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0Data Science Live Book



Data Science Live Book

An intuitive and practical approach in data analysis, data preparation and predictive modeling, suitable for all ages!

by Pablo Casas

0.1A book to learn data science, data analysis and machine learning, suitable for all ages!

0.1.1Last update: 2017-04-21

0.2*What does it cover?*

This live book (`#dsLiveBook`) covers common aspects in predictive modeling:

- A. Exploratory Data Analysis
- B. Data Preparation
- C. Selecting Best Variables
- D. Scoring Data
- E. Assessing Model Performance

0.3Upcoming updates

More info about methodological aspects in data preparation.

0.4What programming language do I need?

Most of the concepts are independent from the language, the focus is on general concepts. But when technical example is required it is done in [R language](#), using the `funModeling` package which you can install by doing: `install.packages("funModeling")`

0.5Book Focus

- **Stimulate intuition** behind concepts: The explanation of how to interpret results brings a deeper understanding of **what is being done**, boosting the freedom to use that knowledge in other situations regardless of the language.
- Regarding technical aspects.... model creation consumes around **10%** of almost any predictive modeling project; the **Live Book** and `funModeling` will try to cover remaining 90%.

Why a live book ? Hopefully this book barely has an end, it will be updated periodically. And you can contribute! below the github link.

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1.1 Profiling Data

1.1 What is this about?

Quantity of zeros, NA, Inf, unique values; as well as the data type may lead to a good or bad model. Here's an approach to cover the very first step in data modeling.

```
## Loading funModeling !  
library(funModeling)  
library(dplyr)  
data(heart_disease)
```

1.1 Checking NA, zeros, data type and unique values

```
my_data_status=df_status(heart_disease)
```

```
##          variable q_zeros p_zeros q_na p_na q_inf p_inf   type
## 1             age      0    0.00  0 0.00  0    0 integer
## 2             gender      0    0.00  0 0.00  0    0  factor
## 3         chest_pain      0    0.00  0 0.00  0    0  factor
## 4 resting_blood_pressure      0    0.00  0 0.00  0    0 integer
## 5      serum_cholesterol      0    0.00  0 0.00  0    0 integer
## 6   fasting_blood_sugar    258  85.15  0 0.00  0    0  factor
## 7      resting_electro    151  49.83  0 0.00  0    0  factor
## 8         max_heart_rate      0    0.00  0 0.00  0    0 integer
## 9             exer_angina    204  67.33  0 0.00  0    0 integer
## 10             oldpeak      99  32.67  0 0.00  0    0 numeric
## 11             slope      0    0.00  0 0.00  0    0 integer
## 12   num_vessels_flour    176  58.09  4 1.32  0    0 integer
## 13             thal      0    0.00  2 0.66  0    0  factor
## 14 heart_disease_severity    164  54.13  0 0.00  0    0 integer
## 15             exer_angina    204  67.33  0 0.00  0    0  factor
## 16   has_heart_disease      0    0.00  0 0.00  0    0  factor
##   unique
## 1      41
## 2       2
## 3       4
## 4      50
## 5     152
## 6       2
## 7       3
## 8      91
## 9       2
## 10     40
## 11      3
## 12      4
## 13      3
## 14      5
## 15      2
## 16      2
```

- `q_zeros` : quantity of zeros (`p_zeros` : in percentage)
- `q_inf` : quantity of infinite values (`p_inf` : in percentage)
- `q_na` : quantity of NA (`p_na` : in percentage)
- `type` : factor or numeric
- `unique` : quantity of unique values

1.0.1 Why are these metrics important?

- **Zeros**: Variables with **lots of zeros** may be not useful for modeling, and in some cases it may dramatically bias the model.
- **NA**: Several models automatically exclude rows with NA (**random forest**, for

example). As a result, the final model can be biased due to several missing rows because of only one variable. For example, if the data contains only one out of 100 variables with 90% of NAs, the model will be training with only 10% of original rows.

- **Inf:** Infinite values may lead to an unexpected behavior in some functions in R.
- **Type:** Some variables are encoded as numbers, but they are codes or categories, and the models **don't handle them** in the same way.
- **Unique:** Factor/categorical variables with a high number of different values (~30), tend to do overfitting if categories have low cardinality, (**decision trees**, for example).

1.0.2 Filtering unwanted cases

The function `df_status` takes a data frame and returns a the status table to quickly remove unwanted cases.

Removing variables with high number of NA/zeros

```
# Removing variables with 60% of zero values
vars_to_remove=filter(my_data_status, p_zeros > 60) %>% .$variable
vars_to_remove
```

```
## [1] "fasting_blood_sugar" "exer_angina"          "exter_angina"
```

```
## Keeping all columns except vars_to_remove
heart_disease_2=select(heart_disease, -one_of(vars_to_remove))
```

Ordering data by percentage of zeros

```
arrange(my_data_status, -p_zeros) %>% select(variable, q_zeros, p_zeros)
```

```
##           variable q_zeros p_zeros
## 1   fasting_blood_sugar    258  85.15
## 2         exer_angina    204  67.33
## 3         exter_angina    204  67.33
## 4   num_vessels_flour    176  58.09
## 5 heart_disease_severity    164  54.13
## 6   resting_electro    151  49.83
## 7         oldpeak     99  32.67
## 8         age         0    0.00
## 9         gender         0    0.00
## 10        chest_pain         0    0.00
## 11 resting_blood_pressure         0    0.00
## 12   serum_cholesterol         0    0.00
## 13        max_heart_rate         0    0.00
## 14         slope         0    0.00
## 15         thal         0    0.00
## 16   has_heart_disease         0    0.00
```

1.1 Profiling categorical variable

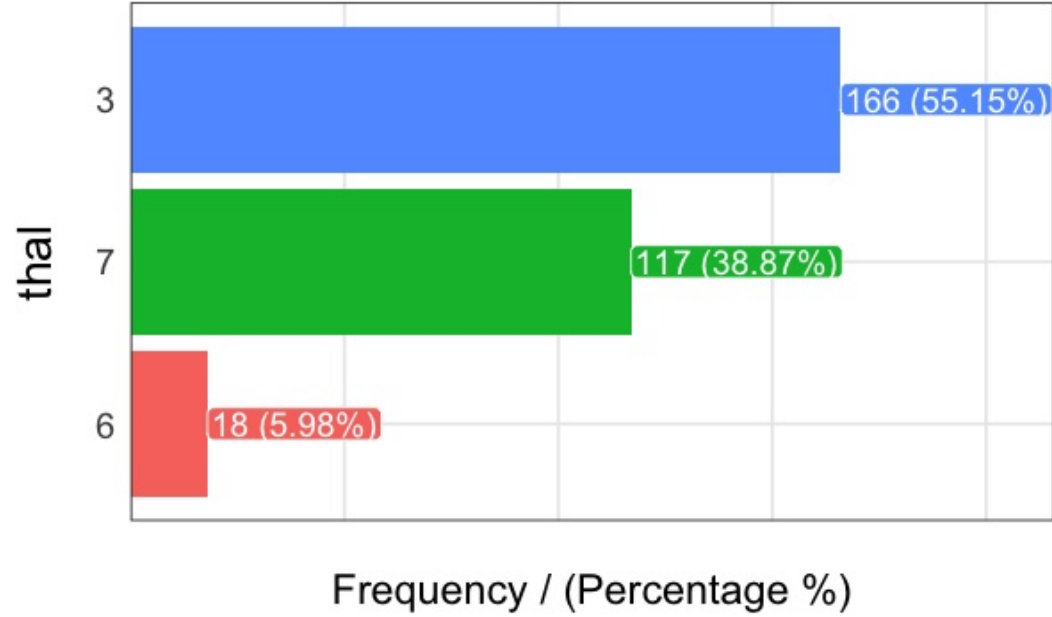
Make sure you have the latest funModeling version (≥ 1.3).

Frequency or distribution analysis is made simple by the `freq` function. It retrieves the distribution in a table and a plot (by default) which shows the distribution in absolute and relative numbers.

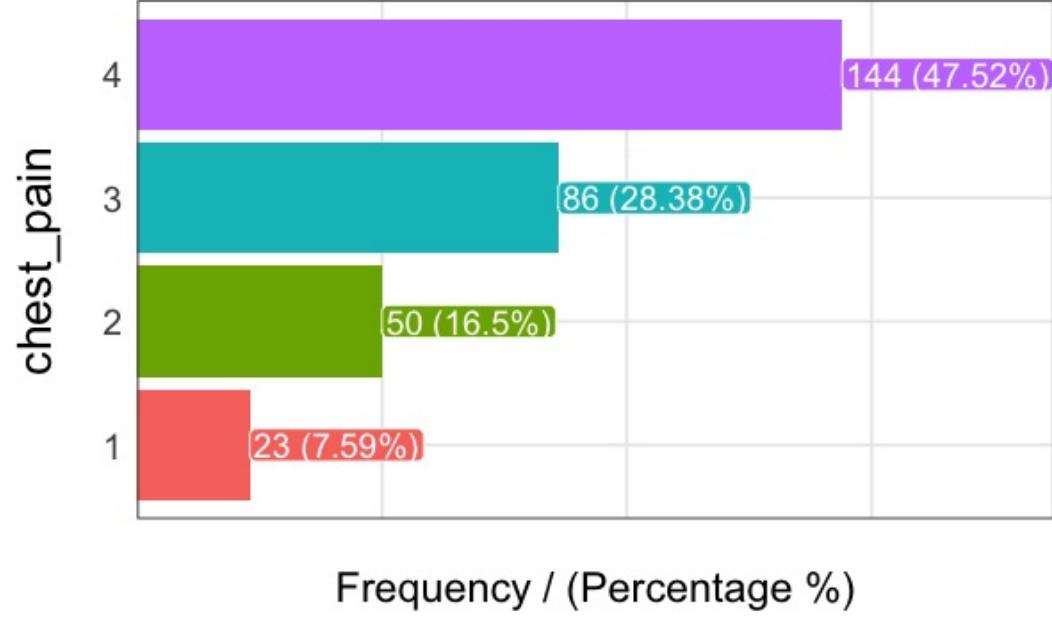
If you want the distribution for two variables:

```
freq(data=heart_disease, str_input = c('thal', 'chest_pain'))
```

```
## Warning in if (is.na(str_input)) {: the condition has length > 1 and only
## the first element will be used
```

```
##      thal frequency percentage cumulative_perc
## 1      3      166      55.15      55.15
## 2      7      117      38.87      94.02
## 3      6       18       5.98     100.00
```



```
##      chest_pain frequency percentage cumulative_perc
## 1          4      144      47.52      47.52
## 2          3       86      28.38      75.90
## 3          2       50      16.50      92.40
## 4          1       23       7.59     100.00
```

```
## [1] "Variables processed: thal, chest_pain"
```

As well as in the remaining `funModeling` functions, if `str_input` is missing it will run for all factor or character variables present in given data frame:

```
freq(data=heart_disease)
```

Also, as the other plot functions in the package, if there is the need of exporting plots, add the `path_out` parameter (it will create the folder if it's not created yet)

```
freq(data=heart_disease, path_out='my_folder')
```

4 High Cardinality Variable in Descriptive Stats

4.1 What is this about?

A **high cardinality** variable is one in which it can take *many* different values. For example country.

This chapter will cover cardinality reduction based on Pareto rule, using the `freq` function which gives a quick view about where the most of values are concentrated and variable distribution.

4.2 High Cardinality in Descriptive Statistics

The following example contains a survey of 910 cases, with 3 columns: `person`, `country` and `has_flu`, which indicates having such illness in the last month.

```
library(funModeling)
```

`data_country` data comes inside `funModeling` package (please update to release 1.6).

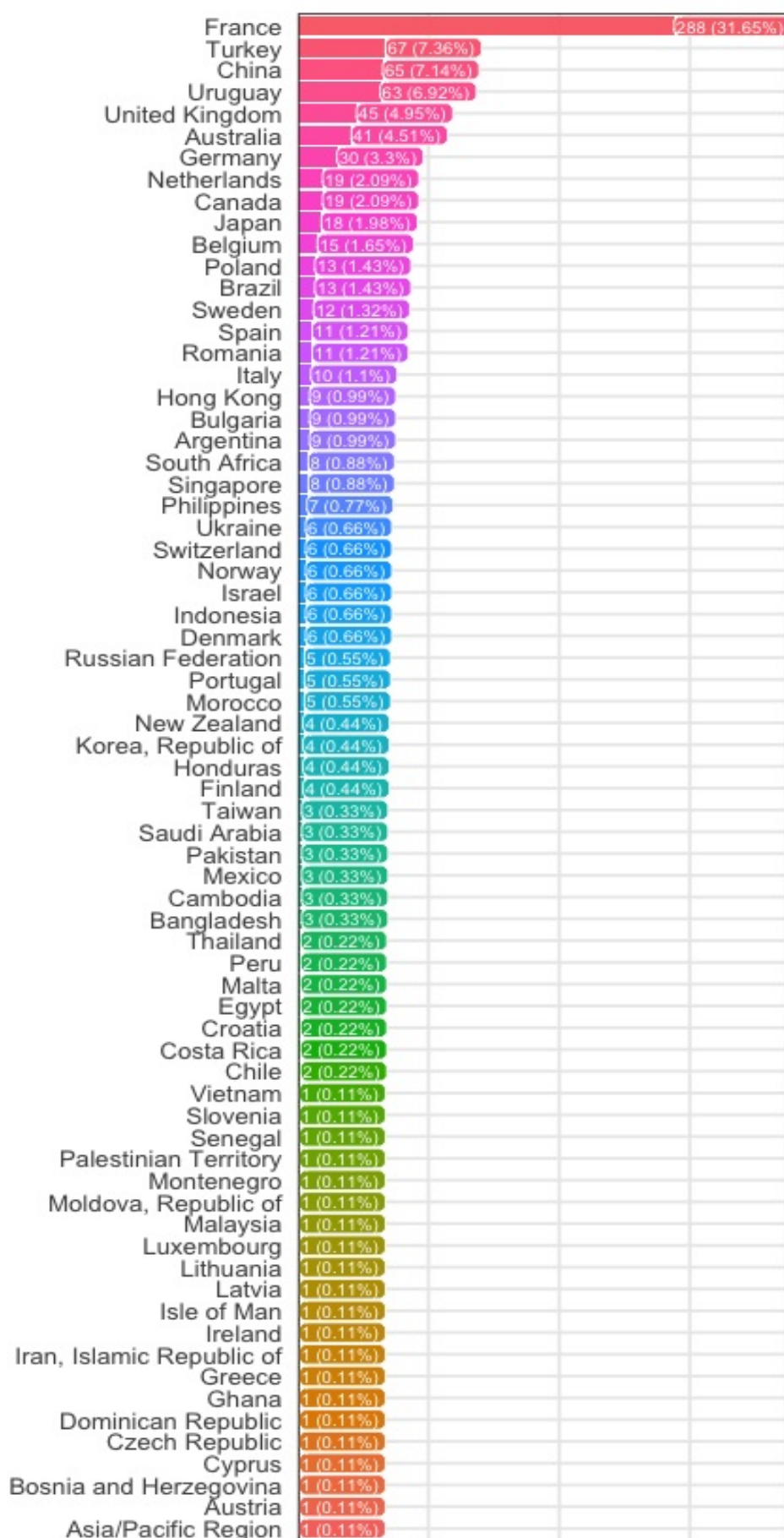
Quick `data_country` profiling (first 10 rows)

```
# plotting first 10 rows  
head(data_country, 10)
```

```
##      person    country has_flu
## 478    478      France      no
## 990    990      Brazil      no
## 606    606      France      no
## 575    575 Philippines      no
## 806    806      France      no
## 232    232      France      no
## 422    422      Poland      no
## 347    347      Romania      no
## 858    858      Finland      no
## 704    704      France      no
```

```
# exploring data, displaying only first 10 rows
head(freq(data_country, "country"), 10)
```

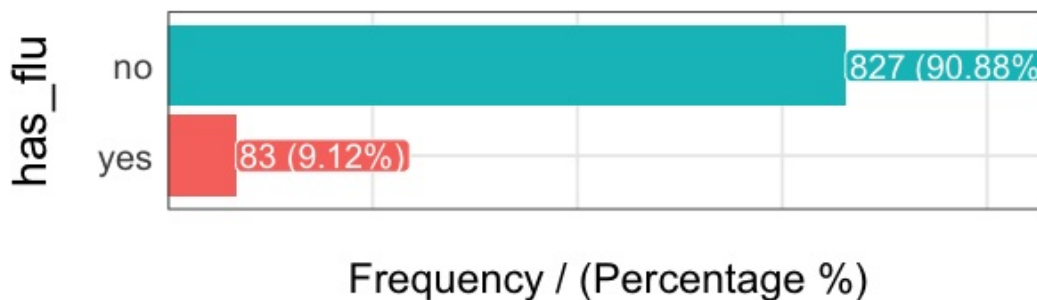
country



Frequency / (Percentage %)

```
##          country frequency percentage cumulative_perc
## 1      France      288      31.65      31.65
## 2      Turkey       67       7.36      39.01
## 3       China       65       7.14      46.15
## 4    Uruguay       63       6.92      53.07
## 5  United Kingdom   45       4.95      58.02
## 6    Australia     41       4.51      62.53
## 7      Germany     30       3.30      65.83
## 8      Canada      19       2.09      67.92
## 9   Netherlands    19       2.09      70.01
## 10     Japan       18       1.98      71.99
```

```
# exploring data
freq(data_country, "has_flu")
```



```
##   has_flu frequency percentage cumulative_perc
## 1     no      827      90.88      90.88
## 2     yes       83       9.12     100.00
```

The last table shows there are **70 different countries**, and ~9% of people who had flu - `has_flu="yes"` .

But many of them have almost no participation in the data. This is the *long tail*, so one technique to reduce cardinality is to keep those categories that are present the a high percentahge of data share, for example 70, 80 or 90%, the Pareto principle.

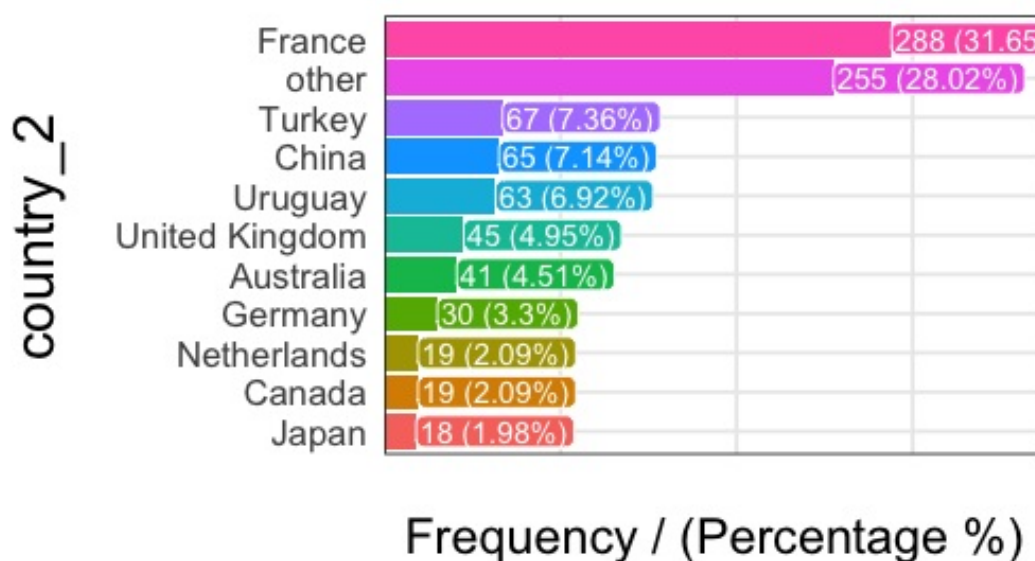
```
# 'freq' function, from 'funModeling' package, retrieves the cumulative_percentage
that will help to do the cut.
country_freq=freq(data_country, 'country', plot = F)

# Since 'country_freq' is an ordered table by frequency, let's inspect the first 10
rows with the most share.
country_freq[1:10,]
```

| ## | country | frequency | percentage | cumulative_perc |
|-------|----------------|-----------|------------|-----------------|
| ## 1 | France | 288 | 31.65 | 31.65 |
| ## 2 | Turkey | 67 | 7.36 | 39.01 |
| ## 3 | China | 65 | 7.14 | 46.15 |
| ## 4 | Uruguay | 63 | 6.92 | 53.07 |
| ## 5 | United Kingdom | 45 | 4.95 | 58.02 |
| ## 6 | Australia | 41 | 4.51 | 62.53 |
| ## 7 | Germany | 30 | 3.30 | 65.83 |
| ## 8 | Canada | 19 | 2.09 | 67.92 |
| ## 9 | Netherlands | 19 | 2.09 | 70.01 |
| ## 10 | Japan | 18 | 1.98 | 71.99 |

So 10 countries represent more the 70% of cases. We can assign the category `other` to the remaining cases and plot:

```
data_country$country_2=ifelse(data_country$country %in% country_freq[1:10,'country'],
data_country$country, 'other')
freq(data_country, 'country_2')
```



| ## | country_2 | frequency | percentage | cumulative_perc |
|-------|----------------|-----------|------------|-----------------|
| ## 1 | France | 288 | 31.65 | 31.65 |
| ## 2 | other | 255 | 28.02 | 59.67 |
| ## 3 | Turkey | 67 | 7.36 | 67.03 |
| ## 4 | China | 65 | 7.14 | 74.17 |
| ## 5 | Uruguay | 63 | 6.92 | 81.09 |
| ## 6 | United Kingdom | 45 | 4.95 | 86.04 |
| ## 7 | Australia | 41 | 4.51 | 90.55 |
| ## 8 | Germany | 30 | 3.30 | 93.85 |
| ## 9 | Canada | 19 | 2.09 | 95.94 |
| ## 10 | Netherlands | 19 | 2.09 | 98.03 |
| ## 11 | Japan | 18 | 1.98 | 100.00 |

4.3 Final comments

Low representative categories are sometimes errors in data, such as having: `Egypt` , `Egypt.` , and may give some evidence in bad habits collecting data and/or possible errors when collecting from the source.

There is no general rule to shrink data, it depends on each case.

Next recommended chapter: [High Cardinality Variable in Predictive Modeling](#)