa") %>% slice(1:5)
```

```
## # A tibble: 5 x 5
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
##          <dbl>       <dbl>        <dbl>       <dbl> <fct>
## 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
```

```
iris.tbl %>%
    filter(Sepal.Length < 7 & Species ==  "setosa") %>% slice(1:5)

iris.tbl %>%
    filter(Sepal.Length < 7,Species ==  "setosa") %>% slice(1:5)
```

Summarise observations using dplyr::summarise()

```
iris.tbl %>% summarise(mean = mean(Petal.Length), sd = sd(Petal.Length))
```

```
## # A tibble: 1 x 2
##    mean    sd
##   <dbl> <dbl>
## 1  3.76  1.77
```

```
iris.tbl %>% select(-Species) %>%summarise_all(mean)
```

```
## # A tibble: 1 x 4
##   Sepal.Length Sepal.Width Petal.Length Petal.Width
##          <dbl>       <dbl>        <dbl>       <dbl>
## 1         5.84        3.06         3.76        1.20
```

```
iris.tbl %>% summarise(n = n())
```

```
## # A tibble: 1 x 1
##       n
##   <int>
## 1   150
```

Summarise observations using dplyr::group_by()

```
iris.tbl %>% group_by(Species) %>% summarise(mean = mean(Petal.Length), sd = sd(Pet
```

```
## # A tibble: 3 x 3
##   Species     mean    sd
##   <fct>      <dbl> <dbl>
## 1 setosa      1.46 0.174
## 2 versicolor  4.26 0.470
## 3 virginica   5.55 0.552
```

```
iris.tbl %>% group_by(Species) %>% summarise(n = n())
```

```
## # A tibble: 3 x 2
##   Species        n
##   <fct>      <int>
## 1 setosa        50
## 2 versicolor    50
## 3 virginica     50
```

```
iris.tbl %>% group_by(Species) %>% tally()
iris.tbl %>% count(Species)
```

Summarise observations using dplyr::group_by()

```
iris.tbl %>% group_by(Species) %>% filter(Petal.Length >= max(Petal.Length))
```

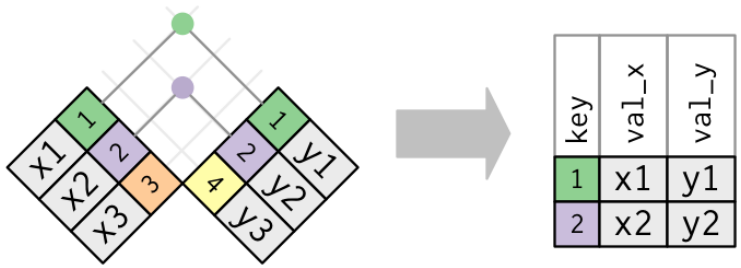
```
## # A tibble: 4 x 5
## # Groups:   Species [3]
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
##          <dbl>       <dbl>        <dbl>       <dbl> <fct>
## 1          4.8         3.4          1.9         0.2 setosa
## 2          5.1         3.8          1.9         0.4 setosa
## 3          6           2.7          5.1         1.6 versicolor
## 4          7.7         2.6          6.9         2.3 virginica
```

```
iris.tbl %>% group_by(Species) %>% top_n(1,Petal.Length)
```

```
## # A tibble: 4 x 5
## # Groups:   Species [3]
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
##          <dbl>       <dbl>        <dbl>       <dbl> <fct>
## 1          4.8         3.4          1.9         0.2 setosa
## 2          5.1         3.8          1.9         0.4 setosa
## 3          6           2.7          5.1         1.6 versicolor
## 4          7.7         2.6          6.9         2.3 virginica
```

Inner join

Inner join : return all rows from `x` where there are matching values in `y`, and all columns from `x` and `y`. If there are multiple matches between `x` and `y`, all combination of the matches are returned.

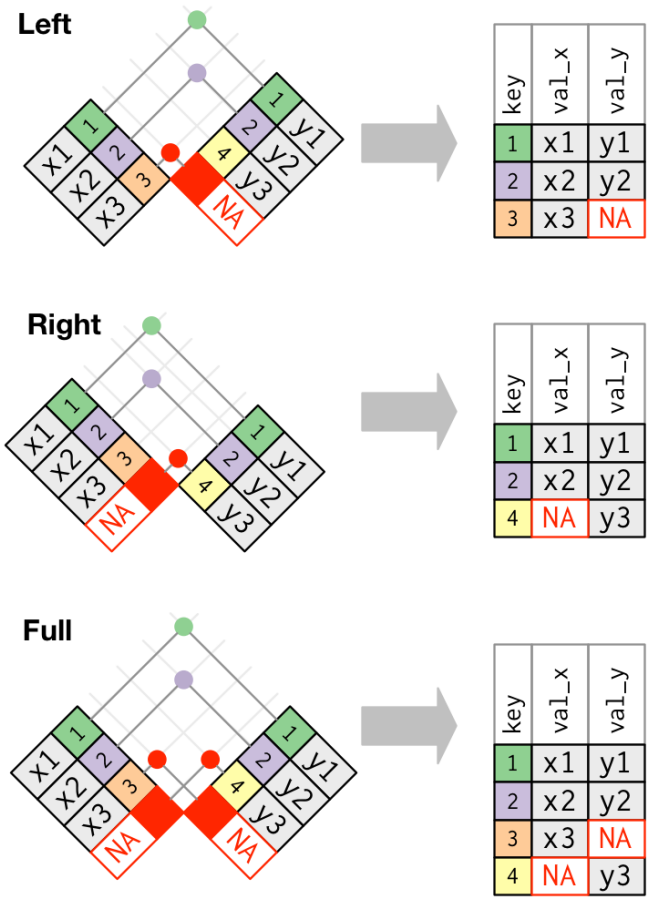



```
iris.meta.nosetosa <- iris.meta %>% filter(Species !="setosa")
iris.tbl %>% inner_join(iris.meta.nosetosa,by = "Species") %>% print(n=5)
```

```
## # A tibble: 100 x 8
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species Colony Ploidy
##          <dbl>       <dbl>        <dbl>       <dbl> <fct>   <chr>  <chr>
## 1          7           3.2          4.7         1.4 versic~ A      hexap~
## 2          6.4         3.2          4.5         1.5 versic~ A      hexap~
## 3          6.9         3.1          4.9         1.5 versic~ A      hexap~
## 4          5.5         2.3          4           1.3 versic~ A      hexap~
## 5          6.5         2.8          4.6         1.5 versic~ A      hexap~
## # ... with 95 more rows, and 1 more variable: `Common name` <chr>
```

Outer joins

- A **left join** keeps all observations in `x`.
- A **right join** keeps all observations in `y`.
- A **full join** keeps all observations in `x` and `y`.



Outer joins

left join :

```
iris.meta.nosetosa <- iris.meta %>% filter(Species !="setosa")
iris.tbl %>% left_join(iris.meta.nosetosa,by = "Species") %>% print(n=5)
```

```
## # A tibble: 150 x 8
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species Colony Ploidy
##          <dbl>       <dbl>        <dbl>       <dbl> <fct>   <chr>  <chr>
## 1          5.1         3.5          1.4         0.2 setosa  <NA>   <NA>
## 2          4.9         3            1.4         0.2 setosa  <NA>   <NA>
## 3          4.7         3.2          1.3         0.2 setosa  <NA>   <NA>
## 4          4.6         3.1          1.5         0.2 setosa  <NA>   <NA>
## 5          5           3.6          1.4         0.2 setosa  <NA>   <NA>
## # ... with 145 more rows, and 1 more variable: `Common name` <chr>
```

right join :

```
iris.tbl.nosetosa <- iris.tbl %>% filter(Species !="setosa")
iris.tbl.nosetosa %>% right_join(iris.meta,by = "Species") %>% print(n=5)
```

```
## # A tibble: 101 x 8
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species Colony Ploidy
##          <dbl>       <dbl>        <dbl>       <dbl> <fct>   <chr>  <chr>
## 1           NA          NA           NA          NA setosa  A      diplo~
## 2            7           3.2          4.7         1.4 versic~ A      hexap~
## 3            6.4         3.2          4.5         1.5 versic~ A      hexap~
## 4            6.9         3.1          4.9         1.5 versic~ A      hexap~
## 5            5.5         2.3          4           1.3 versic~ A      hexap~
```

Outer joins

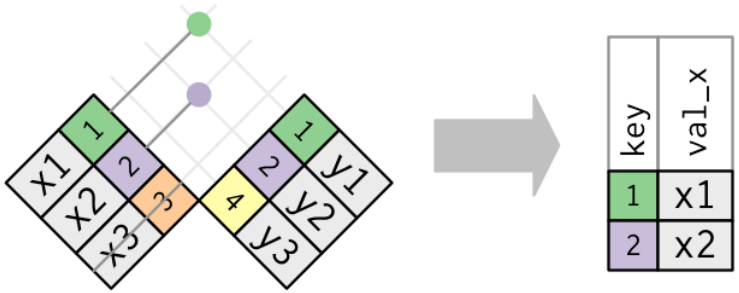
full join :

```
iris.meta.nosetosa <- iris.meta %>% filter(Species !="setosa")
iris.tbl %>% filter(Species != "virginica") %>% full_join(iris.meta.nosetosa,by = "Species") %
```

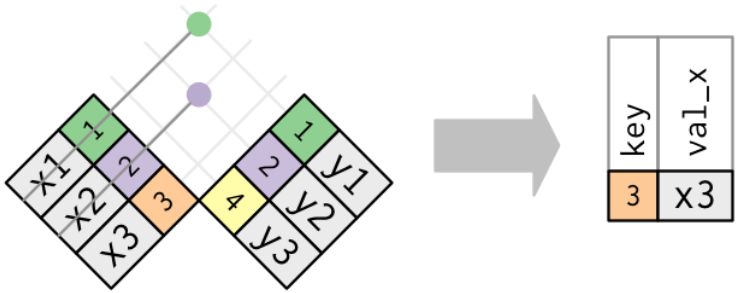
```
## # A tibble: 11 x 8
## # Groups:   Species [3]
##    Sepal.Length Sepal.Width Petal.Length Petal.Width Species Colony Ploidy
##           <dbl>       <dbl>        <dbl>       <dbl> <fct>   <chr>  <chr>
##  1          5.1         3.5          1.4         0.2 setosa  <NA>   <NA>
##  2          4.9         3            1.4         0.2 setosa  <NA>   <NA>
##  3          4.7         3.2          1.3         0.2 setosa  <NA>   <NA>
##  4          4.6         3.1          1.5         0.2 setosa  <NA>   <NA>
##  5          5           3.6          1.4         0.2 setosa  <NA>   <NA>
##  6          7           3.2          4.7         1.4 versic~ A      hexap~
##  7          6.4         3.2          4.5         1.5 versic~ A      hexap~
##  8          6.9         3.1          4.9         1.5 versic~ A      hexap~
##  9          5.5         2.3          4           1.3 versic~ A      hexap~
## 10          6.5         2.8          4.6         1.5 versic~ A      hexap~
## 11         NA          NA           NA          NA   virgin~ B      tetra~
## # ... with 1 more variable: `Common name` <chr>
```

Filtering joins

- `semi_join(x, y)` keeps all observations in `x` that have a match in `y`.



- `anti_join(x, y)` drops all observations in `x` that have a match in `y`.



Filtering joins

Table 6 – Patients files

First_Name	Last_Name	age	sex	adress
John	Smith	46	M	221B Baker Street
Jane	Doe	33	F	57 Rue de Varenne

```
treatments.3 %>%
    separate(person,into = c("First_Name","Last_Name"),sep=" ") %>%
    semi_join(treatment.meta,by = c("First_Name","Last_Name"))
```

```
##   First_Name Last_Name   treatment result
## 1       John     Smith treatment_a     17
## 2       Jane       Doe treatment_a     21
## 3       John     Smith treatment_b     21
## 4       Jane       Doe treatment_b     24
## 5       John     Smith treatment_c     24
## 6       Jane       Doe treatment_c     19
```

Use multiple command together

```
iris.tbl
```

```
## # A tibble: 150 x 5
##    Sepal.Length Sepal.Width Petal.Length Petal.Width Species
##           <dbl>       <dbl>        <dbl>       <dbl> <fct>
##  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
##  7          4.6         3.4          1.4         0.3 setosa
##  8          5           3.4          1.5         0.2 setosa
##  9          4.4         2.9          1.4         0.2 setosa
## 10          4.9         3.1          1.5         0.1 setosa
## # ... with 140 more rows
```

Use multiple command together

```
iris.tbl %>%
    gather(key = "Type",value = "obs",-Species) %>%
    separate(Type,into = c("Type_1","Type_2"),se="\\.")
```

```
## # A tibble: 600 x 4
##    Species Type_1 Type_2   obs
##    <fct>   <chr>  <chr>  <dbl>
##  1 setosa  Sepal  Length   5.1
##  2 setosa  Sepal  Length   4.9
##  3 setosa  Sepal  Length   4.7
##  4 setosa  Sepal  Length   4.6
##  5 setosa  Sepal  Length   5
##  6 setosa  Sepal  Length   5.4
##  7 setosa  Sepal  Length   4.6
##  8 setosa  Sepal  Length   5
##  9 setosa  Sepal  Length   4.4
## 10 setosa  Sepal  Length   4.9
## # ... with 590 more rows
```

Use multiple command together

```
iris.tbl %>%
    gather(key = "Type",value = "obs",-Species) %>%
    separate(Type,into = c("Type_1","Type_2"),se="\\.") %>%
    group_by(Species,Type_1,Type_2) %>%
    mutate(med = median(obs))
```

```
## # A tibble: 600 x 5
## # Groups:   Species, Type_1, Type_2 [12]
##    Species Type_1 Type_2   obs   med
##    <fct>   <chr>  <chr>  <dbl> <dbl>
##  1 setosa  Sepal  Length   5.1     5
##  2 setosa  Sepal  Length   4.9     5
##  3 setosa  Sepal  Length   4.7     5
##  4 setosa  Sepal  Length   4.6     5
##  5 setosa  Sepal  Length   5       5
##  6 setosa  Sepal  Length   5.4     5
##  7 setosa  Sepal  Length   4.6     5
##  8 setosa  Sepal  Length   5       5
##  9 setosa  Sepal  Length   4.4     5
## 10 setosa  Sepal  Length   4.9     5
## # ... with 590 more rows
```

Use multiple command together

```
iris.tbl %>%
    gather(key = "Type",value = "obs",-Species) %>%
    separate(Type,into = c("Type_1","Type_2"),se="\\.") %>%
    group_by(Species,Type_1,Type_2) %>%
    mutate(med = median(obs)) %>%
    mutate(Size = ifelse(obs < med,"Small","Big")) %>%
    left_join(iris.meta,by = "Species")
```

```
## # A tibble: 600 x 9
## # Groups:   Species, Type_1, Type_2 [?]
##    Species Type_1 Type_2   obs   med Size  Colony Ploidy  `Common name`
##    <fct>   <chr>  <chr>  <dbl> <dbl> <chr> <chr>  <chr>   <chr>
##  1 setosa  Sepal  Length   5.1     5 Big   A      diploid Beachhead iris
##  2 setosa  Sepal  Length   4.9     5 Small A      diploid Beachhead iris
##  3 setosa  Sepal  Length   4.7     5 Small A      diploid Beachhead iris
##  4 setosa  Sepal  Length   4.6     5 Small A      diploid Beachhead iris
##  5 setosa  Sepal  Length   5       5 Big   A      diploid Beachhead iris
##  6 setosa  Sepal  Length   5.4     5 Big   A      diploid Beachhead iris
##  7 setosa  Sepal  Length   4.6     5 Small A      diploid Beachhead iris
##  8 setosa  Sepal  Length   5       5 Big   A      diploid Beachhead iris
##  9 setosa  Sepal  Length   4.4     5 Small A      diploid Beachhead iris
## 10 setosa  Sepal  Length   4.9     5 Small A      diploid Beachhead iris
## # ... with 590 more rows
```

Use multiple command together

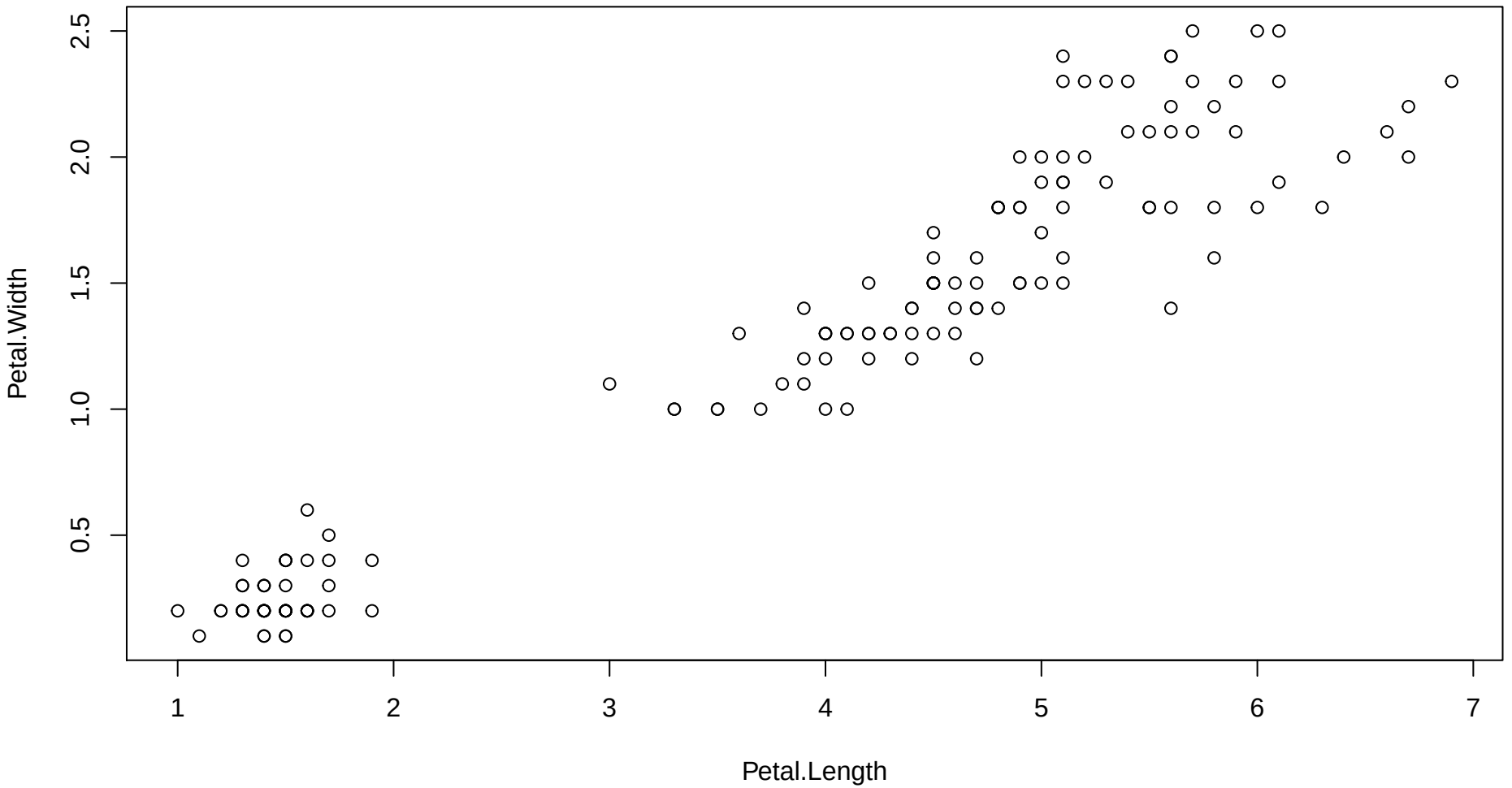
```
iris.tbl %>%
    gather(key = "Type",value = "obs",-Species) %>%
    separate(Type,into = c("Type_1","Type_2"),se="\\.") %>%
    group_by(Species,Type_1,Type_2) %>%
    mutate(med = median(obs)) %>%
    mutate(Size = ifelse(obs < med,"Small","Big")) %>%
    left_join(iris.meta,by = "Species") %>%
    arrange(desc(obs)) %>% slice(1)
```

```
## # A tibble: 12 x 9
## # Groups:   Species, Type_1, Type_2 [12]
##    Species   Type_1 Type_2   obs   med Size  Colony Ploidy  `Common name`
##    <fct>     <chr>  <chr>  <dbl> <dbl> <chr> <chr>  <chr>   <chr>
##  1 setosa    Petal  Length   1.9  1.5  Big   A      diploid Beachhead iris
##  2 setosa    Petal  Width    0.6  0.2  Big   A      diploid Beachhead iris
##  3 setosa    Sepal  Length   5.8  5    Big   A      diploid Beachhead iris
##  4 setosa    Sepal  Width    4.4  3.4  Big   A      diploid Beachhead iris
##  5 versicol~ Petal  Length   5.1  4.35 Big   A      hexapl~ Harlequin blue~
##  6 versicol~ Petal  Width    1.8  1.3  Big   A      hexapl~ Harlequin blue~
##  7 versicol~ Sepal  Length   7    5.9  Big   A      hexapl~ Harlequin blue~
##  8 versicol~ Sepal  Width    3.4  2.8  Big   A      hexapl~ Harlequin blue~
##  9 virginica Petal  Length   6.9  5.55 Big   B      tetrap~ Virginia iris
## 10 virginica Petal  Width    2.5  2    Big   B      tetrap~ Virginia iris
## 11 virginica Sepal  Length   7.9  6.5  Big   B      tetrap~ Virginia iris
## 12 virginica Sepal  Width    3.8  3    Big   B      tetrap~ Virginia iris
```

Data visualisation using ggplot2

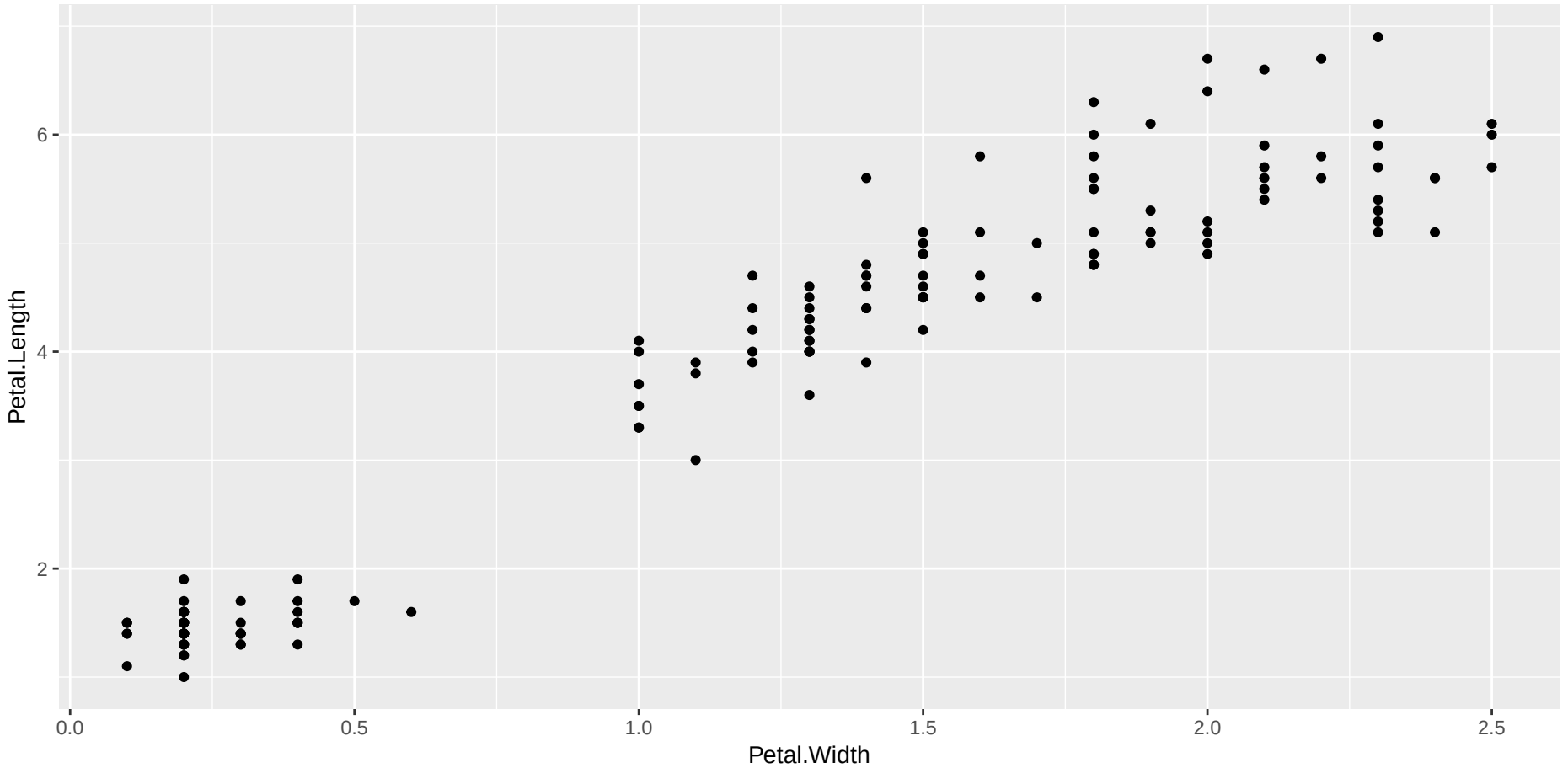
A base plot

```
plot(Petal.Width~Petal.Length,data=iris.tbl)
```



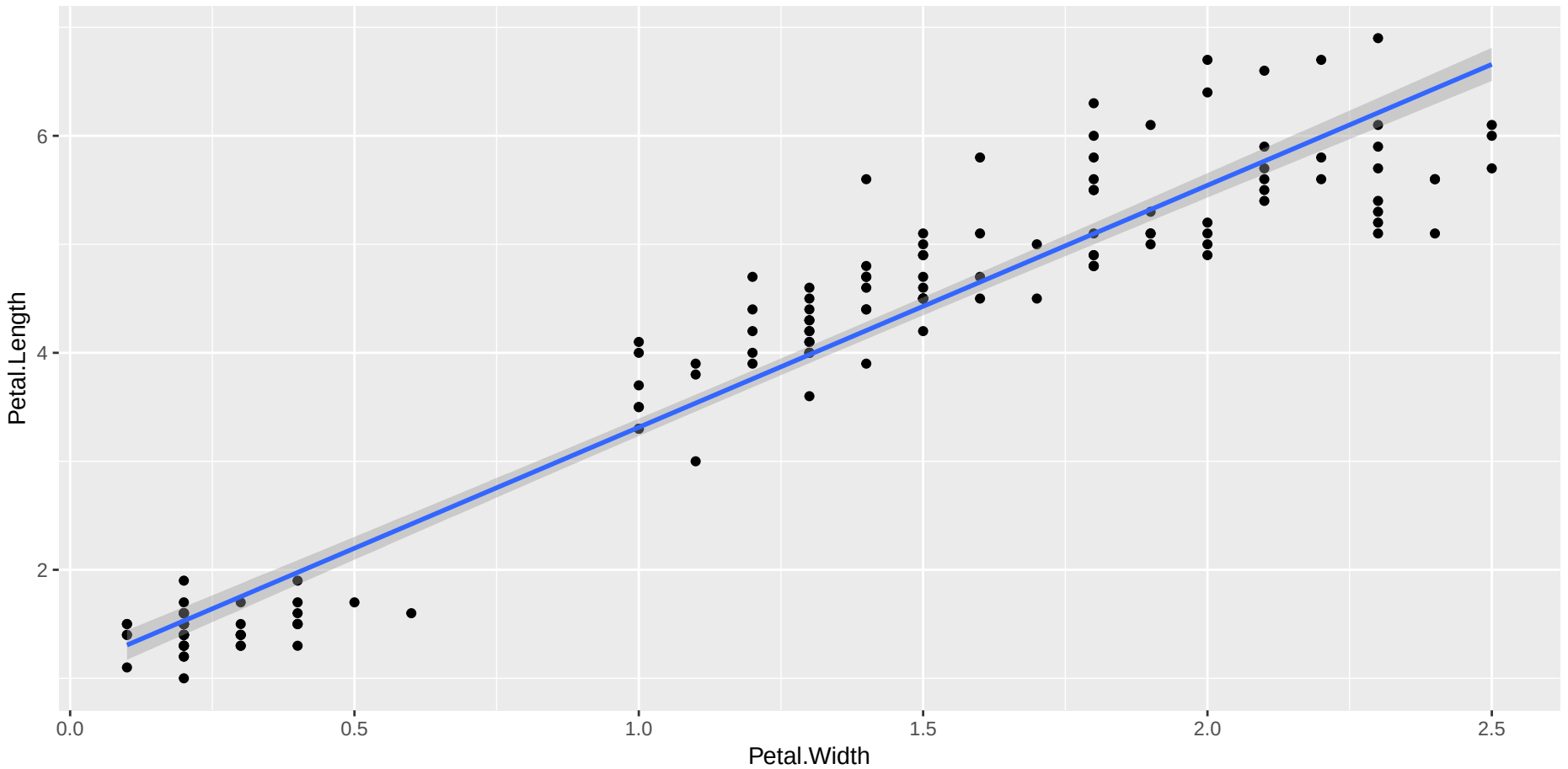
A ggplot2 plot

```
iris.tbl %>% ggplot(aes(x=Petal.Width,y=Petal.Length)) +
    geom_point()
```



A ggplot2 plot

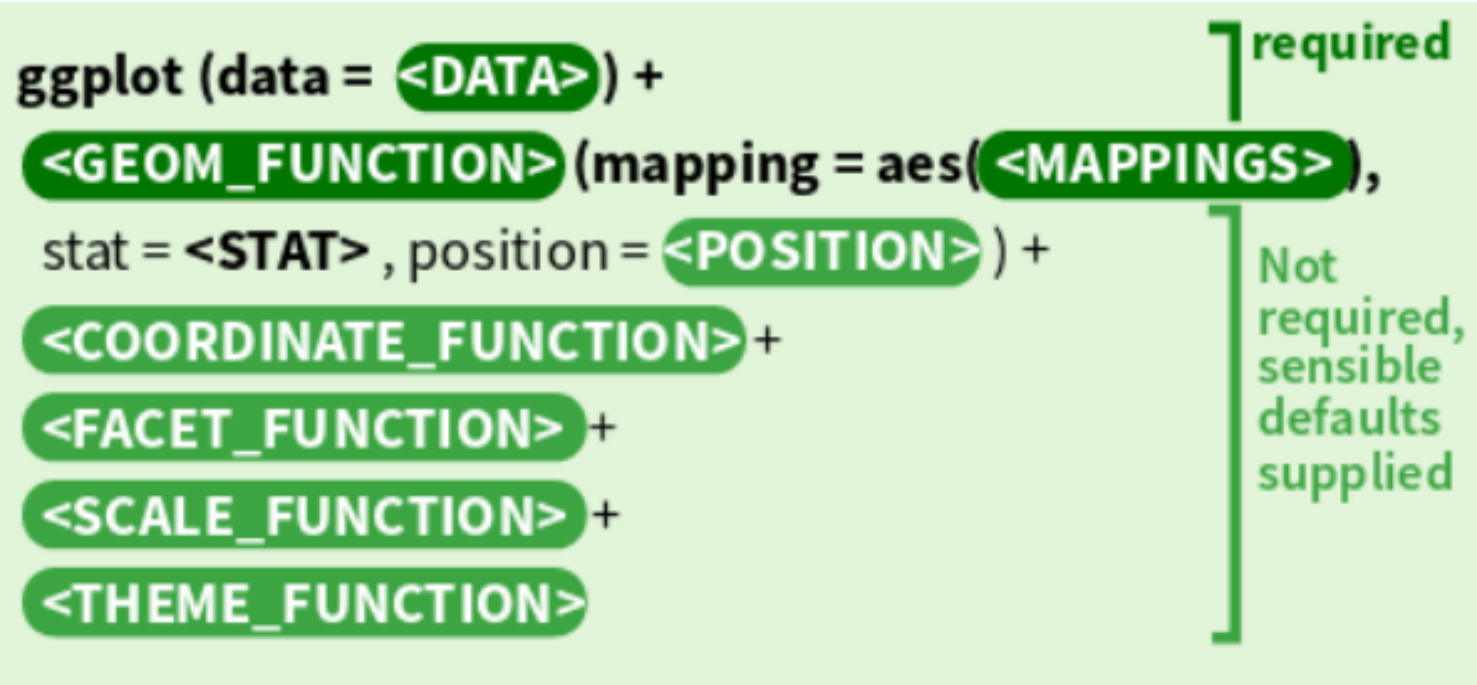
```
iris.tbl %>% ggplot(aes(x=Petal.Width,y=Petal.Length)) +
    geom_point() +
    geom_smooth(method = "lm")
```



The three key components of every ggplot2

The three components of every graphics :

- **data** : the dataset who's need to be plotted.
- **aesthetics** : aesthetics mapping between variables in the data (x,y,visuals properties, . . .).
- **geoms** : one or more layers to render each observations.



The three key components of every ggplot2

The three components of every graphics :

- **data** : the dataset who's need to be plotted.
- **aesthetics** : aesthetics mapping between variables in the data (x,y,visuals properties, . . .).
- **geoms** : one or more layers to render each observations.

```
p <- iris.tbl %>%# Data
    ggplot(aes(x=Petal.Width,y=Petal.Length)) +# aesthetics
    geom_point()# Layer: points
```

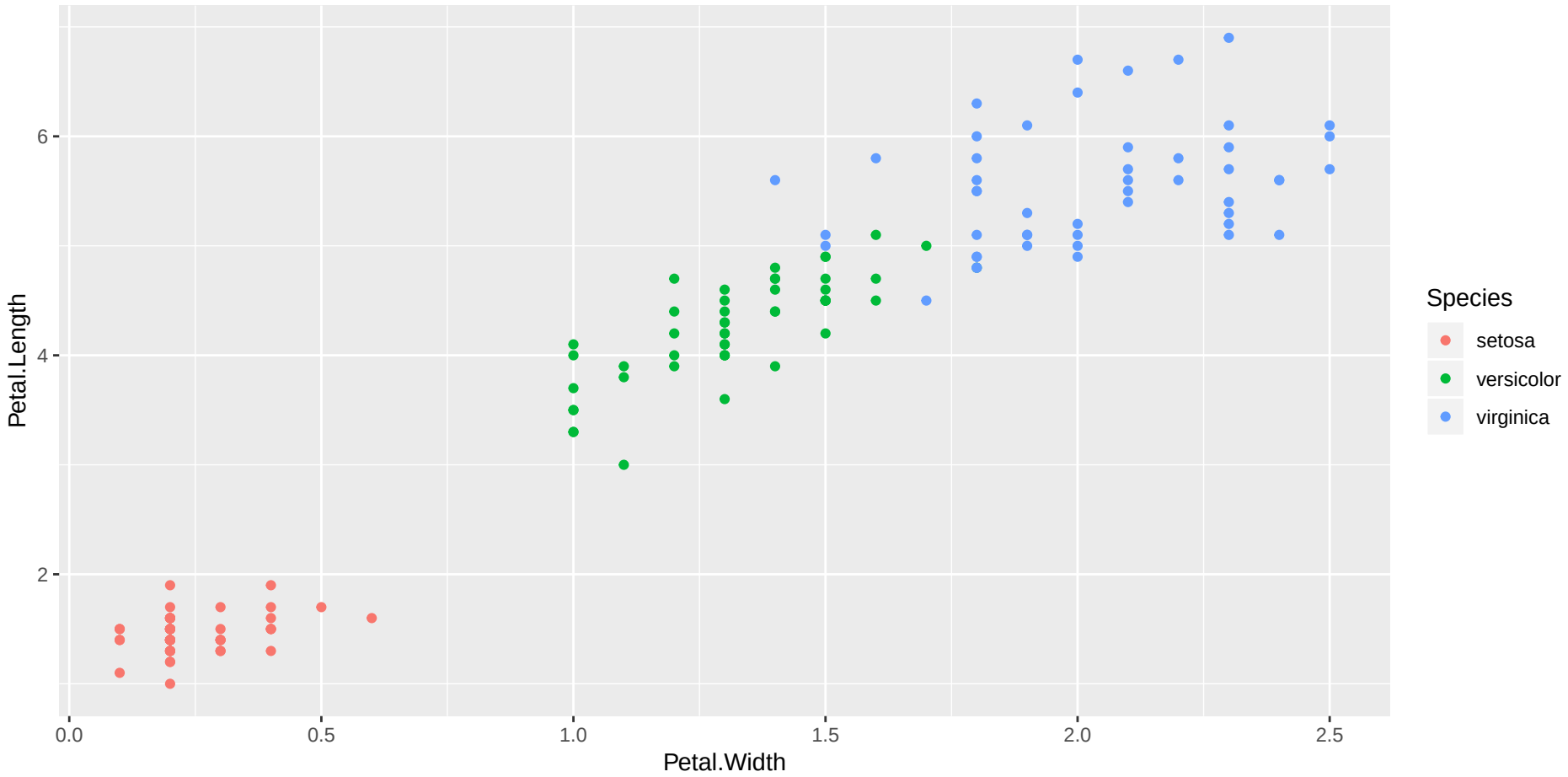
Add layer : smooth with linear model

```
p + geom_smooth(method = "lm")
```

More you add components with +, more you'll build sophisticated plots.

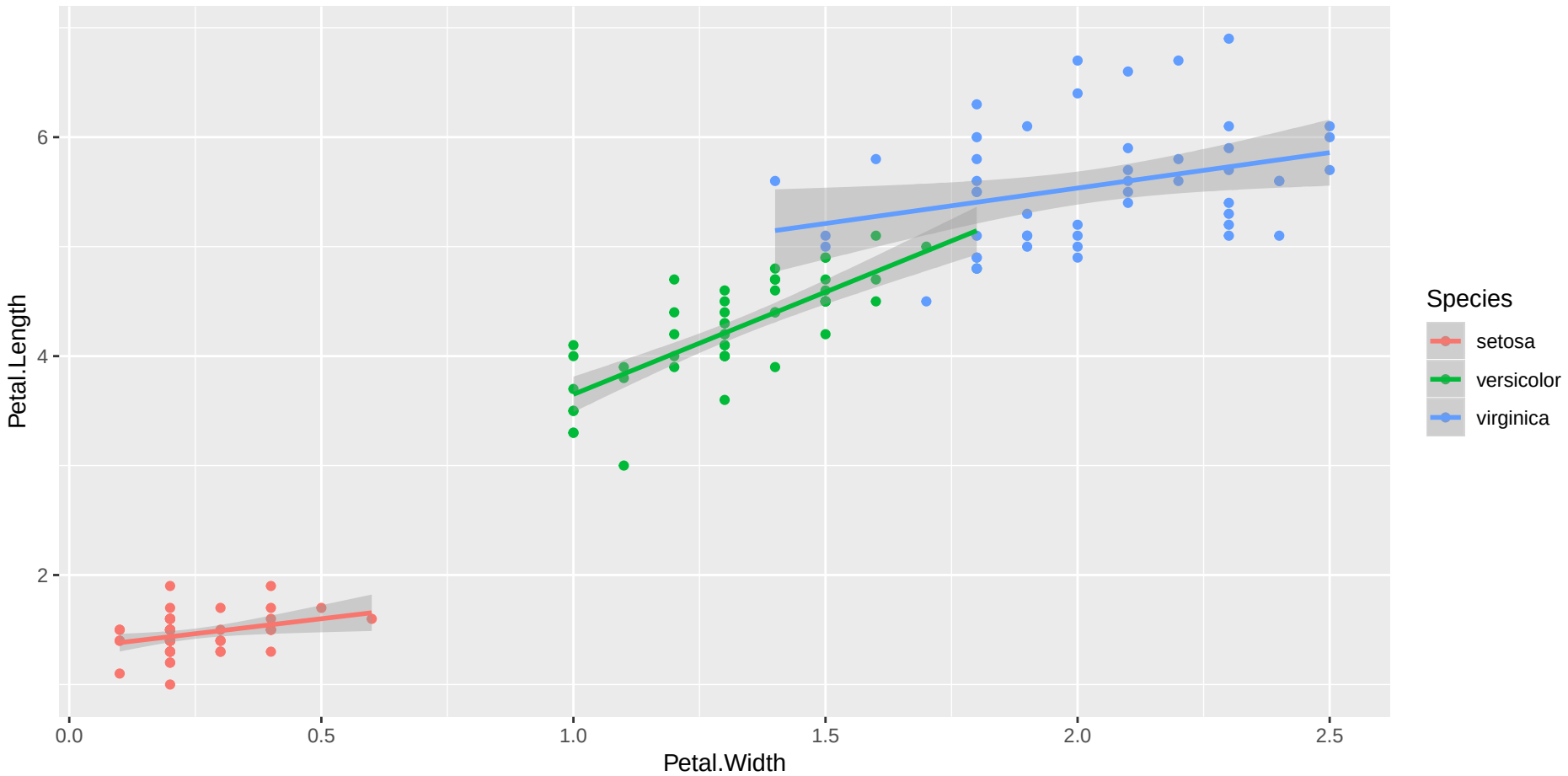
Add more aesthetics

```
p <- iris.tbl %>%# Data
    ggplot(aes(x=Petal.Width,y=Petal.Length,col=Species)) +# aesthetics
    geom_point()# Layer: points
print(p)
```



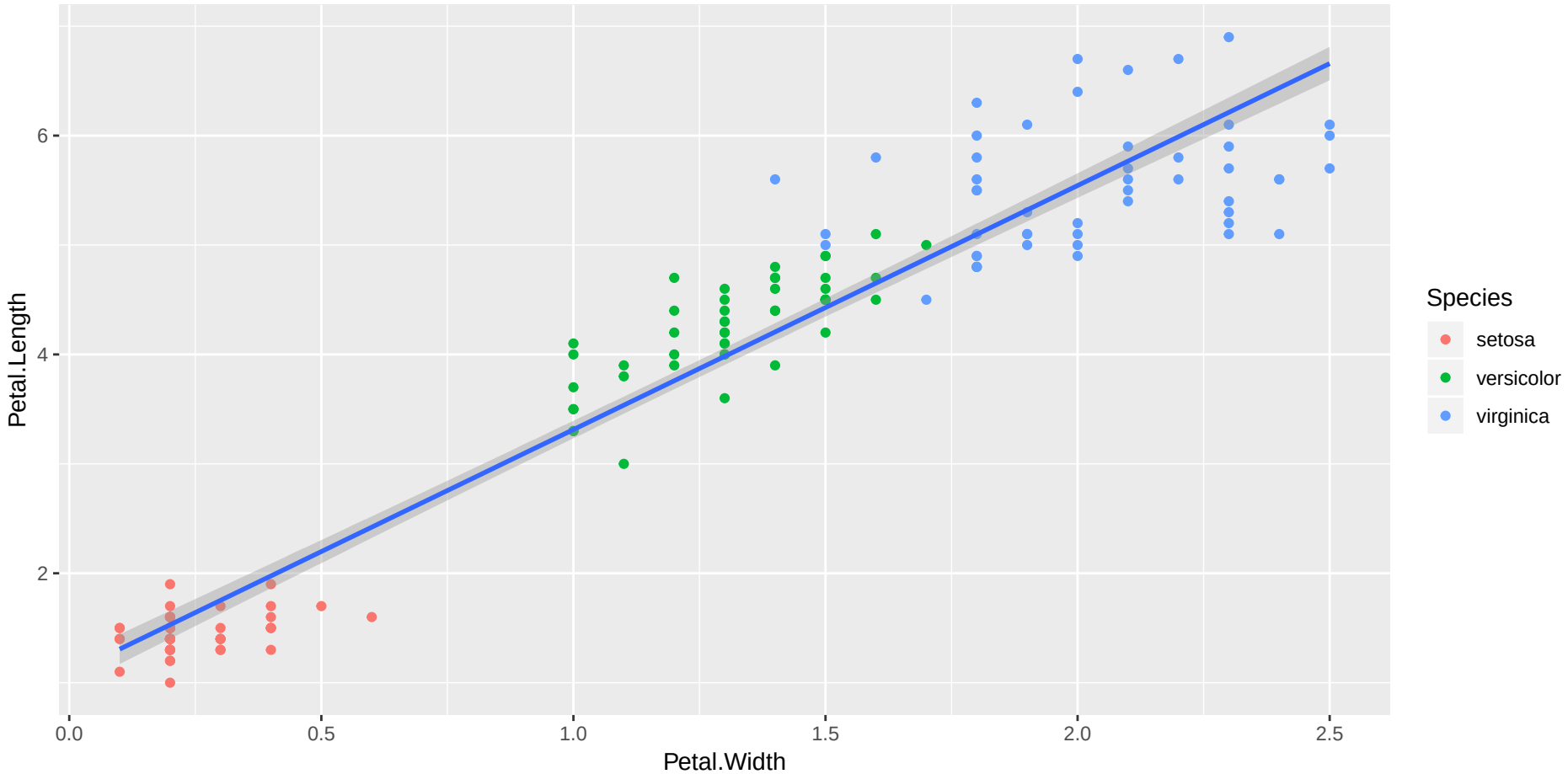
Add more aesthetics

```
p + geom_smooth(method = "lm")
```



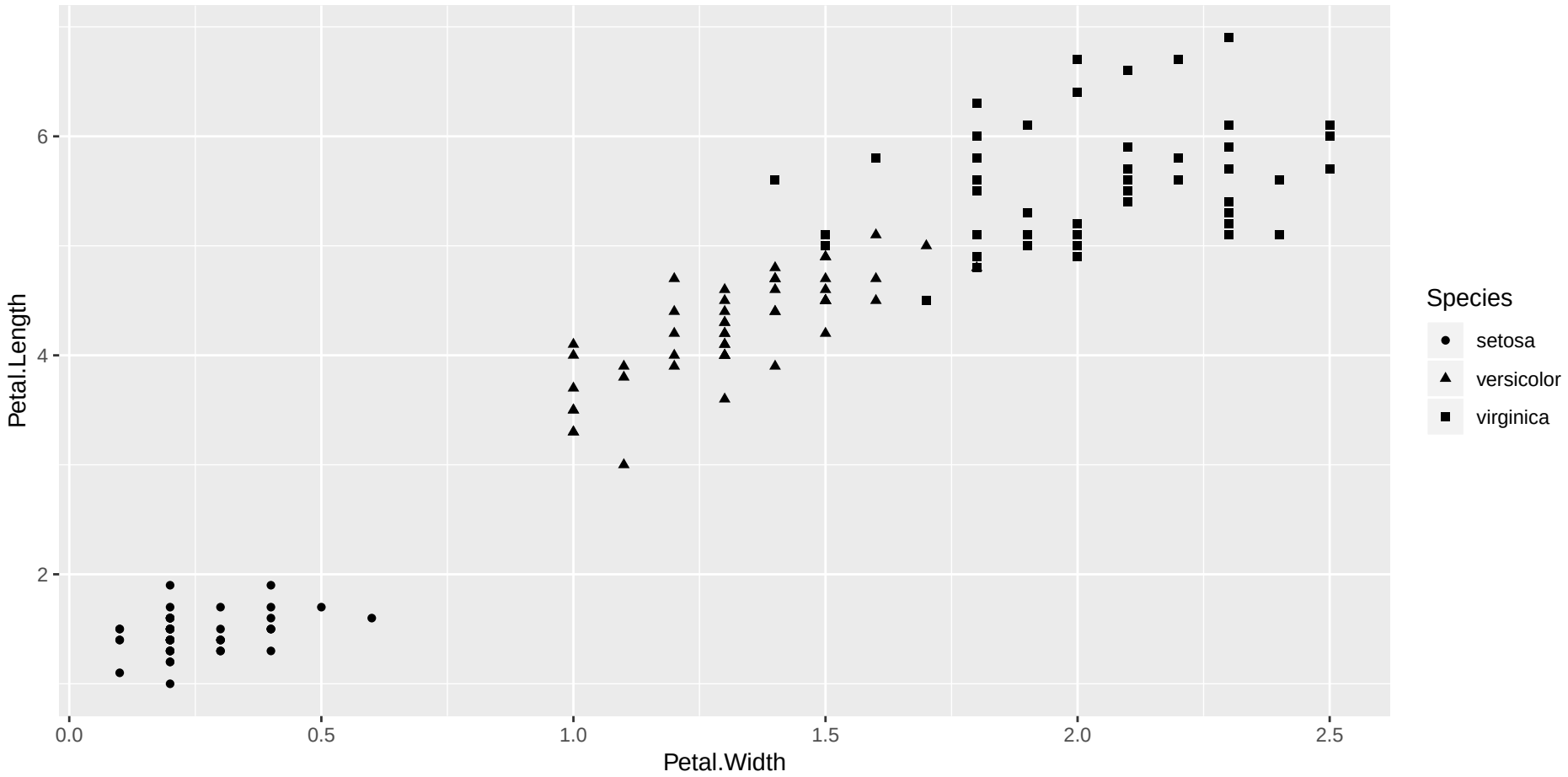
Add more aesthetics

```
p <- iris.tbl %>%# Data
    ggplot(aes(x=Petal.Width,y=Petal.Length)) +# aesthetics
    geom_point(aes(col=Species)) +# Layer: points
    geom_smooth(method = "lm")
print(p)
```



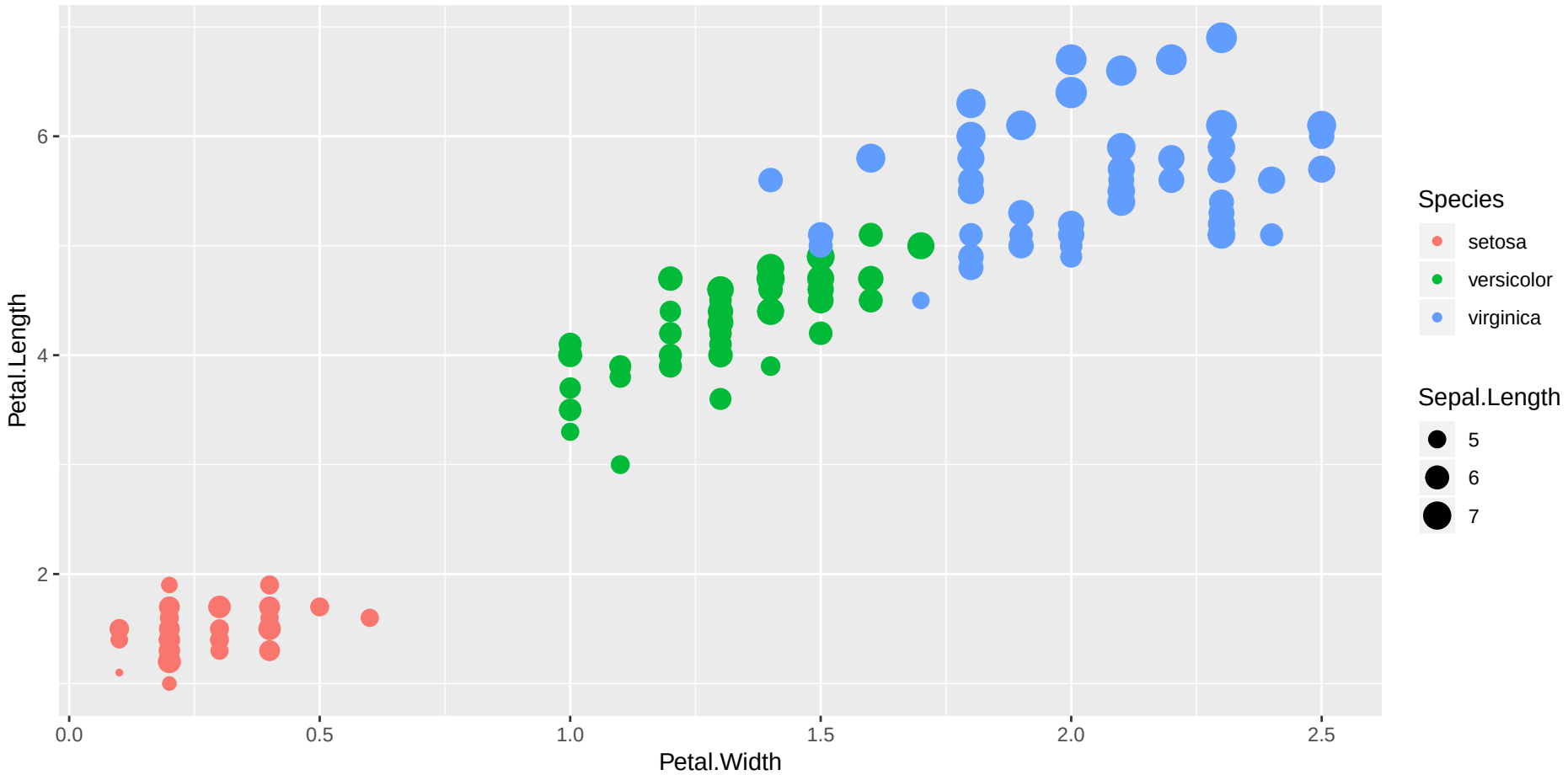
Other aesthetics attributes

```
p <- iris.tbl %>%# Data
    ggplot(aes(x=Petal.Width,y=Petal.Length)) +# aesthetics
    geom_point(aes(shape=Species))# Layer: points
print(p)
```



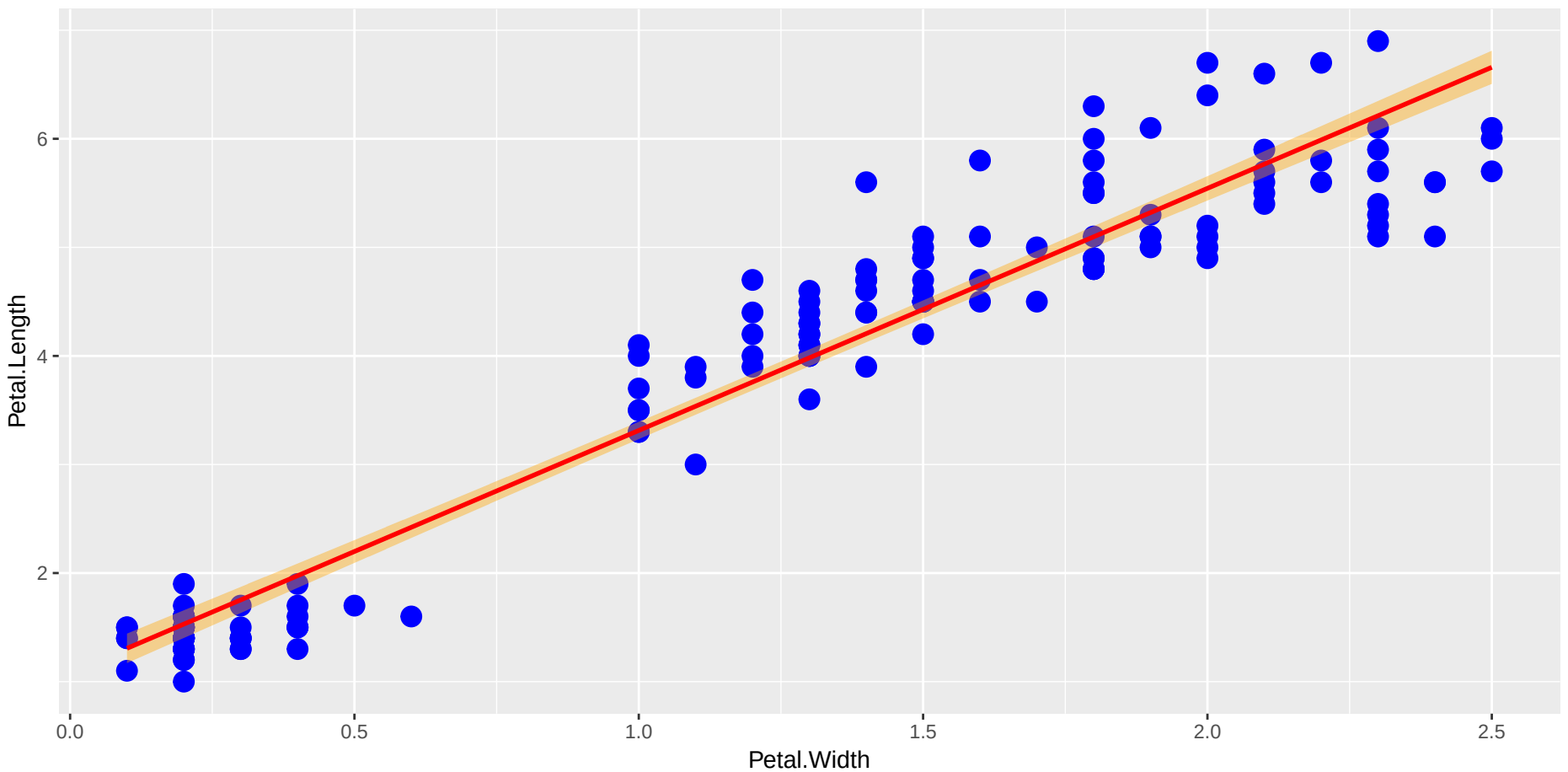
Other aesthetics attributes

```
p <- iris.tbl %>%# Data
    ggplot(aes(x=Petal.Width,y=Petal.Length)) +# aesthetics
    geom_point(aes(col=Species,size = Sepal.Length))# Layer: points
print(p)
```



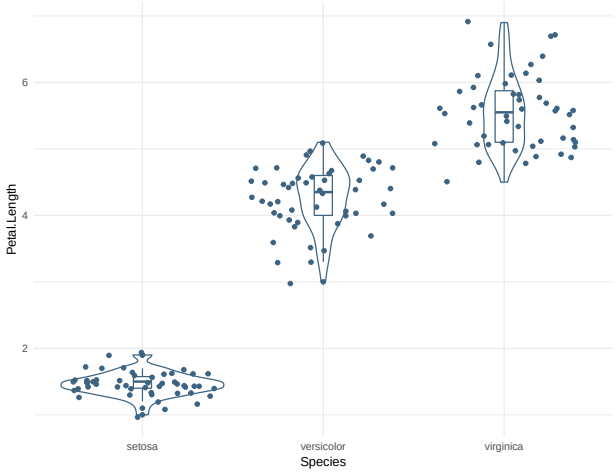
Use fixed value

```
p <- iris.tbl %>%# Data
    ggplot(aes(x=Petal.Width,y=Petal.Length)) +# aesthetics
    geom_point(col="blue",size=4) +# Layer: points
    geom_smooth(method = "lm",col="red",fill="orange")
print(p)
```

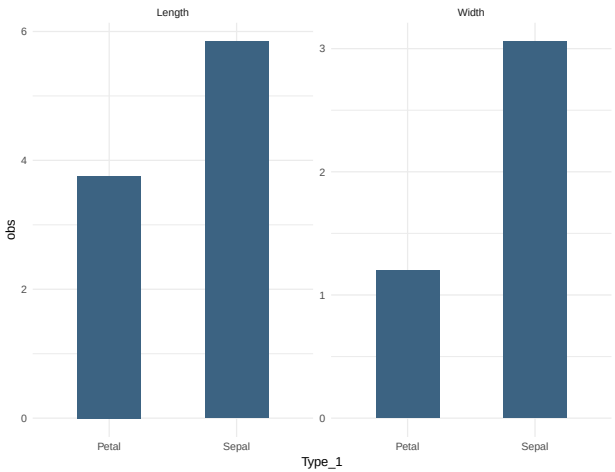


Plot geoms

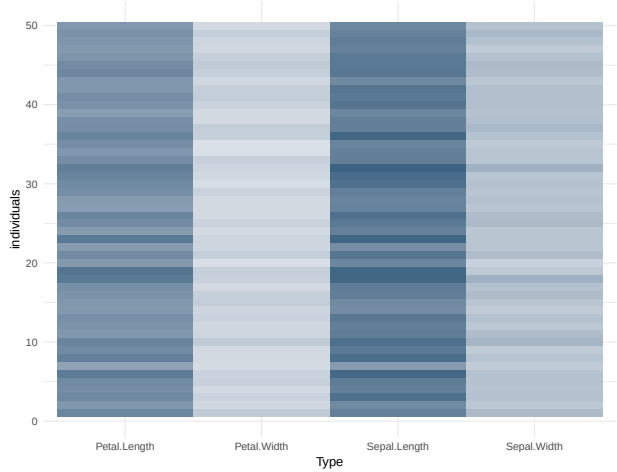
discrete x, continous y



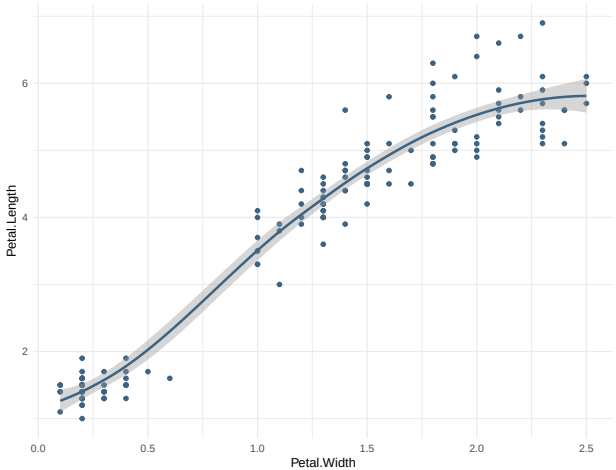
discrete x, continous y



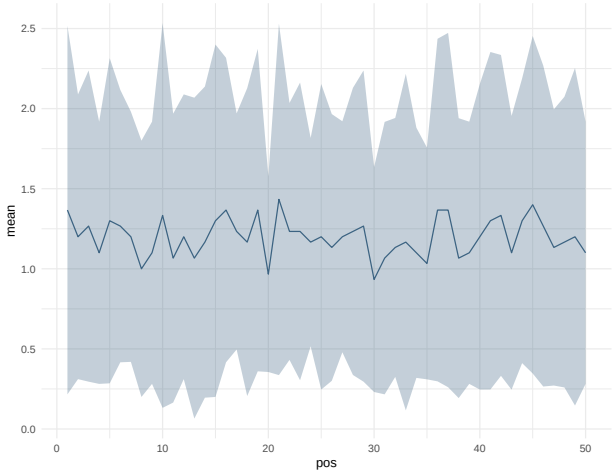
discrete x, discrete y



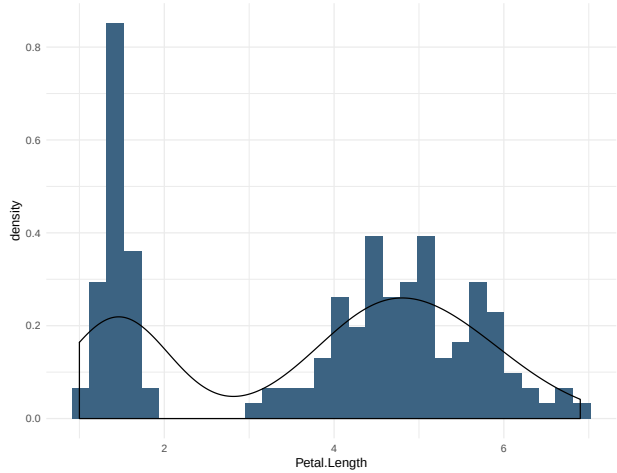
continous x, continous y



continous x, continous y



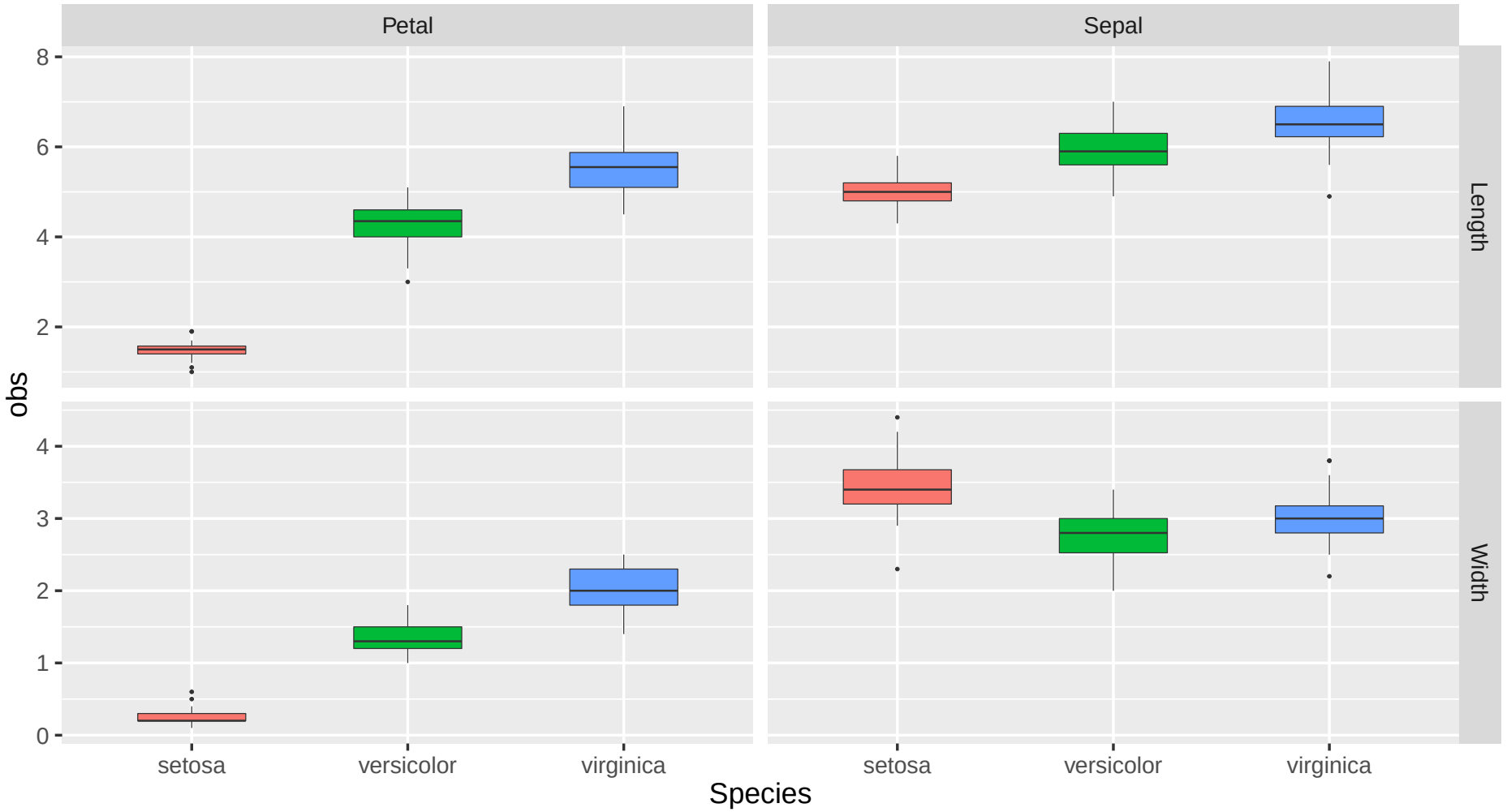
one variable continous



Facetting

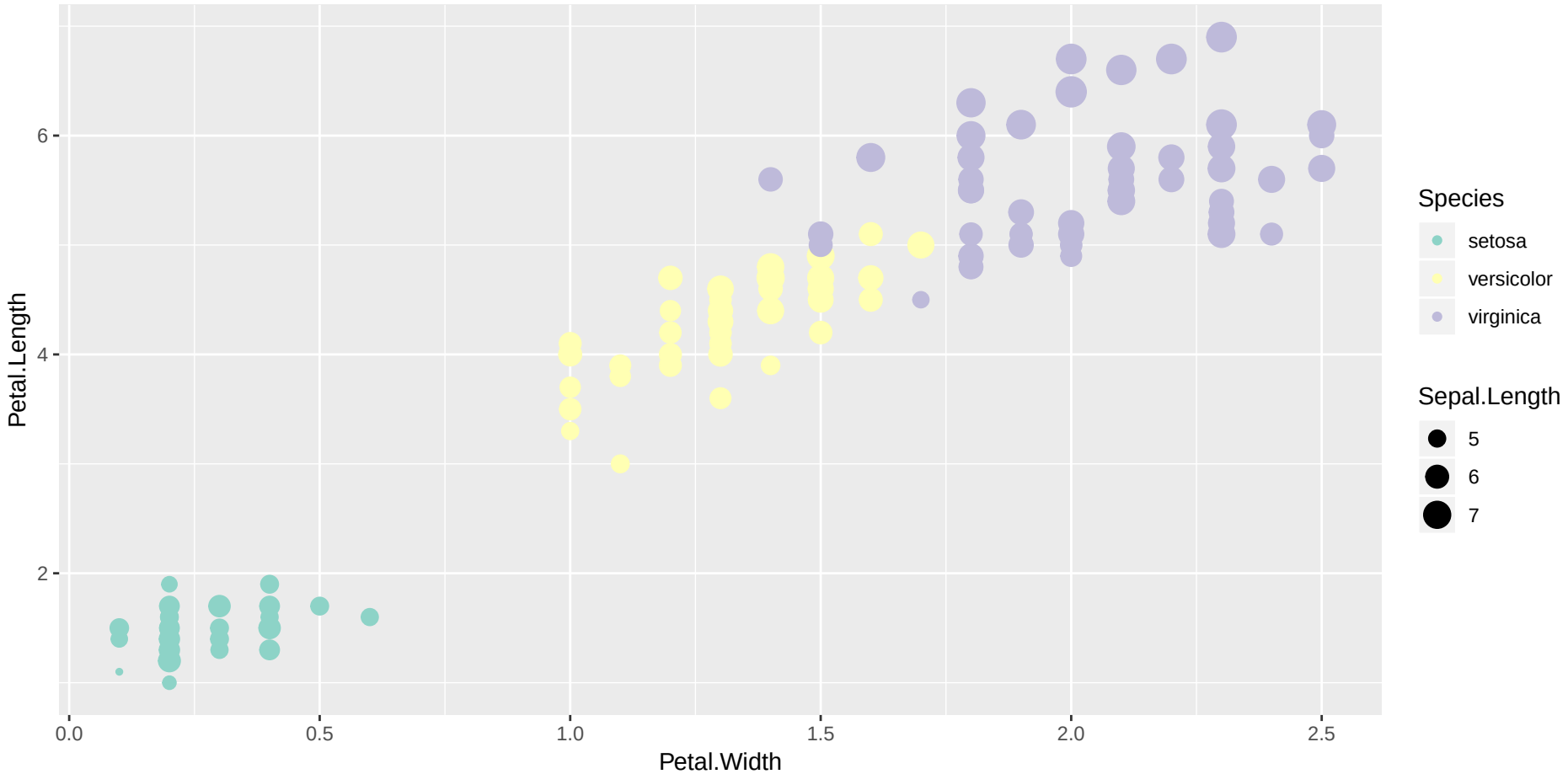
Facetting :

- `facet_grid(variable~foliaces)` : Display all possibility even if some plots are **empty**.
- `facet_wrap(variable~foliaces)` : Display only the plots having actual values.



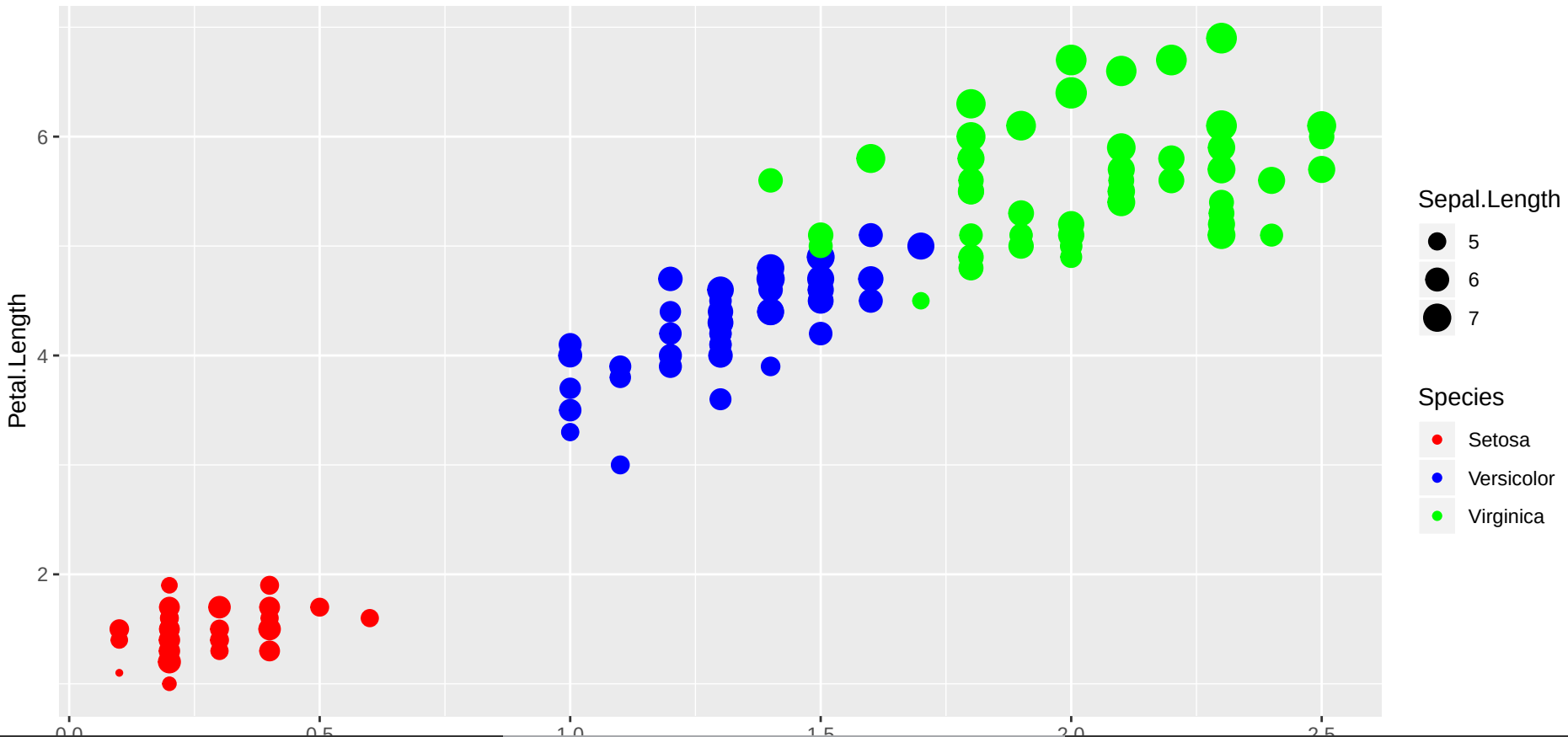
Graphical options

```
p <- iris.tbl %>%# Data
    ggplot(aes(x=Petal.Width,y=Petal.Length)) +# aesthetics
    geom_point(aes(col=Species,size = Sepal.Length)) +# Layer: points
    scale_color_brewer(palette="Set3") #A new palette
print(p)
```

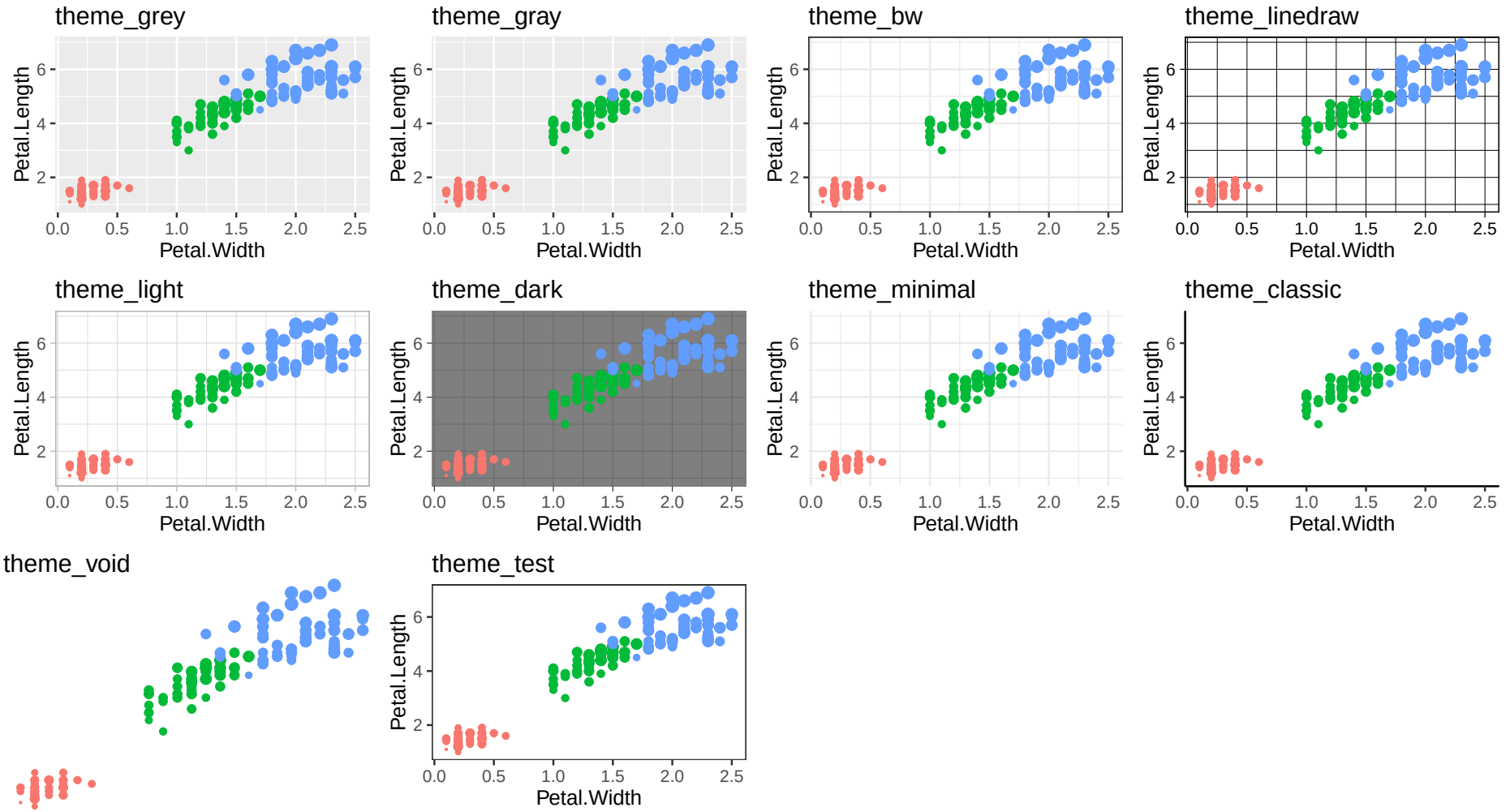


Graphical options

```
p <- iris.tbl %>%# Data
    ggplot(aes(x=Petal.Width,y=Petal.Length)) +# aesthetics
    geom_point(aes(col=Species,size = Sepal.Length)) +# Layer: points
    scale_color_manual(values = c("red","blue","green"),  #A new palette
                       labels = c("Setosa","Versicolor","Virginica"))
print(p)
```

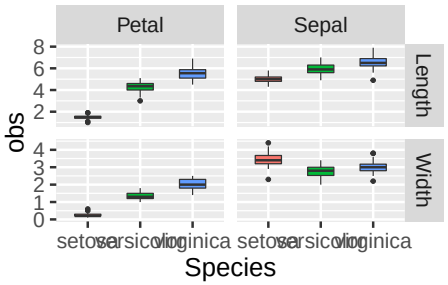


Themes

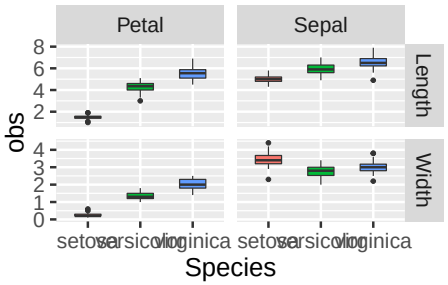

theme_grey
theme_gray
theme_bw
theme_linedraw
theme_light
theme_dark
theme_minimal
theme_classic
theme_void
theme_test
Petal.Length
Petal.Width

Themes

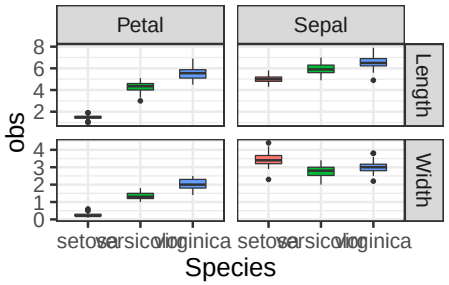
theme_grey



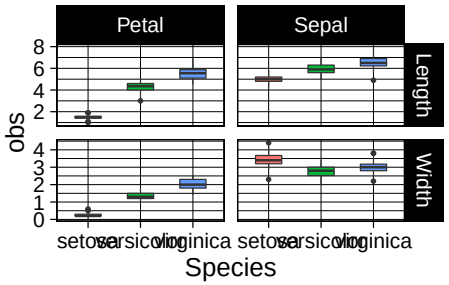
theme_gray



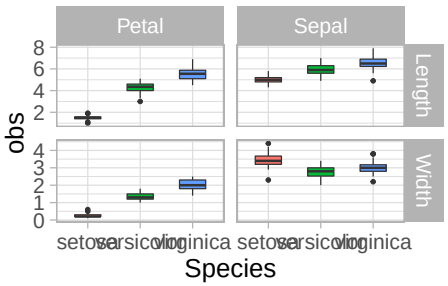
theme_bw



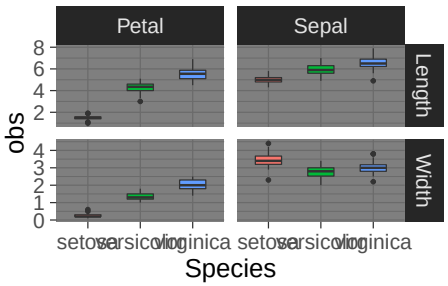
theme_linedraw



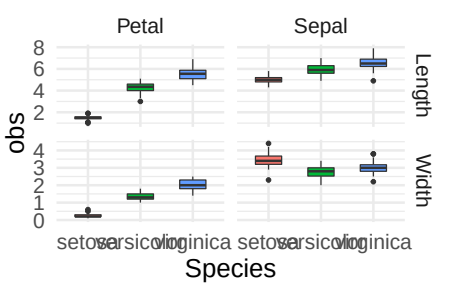
theme_light



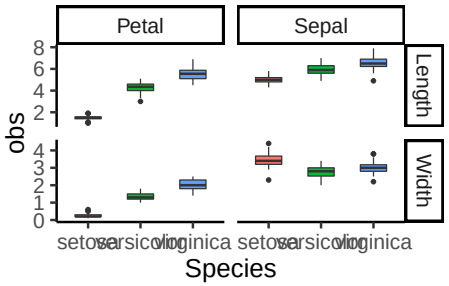
theme_dark



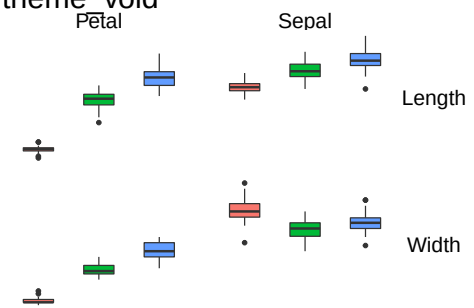
theme_minimal



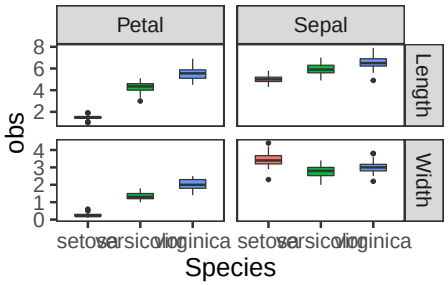
theme_classic



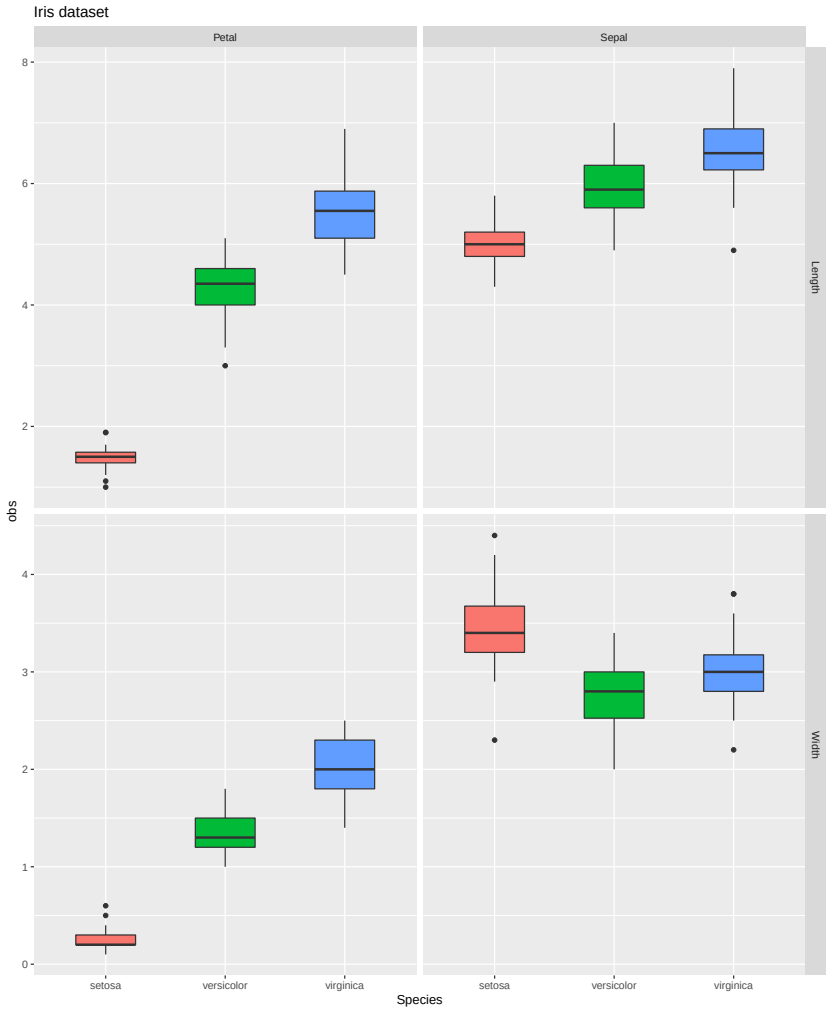
theme_void

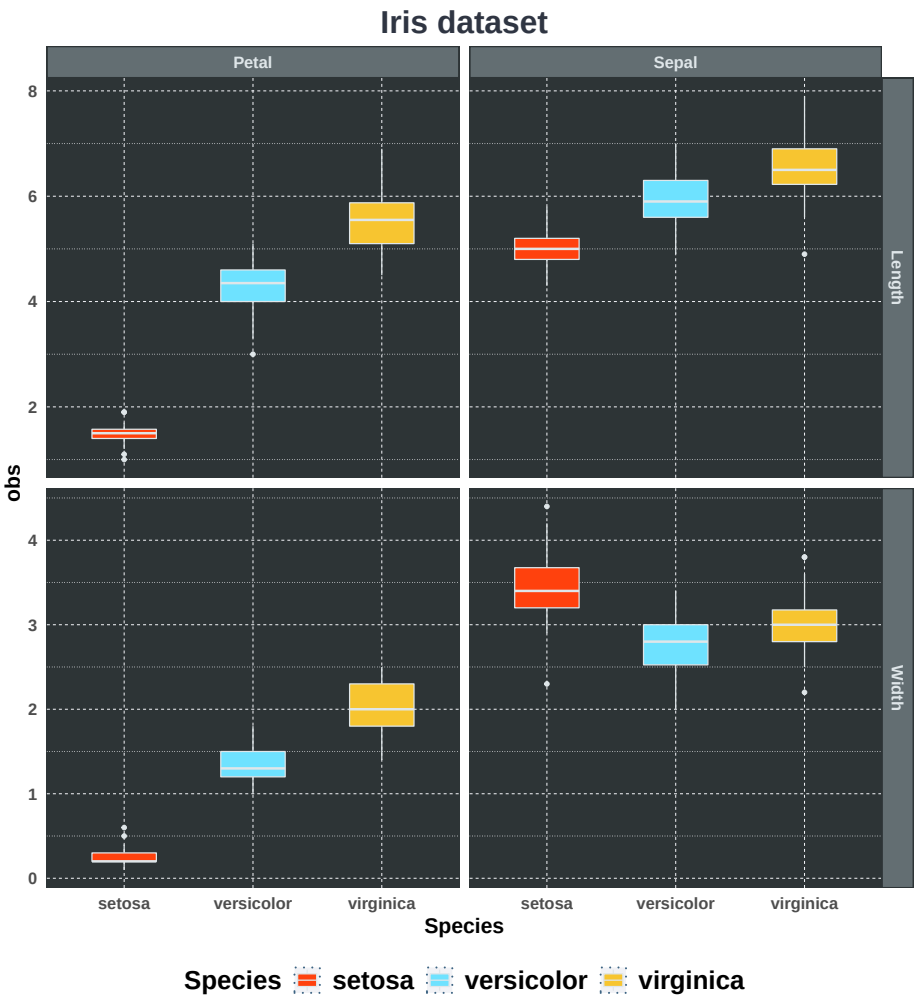


theme_test



Themes


Iris dataset
Petal
Sepal
Length
Width
obs
Species
setosa
versicolor
virginica


Iris dataset
Petal
Sepal
Length
Width
obs
setosa
versicolor
virginica
Species

Extensions

- **ggplot2** extensions : This site tracks and lists ggplot2 extensions developed by R users in the community. https://www.ggplot2-exts.org/.
- **cowplot** : Arranging graphs into a grid and improve plot design.
- **ggpubr** & ___ ggstatsplot___ : Publication ready plots & add statistical tests.
- **ggrepel** : Automatic label placement.
- **esquisse** : Explore and Visualize Your Data Interactively with ggplot2.
- **ggvis** : Create rich interactive graphics with a syntax similar in spirit to ggplot2.

Why I use ggplot2

- The "default" output is much nicer than with base graphics.
- Automatic legend, color with mapping to the variables.
- Easy to combine multiple plot.
- Easy facetting.
- A lot of themes.
- A lot of extensions ...