

# Journal Club Bioinfo

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

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# R for data science

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## R for Data Science

VISUALIZE, MODEL, TRANSFORM, TIDY, AND IMPORT DATA

Hadley Wickham &  
Garrett Golemund

- **R for data science** : The best place to start learning the tidyverse by Hadley Wickham and Garrett Golemund<sup>a</sup>.
- **ggplot2 : elegant graphics for data science** by Hadley Wickham. Goes into greater depth into the ggplot2 visualisation system.

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

- 1 Tidyverse & tidy data
- 2 Pipe and tibble
- 3 Tidying dataset
- 4 Manipulate a dataset using dplyr
- 5 Data visualisation using ggplot2
- 6 Sources

## Tidyverse & tidy data



# 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 :

country	year	cases	population
Afghanistan	1999	181	19987071
Afghanistan	2000	2666	20095360
Brazil	1999	30737	17206362
Brazil	2000	80488	17404898
China	1999	212258	127015272
China	2000	213066	128023583

variables

country	year	cases	population
Afghanistan	1999	181	19987071
Afghanistan	2000	2666	20095360
Brazil	1999	30737	17206362
Brazil	2000	80488	17404898
China	1999	212258	127015272
China	2000	213066	128023583

observations

country	year	cases	population
Afghanistan	1999	181	19987071
Afghanistan	2000	2666	20095360
Brazil	1999	30737	17206362
Brazil	2000	80488	17404898
China	1999	212258	127015272
China	2000	213066	128023583

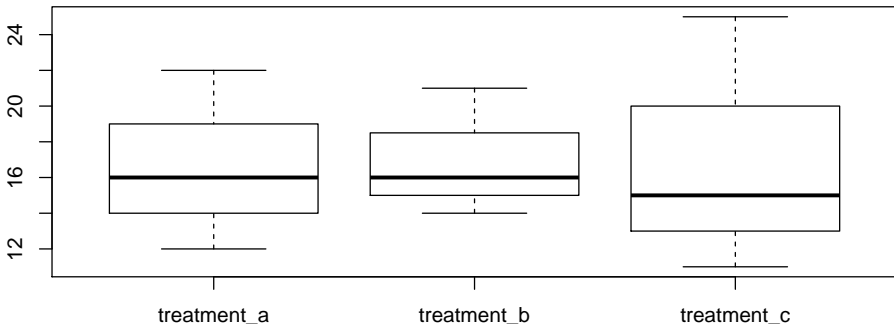
values

# Why tidying a dataset ?

TABLE 1 – Typical presentation dataset

	treatment_a	treatment_b	treatment_c
John Smith	12	14	15
Jane Doe	22	16	11
Mary Johnson	16	21	25

```
boxplot(treatments)
```





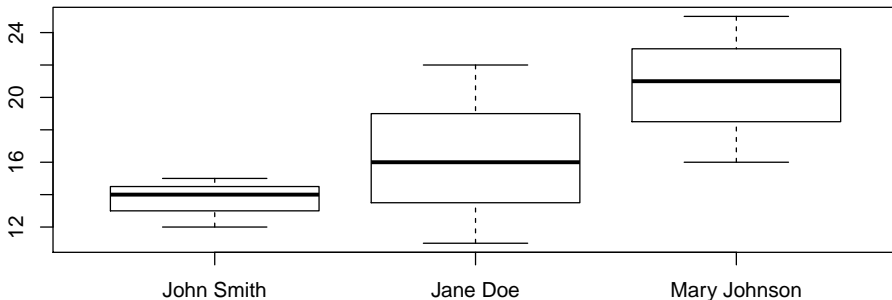
# Why tidying a dataset ?

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

TABLE 2 – The same data but structured differently

	John Smith	Jane Doe	Mary Johnson
treatment_a	12	22	16
treatment_b	14	16	21
treatment_c	15	11	25

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

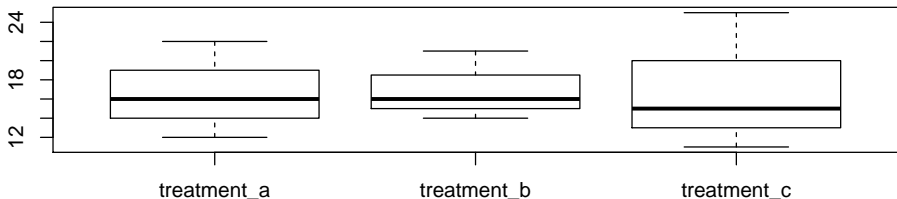


# Why tidying a dataset ?

TABLE 3 – An exemple of a tidy dataset

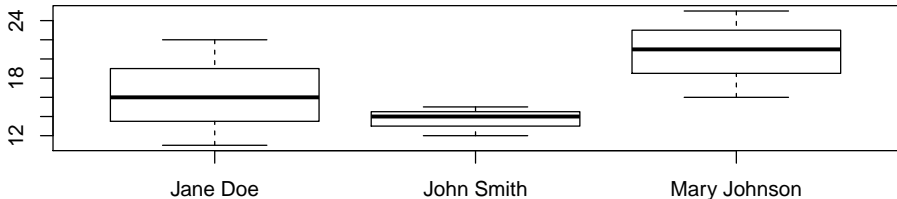
person	treatment	result
John Smith	treatment_a	12
Jane Doe	treatment_a	22
Mary Johnson	treatment_a	16
John Smith	treatment_b	14
Jane Doe	treatment_b	16
Mary Johnson	treatment_b	21
John Smith	treatment_c	15
Jane Doe	treatment_c	11
Mary Johnson	treatment_c	25

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

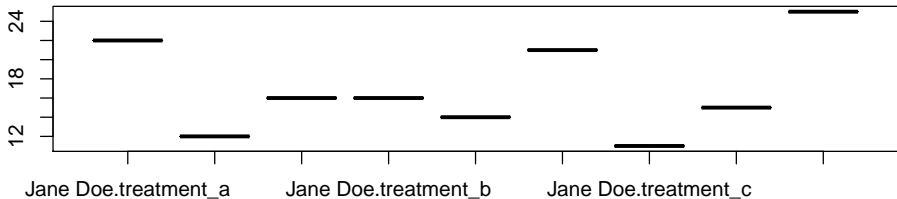


## Why tidying a dataset ?

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



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





# 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
```

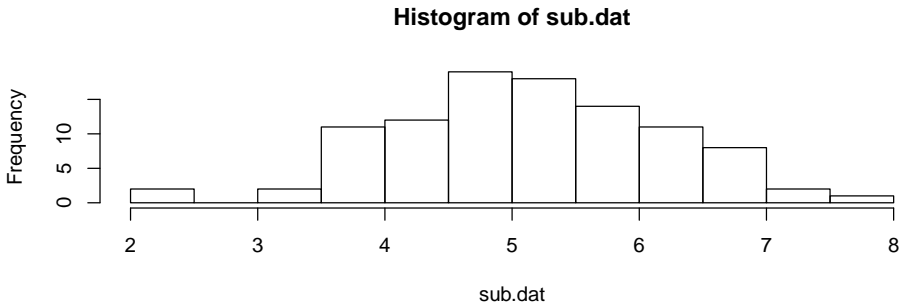
```
## Species  
## Setosa  
## Setosa  
## Setosa  
## Setosa  
## Setosa  
## Setosa  
## Setosa  
## Setosa  
## Setosa
```

```
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

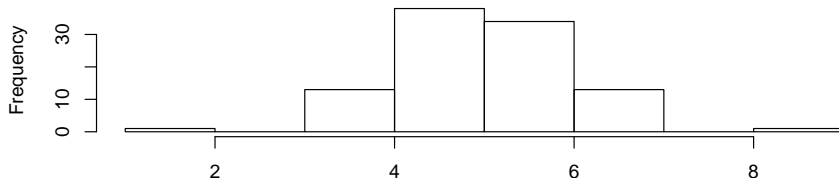
```
ex.dat <- rnorm(n = 1000, mean = 5, sd=1)
sub.dat <- sample(ex.dat, size = 100, replace=F)
hist(sub.dat)
```



# Pipes vs no pipes : without pipe

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

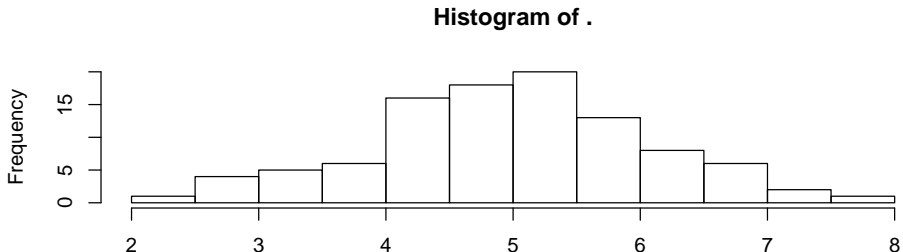
**Histogram of `sample(rnorm(n = 1000, mean = 5, sd = 1), size = 100, replace = F)`**



`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      12        14        15
## 2 Jane Doe        22        16        11
## 3 Mary Johnson    16        21        25
```

# 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     12
## 2    Jane Doe treatment_a     22
## 3 Mary Johnson treatment_a     16
## 4   John Smith treatment_b     14
## 5    Jane Doe treatment_b     16
## 6 Mary Johnson treatment_b     21
## 7   John Smith treatment_c     15
## 8    Jane Doe treatment_c     11
## 9 Mary Johnson treatment_c     25
```

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

```
##           person treatment_a treatment_b treatment_c
## 1    Jane Doe           22           16           11
## 2   John Smith           12           14           15
## 3 Mary Johnson           16           21           25
```

# 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     12
## 2      Jane       Doe treatment_a     22
## 3      Mary    Johnson treatment_a     16
## 4      John      Smith treatment_b     14
## 5      Jane       Doe treatment_b     16
## 6      Mary    Johnson treatment_b     21
## 7      John      Smith treatment_c     15
## 8      Jane       Doe treatment_c     11
## 9      Mary    Johnson treatment_c     25
```



## Manipulate a dataset using dplyr



# 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(Petal.Length))
```

```
## # 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))
```

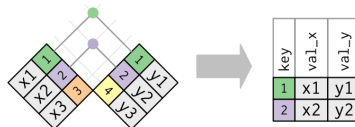
```
## # A tibble: 4 x 5
## # Groups:   Species [3]
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
##         <dbl>         <dbl>         <dbl>         <dbl> <fct>
## 1         4.8           3.4           1.9           0.2 setosa
## 2         5.1           3.8           1.9           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.



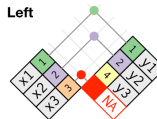
```
iris.meta.nosetosa <- iris.meta %>% filter(Species != "setosa")
iris.tbl %>% inner_join(iris.meta.nosetosa, by = "Species") %>% print(n=5)
```

```
## # 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

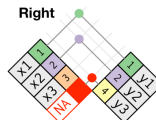
- A **left join** keeps all observations in *x*.
- A **right join** keeps all observations in *y*.
- A **full join** keeps all observations in *x* and *y*.

Left



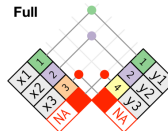
key	val_x	val_y
1	x1	y1
2	x2	y2
3	x3	NA

Right



key	val_x	val_y
1	x1	y1
2	x2	y2
4	NA	y3

Full



key	val_x	val_y
1	x1	y1
2	x2	y2
3	x3	NA
4	NA	y3



# 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

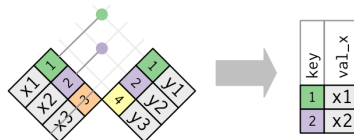
full join :

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

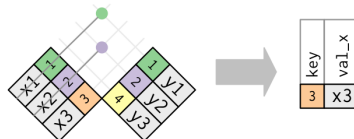
```
## # A tibble: 11 x 8
## # Groups:   Species [3]
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species Colony Ploidy
##         <dbl>      <dbl>      <dbl>      <dbl> <fct>   <chr>   <chr>
## 1         5.1         3.5         1.4         0.2 setosa  <NA>   <NA>
## 2         4.9         3         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     12  
## 2      Jane       Doe treatment_a     22  
## 3      John      Smith treatment_b     14  
## 4      Jane       Doe treatment_b     16  
## 5      John      Smith treatment_c     15  
## 6      Jane       Doe treatment_c     11
```

# 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

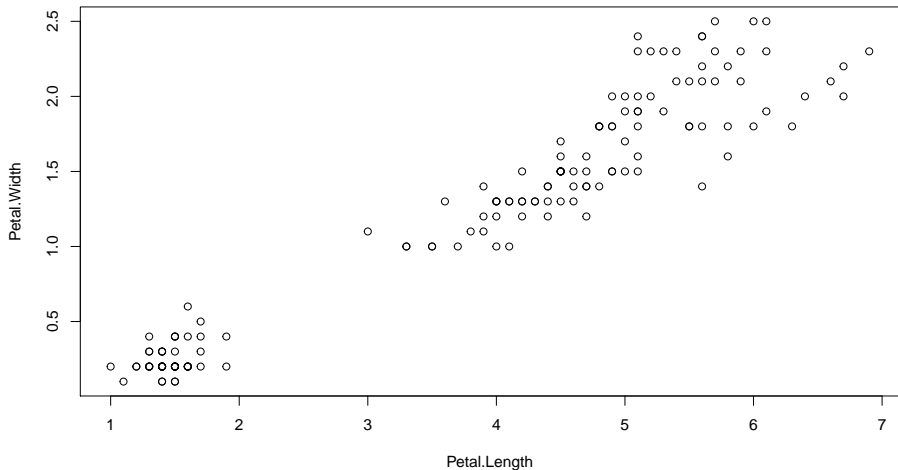
## # Groups: Species, Type\_1, Type\_2 [12]

##	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

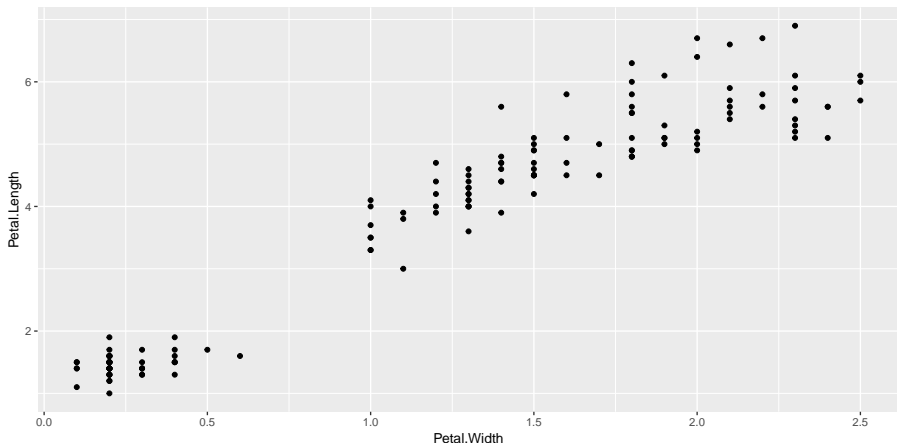
# A base plot

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



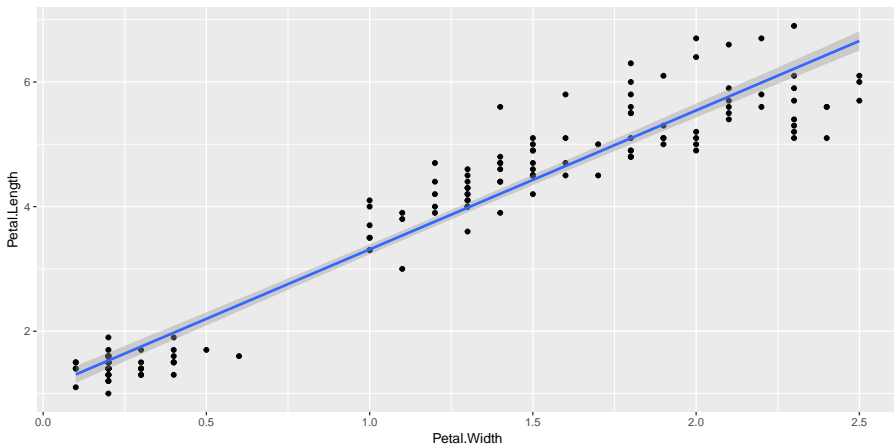
# A ggplot2 plot

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



# A ggplot2 plot

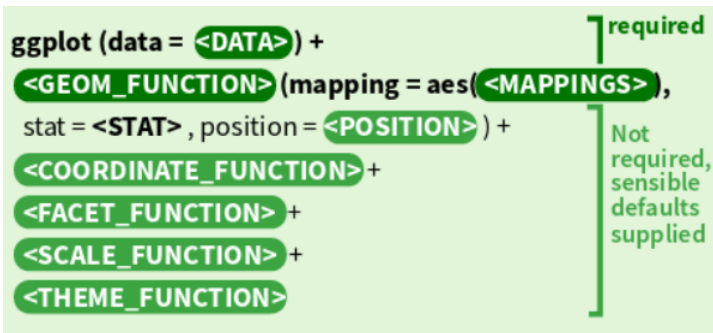
```
iris.tbl %>% ggplot(aes(x=Petal.Width,y=Petal.Length)) +  
  geom_point() +  
  geom_smooth(method = "lm")
```



# 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
```

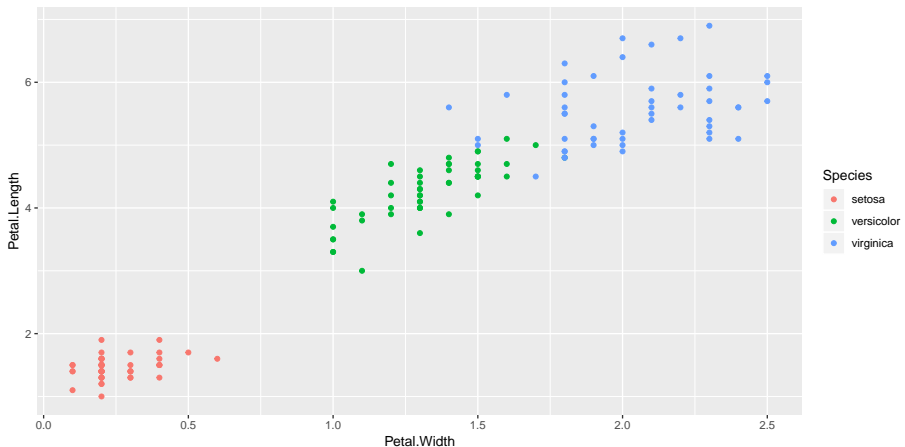
Add layer : smooth with linear model

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

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

## Add more aesthetics

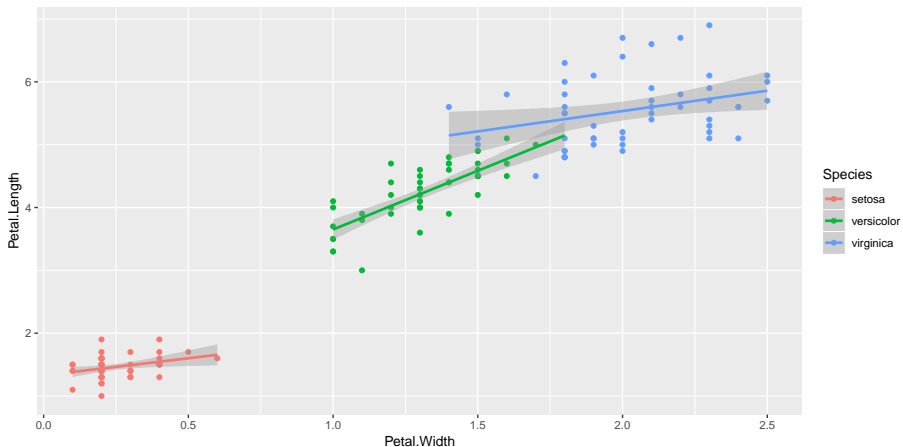
```
p <- iris.tbl %>%# Data
  ggplot(aes(x=Petal.Width,y=Petal.Length,col=Species)) +# aesthetics
  geom_point()# Layer: points
print(p)
```





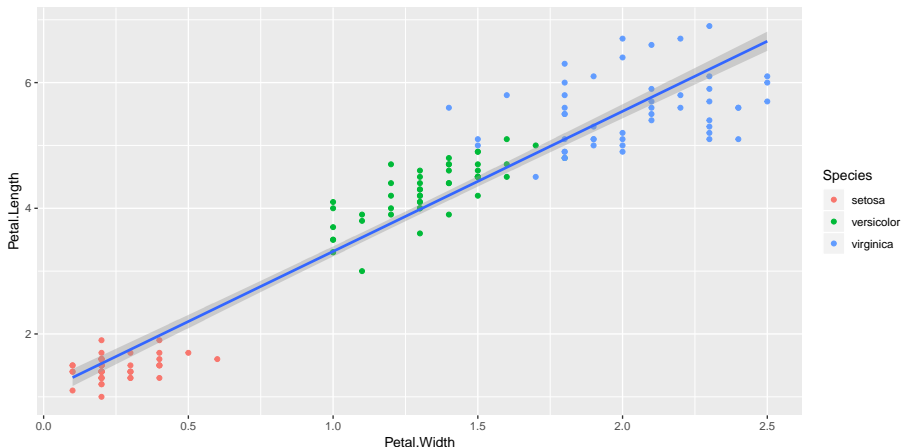
# Add more aesthetics

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



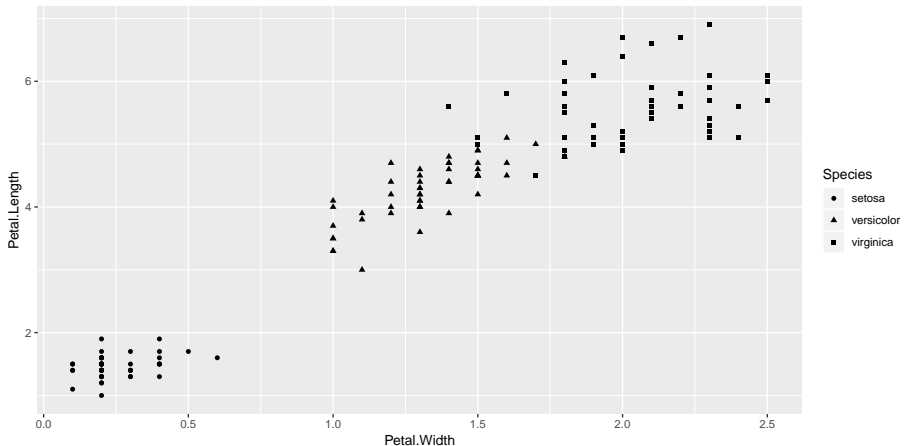
## Add more aesthetics

```
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)
```



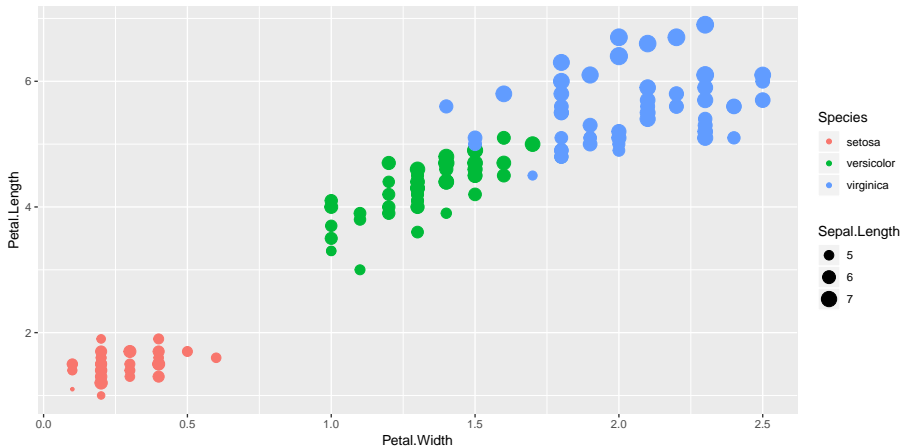
## Other aesthetics attributes

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



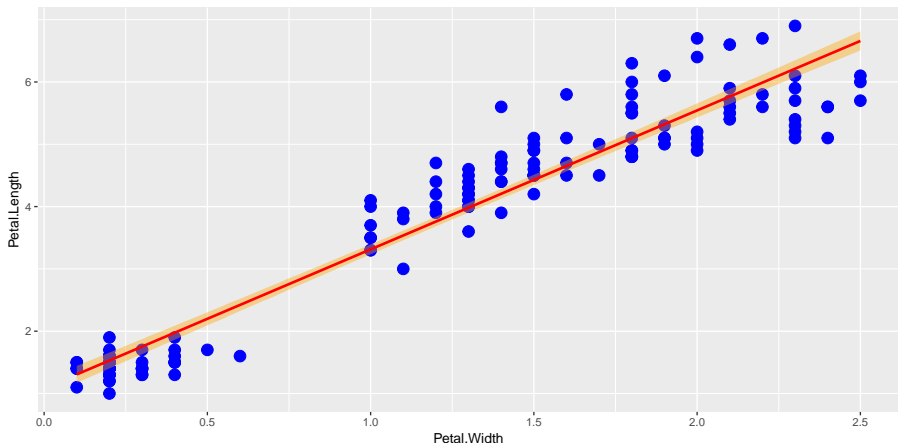
## Other aesthetics attributes

```
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)
```



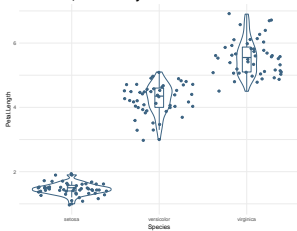
## Use fixed value

```
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)
```

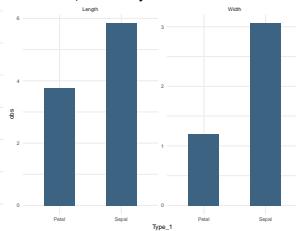


# Plot geoms

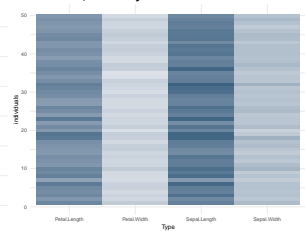
discrete x, continous y



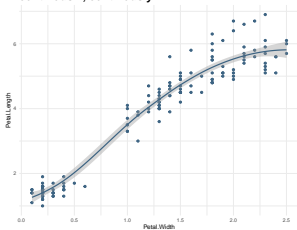
discrete x, continous y



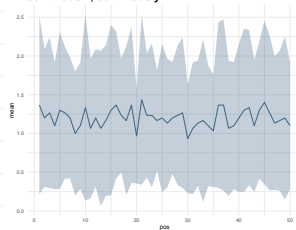
discrete x, discrete y



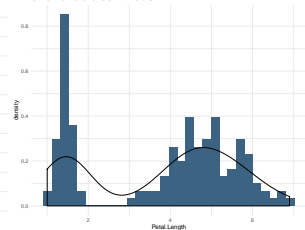
continous x, continous y



continous x, continous y



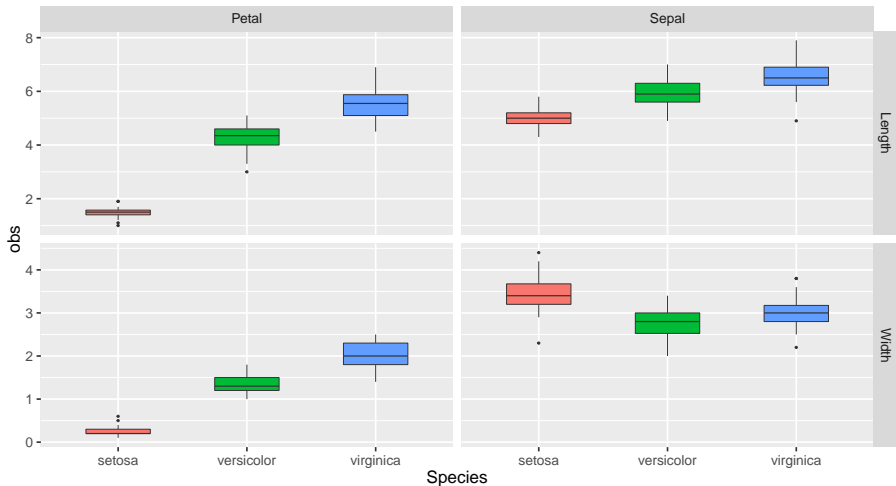
one variable continous



# Facetting

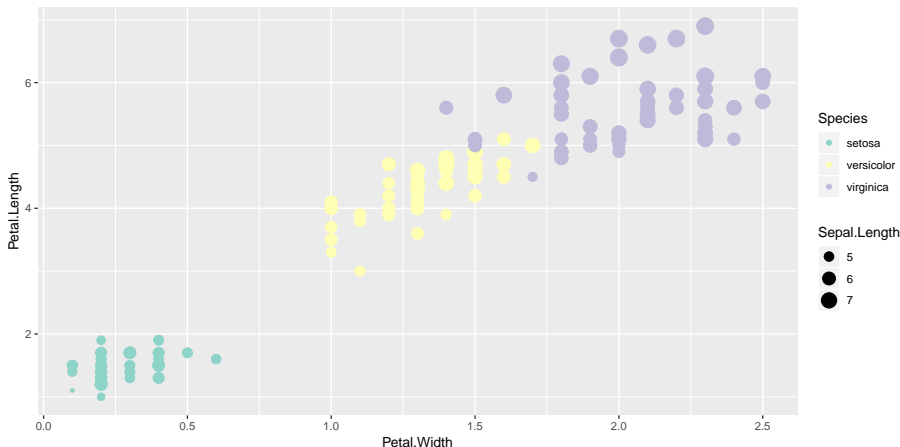
## Facetting :

- `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

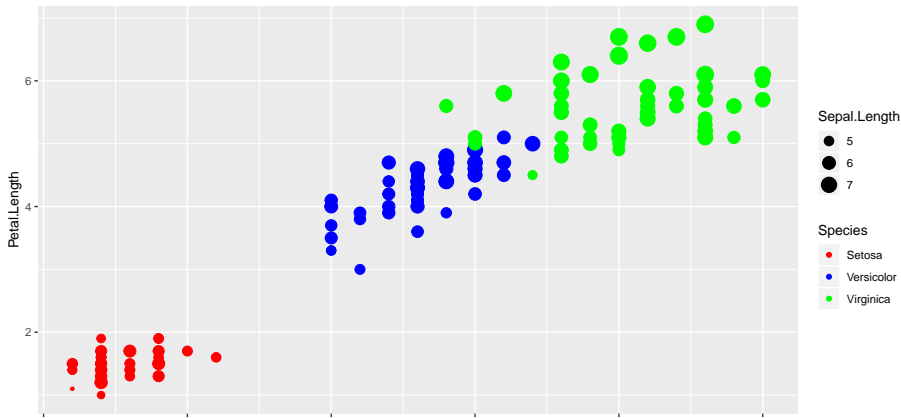
```
p <- iris.tbl %>%# Data
  ggplot(aes(x=Petal.Width,y=Petal.Length)) +# aesthetics
  geom_point(aes(col=Species,size = Sepal.Length)) +# Layer: points
  scale_color_brewer(palette="Set3") #A new palette
print(p)
```



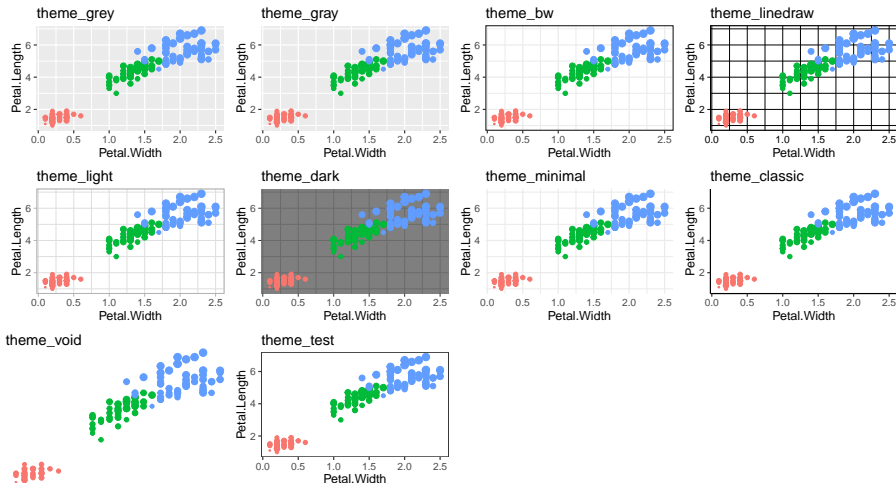


# Graphical options

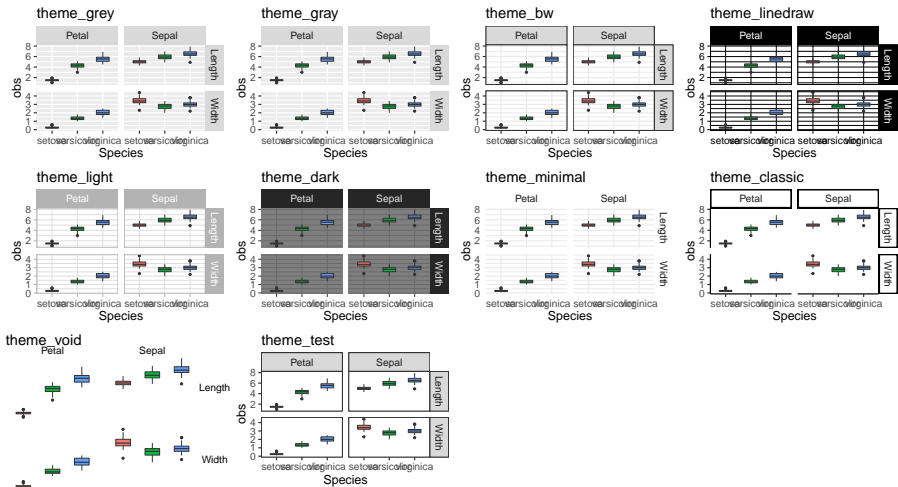
```
p <- iris.tbl %>% # Data
  ggplot(aes(x=Petal.Width,y=Petal.Length)) + # aesthetics
  geom_point(aes(col=Species,size = Sepal.Length)) + # Layer: points
  scale_color_manual(values = c("red","blue","green"), #A new palette
                    labels = c("Setosa","Versicolor","Virginica"))
print(p)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



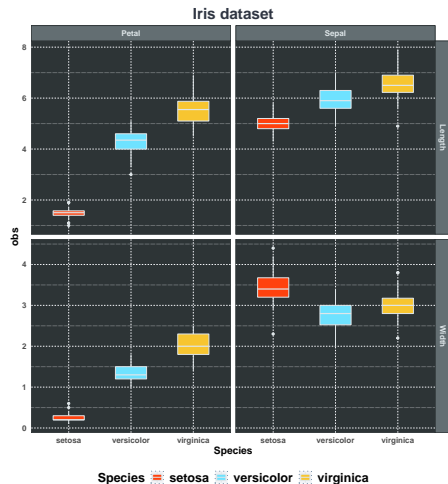
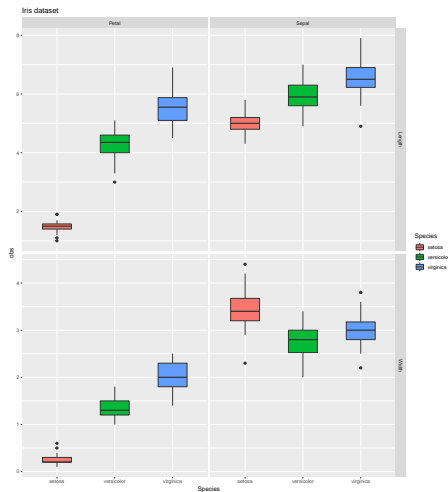
# Themes



# Themes



# Themes



## 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 ...



# Sources

## Sources :

- **PDF and sources :**

[https://github.com/rochevin/tidyverse\\_journal\\_club](https://github.com/rochevin/tidyverse_journal_club)

- **Web version :** [https://rochevin.github.io/tidyverse\\_journal\\_club](https://rochevin.github.io/tidyverse_journal_club)