TNDS_2021_Comp_Across_Langs

Kees Schipper

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Set up libraries and working directory

```
knitr::opts_chunk$set(
    echo = TRUE,
    message = FALSE,
    warnings = FALSE,
    tidy.opts=list(width.cutoff=80),
    tidy=TRUE
)

options(width = 80)
setwd("C:/Users/keess/Box/TNDS Workshop/R")

library(tidyverse)
library(readxl)
library(haven)
library(plotrix)
library(expss)
library(moments)
```

Read in data

```
# load("Input_Data/workshop_data.RData")
# write_csv(x = workshop_data, "Input_Data/workshop_data.csv")
getwd() # workind directory is different in Rmarkdown than in an R script
```

```
## [1] "C:/Users/keess/Box/TNDS Workshop/R/R scripts"
```

```
# load("../../data for workshop/workshop_data.RData")
df <- read_csv("../../data for workshop/workshop_data.csv")
```

Describe, view, and edit data once imported

```r
names(df) # variable names in df
```

```
##  [1] "study_id"    "study_arm"   "agedays"     "agemonths"   "gender"
##  [6] "cgage"       "edu"         "av_weight"   "av_len"      "av_muac"
## [11] "_zwei"       "_zwfl"       "hfias_score" "hfias_cat"   "ageyears"
```

```r
nrow(df) # number of rows in df
```

```
## [1] 2653
```

```r
ncol(df) # number of columns in df
```

```
## [1] 15
```

```r
str(df) # structure
```

```
## tibble [2,653 x 15] (S3: spec_tbl_df/tbl_df/tbl/data.frame)
##  $ study_id   : num [1:2653] 1 2 3 4 5 6 7 8 9 10 ...
##  $ study_arm  : num [1:2653] 1 1 1 1 1 1 1 1 1 1 ...
##  $ agedays    : num [1:2653] 399 477 1506 429 527 ...
##  $ agemonths  : num [1:2653] 13.1 15.7 49.5 14.1 17.3 ...
##  $ gender     : num [1:2653] 1 1 1 1 0 0 0 1 0 0 ...
##  $ cgage      : num [1:2653] 21 25 46 29 20 25 23 20 35 25 ...
##  $ edu        : num [1:2653] 0 3 0 0 0 0 3 3 0 1 ...
##  $ av_weight  : num [1:2653] 7.14 7.2 12.79 6.76 6.93 ...
##  $ av_len     : num [1:2653] 70.6 70.6 103.3 68.2 72.3 ...
##  $ av_muac    : num [1:2653] 11.8 11.9 11.9 12 12 ...
##  $ _zwei      : num [1:2653] -2.95 -3.33 -2.06 -3.59 -3.19 -2.39 -2.91 -2.6 -2.89 -2.55 ...
##  $ _zwfl      : num [1:2653] -2.26 -2.16 -2.89 -2.14 -2.53 -1.55 -1.96 -1.45 -2.15 -1.63 ...
##  $ hfias_score: num [1:2653] 16 21 15 0 10 12 15 16 11 26 ...
##  $ hfias_cat  : num [1:2653] 1 1 1 4 2 2 1 1 2 1 ...
##  $ ageyears   : num [1:2653] 1.09 1.31 4.12 1.17 1.44 ...
##  - attr(*, "spec")=
##   .. cols(
##   ..   study_id = col_double(),
##   ..   study_arm = col_double(),
##   ..   agedays = col_double(),
##   ..   agemonths = col_double(),
##   ..   gender = col_double(),
##   ..   cgage = col_double(),
##   ..   edu = col_double(),
##   ..   av_weight = col_double(),
##   ..   av_len = col_double(),
##   ..   av_muac = col_double(),
##   ..   `_zwei` = col_double(),
##   ..   `_zwfl` = col_double(),
##   ..   hfias_score = col_double(),
##   ..   hfias_cat = col_double(),
##   ..   ageyears = col_double()
##   .. )
```

```r
## find all unique values of gender
unique(df$gender)
```

```
## [1]   1   0 -99
```

```r
# find the number of unique values of age in days
n_distinct(df$agedays)
```

```
## [1] 690
```

```r
# the number of rows with complete observations
sum(complete.cases(df))
```

```
## [1] 2623
```

```r
# the number of missing observations with agedays
sum(is.na(df$agedays))
```

```
## [1] 13
```

```r
## lapply can take a function (like unique), and apply it to all columns of a dataframe (df)
unique_vals <- lapply(df, unique)
distinct_vals <- lapply(df, n_distinct)
## missing vals for each column:
missing <- lapply(df, function(x) sum(is.na(x)))
```

Generate and label variables and observations

```r
# creating variables in base R: do simple operations on already existing variables
df$ageyears <- df$agedays/365.25

# you can also create completely new variables, like this nonsensical one below
# df$nonsense <- "this variable means nothing"

# labelling categorical variables as factors
df$gender <- factor(df$gender, levels = c(-99, 0, 1),
                    labels = c("not documented", "female", "male"))
summary(df$gender)
```

```
## not documented         female           male
##              3           1523           1127
```

```r
# let's do the same with edu level
df$edu <- factor(df$edu, levels = c(-99, 0, 1, 2, 3, 4, 5),
                 labels = c("not documented", "none", "some primary", "completed primary",
                            "some secondary", "completed secondary", "more than secondary"))
summary(df$edu)
```

```
##      not documented                 none        some primary   completed primary 
##                  14                 1419                 574                  59 
##      some secondary completed secondary more than secondary 
##                 563                   21                   3 
```

Get summary statistics

```
# simple base R summary function, giving min, mean, median, max, and Q1/Q3 for continuous variables, an
summary(df)
```

```
##     study_id      study_arm        agedays         agemonths     
##  Min.   :   1   Min.   :1.000   Min.   : 171.0   Min.   : 5.622  
##  1st Qu.:2595   1st Qu.:2.000   1st Qu.: 231.0   1st Qu.: 7.595  
##  Median :5115   Median :3.000   Median : 326.0   Median :10.718  
##  Mean   :4430   Mean   :2.611   Mean   : 403.1   Mean   :13.254  
##  3rd Qu.:7624   3rd Qu.:4.000   3rd Qu.: 493.2   3rd Qu.:16.216  
##  Max.   :8500   Max.   :4.000   Max.   :1809.0   Max.   :59.474  
##                                 NA's   :13       NA's   :13      
##             gender         cgage                         edu      
##  not documented:   3   Min.   :-99.00   not documented     :  14  
##  female        :1523   1st Qu.: 21.00   none               :1419  
##  male          :1127   Median : 26.00   some primary       : 574  
##                        Mean   : 26.59   completed primary  :  59  
##                        3rd Qu.: 32.00   some secondary     : 563  
##                        Max.   : 80.00   completed secondary:  21  
##                                         more than secondary:   3  
##    av_weight          av_len          av_muac          _zwei       
##  Min.   : 4.085   Min.   : 53.15   Min.   :11.50   Min.   :-6.140  
##  1st Qu.: 5.955   1st Qu.: 63.55   1st Qu.:11.73   1st Qu.:-3.390  
##  Median : 6.510   Median : 66.85   Median :11.97   Median :-2.870  
##  Mean   : 6.677   Mean   : 68.03   Mean   :11.97   Mean   :-2.882  
##  3rd Qu.: 7.220   3rd Qu.: 71.45   3rd Qu.:12.20   3rd Qu.:-2.330  
##  Max.   :15.010   Max.   :108.20   Max.   :12.47   Max.   : 1.260  
##  NA's   :1        NA's   :3                        NA's   :17      
##      _zwfl         hfias_score       hfias_cat      ageyears     
##  Min.   :-4.840   Min.   : 0.000   Min.   :1.0   Min.   :0.4682  
##  1st Qu.:-2.270   1st Qu.: 1.000   1st Qu.:1.0   1st Qu.:0.6324  
##  Median :-1.790   Median :10.000   Median :2.0   Median :0.8925  
##  Mean   :-1.799   Mean   : 9.451   Mean   :2.4   Mean   :1.1037  
##  3rd Qu.:-1.320   3rd Qu.:14.000   3rd Qu.:3.0   3rd Qu.:1.3504  
##  Max.   : 1.370   Max.   :27.000   Max.   :4.0   Max.   :4.9528  
##  NA's   :8        NA's   :9        NA's   :9     NA's   :13      
```

```
# individual summary functions. We need to use the na.rm option to remove NA values, because if we don'
mean(df$agemonths, na.rm = T)
```

```
## [1] 13.254
```

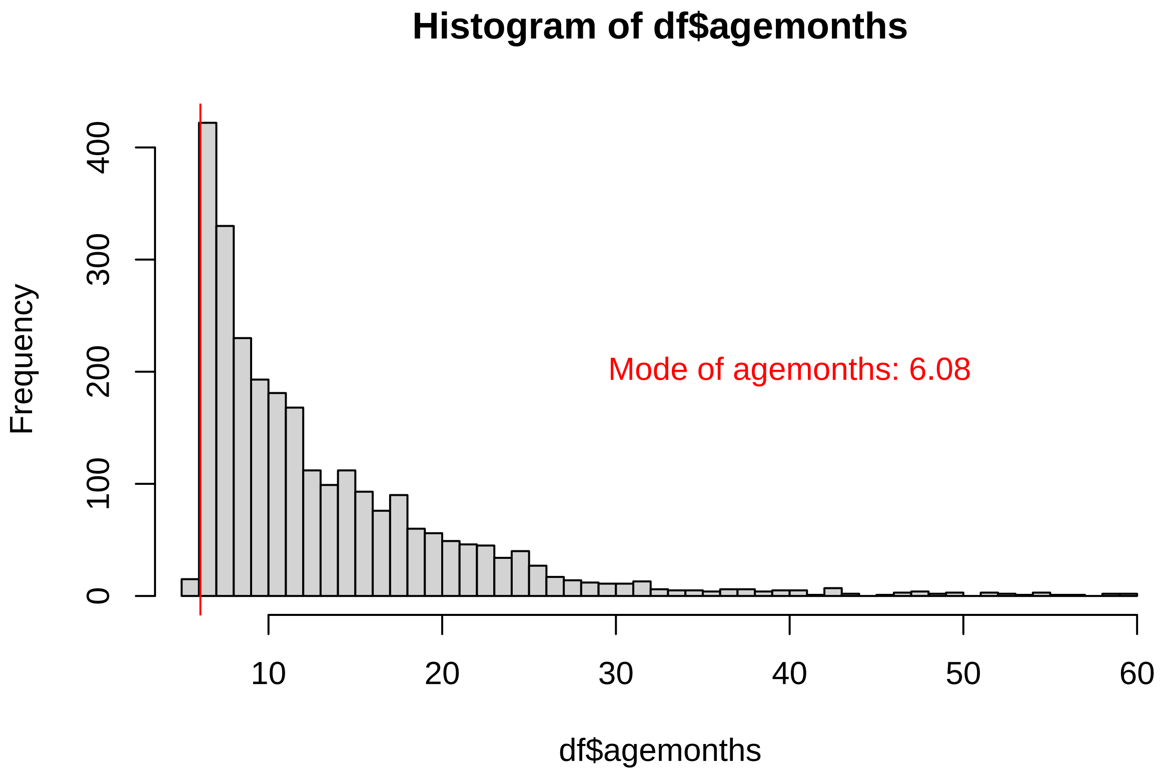
```r
median(df$agemonths, na.rm = T)
```

```
## [1] 10.7178
```

```r
sd(df$agemonths, na.rm = T)
```

```
## [1] 7.900913
```

```r
# no explicit function for the mode of a vector, but R allows you to make functions to suit whatever op
getmode <- function(x){
  uniquev <- unique(x)
  uniquev[which.max(tabulate(match(x, uniquev)))]
}
hist(df$agemonths, breaks = 50, xlim = c(min(df$agemonths, na.rm = T), max(df$agemonths, na.rm = T)))
abline(v = getmode(df$agemonths), col = "red")
text(x = 40, y = 200, paste0("Mode of agemonths: ", round(getmode(df$agemonths), 2)), col = "red")
```



```r
## REMEMBER: getmode is not an actual R function, it is made up for the purposes of displaying R's func

# some other useful aggregation functions. You can think or range as returning the results of min and m
range(df$agemonths, na.rm = T)
```

```
## [1]  5.621912 59.473907
```

```r
min(df$agemonths, na.rm = T)
```

```
## [1] 5.621912
```

```r
max(df$agemonths, na.rm = T)
```

```
## [1] 59.47391
```

```r
## skewness and kurtosis are from the "moments" package
skewness(df$agemonths, na.rm = T)
```

```
## [1] 2.149153
```

```r
kurtosis(df$agemonths, na.rm = T)
```

```
## [1] 9.280115
```

```r
quantile(df$agemonths, probs = c(.10, .25, .50, .75, .90), na.rm = T)
```

```
##       10%       25%       50%       75%       90%
##  6.542459  7.594512 10.717796 16.216421 22.921619
```

```r
# ?quantile()
```

Frequency table with row/column percentages

```r
# to make a table, use the table function. You can then input two vectors that you want to cross-tabula
mytable <- table(df$gender, df$edu)
mytable
```

```
##
##                    not documented none some primary completed primary
##   not documented                0    2            0                 0
##   female                        8  820          336                31
##   male                          6  597          238                28
##
##                    some secondary completed secondary more than secondary
##   not documented                1                   0                   0
##   female                      315                  11                   2
##   male                        247                  10                   1
```

```r
# tidyverse function that does the same thing. Input your data frame (df), and the variable that you wa
count(df, gender, sort = T)
```

```
## # A tibble: 3 x 2
##   gender              n
##   <fct>           <int>
## 1 female           1523
## 2 male             1127
## 3 not documented      3
```

```
# can also tabulate by multiple variables
count(df, gender, edu, sort =  T)
```

```
## # A tibble: 16 x 3
##    gender         edu                    n
##    <fct>          <fct>              <int>
##  1 female         none                 820
##  2 male           none                 597
##  3 female         some primary         336
##  4 female         some secondary       315
##  5 male           some secondary       247
##  6 male           some primary         238
##  7 female         completed primary     31
##  8 male           completed primary     28
##  9 female         completed secondary   11
## 10 male           completed secondary   10
## 11 female         not documented         8
## 12 male           not documented         6
## 13 not documented none                   2
## 14 female         more than secondary    2
## 15 not documented some secondary         1
## 16 male           more than secondary    1
```

```
# only needed if we haven't already defined labels for our variables
# rownames(mytable) = c("missing", "male", "female")
# colnames(mytable) = c("missing", "none", "primary school", "secondary school",
#                        "some high school", "some college", "graduate school")

# back to our original, base R tables:
# summarize table across rows with margin.table
margin.table(mytable, 1)
```

```
##
## not documented         female           male
##              3           1523           1127
```

```
# summarize table across columns
margin.table(mytable, 2)
```

```
##
##      not documented                none        some primary   completed primary
##                  14                1419                 574                  59
##      some secondary completed secondary more than secondary
##                 563                  21                   3
```

```r
# margin.table aggregates your data across the dimension that you provide (where 1 = sum across rows, a

# calculate row percentages
round(prop.table(mytable, 1), 2)
```

```
##
##                    not documented none some primary completed primary
##   not documented             0.00 0.67         0.00              0.00
##   female                     0.01 0.54         0.22              0.02
##   male                       0.01 0.53         0.21              0.02
##
##                    some secondary completed secondary more than secondary
##   not documented             0.33                0.00                0.00
##   female                     0.21                0.01                0.00
##   male                       0.22                0.01                0.00
```

```r
# calculate column percentages
round(prop.table(mytable, 2), 2)
```

```
##
##                    not documented none some primary completed primary
##   not documented             0.00 0.00         0.00              0.00
##   female                     0.57 0.58         0.59              0.53
##   male                       0.43 0.42         0.41              0.47
##
##                    some secondary completed secondary more than secondary
##   not documented             0.00                0.00                0.00
##   female                     0.56                0.52                0.67
##   male                       0.44                0.48                0.33
```

```r
# prop.table calculates row and column percentages, based on the dimension you give it (1 = row percent
# the round function is just there to reduce the number of significant figures we keep
```

Convert continuous to categorical variables with if/then statements

```r
## tidyverse version. ifelse is a vectorized if/else statement, meaning it applies if/else logic across
df_cat <- df %>%
  mutate(hfias_cat = ifelse(hfias_score < 1, 4,
                            ifelse(hfias_score >= 1 & hfias_score < 10, 3,
                                   ifelse(hfias_score >= 10 & hfias_score < 14, 2,
                                          ifelse(hfias_score >= 14, 1, NA)))),
         hfias_cat = factor(hfias_cat))


## base r version. We are indexing all of the columns where our conditions are satisfied, and assigning
df$hfias_cat[df$hfias_score < 1] <- 4
df$hfias_cat[df$hfias_score >= 1 & df$hfias_score < 10] <- 3
df$hfias_cat[df$hfias_score >= 10 & df$hfias_score < 14] <- 2
```

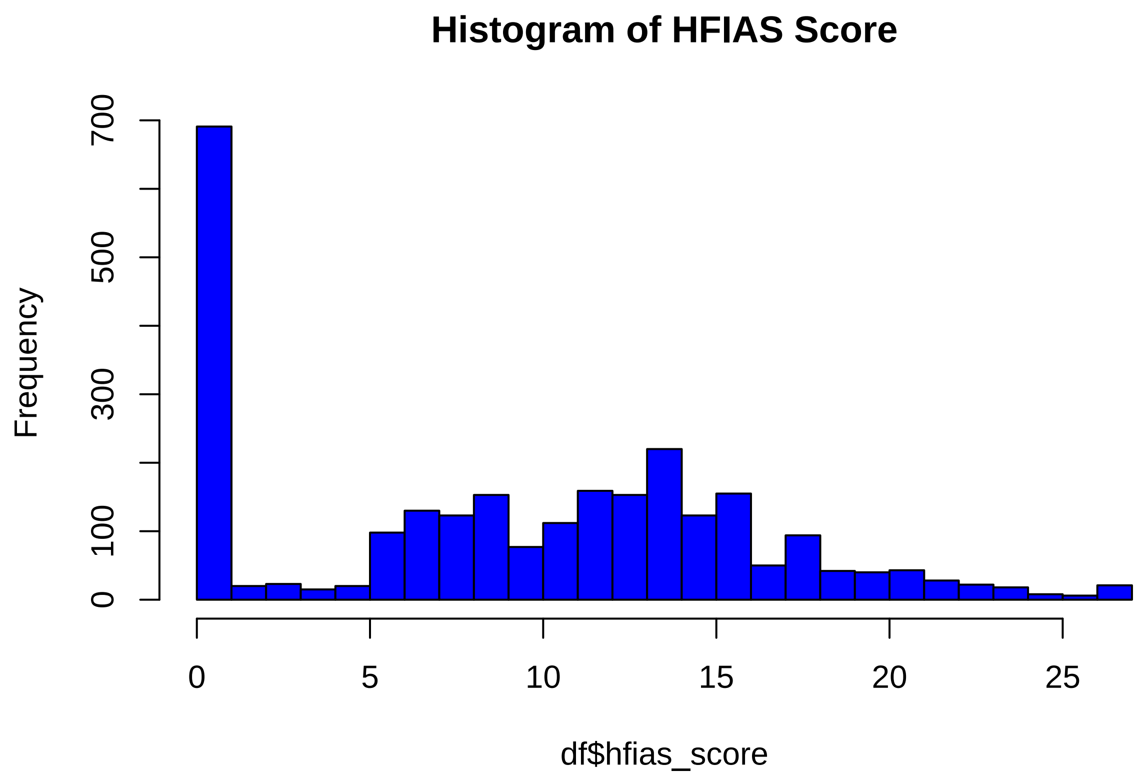
```r
df$hfias_cat[df$hfias_score >= 14] <- 1

## save your output as a permanent RData file with the save function
save(df_cat, file = "../output/output_df.RData")

## or save as a csv
write.csv(df_cat, file = "../output/output_df.csv")

## csv files are more memory intensive than RData files, so if you are working with large data sets, us
```

Producing a histogram to inspect variables

```r
n_distinct(df$hfias_score)
```

```
## [1] 29
```

```r
## use breaks to specify the number of bins you want in your histogram.
hist(df$hfias_score, breaks = 29, main = "Histogram of HFIAS Score",
     freq = TRUE, col = "blue")
```



```
# as each score has its own bin, this is technically a barplot, just made with the hist() function
```

Comparison tests (t-test and Wilcoxon)

```
df_ttest <- df[df$gender == "female" | df$gender == "male",]

# simple unpaired t test
t.test(df_ttest$av_len ~ df_ttest$gender, conf.level = 0.95, paired = FALSE, var.equal = FALSE)
```

```
##
##  Welch Two Sample t-test
##
## data:  df_ttest$av_len by df_ttest$gender
## t = -5.4411, df = 2337.4, p-value = 5.848e-08
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -1.7902305 -0.8416832
## sample estimates:
## mean in group female   mean in group male
##             67.46464             68.78060
```

```
# simple Wilcoxon rank sum
wilcox.test(df_ttest$av_len ~ df_ttest$gender, conf.int = T, conf.level = 0.95, exact = F,
            correct = T)
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  df_ttest$av_len by df_ttest$gender
## W = 736851, p-value = 8.454e-10
## alternative hypothesis: true location shift is not equal to 0
## 95 percent confidence interval:
##  -1.7500611 -0.9000049
## sample estimates:
## difference in location
##              -1.300048
```

Measures of association (pearson vs. spearman)

```
mean(df$av_len, na.rm = T)
```

```
## [1] 68.02908
```

```r
# pearson correlation
p_corr <- cor(df$av_weight, df$av_len, use = "complete.obs", method = c("pearson"))
# spearman correlation
s_corr <- cor(df$av_weight, df$av_len, use = "complete.obs", method = c("spearman"))
p_corr
```

```
## [1] 0.9449736
```

```r
s_corr
```

```
## [1] 0.9309364
```

Simple Linear Regression

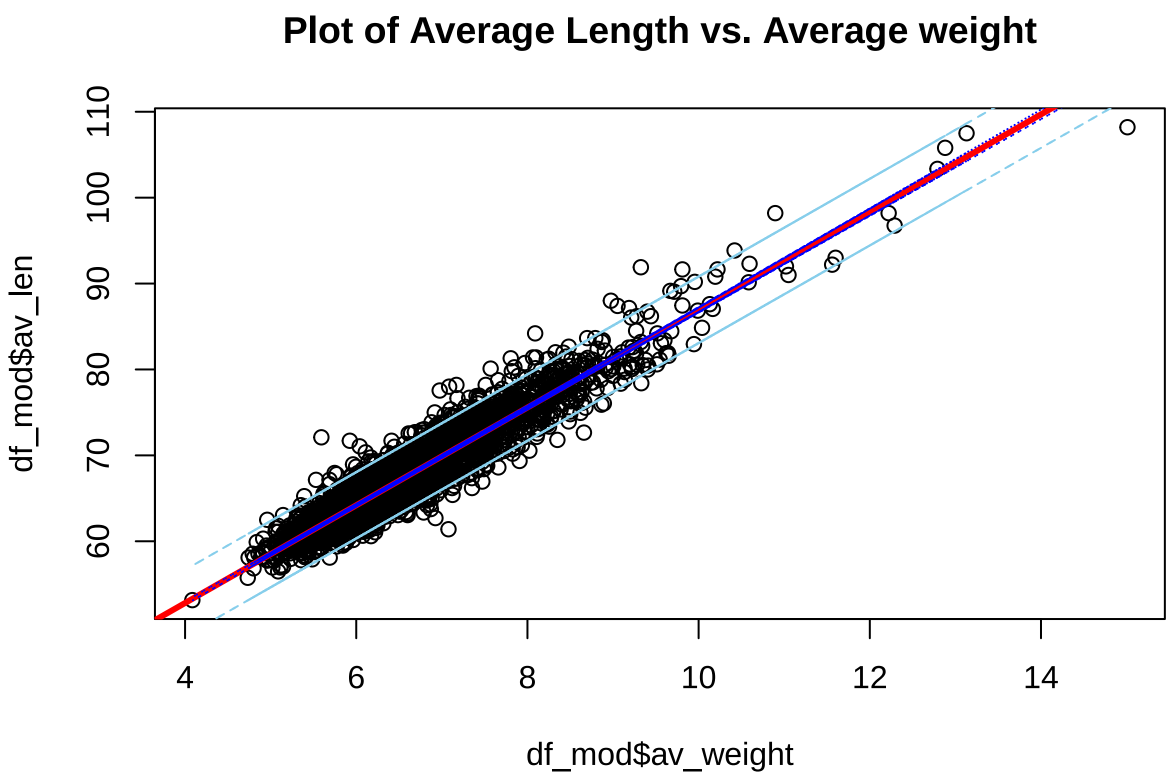
```r
## using complete observations for the sake of simplicity
df_mod <- df[complete.cases(df),]

# model of average length compared to weight
length_model <- lm(av_len ~ av_weight, data = df_mod)
summary(length_model) # get description of model
```

```
##
## Call:
## lm(formula = av_len ~ av_weight, data = df_mod)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -8.9180 -1.2868 -0.0845  1.2361 10.2290
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 30.05976    0.25404   118.3   <2e-16 ***
## av_weight    5.68820    0.03765   151.1   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.967 on 2621 degrees of freedom
## Multiple R-squared:  0.897,  Adjusted R-squared:  0.897
## F-statistic: 2.283e+04 on 1 and 2621 DF,  p-value: < 2.2e-16
```

```r
# calculate prediction intervals for your model
pred_ints <- predict(length_model, interval = "prediction", level = 0.95)
```

```
## Warning in predict.lm(length_model, interval = "prediction", level = 0.95): predictions on current da
```

```r
# calculate confidence intervals as well
conf_ints <- predict(length_model, interval = "confidence", level = 0.95)

# plot model with prediction and confidence intervals, along with model fit
plot(df_mod$av_weight, df_mod$av_len, main = "Plot of Average Length vs. Average weight")
abline(length_model, col = "red", lwd = 3)
lines(df_mod$av_weight, pred_ints[,2], col = "skyblue", lty = 2)
lines(df_mod$av_weight, pred_ints[,3], col = "skyblue", lty = 2)
lines(df_mod$av_weight, conf_ints[,2], col = "blue", lty = 3)
lines(df_mod$av_weight, conf_ints[,3], col = "blue", lty = 3)
```



Multivariable Linear Regression

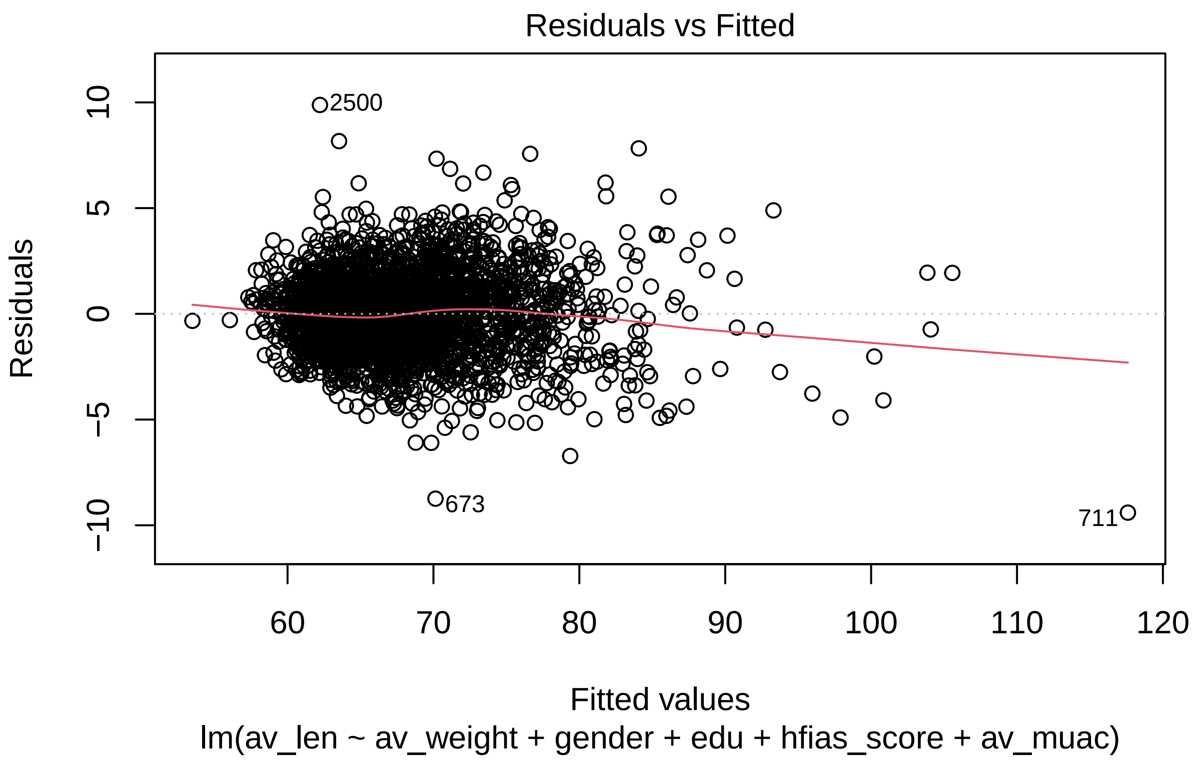
```r
library(car)
library(MASS)
library(corrplot)

# if you want to look at the correlations between variables
# corrplot(cor(df_mod[c("av_len", "av_weight", "hfias_score", "av_muac")], method = "pearson"))

mv_length_model <- lm(av_len ~ av_weight + gender + edu + hfias_score + av_muac, data = df_mod)
summary(mv_length_model)
```

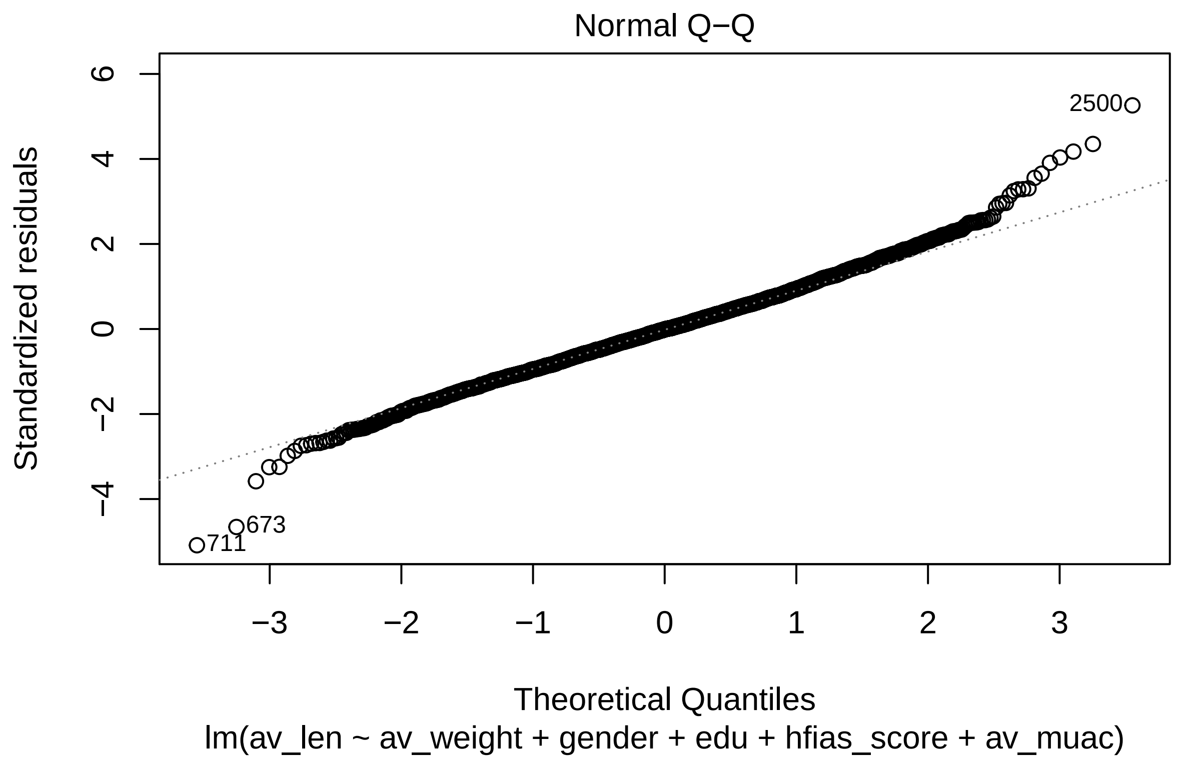
```
##
## Call:
## lm(formula = av_len ~ av_weight + gender + edu + hfias_score +
##     av_muac, data = df_mod)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -9.4016 -1.1998 -0.0151  1.1311  9.8783
##
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)
## (Intercept)            54.461058   1.741776  31.268  < 2e-16 ***
## av_weight               5.898436   0.038474 153.311  < 2e-16 ***
## gendermale             -0.321876   0.075036  -4.290 1.85e-05 ***
## edunone                 0.586457   0.524135   1.119    0.263
## edusome primary         0.630966   0.528072   1.195    0.232
## educompleted primary    0.715381   0.577402   1.239    0.215
## edusome secondary       0.601719   0.528418   1.139    0.255
## educompleted secondary  0.685406   0.664244   1.032    0.302
## edumore than secondary  0.413619   1.204779   0.343    0.731
## hfias_score             0.007117   0.005307   1.341    0.180
## av_muac                -2.200577   0.143265 -15.360  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.88 on 2612 degrees of freedom
## Multiple R-squared:  0.9063, Adjusted R-squared:  0.9059
## F-statistic:  2527 on 10 and 2612 DF,  p-value: < 2.2e-16
```

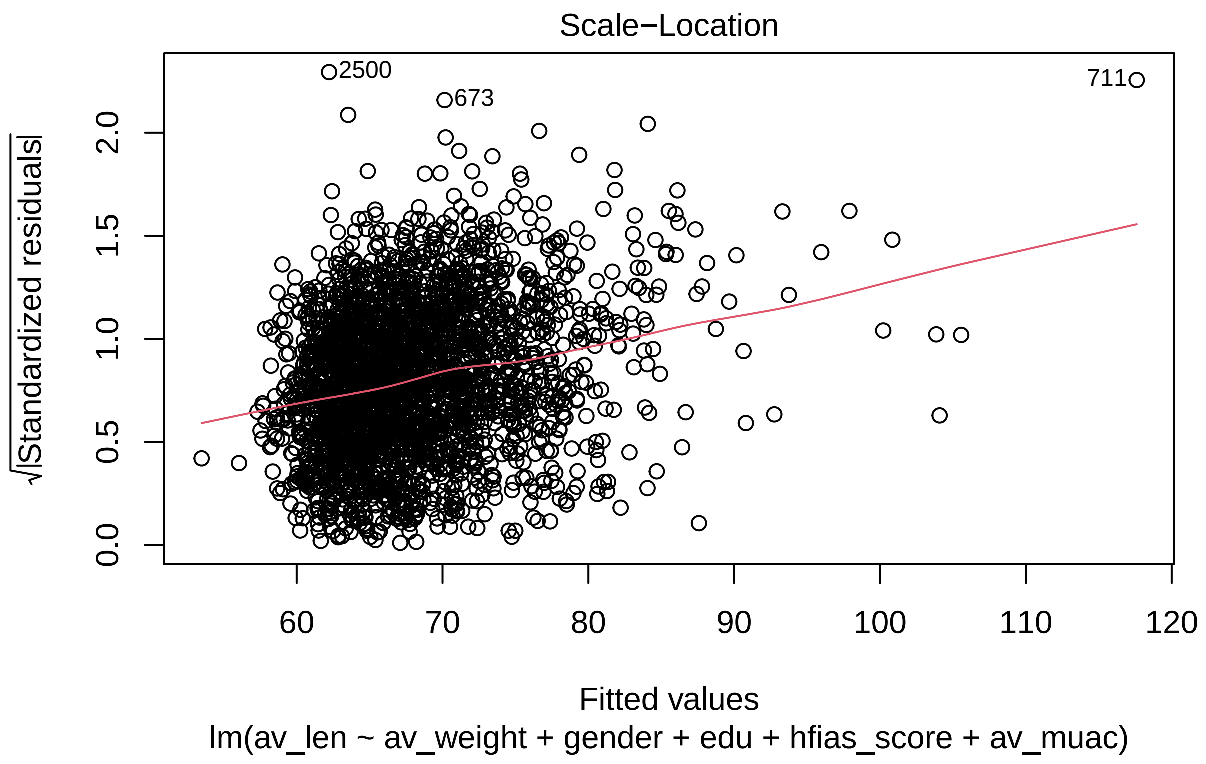
```
## to check linear model assumptions
vif(mv_length_model) # variance inflation factor
```

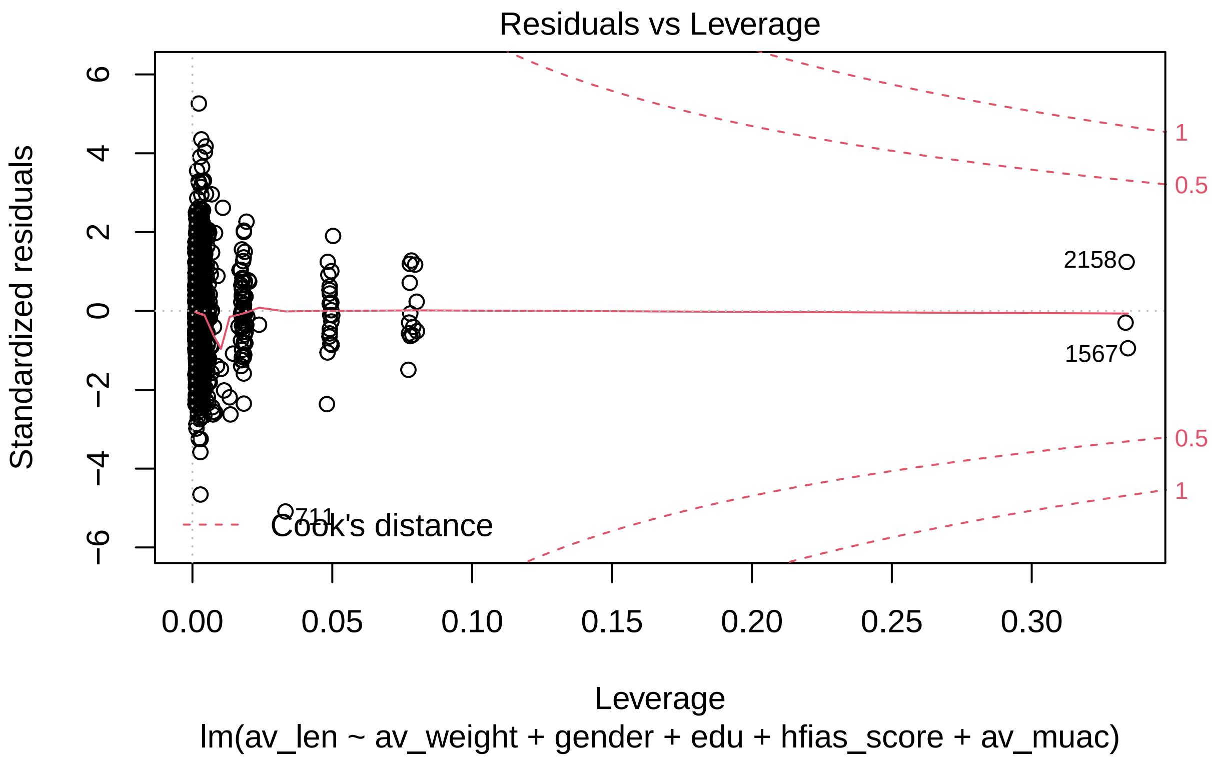
```
##                 GVIF Df GVIF^(1/(2*Df))
## av_weight   1.144008  1        1.069583
## gender      1.021336  1        1.010612
## edu         1.035453  6        1.002907
## hfias_score 1.032338  1        1.016041
## av_muac     1.119802  1        1.058207
```

```
plot(mv_length_model) # plots residuals vs fitted, normal q-q, cook's distance, and std residuals
```

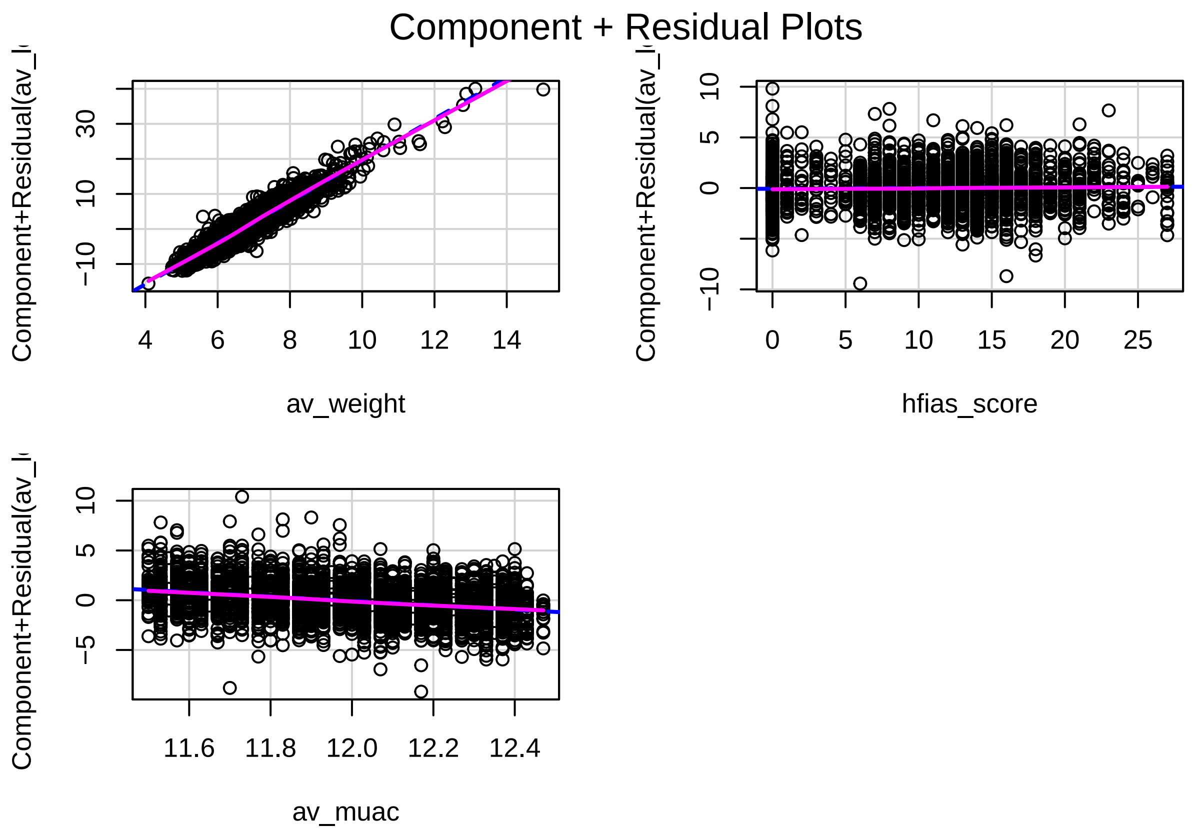

Residuals vs Fitted
Residuals
Fitted values
lm(av_len ~ av_weight + gender + edu + hfias_score + av_muac)
2500
673
711
10
5
0
−5
−10
60
70
80
90
100
110
120


Normal Q−Q
Standardized residuals
Theoretical Quantiles
lm(av_len ~ av_weight + gender + edu + hfias_score + av_muac)
2500
673
711
6
4
2
0
−2
−4
−3
−2
−1
0
1
2
3


Scale−Location
2500
673
711
$\sqrt{|\text{Standardized residuals}|}$
0.0
0.5
1.0
1.5
2.0
60
70
80
90
100
110
120
Fitted values
lm(av_len ~ av_weight + gender + edu + hfias_score + av_muac)



```
crPlots(mv_length_model, terms = ~av_weight + hfias_score + av_muac, smooth = T)
```



```
# shows the smoothed relationship of each variable with the outcome of interest
```