

Workflow en Biologie - Biométrie humaine

Deschuyteneer Audry

...

```
knitr::opts_chunk$set(echo = TRUE)
SciViews::R

## -- Attaching packages -----
## v SciViews  1.1.1      v purrr    0.3.4
## v chart     1.3.0      v readr    1.3.1
## v flow      1.0.0      v tidyr    1.0.2
## v data.io   1.2.2      v tibble   3.0.1
## v svMisc    1.1.0      v ggplot2  3.3.0
## v forcats   0.5.0      v tidyverse 1.3.0
## v stringr   1.4.0      v lattice  0.20.41
## v dplyr     0.8.5      v MASS     7.3.51.5

## -- Conflicts -----
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()     masks stats::lag()
## x dplyr::select() masks MASS::select()

# Importation des données
biometry <- read("../data/biometry_2014.xlsx")

## New names:
## * ‘ ’ -> ...1

# Ajout des labels pour une variable 2 niveaux
biometry %>%
  mutate(., gender = factor(gender, levels = c("H", "F"),
    labels = c("Homme", "Femme"))
  ) -> biometry
# Ajout des labels et unités
biometry <- labelise(biometry, self = FALSE,
  label = list(
    gender = "Genre",
    db = "Date de naissance",
    yb = "Année de naissance",
    weight = "Masse",
    height = "Taille",
    wrist = "Circonférence du poignet",
    measurement_date = "Année de la mesure"),
  units = list(
    gender = NA,
    db = NA,
    yb = NA,
    weight = "kg",
```

```
height = "cm",  
wrist = "mm",  
measurement_date = "année")  
)
```

```
SciViews::R  
chart(biometry, height ~ weight) +  
  geom_point(na.rm = TRUE)
```

