

Statistical Analysis using R

Graphics in R with ggplot2

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Course overview

1. ~~Short Introduction to R and RStudio~~
2. ~~Preparation of Data for Statistical Analysis~~
3. ~~Data wrangling~~
4. ~~Experimental Designs for Plant Breeding~~
5. ~~ANOVA and MET analysis~~
6. ~~Multivariate analysis~~
7. Graphics in R with ggplot2

Recap: Data Import

- To import a **csv** file into R

```
library(tidyverse)
mydata <- read_csv("mydata.csv")
```

- To import a **xlsx** file into R

```
library(readxl)
mydata <- read_excel("mydata.xlsx", sheet = "Sheet1")
```

Recap: Data Wrangling

- There are five key **dplyr** functions in **tidyverse** to solve most of data manipulation challenges:
 - Pick observations by their values – **filter()**
 - Reorder (sort) the rows – **arrange()**
 - Pick variables by their names – **select()**
 - Create new variables with functions of existing variables – **mutate()**
 - Collapse many values down to a summary – **summarize()**



Introduction

Remove
to improve
(the **data-ink** ratio)

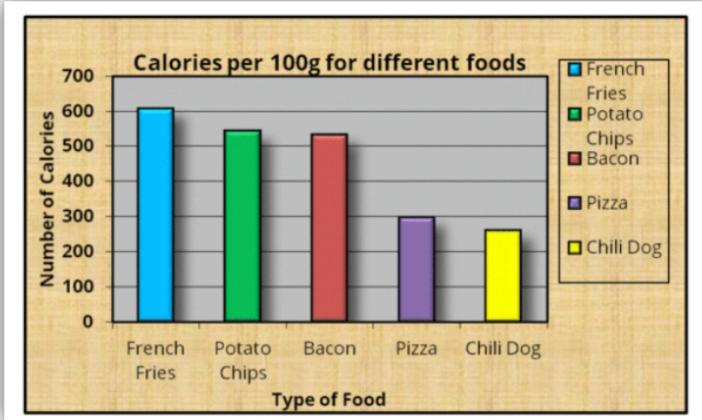
Created by Darkhorse Analytics

www.darkhorseanalytics.com

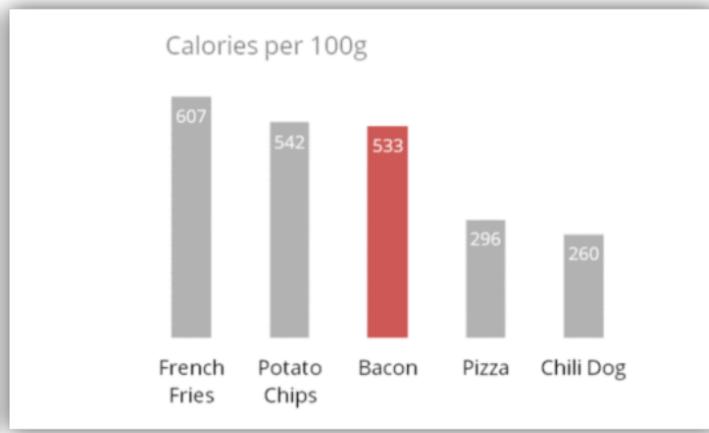
<https://www.darkhorseanalytics.com/blog/data-looks-better-naked>

Introduction

Before



After



Graphics: Less is more effective, attractive, impactive

Introduction

- R is a powerful programming language for graphics and visualizations
- Graphics in R can be done in three ways, via the:
 - `graphics` package: the base graphics in R, loaded by default
 - `lattice` package: which adds more functionalities to the base package
 - `ggplot2` package in the `tidyverse` package

The ggplot2

- The `graphics` package has large choice of plots: `plot`, `hist`, `barplot`, `boxplot`, `pie`, `mosaicplot`, etc. and additional features (e.g. `abline`, `lines`, `legend`, `mtext`, `rect`, etc.). Sometimes the preferred way to plotting for most R users
- `ggplot2` created by Hadley Wickham in 2005, is becoming one of the most popular R packages and the most popular package for graphics and data visualizations
- The `ggplot2` package is a much more modern approach to creating professional-quality graphics

The ggplot2

- The **ggplot2** package is based on the principles of the "grammar of graphics", a coherent system for describing and building graphs as a succession of layers
 - The **dataset** with the variables to represent. Done with the `ggplot()` function and comes first
 - The **variable(s)** to represent on the axes, and the aesthetic elements (such as `color`, `size`, `fill`, `shape` and `transparency`) of the objects to be represented. Done with the `aes()` function.
 - The **type of graphical representation** (`scatter` `plot`, `line` `plot`, `barplot`, `histogram`, etc.). Done with the functions `geom_point()`, `geom_line()`, `geom_bar()`, etc.
 - Additional layers (such as `labels`, `annotations`, `scales`, `axis ticks`, `legends`, `themes`, `facets`, etc.) can be added to **personalize** the plot

The ggplot2

- To create a plot, specify the data in the `ggplot()` function and add the required layers: variables, aesthetic elements and the type of plot:

```
ggplot(data) +  
  aes(x = var_x, y = var_y) +  
  geom_x()
```

- `data` in `ggplot()` is the name of the data frame which contains the variables `var_x` and `var_y`
- The `+` symbol used to indicate the different layers
- The layer `aes()` indicates the variables to be used in the plot and more generally, the aesthetic elements of the plot
- `x` in `geom_x()` represents the type of plot: `geom_point()`, `geom_line()`, etc.

The ggplot2: the data

- The `agridat` package with datasets from small-plot trials, multi-environment trials, uniformity trials, yield monitors, and more
- The `australia.soybean` is a multi-environment trial of 58 varieties of soybeans, in 4 locations across 2 years in Australia.
 - **env** (environment), 8 levels, location-year
 - **loc** (location)
 - **year**
 - **gen** (genotype) of soybeans,
 - **yield**, metric tons/hectare
 - **height**, meters
 - **lodging**
 - **size seed**, millimetres
 - **protein**, percentage
 - **oil**, percentage

The ggplot2: the data

- Data can be accessed using these commands

```
libraryagridat)
data(australia.soybean)
dat <- australia.soybean
str(dat)
```

```
## 'data.frame': 464 obs. of 10 variables:
## $ env    : Factor w/ 8 levels "B70","B71","L70",...: 3 3 3 3 3 3 3 3 3 3 ...
## $ loc    : Factor w/ 4 levels "Brookstead","Lawes",...: 2 2 2 2 2 2 2 2 2 2 ...
## $ year   : int 1970 1970 1970 1970 1970 1970 1970 1970 1970 1970 ...
## $ gen    : Factor w/ 58 levels "G01","G02","G03",...: 1 2 3 4 5 6 7 8 9 10 ...
## $ yield  : num 2.39 2.28 2.57 2.88 2.39 ...
## $ height : num 1.45 1.45 1.46 1.26 1.33 ...
## $ lodging: num 4.25 4.25 3.75 3.5 3.5 4 3 3.25 3 3.75 ...
## $ size   : num 8.45 9.95 10.85 10.05 11 ...
## $ protein: num 36.7 37.5 37.8 38.5 37.5 ...
## $ oil    : num 20.9 20.7 21.3 22 22.1 ...
```

The ggplot2: the data

- The data is available in the agridat package as a data frame. We have opted to work with tibble, let's convert this to a tibble

```
library(tidyverse)
dat <- as_tibble(dat)
dat
```

```
## # A tibble: 464 x 10
##   env    loc  year  gen  yield height lodging size protein oil
##   <fct> <fct> <int> <fct> <dbl>  <dbl>   <dbl> <dbl>   <dbl> <dbl>
## 1 L70    Lawes 1970 G01    2.39   1.44    4.25   8.45   36.7  20.9
## 2 L70    Lawes 1970 G02    2.28   1.45    4.25   9.95   37.6  20.7
## 3 L70    Lawes 1970 G03    2.57   1.46    3.75  10.8    37.8  21.3
## 4 L70    Lawes 1970 G04    2.88   1.26    3.5    10.0    38.4  22.0
## 5 L70    Lawes 1970 G05    2.39   1.34    3.5    11      37.5  22.1
## 6 L70    Lawes 1970 G06    2.41   1.36     4     11.8    38.2  21.2
## 7 L70    Lawes 1970 G07    2.70   1.3     3     11.8    37.4  21.7
## 8 L70    Lawes 1970 G08    2.46   0.955   3.25  10      35.2  21.1
## 9 L70    Lawes 1970 G09    2.57   1.03     3     11.2    35.9  21.5
## 10 L70   Lawes 1970 G10   2.98   1.16    3.75  10.8    39.7  20.4
## # ... with 454 more rows
```

The ggplot2: the data

- The env, loc, year, and gen are the factors but as year was considered as integer, let's convert it to a factor

```
library(tidyverse)
dat$year <- as.factor(dat$year)
dat
```

```
## # A tibble: 464 x 10
##   env    loc  year   gen   yield height lodging size protein oil
##   <fct> <fct> <fct> <fct> <dbl>  <dbl>   <dbl> <dbl>   <dbl> <dbl>
## 1 L70    Lawes 1970  G01    2.39   1.44    4.25  8.45   36.7  20.9
## 2 L70    Lawes 1970  G02    2.28   1.45    4.25  9.95   37.6  20.7
## 3 L70    Lawes 1970  G03    2.57   1.46    3.75  10.8   37.8  21.3
## 4 L70    Lawes 1970  G04    2.88   1.26    3.5   10.0   38.4  22.0
## 5 L70    Lawes 1970  G05    2.39   1.34    3.5   11     37.5  22.1
## 6 L70    Lawes 1970  G06    2.41   1.36    4     11.8   38.2  21.2
## 7 L70    Lawes 1970  G07    2.70   1.3    3     11.8   37.4  21.7
## 8 L70    Lawes 1970  G08    2.46   0.955   3.25  10     35.2  21.1
## 9 L70    Lawes 1970  G09    2.57   1.03    3     11.2   35.9  21.5
## 10 L70   Lawes 1970  G10    2.98   1.16    3.75  10.8   39.7  20.4
## # ... with 454 more rows
```

The ggplot2: scatter plot

- A scatter plot is used to visualize the relation between two quantitative variables Often used to visualize a potential correlation between the two variables

```
library(tidyverse)
ggplot(dat) +
  aes(x = oil, y = yield) +
  geom_point()
```

- We can sometimes see the `aes()` inside the `ggplot()` function

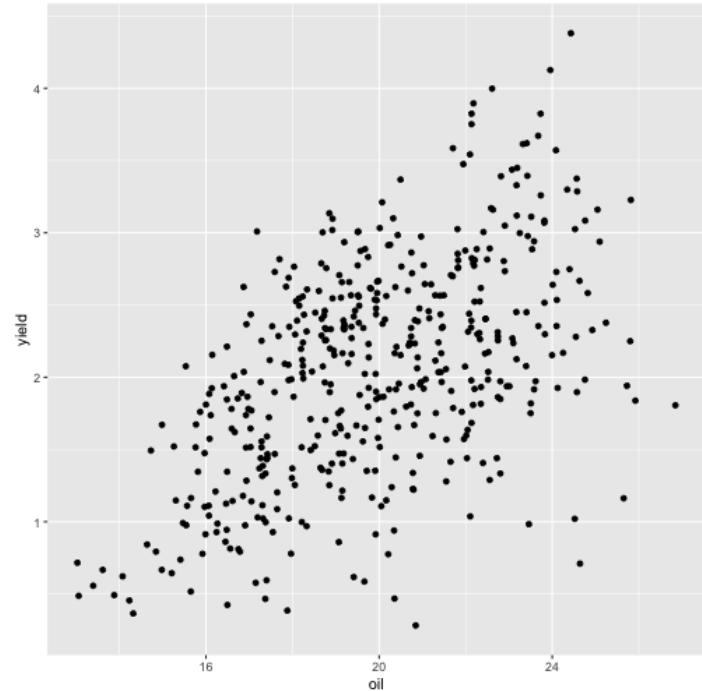
```
library(tidyverse)
ggplot(dat , aes(x = oil, y = yield)) +
  geom_point()
```

- I believe the first option (highlighted in yellow) is better for readability

The ggplot2: scatter plot

```
ggplot(dat) +  
  aes(x = oil, y = yield) +  
  geom_point()
```

That's fine! But we can do better: personalize the plot to make it more informative. We can add a title, subtitle, caption and edit axis labels with the `labs()` function



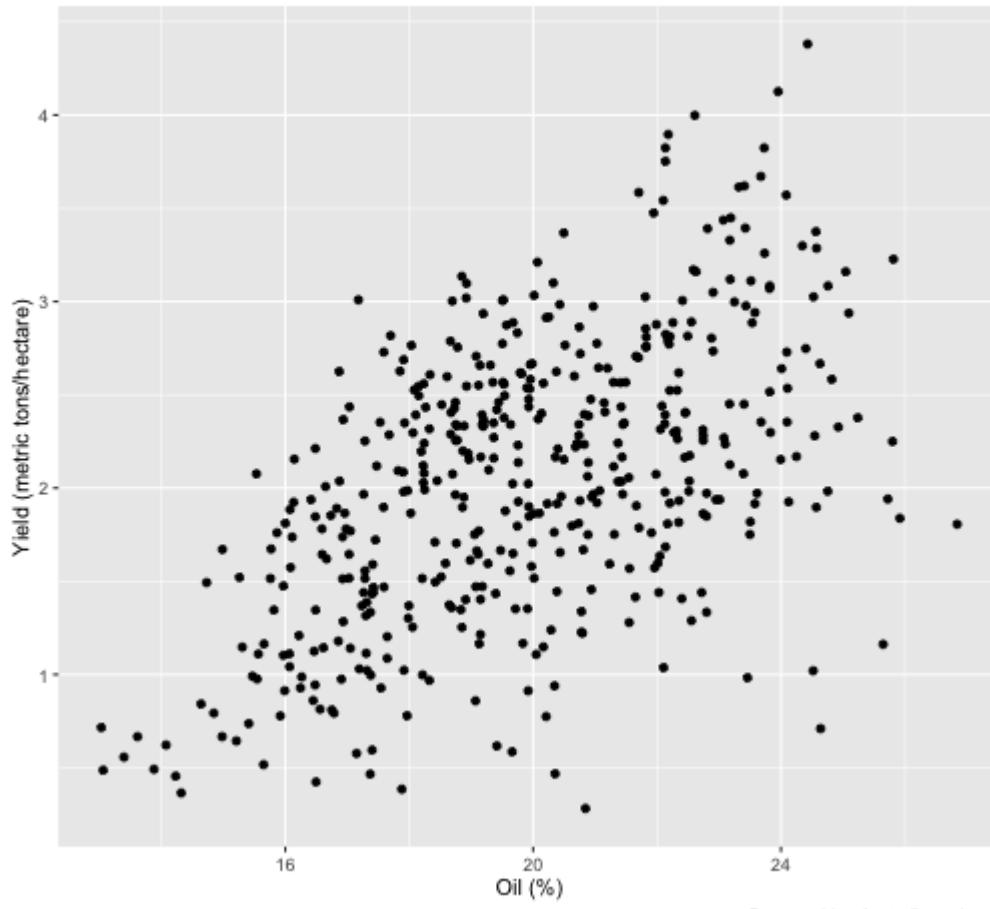
The ggplot2: scatter plot

```
ggplot(dat) +  
  aes(x = oil, y = yield) +  
  geom_point() +  
  labs(title = "Soybeans, yield and oil in Australia",  
       subtitle = "Period 1970-1971",  
       caption = "Data: agridat::Australia.soybean",  
       x = "Oil (%)",  
       y = "Yield (metric tons/hectare)"  
  )
```

The ggplot2: scatter plot

Soybeans, yield and oil in Australia

Period 1970-1971



Data: agridat::Australia.soybean

The ggplot2: scatter plot

- We can save the "basic" plot in an object and add layer(s) by cascades for more readability

```
p <- ggplot(dat) +
  aes(x = oil, y = yield) +
  geom_point()

p <- p +
  labs(title = "Soybeans, yield and oil in Australia",
       subtitle = "Period 1970-1971",
       caption = "Data: agridat::Australia.soybean",
       x = "Oil (%)",
       y = "Yield (metric tons/hectare)" )
```

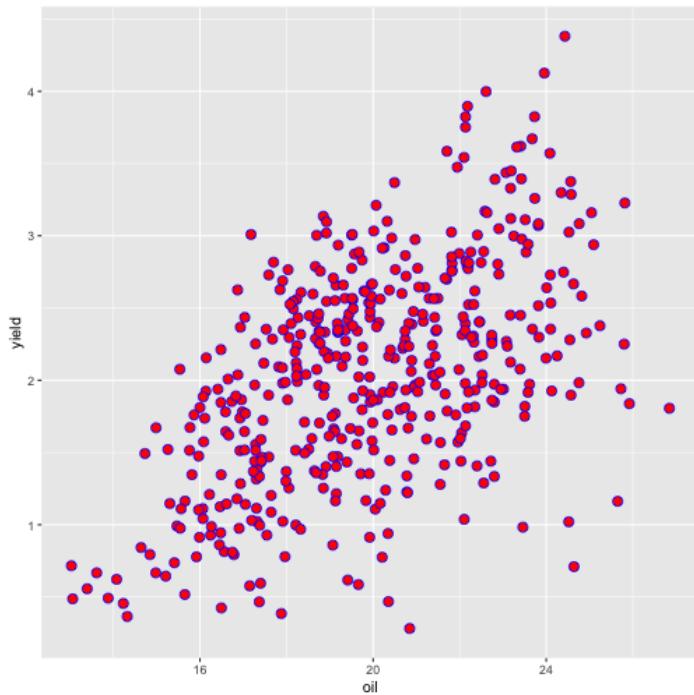
The ggplot2: scatter plot

- `geom_point()` understands also the following aesthetics
 - `alpha`
 - `colour`
 - `fill`
 - `shape`
 - `size`
 - `stroke`

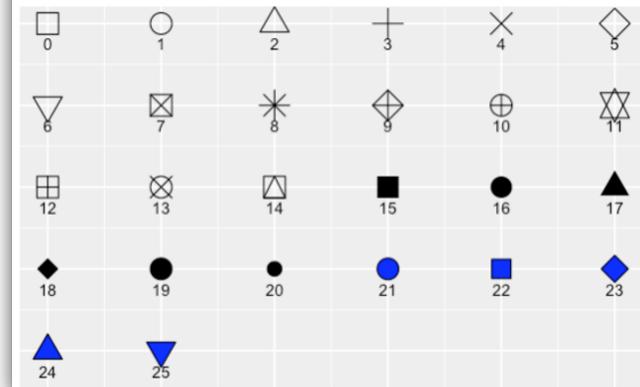
The ggplot2: scatter plot

```
p <- ggplot(dat) +  
  aes(x = oil, y = yield) +  
  geom_point(shape=21, color="blue", fill="red", size=3)
```

```
p
```



Point shapes available in R



The ggplot2: scatter plot

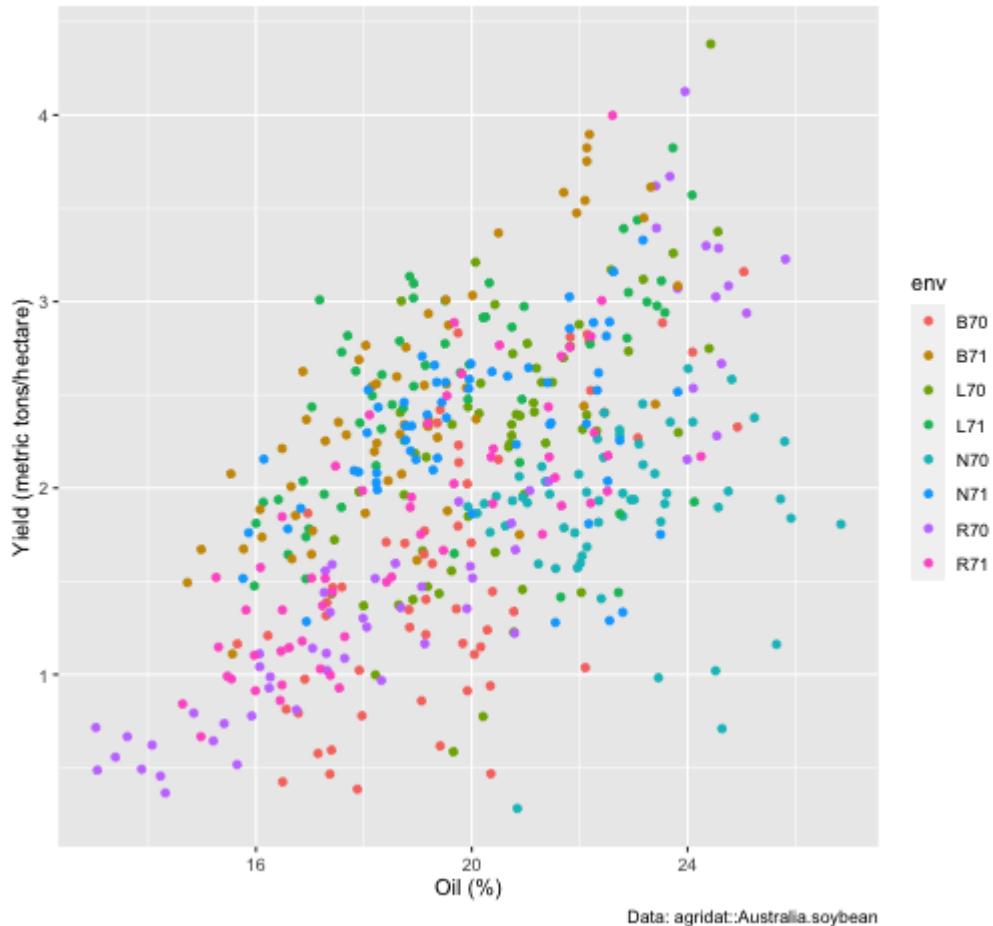
The plot of the yield and oil content of the 58 varieties is across environments. We may be interested to see it by environment

```
p <- ggplot(dat) +  
  aes(x = oil, y = yield, color=env) +  
  geom_point()  
  
p <- p +  
  labs(title = "Soybeans, yield and oil in Australia",  
       subtitle = "Period 1970-1971",  
       caption = "Data: agricidat::Australia.soybean",  
       x = "Oil (%)",  
       y = "Yield (metric tons/hectare)"  
     )  
p
```

The ggplot2: scatter plot

Soybeans, yield and oil in Australia

Period 1970-1971



The ggplot2: scatter plot

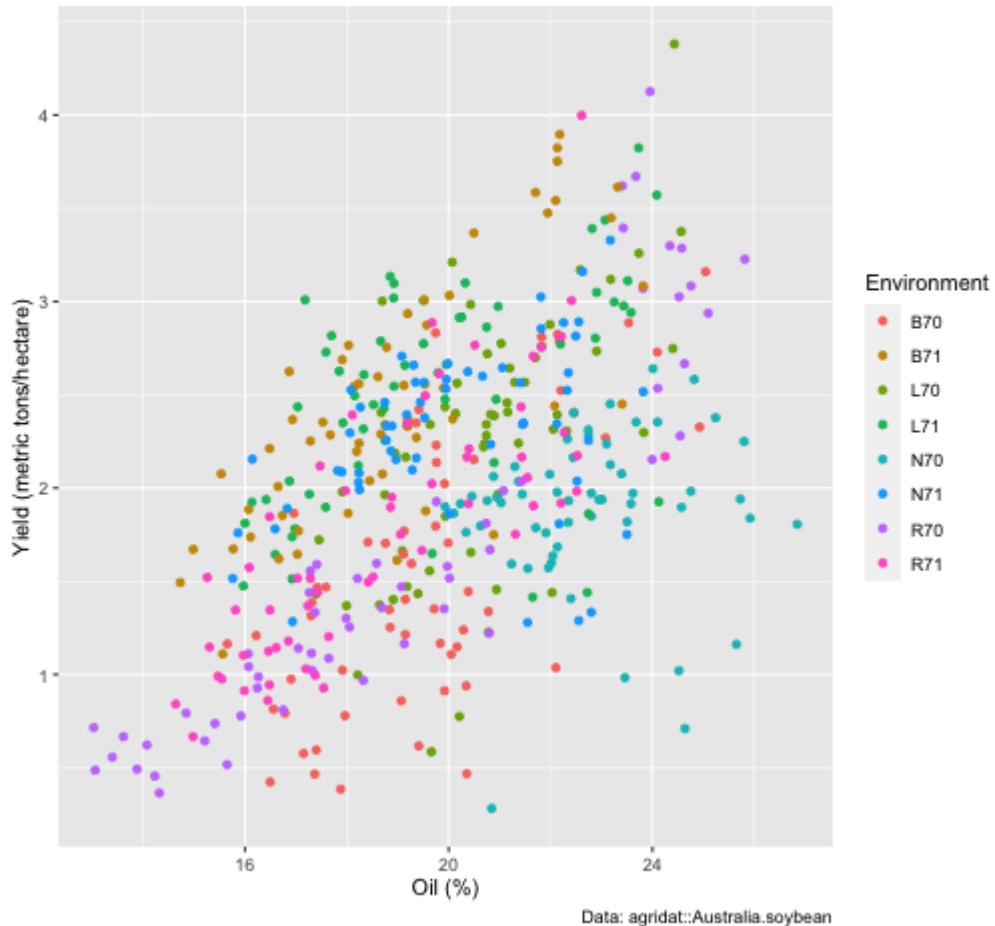
We can do better by changing the title of the legend: “Environment” instead of “env”

```
p <- ggplot(dat) +  
  aes(x = oil, y = yield, color=env) +  
  geom_point()  
  
p <- p +  
  labs(title = "Soybeans, yield and oil in Australia",  
       subtitle = "Period 1970-1971",  
       caption = "Data: agridat::Australia.soybean",  
       x = "Oil (%)",  
       y = "Yield (metric tons/hectare)"  
     )  
p <- p + scale_color_discrete(name="Environment")  
p
```

The ggplot2: scatter plot

Soybeans, yield and oil in Australia

Period 1970-1971



The ggplot2: scatter plot

- We can change the default color
- The RColorBrewer package makes it easy to quickly load sensible color palettes

```
library(RColorBrewer)
```

- Three types of palettes: sequential, diverging and qualitative
 - Sequential: palettes are suited to ordered data that progress from low to high.
 - Diverging: palettes are suited to centered data with extremes in either direction.
 - Qualitative: palettes are suited to nominal or categorical data

The ggplot2: scatter plot

- The function below displays the available palettes

```
display.brewer.all()
```



The ggplot2: scatter plot

We can change the palette via the function `scale_color_brewer()`

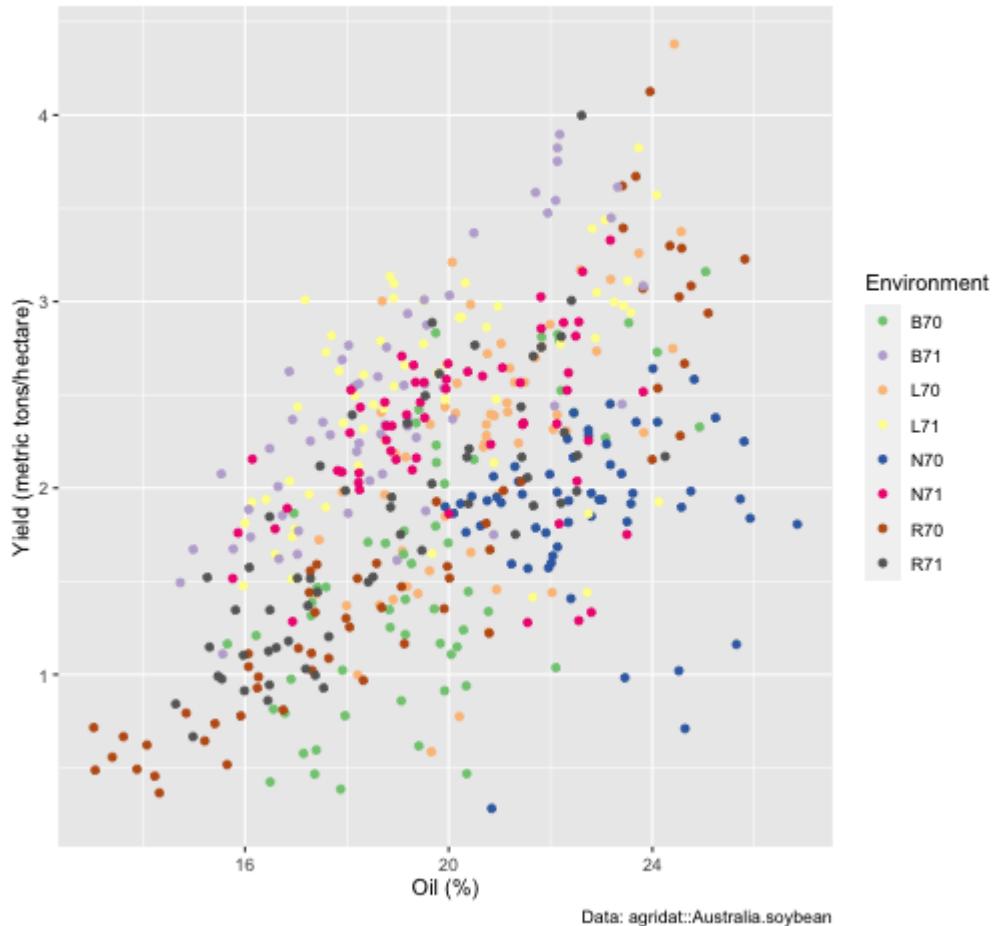
```
p <- ggplot(dat) +
  aes(x = oil, y = yield, color=env) +
  geom_point()

p <- p +
  labs(title = "Soybeans, yield and oil in Australia",
       subtitle = "Period 1970-1971",
       caption = "Data: agridat::Australia.soybean",
       x = "Oil (%)",
       y = "Yield (metric tons/hectare)"
  )
p <- p + scale_color_brewer(name="Environment", palette="Accent")
p
```

The ggplot2: scatter plot

Soybeans, yield and oil in Australia

Period 1970-1971



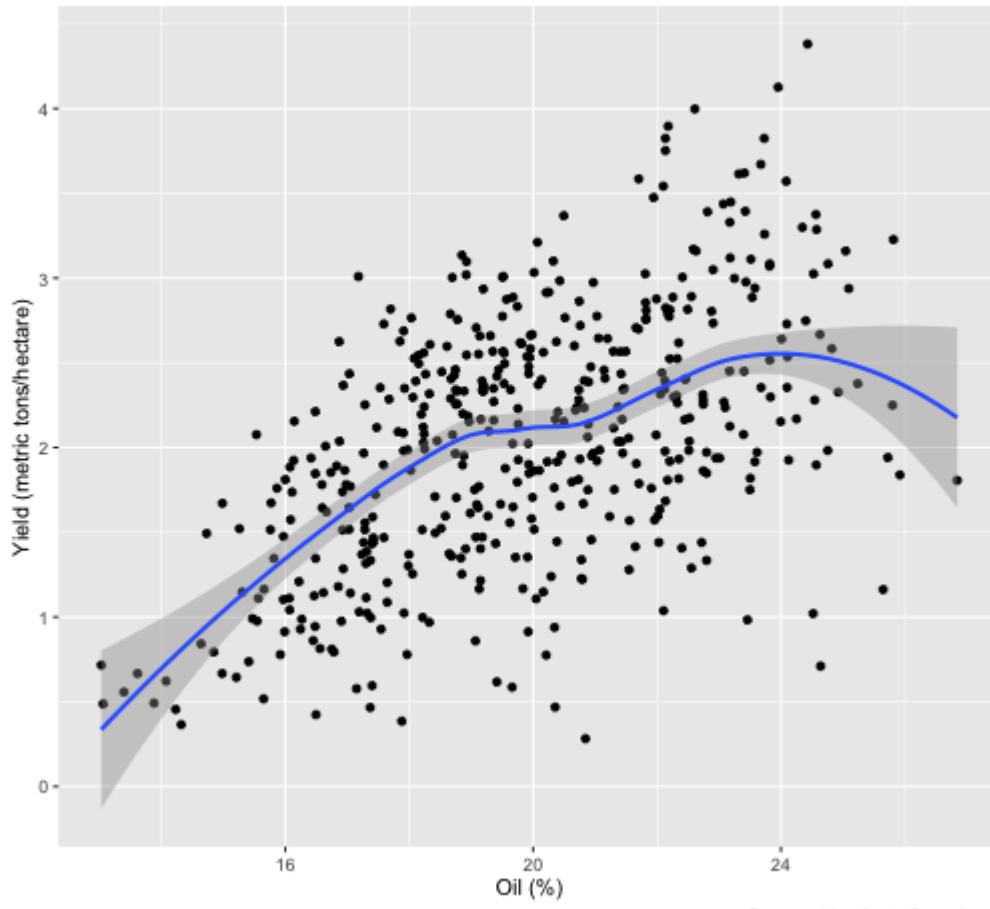
The ggplot2: scatter plot

Possible to add a smooth line fitted to the data

```
p <- ggplot(dat) +  
  aes(x = oil, y = yield) +  
  geom_point()  
  
p <- p +  
  labs(title = "Soybeans, yield and oil in Australia",  
       subtitle = "Period 1970-1971",  
       caption = "Data: agridat::Australia.soybean",  
       x = "Oil (%)",  
       y = "Yield (metric tons/hectare)"  
     )  
p <- p + geom_smooth()  
p
```

The ggplot2: scatter plot

Soybeans, yield and oil in Australia
Period 1970-1971



The ggplot2: scatter plot

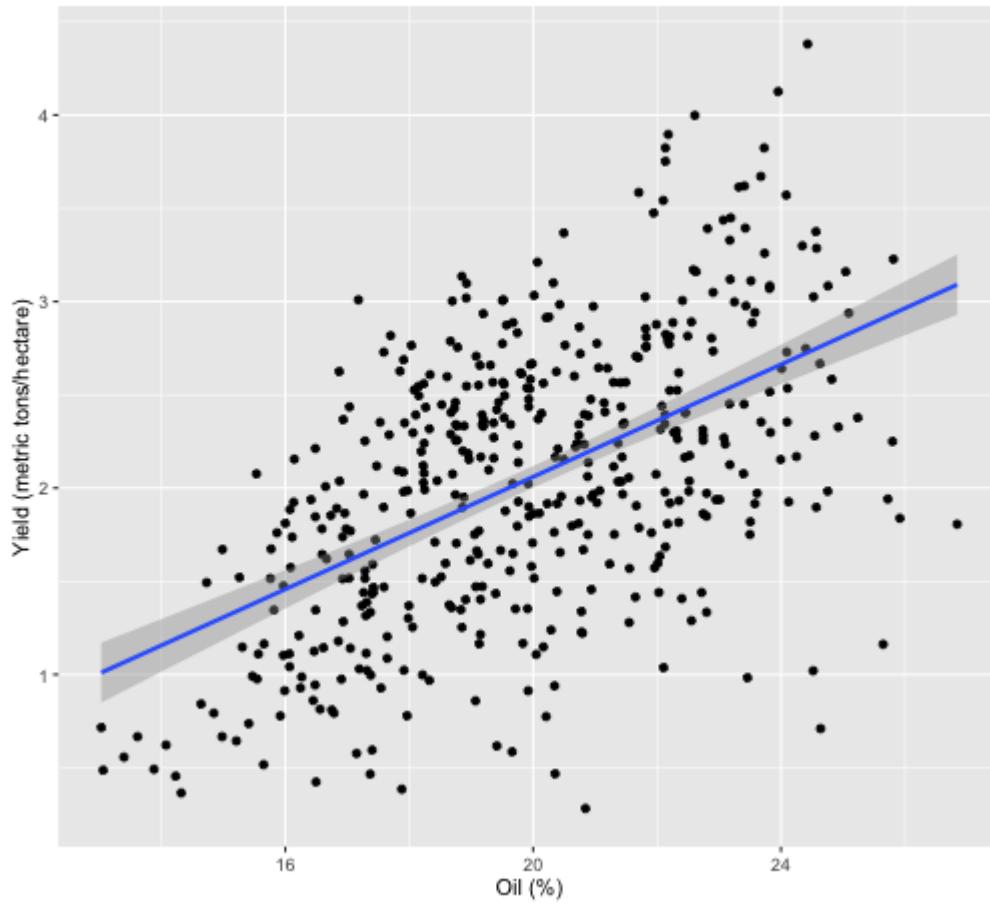
In case of simple linear regression, possible to display the regression line on the plot. Can be done by adding `method = lm` in `geom_smooth()`

```
p <- ggplot(dat) +  
  aes(x = oil, y = yield) +  
  geom_point()  
  
p <- p +  
  labs(title = "Soybeans, yield and oil in Australia",  
       subtitle = "Period 1970-1971",  
       caption = "Data: agridat::Australia.soybean",  
       x = "Oil (%)",  
       y = "Yield (metric tons/hectare)"  
     )  
p <- p + geom_smooth(method = lm)  
p
```

The ggplot2: scatter plot

Soybeans, yield and oil in Australia

Period 1970-1971



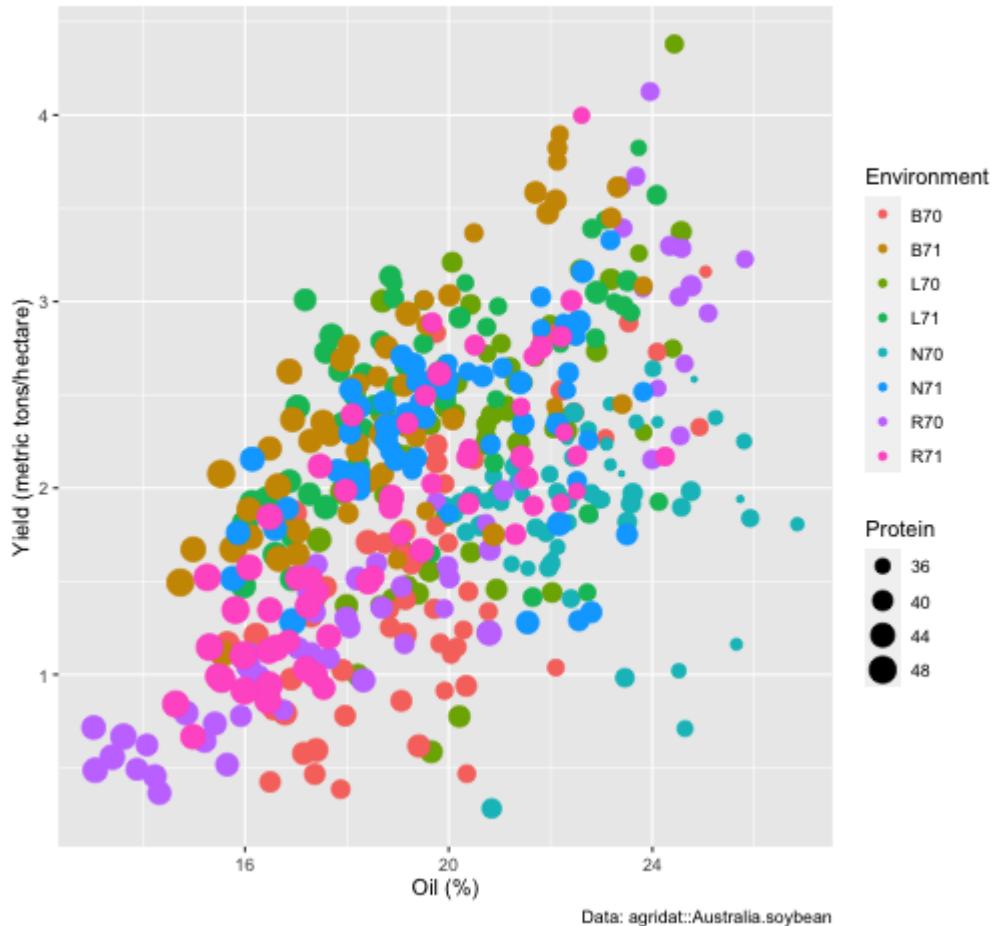
The ggplot2: scatter plot

```
p <- ggplot(dat) +  
  aes(x = oil, y = yield, color=env, size=protein) +  
  geom_point()  
  
p <- p +  
  labs(title = "Soybeans, yield and oil in Australia",  
       subtitle = "Period 1970-1971",  
       caption = "Data: agridat::Australia.soybean",  
       x = "Oil (%)",  
       y = "Yield (metric tons/hectare)"  
     )  
p <- p + scale_color_discrete(name = "Environment")  
p <- p + scale_size_continuous("Protein")  
p
```

The ggplot2: scatter plot

Soybeans, yield and oil in Australia

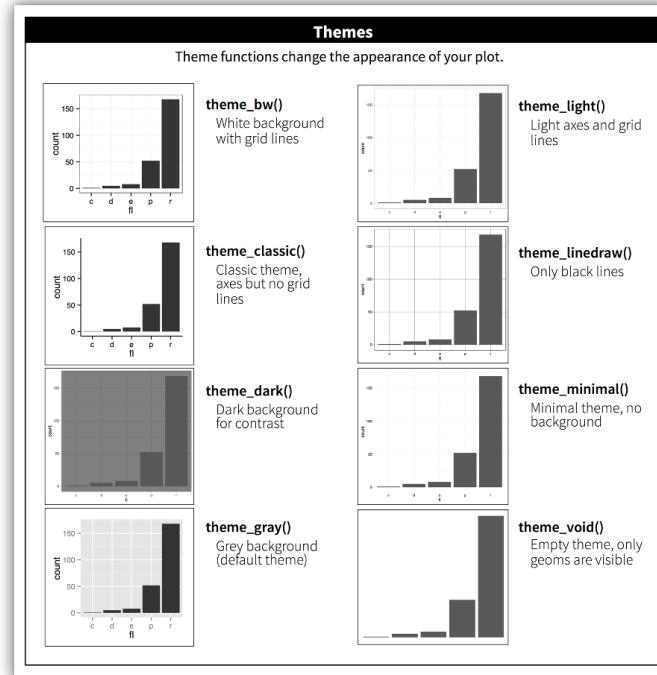
Period 1970-1971



The ggplot2: scatter plot

There are several functions in ggplot2 to change the theme of the plot

- `theme_gray()`: default
- `theme_bw()`: black and white
- `theme_minimal()`: minimal
- `theme_classic()`: classic



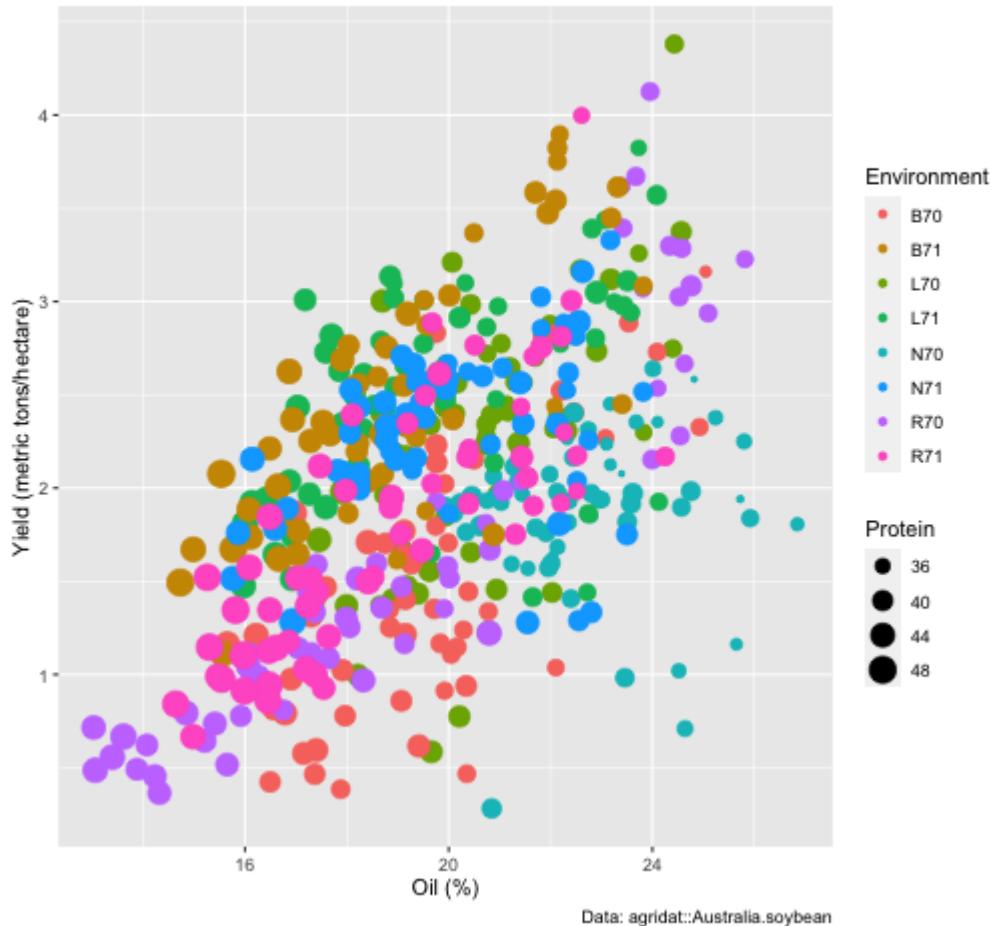
The ggplot2: scatter plot

```
p <- ggplot(dat) +  
  aes(x = oil, y = yield, color=env, size=protein) +  
  geom_point()  
  
p <- p +  
  labs(title = "Soybeans, yield and oil in Australia",  
       subtitle = "Period 1970-1971",  
       caption = "Data: agridat::Australia.soybean",  
       x = "Oil (%)",  
       y = "Yield (metric tons/hectare)"  
     )  
p <- p + scale_color_discrete(name = "Environment")  
p <- p + scale_size_continuous("Protein")  
p <- p + theme_gray()  
p
```

The ggplot2: scatter plot

Soybeans, yield and oil in Australia

Period 1970-1971



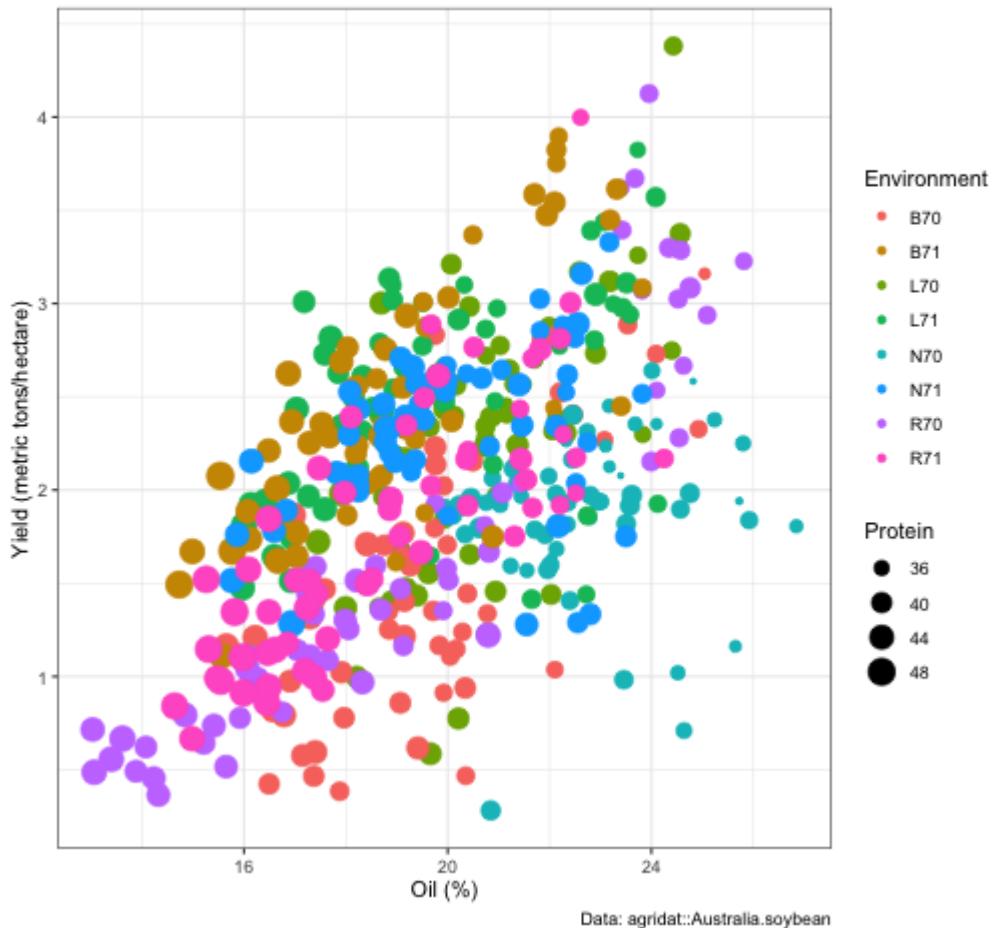
The ggplot2: scatter plot

```
p <- ggplot(dat) +  
  aes(x = oil, y = yield, color=env, size=protein) +  
  geom_point()  
  
p <- p +  
  labs(title = "Soybeans, yield and oil in Australia",  
       subtitle = "Period 1970-1971",  
       caption = "Data: agridat::Australia.soybean",  
       x = "Oil (%)",  
       y = "Yield (metric tons/hectare)"  
     )  
p <- p + scale_color_discrete(name = "Environment")  
p <- p + scale_size_continuous("Protein")  
p <- p + theme_bw()  
p
```

The ggplot2: scatter plot

Soybeans, yield and oil in Australia

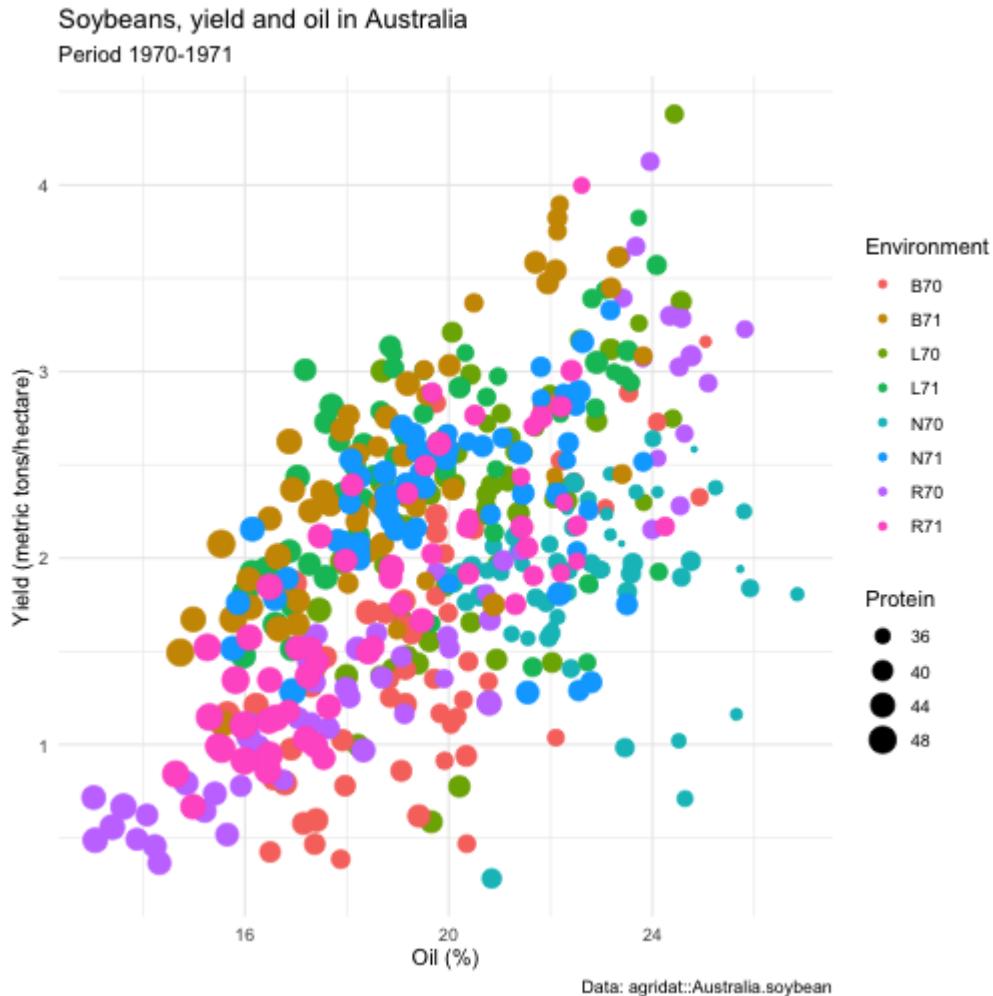
Period 1970-1971



The ggplot2: scatter plot

```
p <- ggplot(dat) +  
  aes(x = oil, y = yield, color=env, size=protein) +  
  geom_point()  
  
p <- p +  
  labs(title = "Soybeans, yield and oil in Australia",  
       subtitle = "Period 1970-1971",  
       caption = "Data: agridat::Australia.soybean",  
       x = "Oil (%)",  
       y = "Yield (metric tons/hectare)"  
     )  
p <- p + scale_color_discrete(name = "Environment")  
p <- p + scale_size_continuous("Protein")  
p <- p + theme_minimal()  
p
```

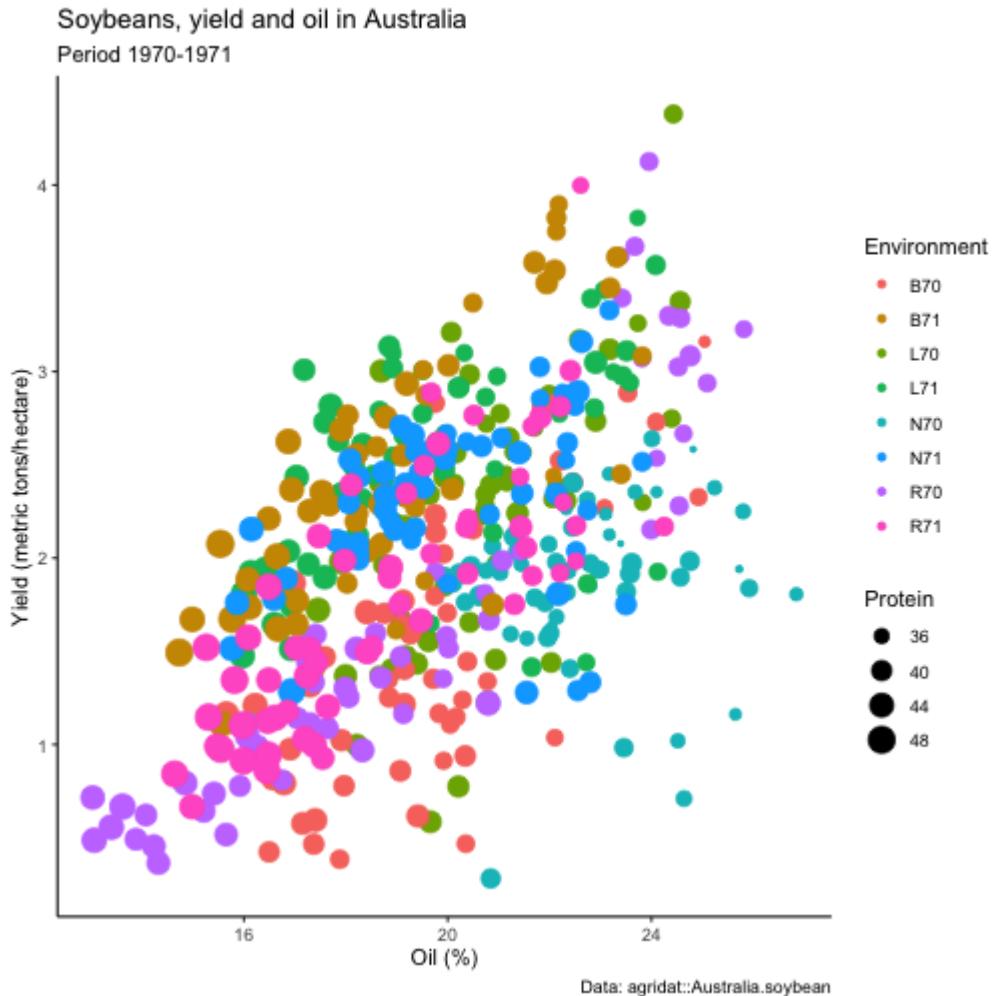
The ggplot2: scatter plot



The ggplot2: scatter plot

```
p <- ggplot(dat) +  
  aes(x = oil, y = yield, color=env, size=protein) +  
  geom_point()  
  
p <- p +  
  labs(title = "Soybeans, yield and oil in Australia",  
       subtitle = "Period 1970-1971",  
       caption = "Data: agridat::Australia.soybean",  
       x = "Oil (%)",  
       y = "Yield (metric tons/hectare)"  
     )  
p <- p + scale_color_discrete(name = "Environment")  
p <- p + scale_size_continuous("Protein")  
p <- p + theme_classic()  
p
```

The ggplot2: scatter plot



The ggplot2: scatter plot

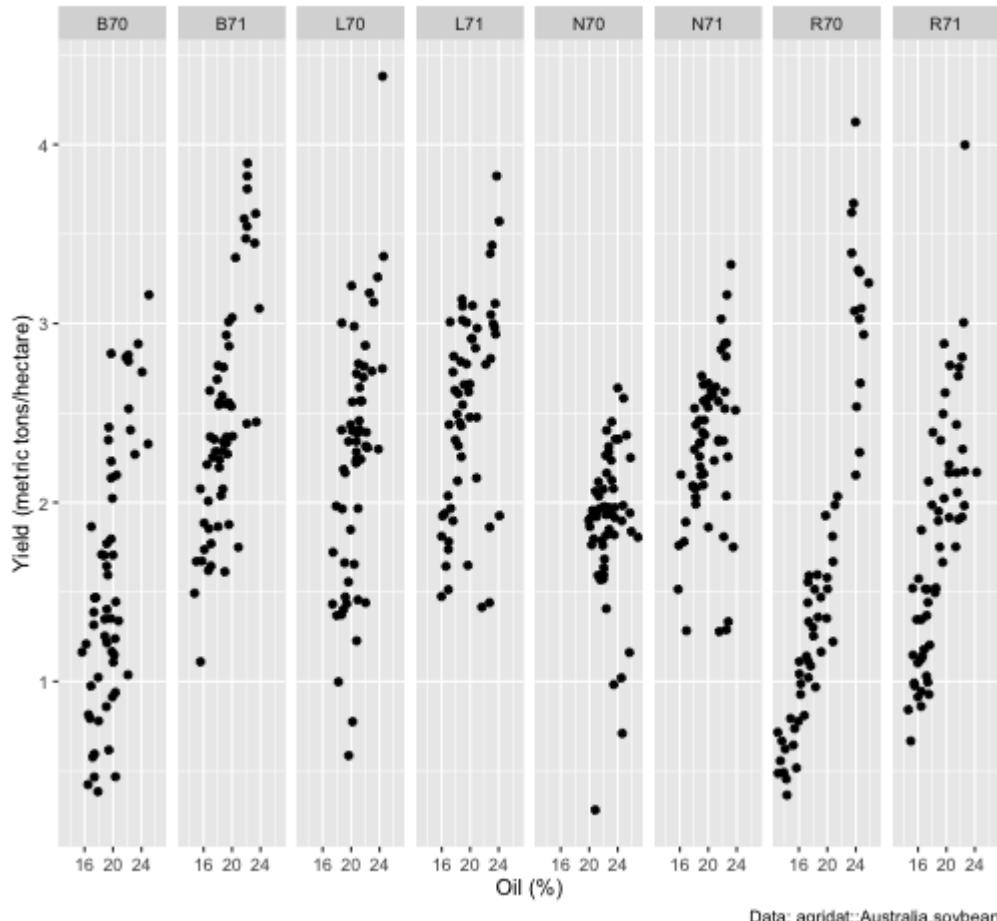
Instead of plotting all the environments in the same plot and using color to differentiate them, we can use `facet_grid()` to divide the same graphic into several panels according to the values of one (environment) or even two qualitative variables

```
p <- ggplot(dat) +  
  aes(x = oil, y = yield, color=env, size=protein) +  
  geom_point()  
  
p <- p +  
  labs(title = "Soybeans, yield and oil in Australia",  
       subtitle = "Period 1970-1971",  
       caption = "Data: agricat::Australia.soybean",  
       x = "Oil (%)",  
       y = "Yield (metric tons/hectare)"  
     )  
  
p + facet_grid(. ~ env)  
p
```

The ggplot2: scatter plot

Soybeans, yield and oil in Australia

Period 1970-1971



The ggplot2: Practical



Your turn

10:00 minutes

- Use the `australia.soybean` in the `agridat` package
- Visualize the relationship between `oil` in the x-axis and `protein` in the y-axis by location
 - change the shape of the points (choose one as you see fit)
 - Add a title
 - sub-title
 - caption
 - change the x-axis and y-axis labels
- Visualize this relationship in a plot with different panels (the number of panels is the number of locations)

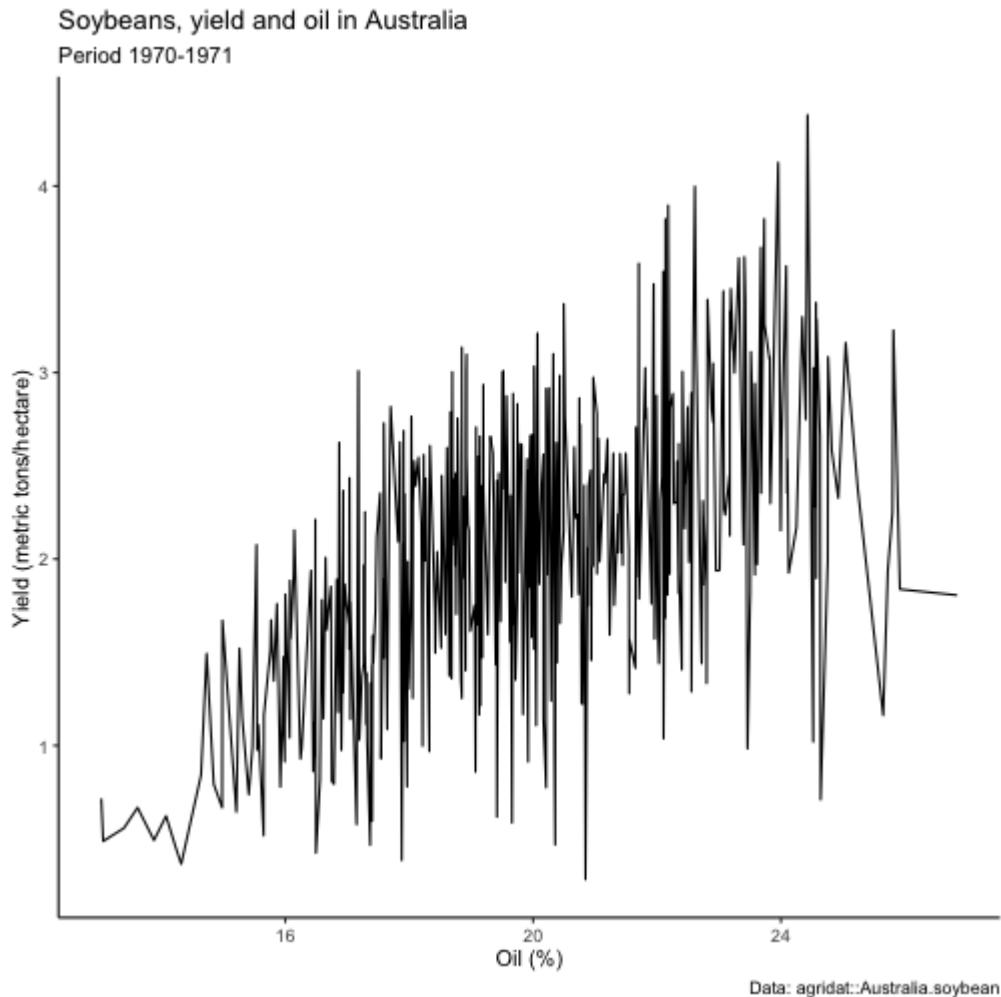
The ggplot2: line plot

Line plots, particularly useful in time series, can be created by using `geom_line()`

```
p <- ggplot(dat) +
  aes(x = oil, y = yield) +
  geom_line()

p <- p +
  labs(title = "Soybeans, yield and oil in Australia",
       subtitle = "Period 1970-1971",
       caption = "Data: agridat::Australia.soybean",
       x = "Oil (%)",
       y = "Yield (metric tons/hectare)"
  )
p <- p + theme_classic()
p
```

The ggplot2: line plot

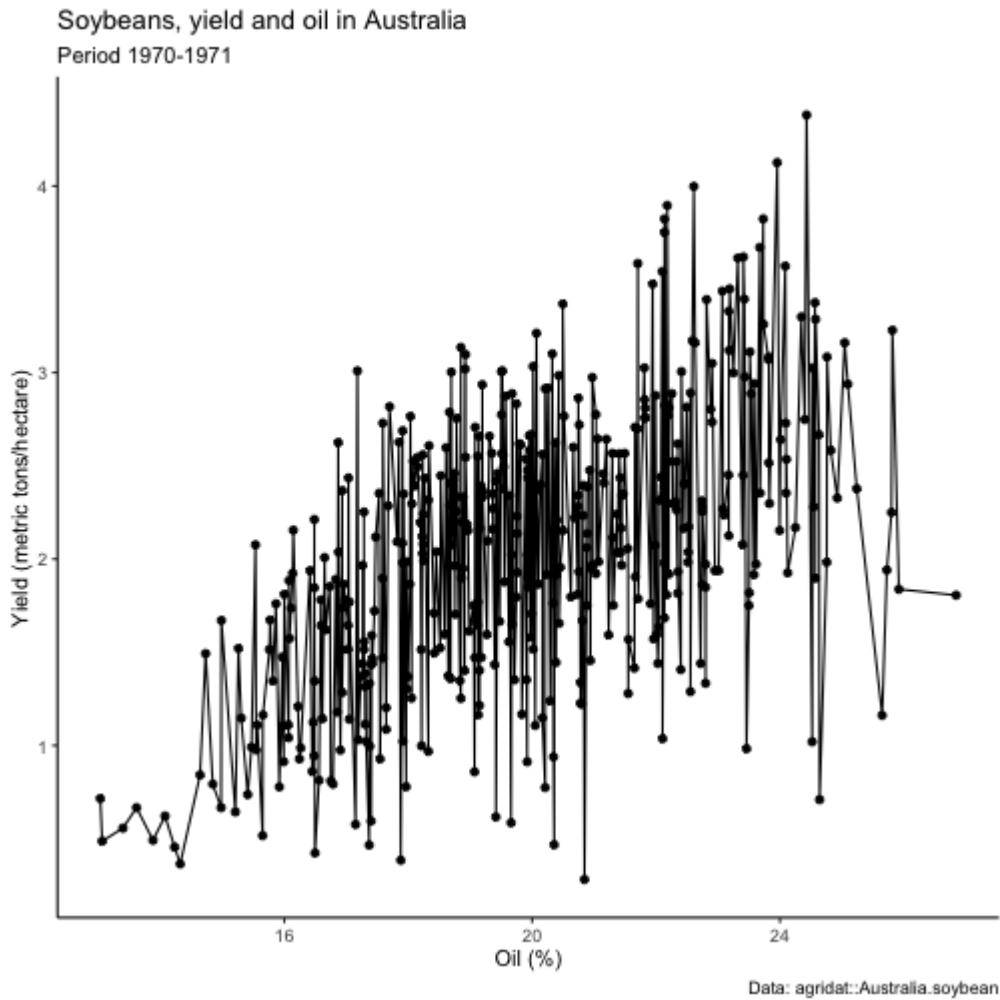


The ggplot2: line plot

We can add a line to a scatter plot by simply adding a layer to the initial scatter plot

```
p <- ggplot(dat) +  
  aes(x = oil, y = yield) +  
  geom_point() +  
  geom_line()  
  
p <- p +  
  labs(title = "Soybeans, yield and oil in Australia",  
       subtitle = "Period 1970-1971",  
       caption = "Data: agricardat::Australia.soybean",  
       x = "Oil (%)",  
       y = "Yield (metric tons/hectare)"  
     )  
p <- p + theme_classic()  
p
```

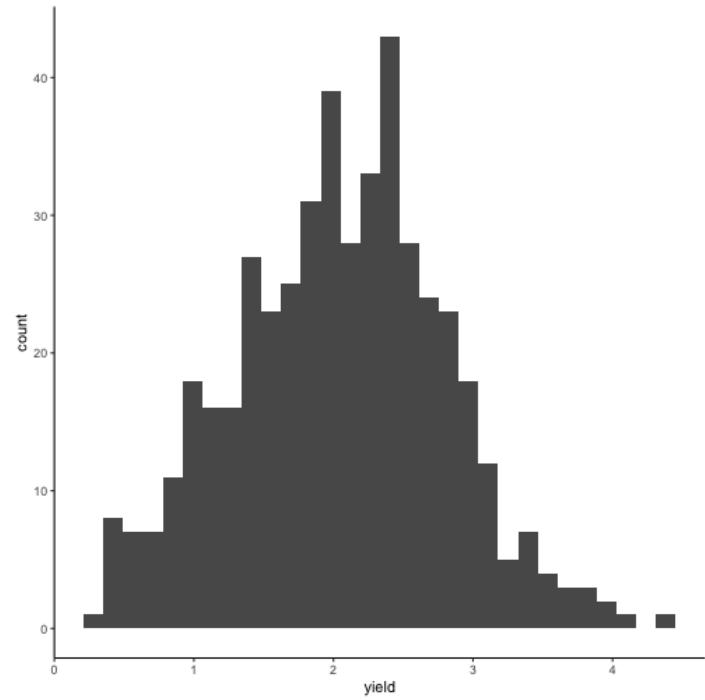
The ggplot2: line plot



The ggplot2: histogram

A histogram can be plotted using `geom_histogram()`

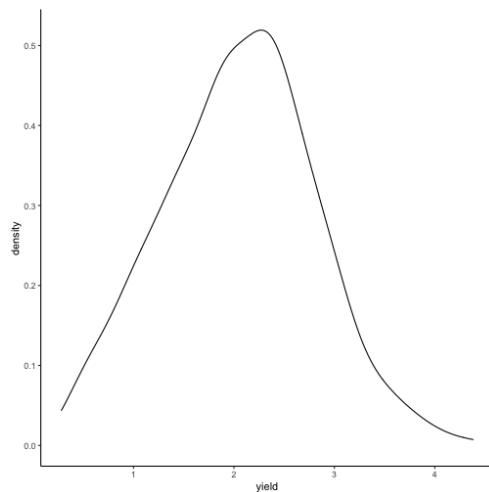
```
p <- ggplot(dat) +  
  aes(x = yield) +  
  geom_histogram()  
p <- p + theme_classic()  
p
```



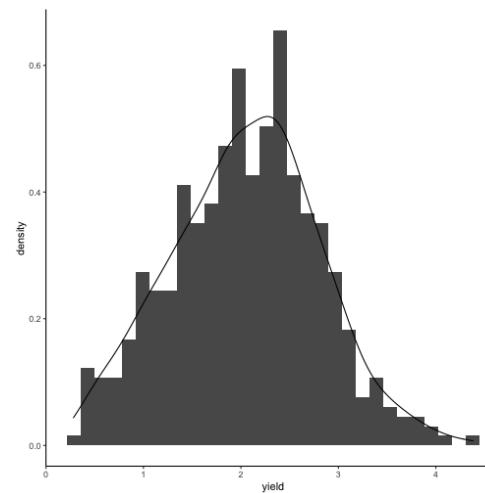
The ggplot2: density plot

Density plots can be created using `geom_density()`

```
p <- ggplot(dat) +  
  aes(x=yield) +  
  geom_density()  
p <- p + theme_classic()  
  
p
```



```
p <- ggplot(dat) +  
  aes(x=yield, y=..density..) +  
  geom_histogram() +  
  geom_density()  
p <- p + theme_classic()  
p
```

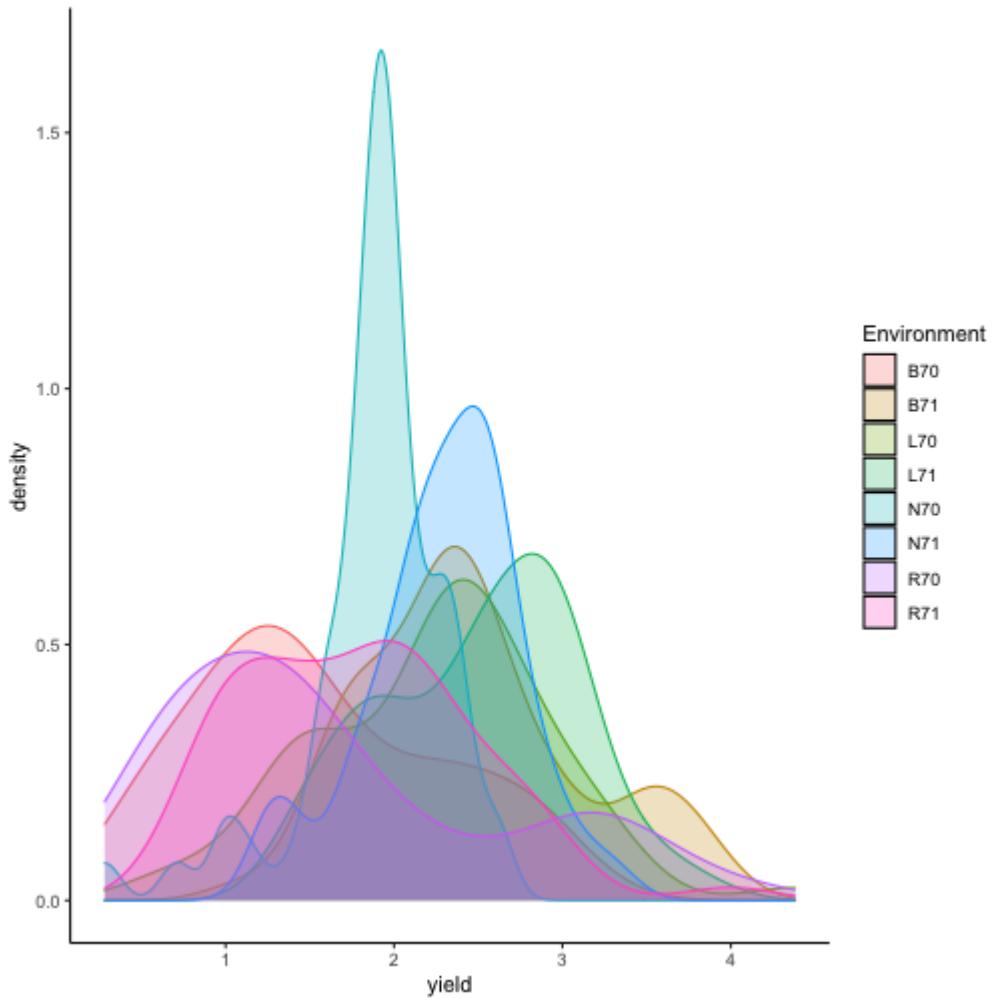


The ggplot2: density plot

Can superimpose several densities by environment

```
p <- ggplot(dat) +  
  aes(x=yield, color=env, fill=env) +  
  geom_density(alpha = 0.25)  
p <- p + scale_fill_discrete(name="Environment")  
p <- p + guides(color=FALSE)  
p <- p + theme_classic()  
p
```

The ggplot2: density plot



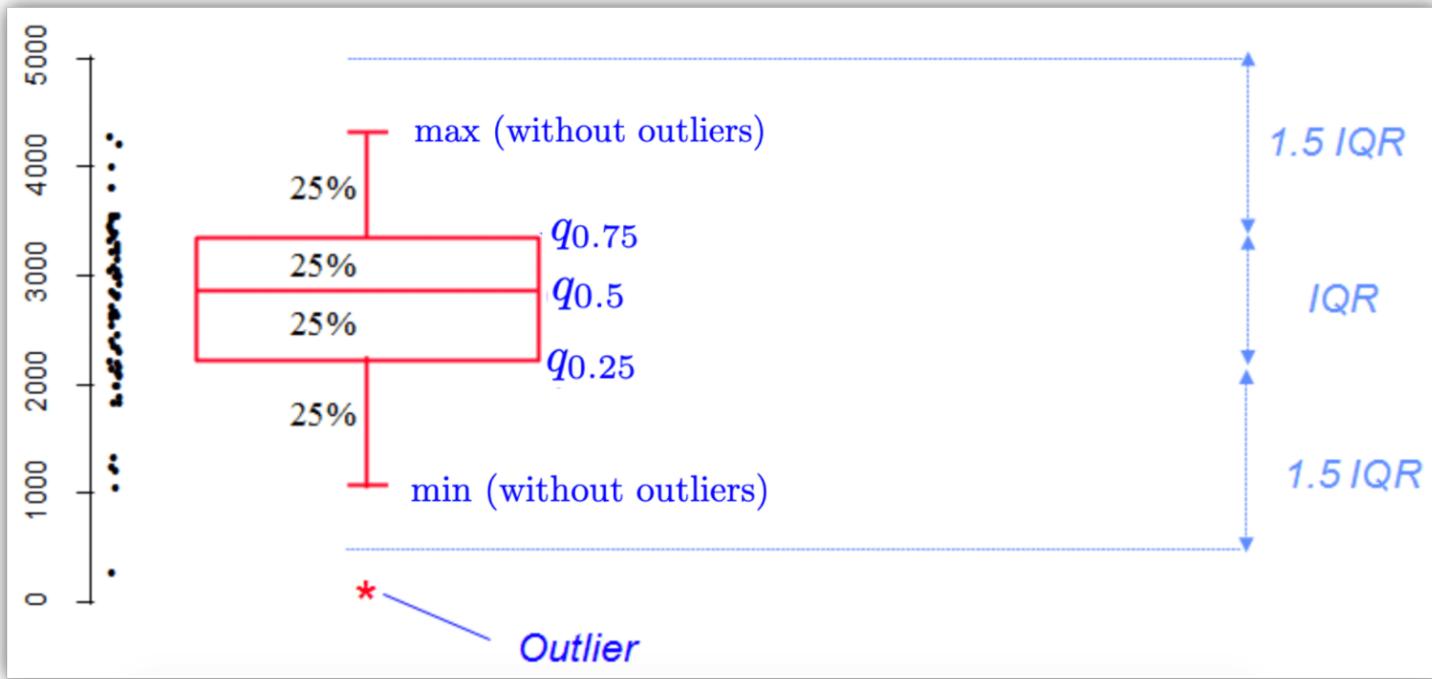
The ggplot2: boxplot

- A boxplot can be plotted using `geom_boxplot()`
- A boxplot graphically represents the distribution of a quantitative variable by visually displaying five common location summary (**minimum, median, first/third quartiles** and **maximum**) and any observation that was classified as a suspected outlier using the interquartile range (IQR) criterion
- All observations
 - above $q0.75 + 1.5 \cdot \text{IQR}$
 - below $q0.25 - 1.5 \cdot \text{IQR}$

where $q0.25$ and $q0.75$ correspond to first and third quartile respectively are considered as potential outliers by R.

- The minimum and maximum in the boxplot are represented without these suspected outliers

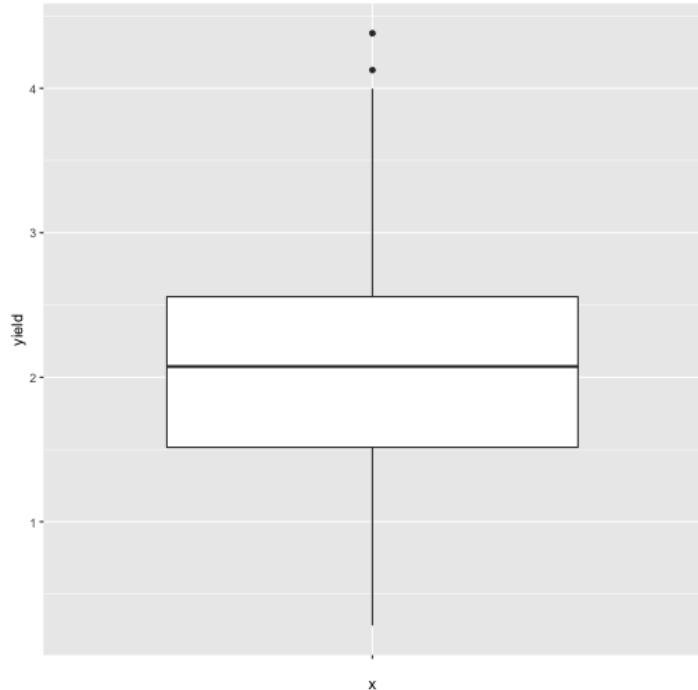
The ggplot2: boxplot



The ggplot2: boxplot

```
p <- ggplot(dat) +  
  aes(x = "", y = yield) +  
  geom_boxplot()
```

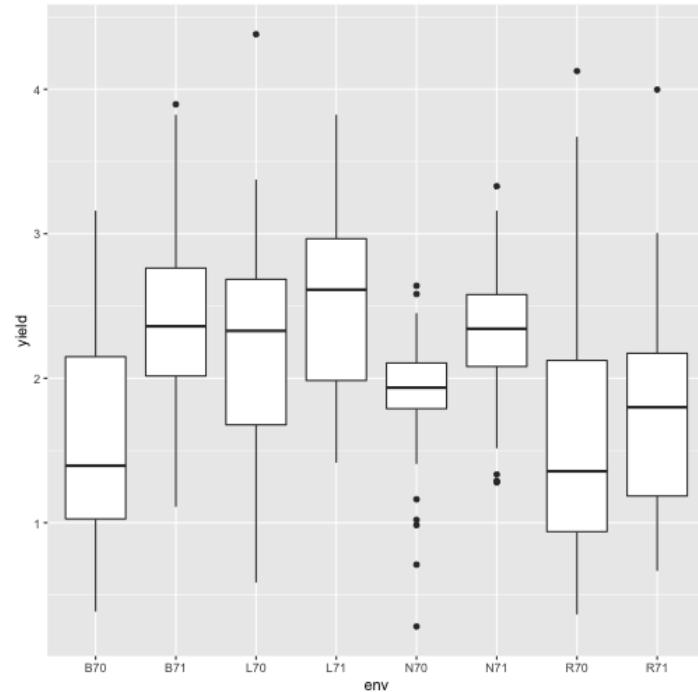
```
p
```



The ggplot2: boxplot

```
p <- ggplot(dat) +  
  aes(x = env, y = yield) +  
  geom_boxplot()
```

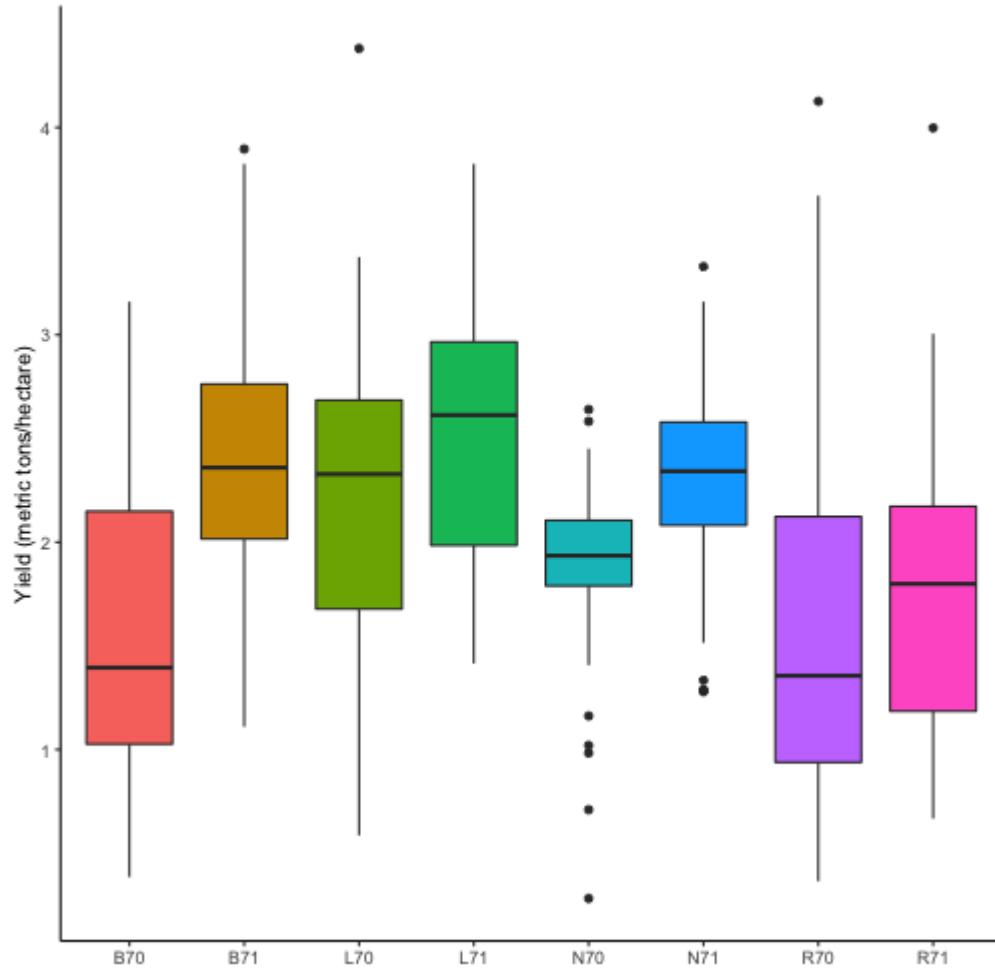
```
p
```



The ggplot2: boxplot

```
p <- ggplot(dat) +  
  aes(x = env, y = yield, fill = env) +  
  geom_boxplot()  
p <- p + labs(x = "", y = "Yield (metric tons/hectare)")  
p <- p + guides(fill=FALSE)  
p <- p + theme_classic()  
p
```

The ggplot2: boxplot

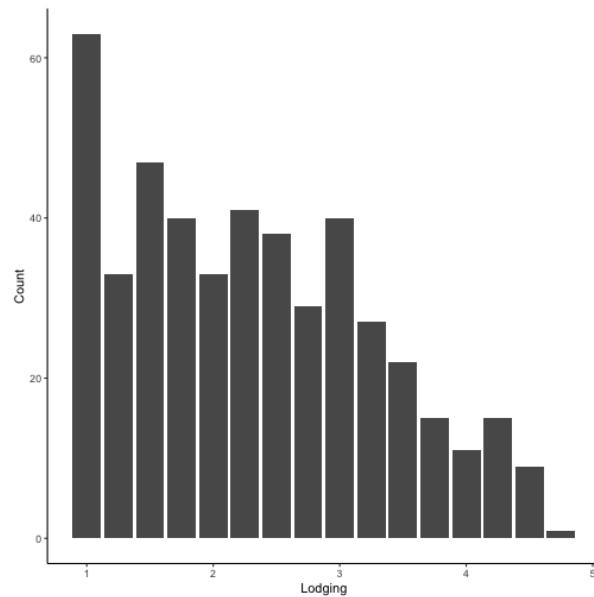


The ggplot2: barplot

- A barplot can be plotted using `geom_bar()`
- A barplot is a tool to visualize the distribution of a qualitative variable (factor). Let's look at the variables in the dataset again
 - **env** (environment), 8 levels, location-year
 - **loc** (location)
 - **year**
 - **gen** (genotype) of soybeans,
 - **yield**, metric tons/hectare
 - **height**, meters
 - **lodging**
 - **size seed**, millimetres
 - **protein**, percentage
 - **oil**, percentage

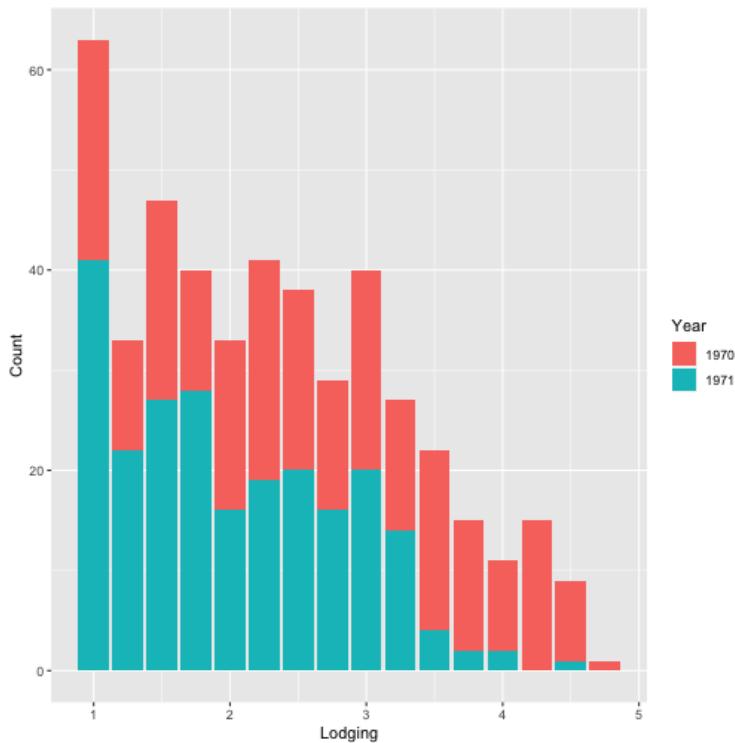
The ggplot2: barplot

```
p <- ggplot(dat) +  
  aes(x = lodging) +  
  geom_bar()  
p <- p + labs(x = "Lodging", y = "Count")  
p <- p + theme_classic()  
p
```



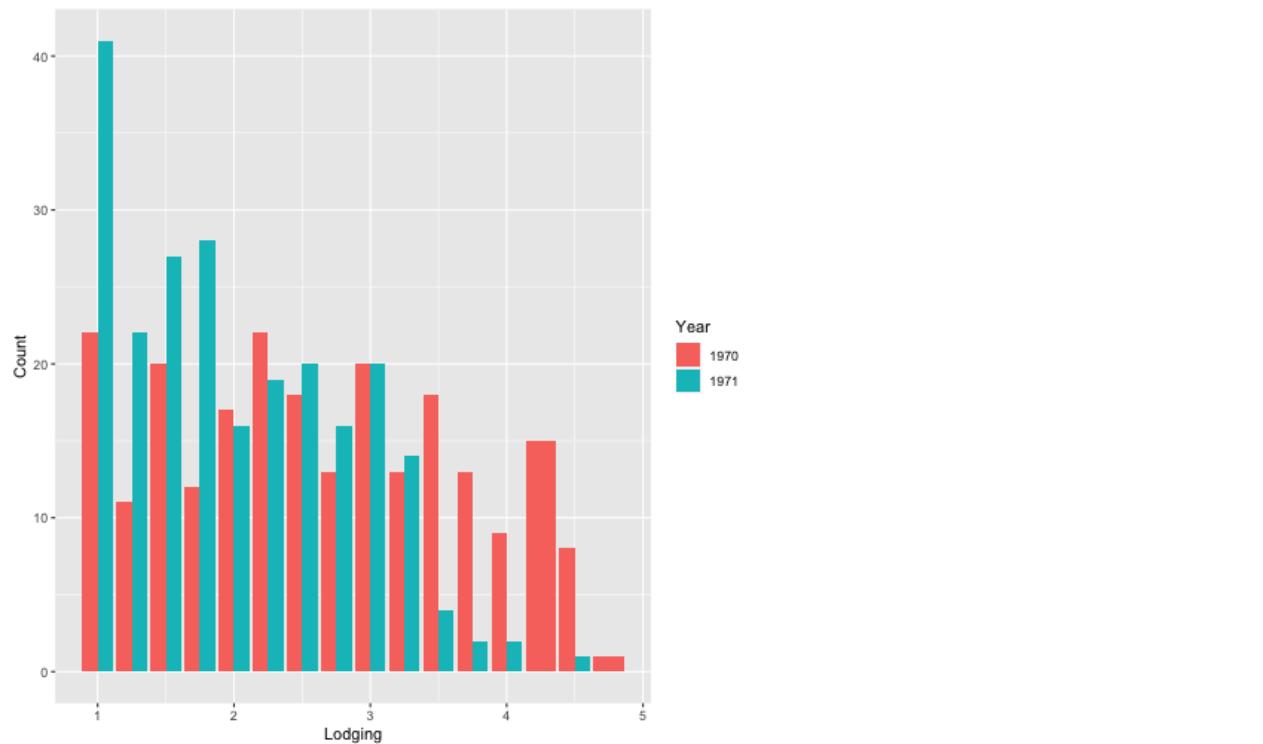
The ggplot2: barplot

```
p <- ggplot(dat) +  
  aes(x = lodging, fill=year) +  
  geom_bar()  
p <- p + labs(x = "Lodging", y = "Count")  
p + scale_fill_discrete(name="Year")
```



The ggplot2: barplot

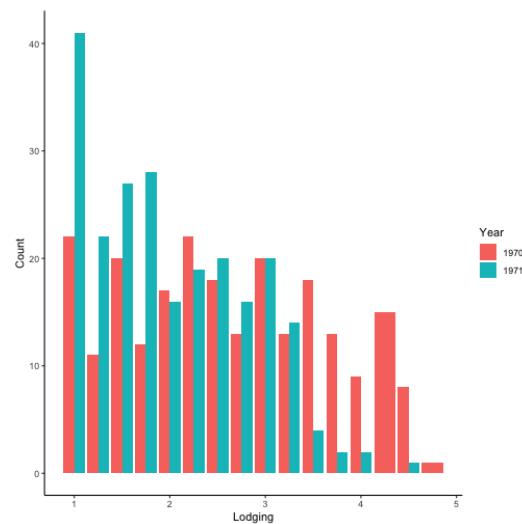
```
p <- ggplot(dat) +  
  aes(x = lodging, fill=year) +  
  geom_bar(position="dodge")  
p <- p + labs(x = "Lodging", y = "Count")  
p + scale_fill_discrete(name="Year")
```



The ggplot2: barplot

The function `ggsave()` will save the most recent plot to disk

```
p <- ggplot(dat) +  
  aes(x = lodging, fill=year) +  
  geom_bar(position="dodge")  
p <- p + labs(x = "Lodging", y = "Count")  
p <- p + scale_fill_discrete(name="Year")  
p + theme_classic()  
ggsave("my-plot.png")
```



The ggplot2: Practical



Your turn

30:00 minutes

- Use the `ars.earlywhitecorn96` in the `agridat` package
- Visualize the relation between `earth` and `yield` by location. Add a title, sub-title, caption; change the x-axis and y-axis labels; conclusion?
- Display together the histogram and the density of `yield` into different panels, each representing a location
- Display the boxplot of `yield` by location using colors

The ggplot2: Practical



Your turn

30:00 minutes

- Import the `iris.xlsx` into **R**
- Make a summary of the table: calculate and display the mean, standard deviation, variance, number of observations by Species
- Visualize the relation between Sepal.Length and Petal.Length by Species
- Add a regression line for each of the Species
- Display the boxplot of Sepal.Width by Species using colors
 - Add a title
 - Change the x-axis label
 - Change the y-axis label