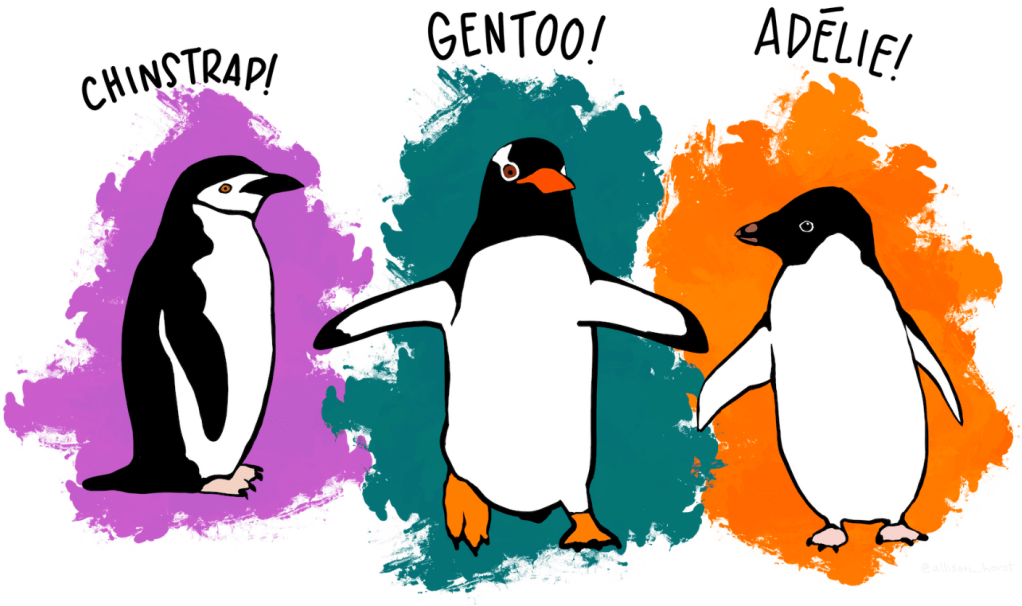
Data Preparation (Penguins)

Delete all variables

```
rm( list = ls() )
```

Meet the Palmer penguins



Data Preparation and first Insights

Import Data

- Download the data from Moodle
- Import the data using the function read.csv()
- Create a dataframe for it using the function data.frame()
- Have a look at the first rows using the function head()
- Have a look at the last rows using the function tail()

```
library(dplyr)
```

```
## Warning: package 'dplyr' was built under R version 4.1.3
```

```
##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
data = read.csv("C:/Users/Dari-Laptop/Desktop/FH Karnten - Master - AppDs/StatisticsAppDSLaptop/penguins
```

What are the column names of the data?

Use the function names()

```
names(data)
```

```
##  [1] "studyName"           "Sample.Number"       "Species"
##  [4] "Region"              "Island"              "Stage"
##  [7] "Individual.ID"       "Clutch.Completion"   "Date.Egg"
## [10] "Culmen.Length..mm."  "Culmen.Depth..mm."   "Flipper.Length..mm."
## [13] "Body.Mass..g."       "Gender"              "Delta.15.N..o.oo."
## [16] "Delta.13.C..o.oo."   "Comments"
```

What are the data types of each column?

```
str(data)
```

```
## 'data.frame':    344 obs. of  17 variables:
##  $ studyName          : chr  "PAL0708" "PAL0708" "PAL0708" "PAL0708" ...
##  $ Sample.Number      : int  1 2 3 4 5 6 7 8 9 10 ...
##  $ Species            : chr  "Adelie Penguin (Pygoscelis adeliae)" "Adelie Penguin (Pygoscelis adelia
##  $ Region             : chr  "Anvers" "Anvers" "Anvers" "Anvers" ...
##  $ Island             : chr  "Torgersen" "Torgersen" "Torgersen" "Torgersen" ...
##  $ Stage              : chr  "Adult, 1 Egg Stage" "Adult, 1 Egg Stage" "Adult, 1 Egg Stage" "Adult,
##  $ Individual.ID      : chr  "N1A1" "N1A2" "N2A1" "N2A2" ...
##  $ Clutch.Completion  : chr  "Yes" "Yes" "Yes" "Yes" ...
##  $ Date.Egg           : chr  "11/11/07" "11/11/07" "11/16/07" "11/16/07" ...
##  $ Culmen.Length..mm. : num  39.1 39.5 40.3 NA 36.7 39.3 38.9 39.2 34.1 42 ...
##  $ Culmen.Depth..mm.  : num  18.7 17.4 18 NA 19.3 20.6 17.8 19.6 18.1 20.2 ...
##  $ Flipper.Length..mm.: int  181 186 195 NA 193 190 181 195 193 190 ...
##  $ Body.Mass..g.      : int  3750 3800 3250 NA 3450 3650 3625 4675 3475 4250 ...
##  $ Gender             : chr  "MALE" "FEMALE" "FEMALE" "" ...
##  $ Delta.15.N..o.oo.  : num  NA 8.95 8.37 NA 8.77 ...
##  $ Delta.13.C..o.oo.  : num  NA -24.7 -25.3 NA -25.3 ...
##  $ Comments           : chr  "Not enough blood for isotopes." "" "" "Adult not sampled." ...
```

Data types:

- Nominal:
  - studyName
  - Species
  - Region
  - Island
  - Gender
  - Comments
  - Clutch.Completion
- Ordinal:
  - Individual.ID
  - Date
- Discrete:
  - Body Mass
  - Sample.Number
  - Flipper.length
- Continuous:
  - Culmen.Length
  - Culmen.Depth
  - Delta.15
  - Delta13

Delete some columns

Delete the following columns since we won't need them in this class:

- studyName,
- Region,
- Stage,
- Clutch.Completion,
- Date.Egg,
- Delta.15.N..o.oo.,
- Delta.13.C..o.oo.,
- Comments

Use therefore the function %in%

```
drop <- c('studyName', 'Region', 'Stage', 'Clutch.Completion', 'Date.Egg', 'Delta.15.N..o.oo.',
          'Delta.13.C..o.oo.', 'Comments')

df = data[,!(names(data) %in% drop)]

head(df)
```

```
##   Sample.Number                             Species    Island Individual.ID
## 1             1 Adelie Penguin (Pygoscelis adeliae) Torgersen          N1A1
## 2             2 Adelie Penguin (Pygoscelis adeliae) Torgersen          N1A2
## 3             3 Adelie Penguin (Pygoscelis adeliae) Torgersen          N2A1
## 4             4 Adelie Penguin (Pygoscelis adeliae) Torgersen          N2A2
## 5             5 Adelie Penguin (Pygoscelis adeliae) Torgersen          N3A1
```

```
## 6             6 Adelie Penguin (Pygoscelis adeliae) Torgersen          N3A2
##   Culmen.Length..mm. Culmen.Depth..mm. Flipper.Length..mm. Body.Mass..g. Gender
## 1               39.1              18.7                 181          3750   MALE
## 2               39.5              17.4                 186          3800 FEMALE
## 3               40.3              18.0                 195          3250 FEMALE
## 4                 NA                NA                  NA            NA
## 5               36.7              19.3                 193          3450 FEMALE
## 6               39.3              20.6                 190          3650   MALE
```

Rearrange the data

Put the column "Individual.ID" to first column

```
reorder = c("Individual.ID", names(df[,names(df)!="Individual.ID"]))
reorder
```

```
## [1] "Individual.ID"       "Sample.Number"       "Species"
## [4] "Island"              "Culmen.Length..mm."  "Culmen.Depth..mm."
## [7] "Flipper.Length..mm." "Body.Mass..g."       "Gender"
```

```
df <- df[, reorder]
head(df)
```

```
##   Individual.ID Sample.Number                              Species    Island
## 1          N1A1             1 Adelie Penguin (Pygoscelis adeliae) Torgersen
## 2          N1A2             2 Adelie Penguin (Pygoscelis adeliae) Torgersen
## 3          N2A1             3 Adelie Penguin (Pygoscelis adeliae) Torgersen
## 4          N2A2             4 Adelie Penguin (Pygoscelis adeliae) Torgersen
## 5          N3A1             5 Adelie Penguin (Pygoscelis adeliae) Torgersen
## 6          N3A2             6 Adelie Penguin (Pygoscelis adeliae) Torgersen
##   Culmen.Length..mm. Culmen.Depth..mm. Flipper.Length..mm. Body.Mass..g. Gender
## 1               39.1              18.7                 181          3750   MALE
## 2               39.5              17.4                 186          3800 FEMALE
## 3               40.3              18.0                 195          3250 FEMALE
## 4                 NA                NA                  NA            NA
## 5               36.7              19.3                 193          3450 FEMALE
## 6               39.3              20.6                 190          3650   MALE
```

Rename columns

Rename the columns to

- IndividualID
- Species
- Island
- CulmenLength(mm)
- CulmenDepth(mm)
- FlipperLength(mm)
- BodyMass(g)
- Gender

```
## Rename
names(df)[1] = "IndividualID"
names(df)[2] = "Species"
names(df)[3] = "Island"
names(df)[4] = "CulmenLength(mm)"
names(df)[5] = "CulmenDepth(mm)"
names(df)[6] = "FlipperLength(mm)"
names(df)[7] = "BodyMass(g)"
names(df)[8] = "Gender"

head(df)
```

```
##   IndividualID Species                                Island CulmenLength(mm)
## 1         N1A1       1 Adelie Penguin (Pygoscelis adeliae)        Torgersen
## 2         N1A2       2 Adelie Penguin (Pygoscelis adeliae)        Torgersen
## 3         N2A1       3 Adelie Penguin (Pygoscelis adeliae)        Torgersen
## 4         N2A2       4 Adelie Penguin (Pygoscelis adeliae)        Torgersen
## 5         N3A1       5 Adelie Penguin (Pygoscelis adeliae)        Torgersen
## 6         N3A2       6 Adelie Penguin (Pygoscelis adeliae)        Torgersen
##   CulmenDepth(mm) FlipperLength(mm) BodyMass(g) Gender Gender
## 1            39.1              18.7         181   3750   MALE
## 2            39.5              17.4         186   3800 FEMALE
## 3            40.3              18.0         195   3250 FEMALE
## 4              NA                NA          NA     NA
## 5            36.7              19.3         193   3450 FEMALE
## 6            39.3              20.6         190   3650   MALE
```

What are the three types of Species?

Use therefore the function unique()

```
# unique

unique(df$Species)
```

```
##   [1]   1   2   3   4   5   6   7   8   9  10  11  12  13  14  15  16  17  18
##  [19]  19  20  21  22  23  24  25  26  27  28  29  30  31  32  33  34  35  36
##  [37]  37  38  39  40  41  42  43  44  45  46  47  48  49  50  51  52  53  54
##  [55]  55  56  57  58  59  60  61  62  63  64  65  66  67  68  69  70  71  72
##  [73]  73  74  75  76  77  78  79  80  81  82  83  84  85  86  87  88  89  90
##  [91]  91  92  93  94  95  96  97  98  99 100 101 102 103 104 105 106 107 108
## [109] 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126
## [127] 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144
## [145] 145 146 147 148 149 150 151 152
```

Rename the Species types

Rename the types to

- Adele
- Chinstrap

- Gentoo

```
# rename species


df$Species[df$Species=="Adelie Penguin (Pygoscelis adeliae)"] = "Adele"
df$Species[df$Species=="Chinstrap penguin (Pygoscelis antarctica)"] = "Chinstrap"
df$Species[df$Species=="Gentoo penguin (Pygoscelis papua)"] = "Gentoo"

unique(df$Species)
```

```
##   [1] "1"   "2"   "3"   "4"   "5"   "6"   "7"   "8"   "9"   "10"  "11"  "12"
##  [13] "13"  "14"  "15"  "16"  "17"  "18"  "19"  "20"  "21"  "22"  "23"  "24"
##  [25] "25"  "26"  "27"  "28"  "29"  "30"  "31"  "32"  "33"  "34"  "35"  "36"
##  [37] "37"  "38"  "39"  "40"  "41"  "42"  "43"  "44"  "45"  "46"  "47"  "48"
##  [49] "49"  "50"  "51"  "52"  "53"  "54"  "55"  "56"  "57"  "58"  "59"  "60"
##  [61] "61"  "62"  "63"  "64"  "65"  "66"  "67"  "68"  "69"  "70"  "71"  "72"
##  [73] "73"  "74"  "75"  "76"  "77"  "78"  "79"  "80"  "81"  "82"  "83"  "84"
##  [85] "85"  "86"  "87"  "88"  "89"  "90"  "91"  "92"  "93"  "94"  "95"  "96"
##  [97] "97"  "98"  "99"  "100" "101" "102" "103" "104" "105" "106" "107" "108"
## [109] "109" "110" "111" "112" "113" "114" "115" "116" "117" "118" "119" "120"
## [121] "121" "122" "123" "124" "125" "126" "127" "128" "129" "130" "131" "132"
## [133] "133" "134" "135" "136" "137" "138" "139" "140" "141" "142" "143" "144"
## [145] "145" "146" "147" "148" "149" "150" "151" "152"
```

```
head(df)
```

```
##   IndividualID Species                                Island CulmenLength(mm)
## 1         N1A1       1 Adelie Penguin (Pygoscelis adeliae)        Torgersen
## 2         N1A2       2 Adelie Penguin (Pygoscelis adeliae)        Torgersen
## 3         N2A1       3 Adelie Penguin (Pygoscelis adeliae)        Torgersen
## 4         N2A2       4 Adelie Penguin (Pygoscelis adeliae)        Torgersen
## 5         N3A1       5 Adelie Penguin (Pygoscelis adeliae)        Torgersen
## 6         N3A2       6 Adelie Penguin (Pygoscelis adeliae)        Torgersen
##   CulmenDepth(mm) FlipperLength(mm) BodyMass(g) Gender Gender
## 1            39.1              18.7         181   3750   MALE
## 2            39.5              17.4         186   3800 FEMALE
## 3            40.3              18.0         195   3250 FEMALE
## 4              NA                NA          NA     NA
## 5            36.7              19.3         193   3450 FEMALE
## 6            39.3              20.6         190   3650   MALE
```

Missing Values

How many rows contain missing values?

```
summary(df)
```

```
##  IndividualID         Species             Island          CulmenLength(mm)
##  Length:344         Length:344         Length:344         Length:344
```

```
##  Class :character   Class :character   Class :character   Class :character
##  Mode  :character   Mode  :character   Mode  :character   Mode  :character
##
##
##
##
##  CulmenDepth(mm) FlipperLength(mm)  BodyMass(g)        Gender
##  Min.   :32.10   Min.   :13.10     Min.   :172.0   Min.   :2700
##  1st Qu.:39.23   1st Qu.:15.60     1st Qu.:190.0   1st Qu.:3550
##  Median :44.45   Median :17.30     Median :197.0   Median :4050
##  Mean   :43.92   Mean   :17.15     Mean   :200.9   Mean   :4202
##  3rd Qu.:48.50   3rd Qu.:18.70     3rd Qu.:213.0   3rd Qu.:4750
##  Max.   :59.60   Max.   :21.50     Max.   :231.0   Max.   :6300
##  NA's   :2       NA's   :2         NA's   :2       NA's   :2
##     Gender
##  Length:344
##  Class :character
##  Mode  :character
##
##
##
##
```

How many rows have empty entries in the qualitative columns?

```
# rows that have empty entries in the qualitative columns

#### first method
# qualitative = dplyr::select_if(df, is.numeric)
# head(qualitative)
# summary(qualitative)


# second method
cnt = rowSums(is.na(df) | df == "") > 0
sum(cnt)
```

```
## [1] 10
```

Data Imputation

What about data imputation? Check the rows with NA values. Can you apply data imputation on it?

```
new_df <- df[-c(4, 340),]

head(new_df)
```

```
##   IndividualID Species                                Island CulmenLength(mm)
## 1         N1A1       1 Adelie Penguin (Pygoscelis adeliae)        Torgersen
## 2         N1A2       2 Adelie Penguin (Pygoscelis adeliae)        Torgersen
## 3         N2A1       3 Adelie Penguin (Pygoscelis adeliae)        Torgersen
```

```
## 5         N3A1       5 Adelie Penguin (Pygoscelis adeliae)        Torgersen
## 6         N3A2       6 Adelie Penguin (Pygoscelis adeliae)        Torgersen
## 7         N4A1       7 Adelie Penguin (Pygoscelis adeliae)        Torgersen
##   CulmenDepth(mm) FlipperLength(mm) BodyMass(g) Gender Gender
## 1            39.1              18.7         181   3750   MALE
## 2            39.5              17.4         186   3800 FEMALE
## 3            40.3              18.0         195   3250 FEMALE
## 5            36.7              19.3         193   3450 FEMALE
## 6            39.3              20.6         190   3650   MALE
## 7            38.9              17.8         181   3625 FEMALE
```

Create Dataframe DataWithoutGender

- Select the rows where the gender is unknown and create a new data set for it. Name it "PenguinsWithoutGender"
- Delete the rows with NA values in the quantitative columns by using the function na.omit()
- replace "." by " " in the column Gender
- save it to a csv file called "DataWithoutGender.csv" (we will classify the missing gender data later).

For the **csv saving**:

- Use either write.csv() or write.csv2() depending on your system's language: if english use write.csv() if german use write.csv2()
- use row.names = FALSE to exclude the row indices –> for a smoother workflow

```
# Select the rows where the gender is unknown and create a new data set for it. Name it "PenguinsWithou
PenguinsWithoutGender <- df[is.na(df$Gender) | df$Gender == "" | df$Gender == ".", ]

PenguinsWithoutGender
```

```
##     IndividualID Species                                Island CulmenLength(mm)
## 4           N2A2       4 Adelie Penguin (Pygoscelis adeliae)        Torgersen
## 340        N38A2     120   Gentoo penguin (Pygoscelis papua)           Biscoe
##     CulmenDepth(mm) FlipperLength(mm) BodyMass(g) Gender Gender
## 4                NA                NA          NA     NA
## 340              NA                NA          NA     NA
```

```
# Delete the rows with NA values in the quantitative columns by using the function na.omit()
na.omit(PenguinsWithoutGender)
```

```
## [1] IndividualID      Species           Island            CulmenLength(mm)
## [5] CulmenDepth(mm)   FlipperLength(mm) BodyMass(g)       Gender
## [9] Gender
## <0 rows> (or 0-length row.names)
```

```
# replace "." by "" in the column Gender
PenguinsWithoutGender$Gender[PenguinsWithoutGender$Gender=="."] = ""

PenguinsWithoutGender
```

```
##     IndividualID Species                                Island CulmenLength(mm)
## 4           N2A2       4 Adelie Penguin (Pygoscelis adeliae)        Torgersen
## 340        N38A2     120   Gentoo penguin (Pygoscelis papua)           Biscoe
##     CulmenDepth(mm) FlipperLength(mm) BodyMass(g) Gender Gender
## 4                NA                NA          NA   <NA>
## 340              NA                NA          NA   <NA>
```

```
write.csv(PenguinsWithoutGender, file='C:/Users/Dari-Laptop/Desktop/FH Karnten - Master - AppDs/Statist
```

Create Dataframe PenguinsWithoutMissingValues

- Delete the rows with NA values in the quantitative columns by using the function na.omit()
- Delete the rows with missing values in the gender column
- save it to a csv file called "PenguinsWithoutMissingValues.csv"

For the **csv saving**:

- Use either write.csv() or write.csv2() depending ob your system's language: if english use write.csv() if german use write.csv2()
- use row.names = FALSE to exclude the row indices –> for a smoother workflow

```
PenguinsWithoutMissingValues = na.omit(df)

PenguinsWithoutMissingValues = PenguinsWithoutMissingValues[-which(PenguinsWithoutMissingValues$Gender==
head(PenguinsWithoutMissingValues)
```

```
## [1] IndividualID      Species           Island            CulmenLength(mm)
## [5] CulmenDepth(mm)   FlipperLength(mm) BodyMass(g)       Gender
## [9] Gender
## <0 rows> (or 0-length row.names)
```

```
write.csv(PenguinsWithoutMissingValues, file='C:/Users/Dari-Laptop/Desktop/FH Karnten - Master - AppDs/S
```