Exploratory Analysis with R

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Outline: Exploratory Analysis with R

- Descriptive Statistics
  - Numerical summaries
  - Graphical exploration

Based on this Course: [*BIMS 8382, University of Virginia School of Medicine (USA)*] (https://bioconnector.github.io/workshops/index.html).

What packages we will use today?

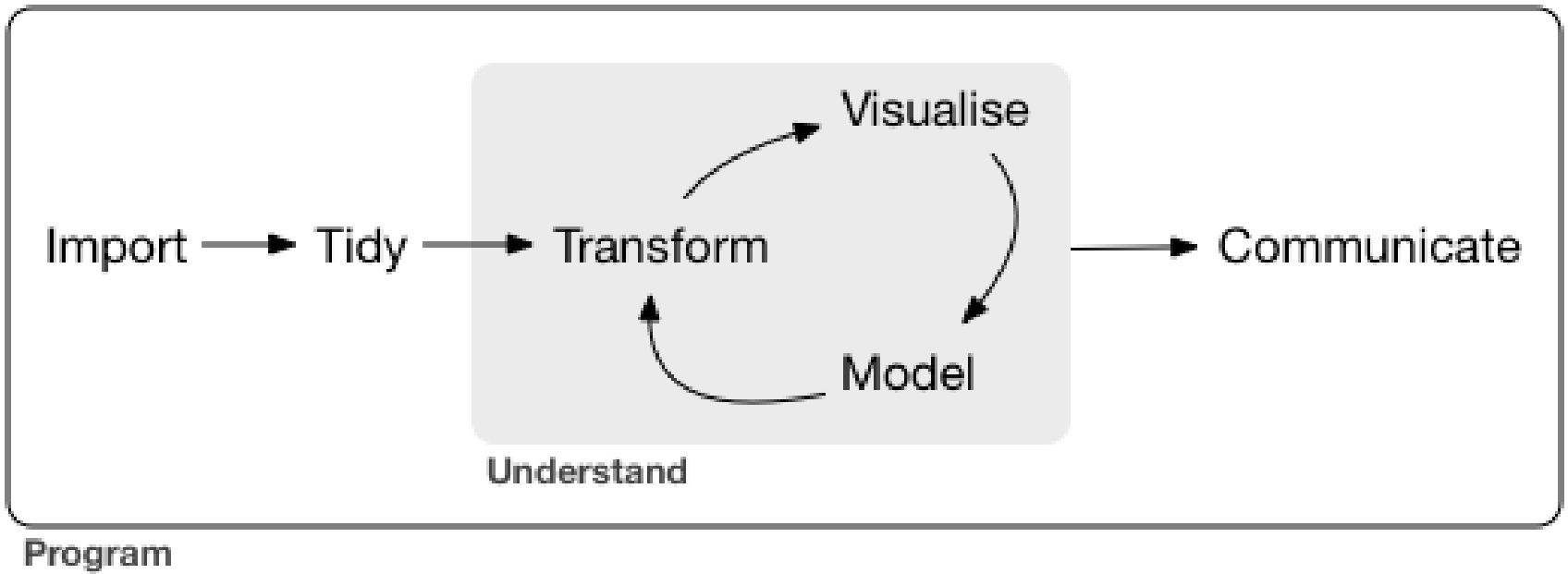
Please be sure you have the following packages installed:

- **dplyr** - subletting, sorting, transforming variables, grouping
- **ggplot2** - system for creating graphics
- **readxl** - reading .xls files

```
# install.packages("dplyr", dependencies = TRUE)
# install.packages("ggplot2", dependencies = TRUE)
# install.packages("readxl", dependencies = TRUE)

library(dplyr)
library(ggplot2)
library(readxl)
```

The Data Science Approach in R



Section 1

Getting started

Getting started (I)

1. Load the dataset *diabetes*:

```
diab <- read_excel("datasets/diabetes_mod.xls")
```

2. Check if we have loaded it correctly:

```
diab[1:4, 1:8]
```

```
## # A tibble: 4 x 8
##   numpacie mort  tempsviu  edat   bmi edatdiag tabac        sbp
##      <dbl> <chr>    <dbl> <dbl> <dbl>    <dbl> <chr>      <dbl>
## 1        1 Vivo      12.4    44  34.2       41 No fumador   132
## 2        2 Vivo      12.4    49  32.6       48 Fumador      130
## 3        3 Vivo       9.6    49  22         35 Fumador      108
## 4        4 Vivo       7.2    47  37.9       45 No fumador   128
```

Getting started (II): functions to check a dataframe:

- Content
  - `head()`: shows the first few rows
  - `tail()`: shows the last few rows
- Size
  - `dim()`: returns the number of rows and the number of columns
  - `nrow()`: returns the number of rows
  - `ncol()`: returns the number of columns
- Summary
  - `colnames()` or names(): returns the column names
  - `glimpse()`: returns a glimpse of your data: structure, class, length and content of each column

Getting started (III)

```
head(diab)
```

```
## # A tibble: 6 x 11
##   numpacie mort  tempsviu  edat   bmi edatdiag tabac       sbp   dbp ecg   chd
##      <dbl> <chr>    <dbl> <dbl> <dbl>    <dbl> <chr>     <dbl> <dbl> <chr> <chr>
## 1        1 Vivo      12.4    44  34.2       41 No fumad~   132    96 Norm~ No
## 2        2 Vivo      12.4    49  32.6       48 Fumador     130    72 Norm~ No
## 3        3 Vivo       9.6    49  22         35 Fumador     108    58 Norm~ Si
## 4        4 Vivo       7.2    47  37.9       45 No fumad~   128    76 Fron~ Si
## 5        5 Vivo      14.1    43  42.2       42 Fumador     142    80 Norm~ No
## 6        6 Vivo      14.1    47  33.1       44 No fumad~   156    94 Norm~ No
```

Getting started (IV)

```
dim(diab)
```

```
## [1] 149  11
```

```
nrow(diab)
```

```
## [1] 149
```

```
colnames(diab)
```

```
##  [1] "numpacie" "mort"     "tempsviu" "edat"     "bmi"      "edatdiag"
##  [7] "tabac"    "sbp"      "dbp"      "ecg"      "chd"
```

Getting started (IV)

```
glimpse(diab)
```

```
## Rows: 149
## Columns: 11
## $ numpacie <dbl> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18~
## $ mort     <chr> "Vivo", "Vivo", "Vivo", "Vivo", "Vivo", "Vivo", "Vivo", "Vivo~
## $ tempsviu <dbl> 12.4, 12.4, 9.6, 7.2, 14.1, 14.1, 12.4, 14.2, 12.4, 14.5, 12.~
## $ edat     <dbl> 44, 49, 49, 47, 43, 47, 50, 36, 50, 49, 50, 54, 42, 44, 40, 4~
## $ bmi      <dbl> 34.2, 32.6, 22.0, 37.9, 42.2, 33.1, 36.5, 38.5, 41.5, 34.1, 3~
## $ edatdiag <dbl> 41, 48, 35, 45, 42, 44, 48, NA, 47, 45, 48, 43, 36, 43, 26, 4~
## $ tabac    <chr> "No fumador", "Fumador", "Fumador", "No fumador", "Fumador", ~
## $ sbp      <dbl> 132, 130, 108, 128, 142, 156, 140, 144, 134, 102, 142, 128, 1~
## $ dbp      <dbl> 96, 72, 58, 76, 80, 94, 86, 88, 78, 68, 84, 74, 86, 58, 98, 6~
## $ ecg      <chr> "Normal", "Normal", "Normal", "Frontera", "Normal", "Normal",~
## $ chd      <chr> "No", "No", "Si", "Si", "No", "No", "Si", "No", "Si", "No", "~
```

Variables and data types

- Data managed in R is stored as *variables*
- Variables can be of distinct types:
  - Numerical
    - numeric (13.7)
    - int (3)
  - Character
    - "R is cute"
  - Factors
    - A,B,C,D
    - WT, Mut
  - Logical
    - TRUE/FALSE

Exercise I

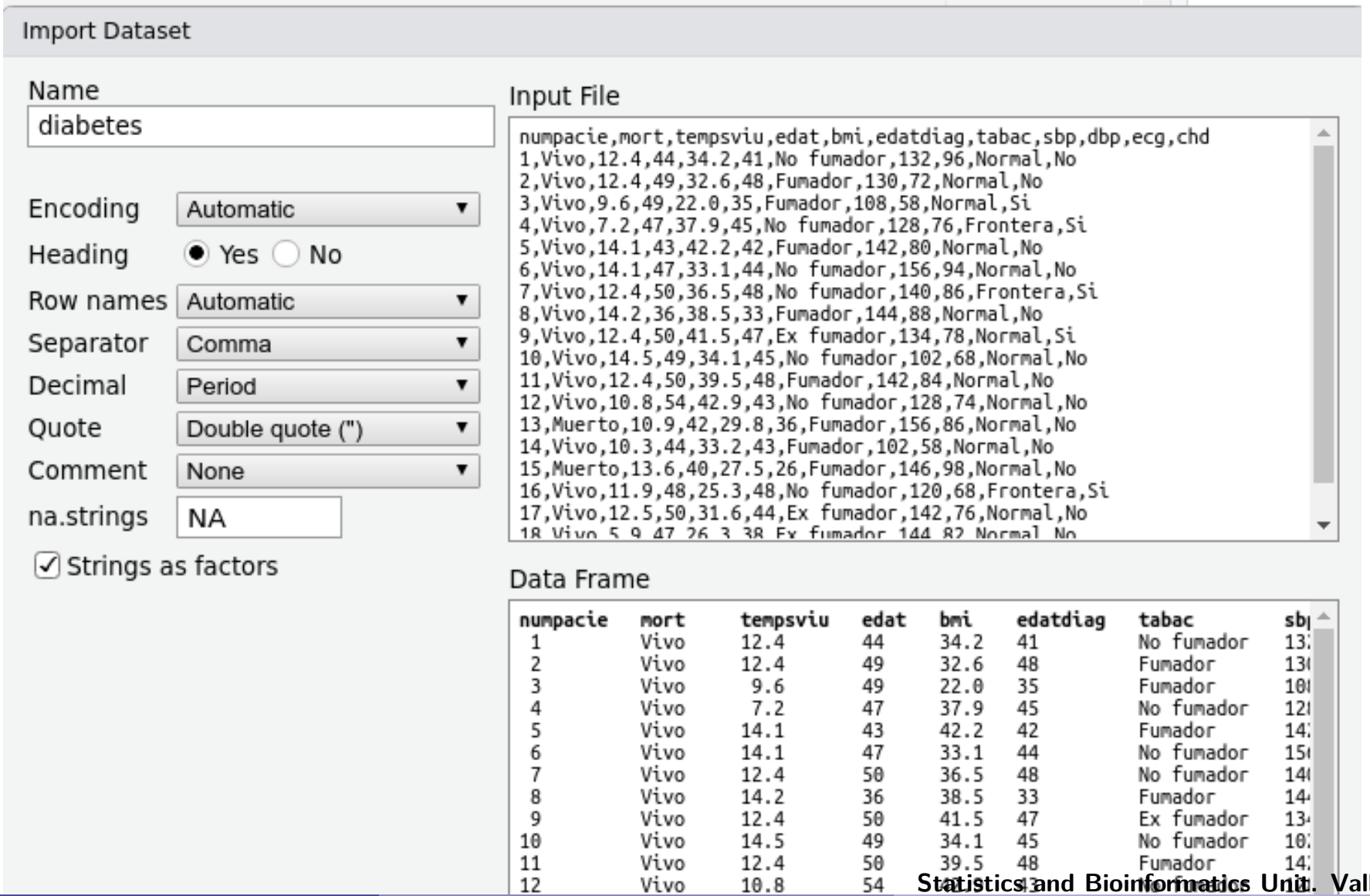
- Load the `osteoporosis` dataset
- Proceed similarly as to what we have done above and obtain information on
  - How many variables and observations
  - How are them (What are their types)

More about factors

- Each data type is what it seems to be, but factors require more explanation.
- Factors are intended to describe categories such as “sex”, “blood group”, but also “risk” or “stage”.
- Factors are useful to describe groups without having to use numeric codes.
- Factors may be created while reading the file or later using the `factor` and `as.factor` commands.

Create factor while reading

- Import the diabetes dataset from the `diabetes.csv` file using the Rstudio dialog.



Check variable type

```
diabetes <- read.csv("datasets/diabetes.csv", stringsAsFactors=TRUE)
class(diabetes$mort)
```

```
## [1] "factor"
```

```
sapply(diabetes, class)
```

```
##  numpacie      mort  tempsviu      edat       bmi  edatdiag     tabac
## "integer"  "factor" "numeric" "integer" "numeric" "integer"  "factor" "i
##       dbp       ecg       chd
## "integer"  "factor"  "factor"
```

Repeat

- Re-read the file from excel or without setting the "stringsAsFactors" to TRUE

Creating factors directly

- Use `factor` or `as.factor`

```
diabetes <- read.csv("datasets/diabetes.csv", stringsAsFactors=FALSE)
class(diabetes$mort)
```

```
## [1] "character"
```

```
diabetes$mort <- as.factor(diabetes$mort)
class(diabetes$mort)
```

```
## [1] "factor"
```

```
levels(diabetes$mort)
```

```
## [1] "Muerto" "Vivo"
```

Warning! by default alphabetic order is used when creating factor levels.

```
vitalStatus <- factor(diabetes$mort, levels=c("Vivo", "Muerto"))
class(vitalStatus)
```

```
## [1] "factor"
```

Change the levels of a factor

- When humans fill the database... many errors can happen :(
  - An answer like "YES", could be entered like:

    `"YES", "yes", "Yes", "Yeah "`
- All this possible answers **will become differents levels for the same factor variable**
- This may be solved using `recode_factor`:

```
diab$mort <- recode_factor(diab$mort, "Muerto" = "muerto")
levels(diab$mort)
```

```
## [1] "muerto" "Vivo"
```

Changing *characters (chr)* to *factors (Factor)*

An alternative way to turn characters into factors is the `mutate_if` function:

```
library(dplyr)
diab <- diabetes %>% mutate_if(is.character, as.factor)
glimpse(diab)
```

```
## Rows: 149
## Columns: 11
## $ numpacie <int> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18~
## $ mort     <fct> Vivo, Vivo, Vivo, Vivo, Vivo, Vivo, Vivo, Vivo, Vivo, Vivo, V~
## $ tempsviu <dbl> 12.4, 12.4, 9.6, 7.2, 14.1, 14.1, 12.4, 14.2, 12.4, 14.5, 12.~
## $ edat     <int> 44, 49, 49, 47, 43, 47, 50, 36, 50, 49, 50, 54, 42, 44, 40, 4~
## $ bmi      <dbl> 34.2, 32.6, 22.0, 37.9, 42.2, 33.1, 36.5, 38.5, 41.5, 34.1, 3~
## $ edatdiag <int> 41, 48, 35, 45, 42, 44, 48, 33, 47, 45, 48, 43, 36, 43, 26, 4~
## $ tabac    <fct> No fumador, Fumador, Fumador, No fumador, Fumador, No fumador~
## $ sbp      <int> 132, 130, 108, 128, 142, 156, 140, 144, 134, 102, 142, 128, 1~
## $ dbp      <int> 96, 72, 58, 76, 80, 94, 86, 88, 78, 68, 84, 74, 86, 58, 98, 6~
## $ ecg      <fct> Normal, Normal, Normal, Frontera, Normal, Normal, Frontera, N~
## $ chd      <fct> No, No, Si, Si, No, No, Si, No, Si, No, No, No, No, No, No, S~
```

Section 2

Exploratory Data Analysis: Numerical summaries

Numerical Summaries (I)

- There are many functions to provide numerical summaries

```
#Mean, median and rang
mean(diab$edat)
```

```
## [1] 52.16779
```

```
median(diab$edat)
```

```
## [1] 50
```

```
sd(diab$edat)
```

```
## [1] 11.77285
```

```
var(diab$edat)
```

```
## [1] 138.6
```

```
range(diab$edat)
```

```
## [1] 31 86
```

Numerical Summaries (II)

A general summary of all variables is provided by distinct functions

```
summary(diab[, 2:11])
```

```
##      mort         tempsviu          edat             bmi           edatdiag
##  Muerto: 25   Min.   : 0.00   Min.   :31.00   Min.   :18.20   Min.   :26.00
##  Vivo  :124   1st Qu.: 7.30   1st Qu.:43.00   1st Qu.:26.60   1st Qu.:38.00
##               Median :11.60   Median :50.00   Median :31.20   Median :45.00
##               Mean   :10.52   Mean   :52.17   Mean   :31.78   Mean   :45.99
##               3rd Qu.:13.90   3rd Qu.:60.00   3rd Qu.:35.20   3rd Qu.:53.00
##               Max.   :16.90   Max.   :86.00   Max.   :59.70   Max.   :81.00
##         tabac          sbp              dbp              ecg       chd
##  Ex fumador:41   Min.   : 98.0   Min.   : 58.00   Anormal : 11   No:99
##  Fumador   :51   1st Qu.:124.0   1st Qu.: 74.00   Frontera: 27   Si:50
##  No fumador:57   Median :138.0   Median : 80.00   Normal  :111
##                  Mean   :139.1   Mean   : 90.04
##                  3rd Qu.:152.0   3rd Qu.: 88.00
##                  Max.   :222.0   Max.   :862.00
```

Improving the `summary` function

- There are many packages to do descriptive statistics.
- See Dabbling with data
- Give a try, for instance to the `skimr` or `summarytools` packages.

More complete descriptions (I)

```
library(summarytools)
dfSummary(diabetes)
```

```
## Data Frame Summary
## diabetes
## Dimensions: 149 x 11
## Duplicates: 1
##
## ------------------------------------------------------------------------------------------------------------------------
## No   Variable      Stats / Values              Freqs (% of Valid)    Graph                 Valid      Missing
## ---- ------------ --------------------------- --------------------- --------------------- ---------- -------
## 1    numpacie     Mean (sd) : 75 (43.2)       148 distinct values   : : : : : : :         149        0
##      [integer]    min < med < max:                                  : : : : : : : :       (100.0%)   (0.0%)
##                   1 < 75 < 149                                      : : : : : : : :
##                   IQR (CV) : 74 (0.6)                               : : : : : : : : :
##                                                                     : : : : : : : : :
##
## 2    mort         1. Muerto                    25 (16.8%)           III                   149        0
##      [factor]     2. Vivo                     124 (83.2%)           IIIIIIIIIIIIIII       (100.0%)   (0.0%)
##
## 3    tempsviu     Mean (sd) : 10.5 (4.1)      84 distinct values                . : .     149        0
##      [numeric]    min < med < max:                                              : : :     (100.0%)   (0.0%)
##                   0 < 11.6 < 16.9                                               : : :
##                   IQR (CV) : 6.6 (0.4)                                . :       : : :
##                                                                     : : : : : : : : .
##
## 4    edat         Mean (sd) : 52.2 (11.8)     45 distinct values          :           149        0
##      [integer]    min < med < max:                                        :           (100.0%)   (0.0%)
##                   31 < 50 < 86                                      : . :   .
##                   IQR (CV) : 17 (0.2)                               : : : . :
##                                                                     : : : : : : : . .
##
## 5    bmi          Mean (sd) : 31.8 (6.8)      105 distinct values       . :           149        0
```

Grouped summeries

If we want to group the descriptive summaries by other variables we can use group_by function:

```
diab %>%
  group_by(tabac, ecg) %>%
  summarize(mean(edat))
```

```
## `summarise()` has grouped output by 'tabac'. You can override using the
## `.groups` argument.
```

```
## # A tibble: 9 x 3
## # Groups:   tabac [3]
##   tabac      ecg      `mean(edat)`
##   <fct>      <fct>           <dbl>
## 1 Ex fumador Anormal          68.5
## 2 Ex fumador Frontera         59.8
## 3 Ex fumador Normal           51.1
## 4 Fumador    Anormal          58
## 5 Fumador    Frontera         44.8
## 6 Fumador    Normal           44.7
## 7 No fumador Anormal          66.5
## 8 No fumador Frontera         53.8
## 9 No fumador Normal           56.0
```

Handling missing data

- What happens if we have missing data in our dataset?
- The file `diabetes_mod.xls` contains some missings

```
diabetes_mod <- read_excel("datasets/diabetes_mod.xls")
diab <- diabetes_mod %>% mutate_if(is.character, as.factor)
mean(diab$sbp)
```

```
## [1] NA
```

NA indicates *missing data* in the variable

Let's look the `sbp` variable:

```
diab$sbp
```

```
##   [1] 132 130 108 128 142 156 140 144 134 102 142 128 156 102 146 120 142 144
##  [19]  NA 134 130 122 132 150 134 142 124 102 134 118 192 122 122 112 142 152
##  [37] 112 118 152 136 134 130 108 126 132 144 126 128  NA 128 142 132 148 170
##  [55] 140 138 112 140 138 130 178 158 168 146 128 132 154 154 122 144 178 162
##  [73] 142 120 124 174 142 160 122 162 132 116 152 144  98 138 138 184 158 176
##  [91] 118 172 182 144 142 154 122 222 150 142 128 122 162 172 132 112 138 128
## [109] 132 120 140 140 172 136 152 126 104 142 128 122 122 122 122 168 162  NA
## [127] 126 180 132 150 106 154 122 120 120 144 134 148 170 160 154 124 130 156
## [145] 162 132 120 160 146
```

Numerical Summaries (VII)

How to work with *missing data*:

```
?mean
```

```
## starting httpd help server ... done
```

```
mean(diab$sbp, na.rm = TRUE)
```

```
## [1] 139.2603
```

```
is.na(diab$sbp)[1:50]
```

```
##  [1] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [13] FALSE FALSE FALSE FALSE FALSE FALSE  TRUE FALSE FALSE FALSE FALSE FALSE
## [25] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [37] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [49]  TRUE FALSE
```

```
sum(is.na(diab$sbp))
```

```
## [1] 3
```

```
sum(is.na(diab$dbp))
```

```
## [1] 0
```

See also: Remove Rows with NA in R Data Frame

EXERCISE

1. With the `diab` dataset

- Show only the rows from 35 to 98 and columns 5, 7, and from 9 to 11
- Change the level of the variable *tabac*, from **No Fumador** to **No_Fumador**
- Display the unique values for the variable *bmi*. Count how many exist.
- Display the mean of *edatdiag*, grouped by *ecg*

Section 3

Exploratory Data Analysis (EDA): Graphical summaries

Exploratory Data Analysis (EDA): Graphical summaries

- We could dedicate one whole course to Data Visualization (at least see our "Statistical Pill on Data Visualization")
- Here we will only see the most common approaches to visualize data:
  - Histograms
  - Barplots
  - Piecharts
  - Boxplots
  - Scatterplots

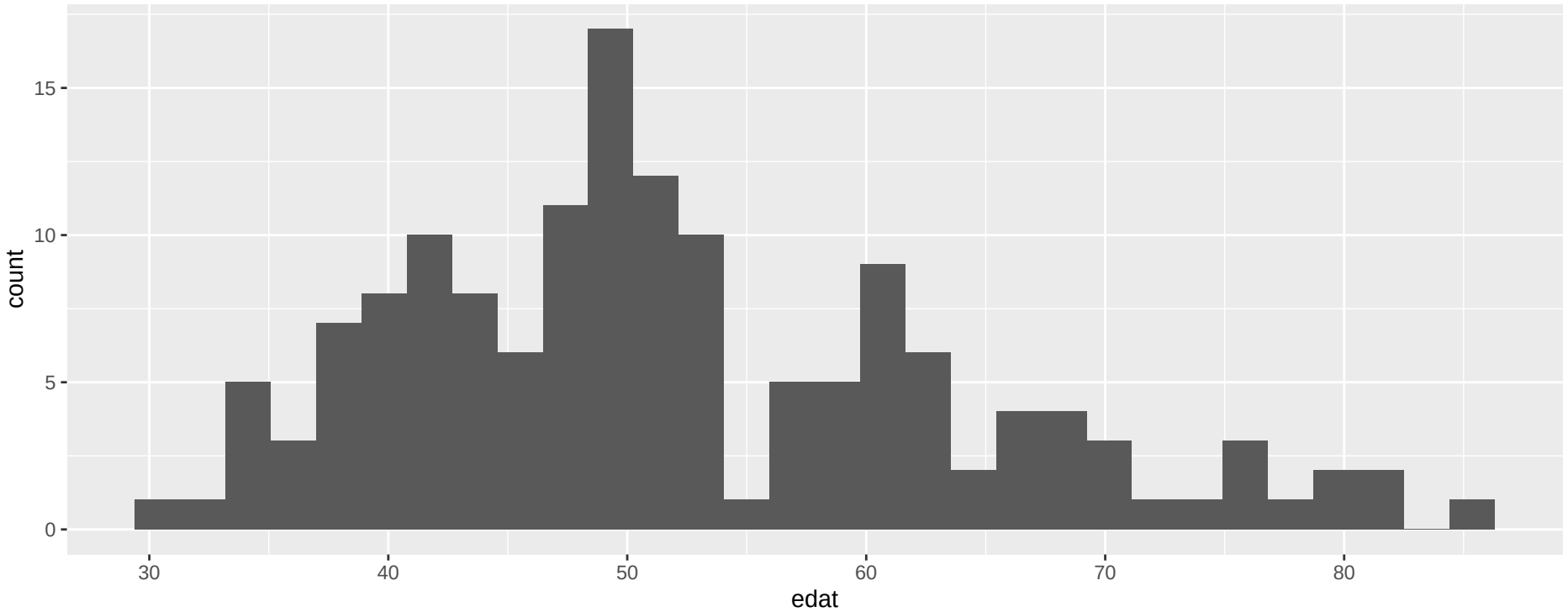
R graphics engines

- R is very powerful and flexible at doing graphics.
- This comes at a price: Complex graphics (that we do not show here) may require sonme extra effort.
- Much work has been done to simplify this
  - There exist graphical tools that allow for the interactive construction of plots.
  - There exist new approaches to plotting that try to be more intuitive than "traditional" ones.
- `ggplot` is one of such approaches.

Histograms

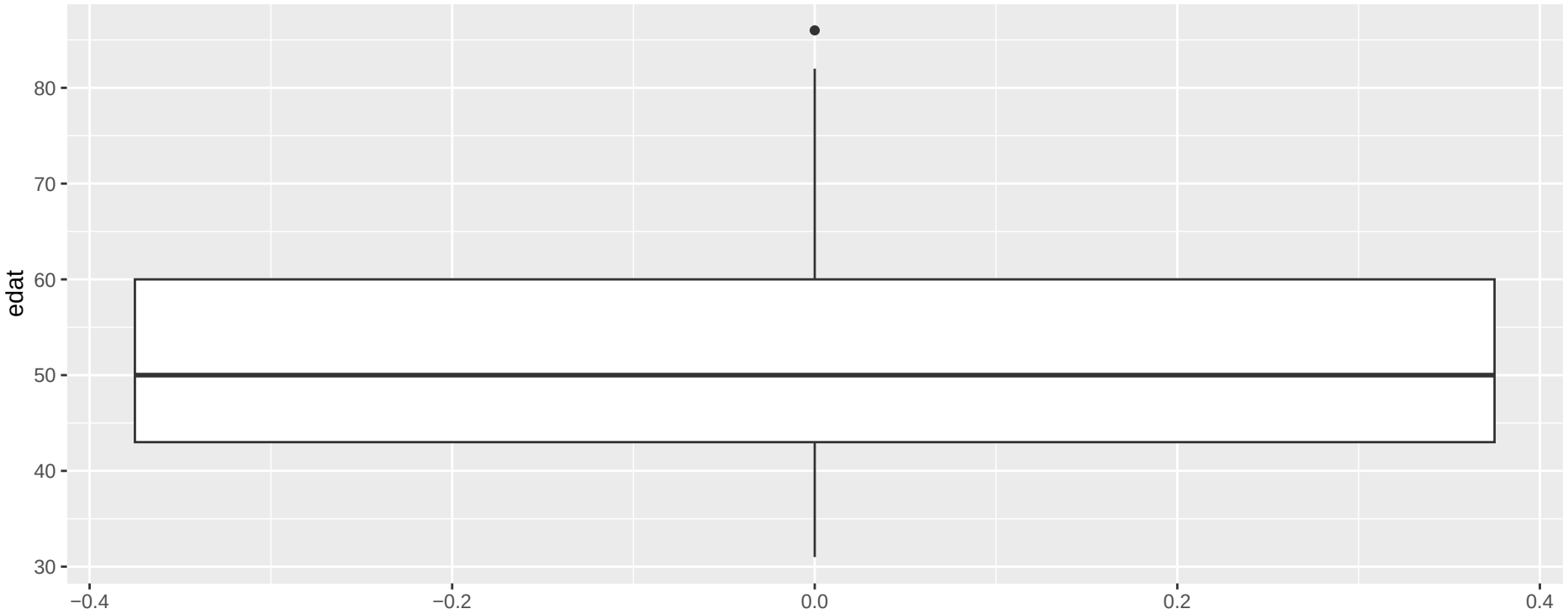
- We will use histograms to plot the frequencies of each range of values in continuous variables.
- These plots provide an approximation to the distribution of the variables being represented.

```
library(ggplot2)
ggplot(data=diab, aes(x=edat))+  geom_histogram()
```



Boxplot. A one-dimensional histogram

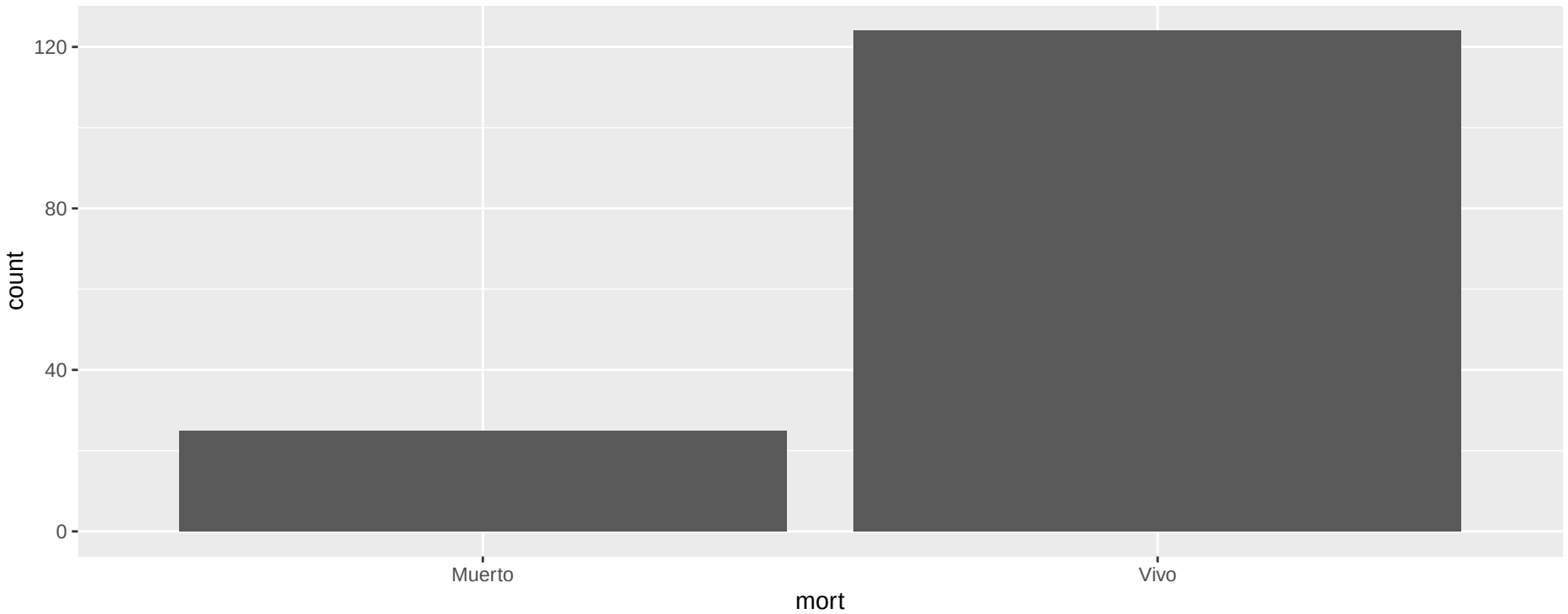
```
ggplot(data=diab, aes(y=edat))+
  geom_boxplot()
```



Plots for categorical variables. Barplots

- Some simple principles
  - Use pie charts only with categorical variables in nominal scale
  - Use barplots for any categorical variable
  - Never use 3D-plots

```
ggplot(data=diab, aes(x=mort))+
  geom_bar()
```



EXERCISE

- Using the *osteoporosis.csv* dataset
- Read the `osteoporosis.csv` data set into R so that character variables are automatically converted into factors.
- Load the dataset and check if it is correctly loaded
- Make a numerical summary of the dataset.
- Calculate the mean and standard deviation of imc grouped by clasific
- Plot the distribution of edat

EXERCISE

- With the variables in the osteoporosis dataset
- Try to represent the different variables using *the most appropriate plot* for each of them.