Data Science Project

For our analysis and the R programming, we will make use of the following R packages:

```
library(dplyr)   # Easy data cleaning, and the very convenient pipe operator <
library(ggplot2) # Beautiful plots
library(mgcv)    # Package to fit generalized additive models
```

```
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


Loading required package: nlme


Attaching package: ‘nlme’


The following object is masked from ‘package:dplyr’:

    collapse


This is mgcv 1.8-40. For overview type 'help("mgcv-package")'.
```

A basic data science project consists of the following six steps:

1. **State the problem** you are trying to solve. It has to be an unambiguous question that can be answered with data and a statistical or machine learning model. At least, specify: What is being observed? What has to be predicted?
2. **Collect the data**, then clean and prepare it. This is commonly the most time-consuming task, but it has to be done in order to fit a prediction model with the data.
3. **Explore the data.** Get to know its properties and quirks. Check numerical summaries of your metric variables, tables of the categorical data, and plot univariate and multivariate representations of your variables. By this, you also get an overview of the quality of the data and can find outliers.
4. **Check if any variables may need to be transformed.** Most commonly, this is a logarithmic transformation of skewed measurements such as concentrations or times. Also, some variables might have to be split up into two or more variables.

5. **Choose a model and train it on the data.** If you have more than one candidate model, apply each and evaluate their goodness-of-fit using independent data that was not used for training the model.

6. **Use the best model to make your final predictions.**

```
data(rivers)
ls()
```

```
'avgpm25' · 'awake_only' · 'filename' · 'msleep' · 'msleep10' · 'msleep5' · 'mtcars' · 'mtcars_data' ·
'plants_data' · 'rivers' · 'sleepData' · 'url'
```

```
data()
```

```
summary(rivers)
sd(rivers)
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
  135.0   310.0   425.0   591.2   680.0  3710.0 
493.87084203459
```

```
dim(rivers)
```

```
NULL
```

```
getwd()
dir()
```

```
'/content'
'avgpm25.csv' · 'sample_data'
```

```
avgpm25<-read.csv('avgpm25.csv')
class(avgpm25)
dim(avgpm25)
```

```
'data.frame'
576 · 5
```

```
str(avgpm25)
```

```
'data.frame':	576 obs. of  5 variables:
 $ pm25     : num  9.77 9.99 10.69 11.34 12.12 ...
 $ fips     : int  1003 1027 1033 1049 1055 1069 1073 1089 1097 1103 ...
 $ region   : chr  "east" "east" "east" "east" ...
 $ longitude: num  -87.7 -85.8 -87.7 -85.8 -86 ...
 $ latitude : num  30.6 33.3 34.7 34.5 34 ...
< table of extent 0 >
```

```
nrow(avgpm25)
ncol(avgpm25)
```

```
object.size(avgpm25)
names(avgpm25)
head(avgpm25)
summary(avgpm25)
table(avgpm25$region)
```

576

5

```
22088 bytes
```

'pm25' · 'fips' · 'region' · 'longitude' · 'latitude'

A data.frame: 6 × 5

	pm25	fips	region	longitude	latitude
	<dbl>	<int>	<chr>	<dbl>	<dbl>
1	9.771185	1003	east	-87.74826	30.59278
2	9.993817	1027	east	-85.84286	33.26581
3	10.688618	1033	east	-87.72596	34.73148
4	11.337424	1049	east	-85.79892	34.45913
5	12.119764	1055	east	-86.03212	34.01860
6	10.827805	1069	east	-85.35039	31.18973

```
      pm25             fips          region            longitude      
 Min.   : 3.383   Min.   : 1003   Length:576         Min.   :-158.04  
 1st Qu.: 8.549   1st Qu.:16038   Class :character   1st Qu.: -97.38  
 Median :10.047   Median :28034   Mode  :character   Median : -87.37  
 Mean   : 9.836   Mean   :28431                      Mean   : -91.65  
 3rd Qu.:11.356   3rd Qu.:41045                      3rd Qu.: -80.72  
 Max.   :18.441   Max.   :56039                      Max.   : -68.26  
    latitude    
 Min.   :19.68  
 1st Qu.:35.30  
 Median :39.09  
 Mean   :38.56  
 3rd Qu.:41.75  
 Max.   :64.82  

east west 
 442  134 
```

```
install.packages('downloader')
```

```
Installing package into ‘/usr/local/lib/R/site-library’
(as ‘lib’ is unspecified)
```

```
library(downloader)
```

```
url <- "https://raw.githubusercontent.com/genomicsclass/dagdata/master/inst/extdata/msleep_
filename <- "msleep_ggplot2.csv"
if (!file.exists(filename)) download(url,filename)
msleep <- read.csv("msleep_ggplot2.csv")
```

```
names(msleep)
```

'name' · 'genus' · 'vore' · 'order' · 'conservation' · 'sleep_total' · 'sleep_rem' · 'sleep_cycle' · 'awake' · 'brainwt' · 'bodywt'

```
head(msleep,2)
tail(msleep,2)
```

A data.frame: 2 × 11

	name	genus	vore	order	conservation	sleep_total	sleep_rem	sleep_cyc
	<chr>	<chr>	<chr>	<chr>	<chr>	<dbl>	<dbl>	<db
1	Cheetah	Acinonyx	carni	Carnivora	lc	12.1	NA	N
2	Owl monkey	Aotus	omni	Primates	NA	17.0	1.8	N

A data.frame: 2 × 11

	name	genus	vore	order	conservation	sleep_total	sleep_rem	sleep_cycle
	<chr>	<chr>	<chr>	<chr>	<chr>	<dbl>	<dbl>	<dbl>
82	Arctic fox	Vulpes	carni	Carnivora	NA	12.5	NA	NA

```
str(msleep)
```

```
'data.frame':	83 obs. of  11 variables:
 $ name        : chr  "Cheetah" "Owl monkey" "Mountain beaver" "Greater short-tailed
 $ genus       : chr  "Acinonyx" "Aotus" "Aplodontia" "Blarina" ...
 $ vore        : chr  "carni" "omni" "herbi" "omni" ...
 $ order       : chr  "Carnivora" "Primates" "Rodentia" "Soricomorpha" ...
 $ conservation: chr  "lc" NA "nt" "lc" ...
 $ sleep_total : num  12.1 17 14.4 14.9 4 14.4 8.7 7 10.1 3 ...
 $ sleep_rem   : num  NA 1.8 2.4 2.3 0.7 2.2 1.4 NA 2.9 NA ...
 $ sleep_cycle : num  NA NA NA 0.133 0.667 ...
 $ awake       : num  11.9 7 9.6 9.1 20 9.6 15.3 17 13.9 21 ...
 $ brainwt     : num  NA 0.0155 NA 0.00029 0.423 NA NA NA 0.07 0.0982 ...
 $ bodywt      : num  50 0.48 1.35 0.019 600 ...
```

```
awake_only<-msleep$awake
head(awake_only,20)
summary(msleep$awake)
table(msleep$conservation)
```

11.9 · 7 · 9.6 · 9.1 · 20 · 9.6 · 15.3 · 17 · 13.9 · 21 · 18.7 · 14.6 · 14 · 11.5 · 13.7 · 15.7 · 14.9 · 6.6 · 18.7 · 6

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
   4.10   10.25   13.90   13.57   16.15   22.10 
```

```
          cd domesticated           en           lc           nt           vu 
           2           10            4           27            4            7 
```

```
summary(msleep)
```

```
    name               genus               vore               order          
Length:83          Length:83          Length:83          Length:83         
Class :character   Class :character   Class :character   Class :character  
Mode  :character   Mode  :character   Mode  :character   Mode  :character  
                                                                           
                                                                           
                                                                           
                                                                           
conservation        sleep_total      sleep_rem      sleep_cycle    
Length:83          Min.   : 1.90   Min.   :0.100   Min.   :0.1167  
Class :character   1st Qu.: 7.85   1st Qu.:0.900   1st Qu.:0.1833  
Mode  :character   Median :10.10   Median :1.500   Median :0.3333  
                   Mean   :10.43   Mean   :1.875   Mean   :0.4396  
                   3rd Qu.:13.75   3rd Qu.:2.400   3rd Qu.:0.5792  
                   Max.   :19.90   Max.   :6.600   Max.   :1.5000  
                                   NA's   :22      NA's   :51      
    awake          brainwt            bodywt        
Min.   : 4.10   Min.   :0.00014   Min.   :   0.005  
1st Qu.:10.25   1st Qu.:0.00290   1st Qu.:   0.174  
Median :13.90   Median :0.01240   Median :   1.670  
Mean   :13.57   Mean   :0.28158   Mean   : 166.136  
3rd Qu.:16.15   3rd Qu.:0.12550   3rd Qu.:  41.750  
Max.   :22.10   Max.   :5.71200   Max.   :6654.000  
                NA's   :27                          
```

```
msleep10 <- select(msleep, -sleep_cycle)
```

```
dim(msleep10)
names(msleep10)
```

83 · 10
'name' · 'genus' · 'vore' · 'order' · 'conservation' · 'sleep_total' · 'sleep_rem' · 'awake' · 'brainwt' · 'bodywt'

```
msleep5 <- select(msleep, -c('name','genus','vore','order','conservation','sleep_cycle'))
```

```
dim(msleep5)
names(msleep5)
```

83 · 5
'sleep_total' · 'sleep_rem' · 'awake' · 'brainwt' · 'bodywt'

```
sleepData <- select(msleep, name, sleep_total)
```

```
str(msleep)
```

```
'data.frame':	83 obs. of  11 variables:
 $ name        : chr  "Cheetah" "Owl monkey" "Mountain beaver" "Greater short-tailed
 $ genus       : chr  "Acinonyx" "Aotus" "Aplodontia" "Blarina" ...
 $ vore        : chr  "carni" "omni" "herbi" "omni" ...
 $ order       : chr  "Carnivora" "Primates" "Rodentia" "Soricomorpha" ...
 $ conservation: chr  "lc" NA "nt" "lc" ...
 $ sleep_total : num  12.1 17 14.4 14.9 4 14.4 8.7 7 10.1 3 ...
 $ sleep_rem   : num  NA 1.8 2.4 2.3 0.7 2.2 1.4 NA 2.9 NA ...
 $ sleep_cycle : num  NA NA NA 0.133 0.667 ...
 $ awake       : num  11.9 7 9.6 9.1 20 9.6 15.3 17 13.9 21 ...
 $ brainwt     : num  NA 0.0155 NA 0.00029 0.423 NA NA NA 0.07 0.0982 ...
 $ bodywt      : num  50 0.48 1.35 0.019 600 ...
'data.frame':	83 obs. of  2 variables:
 $ name       : chr  "Cheetah" "Owl monkey" "Mountain beaver" "Greater short-tailed s
 $ sleep_total: num  12.1 17 14.4 14.9 4 14.4 8.7 7 10.1 3 ...
```

```
str(sleepData)
```

```
'data.frame':	83 obs. of  2 variables:
 $ name       : chr  "Cheetah" "Owl monkey" "Mountain beaver" "Greater short-tailed s
 $ sleep_total: num  12.1 17 14.4 14.9 4 14.4 8.7 7 10.1 3 ...
```

```
head(select(msleep, -c('name','bodywt','vore')))
```

A data.frame: 6 × 8

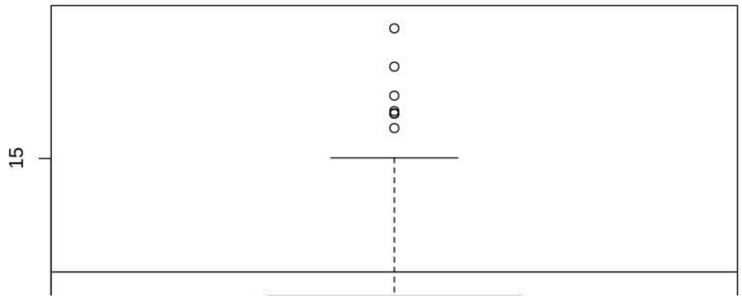
	genus	order	conservation	sleep_total	sleep_rem	sleep_cycle	awake
	<chr>	<chr>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>
1	Acinonyx	Carnivora	lc	12.1	NA	NA	11.9
2	Aotus	Primates	NA	17.0	1.8	NA	7.0
3	Aplodontia	Rodentia	nt	14.4	2.4	NA	9.6
4	Blarina	Soricomorpha	lc	14.9	2.3	0.1333333	9.1
5	Bos	Artiodactyla	domesticated	4.0	0.7	0.6666667	20.0
6	Bradypus	Pilosa	NA	14.4	2.2	0.7666667	9.6

```
ls()
summary(avgpm25$pm25)
```

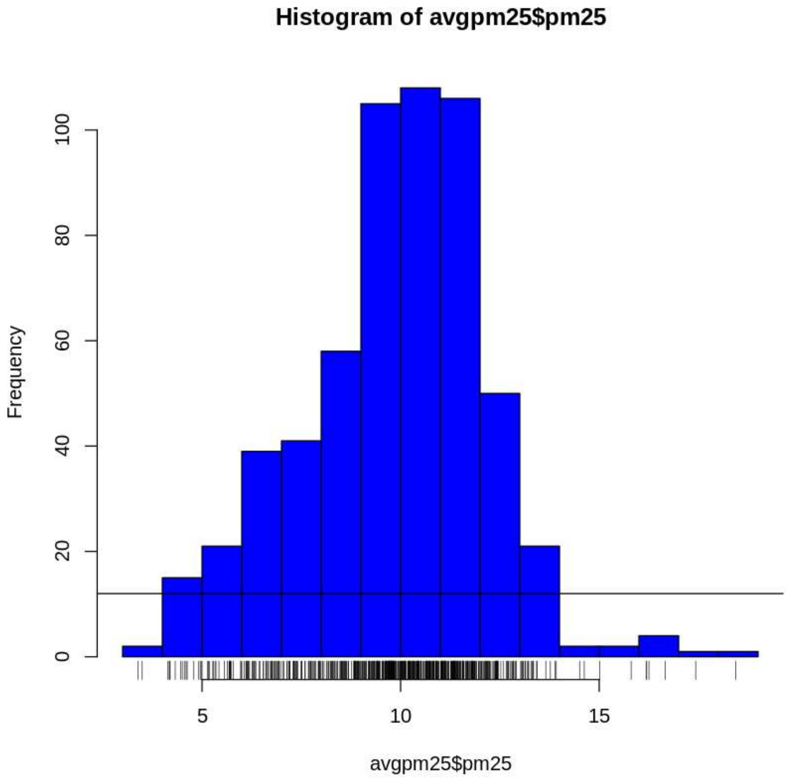
'avgpm25' · 'awake_only' · 'filename' · 'msleep' · 'msleep10' · 'msleep5' · 'mtcars' · 'mtcars_data' · 'plants_data' · 'rivers' · 'sleepData' · 'url'

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
  3.383   8.549  10.047   9.836  11.356  18.441 
```

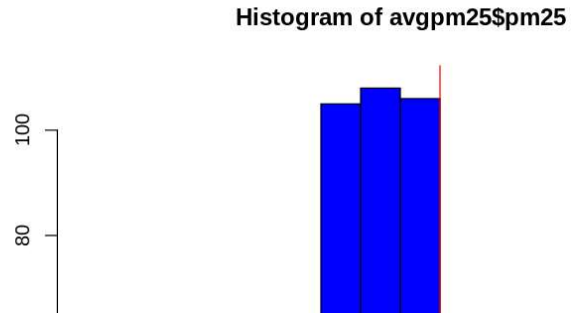
```
boxplot(avgpm25$pm25, col='red')
abline(h=12)
```



```
hist(avgpm25$pm25,col='blue')
rug(avgpm25$pm25)
```

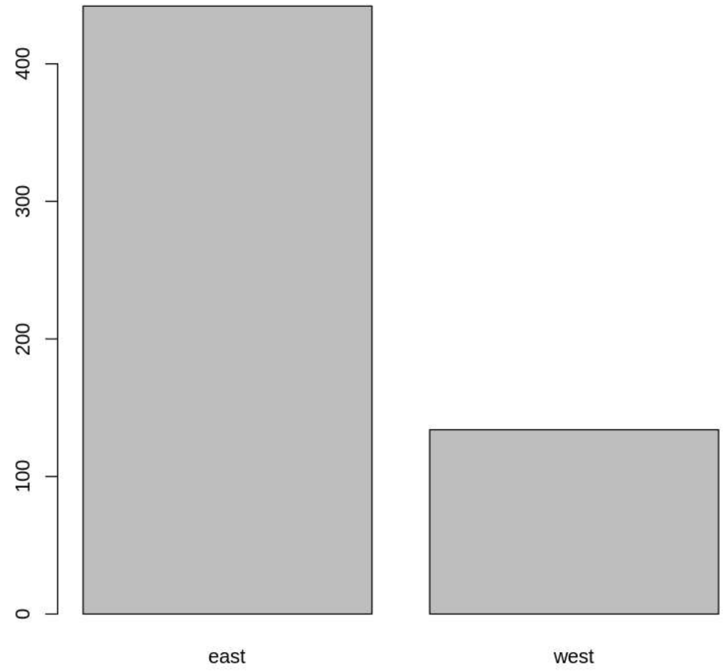


```
hist(avgpm25$pm25,col='blue')
rug(avgpm25$pm25)
abline(v=12, col='red')
```



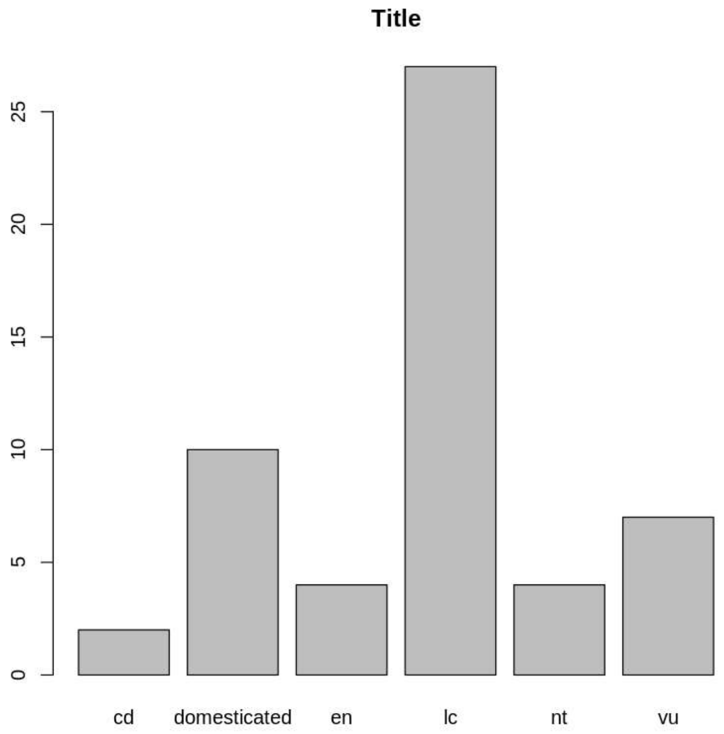
```
barplot(table(avgpm25$region))
table(avgpm25$region)
```

```
east west 
 442  134 
```



```
barplot(table(msleep$conservation), main="Title")
table(msleep$conservation)
```

```
          cd domesticated           en           lc           nt           vu
           2           10            4           27            4            7
```



✓ 2s completed at 01:57