

LSTAT2120 - Project 2022

Linear models of life expectancy

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1 Introduction

We are working with a dataset containing different *health factors* collected from **WHO** (World Health Organization) as well as *economic factors* collected from **ONU** for almost every countries in the world and years between 2000 and 2015. Some countries are not present in this dataset because they had too much missing data.

Since we are dealing with panel data, we chose to only work with data from the year 2012. We removed observations with missing values and we modified the ‘adult mortality’ continuous variable into a qualitative variable. So the final dataset has ??? **observations** and 20 **variables**. For our analysis, we separated the dataset into a training set and a testing set containing respectively 80% and 20% of the observations. This separation is random (*i.e. the dataset is shuffled before separating it*).

2 Research question

We want to understand how different factors affect positively or negatively the life expectancy. We would like to be able to predict the mean life expectancy (response variable : *life.expectancy*) for a given country based on different health, economic and social factors.

Firstly, we will start by doing a descriptive analysis of the different variables. Then we will try different linear models and select the best one based on different relevant criterions. We will check if the classical hypothesis are respected as well as nonlinearity, influential observations. If some hypotheses are not respected, we will fix that. We will finish by making prediction on a testing set with our model.

3 Descriptive statistic

We have 20 variables in our dataset of which 2 are qualitative. The *status* indicates if the country is developed or developing and the *adult.mortality* feature categorize the probability of dying between 15 and 60 years old into five levels : very low, low, middle, high, very high.

More generally, we can classify the different variables into several categories : *economic* (country status, expenditure on health, gdp, hdi), *social* (total population of each country, number of years of schooling), *mortality* (adult mortality, infant death, under five death, under four death because of HIV/AIDS, thinness) and *immunization* factors (immunization of hepatitis b, polio, diphtheria as well as number of reported cases of measles). We will only describe some variables, the curious reader can find a complete description of these in the appendix.

The *hepatitis.b*, *polio* and *diphtheria* variables are respectively the immunization coverages against hepatitis B, polio and DPT3 (diphtheria tetanus toxoid and pertussis) among the 1 year olds and are given in percentage.

The *alcohol* variable is the consumption of alcohol per capita (of 15 years old or more) in litres of pure alcohol.

3.1 Qualitative variables

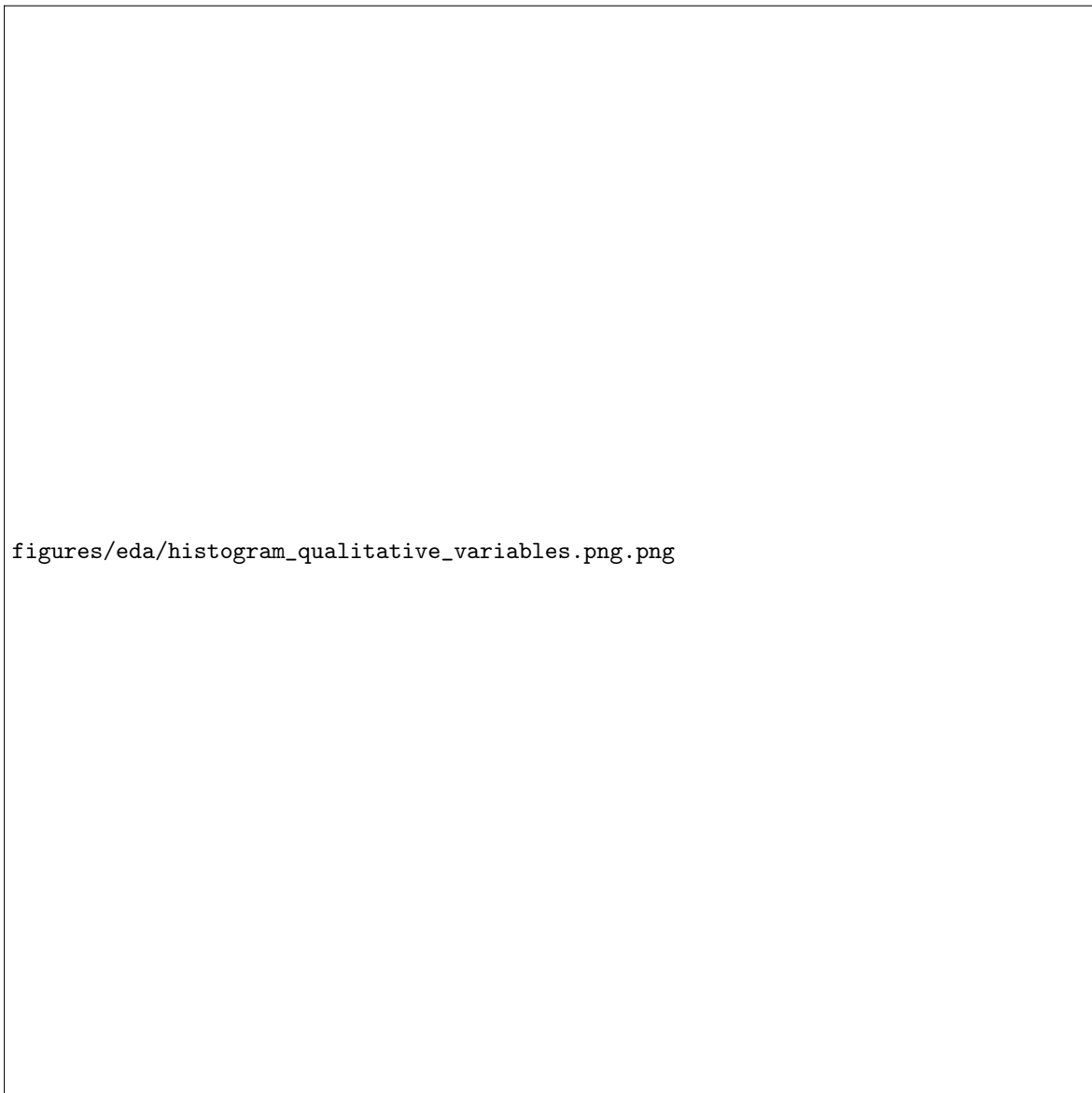


FIGURE 1 – barplot of the qualitative variables

3.2 Quantitative variables

Let's take a look to the table of the 4 moments (*mean*, *standard deviation*, *skewness* and *kurtosis*) for each of the quantitative variables.

4 moments of quantitative variables				
variable	mean	std_dev	skewness	kurtosis
life.expectancy	70.24	8.51	-0.37	2.41
infant.deaths	31.28	112.66	7.52	66.92
alcohol	3.87	4.24	0.76	2.43
percentage.expenditure	900.80	1931.89	3.92	19.17
hepatitis.b	80.57	26.54	-1.94	5.66
measles	967.93	2794.70	4.14	21.96
bmi	38.03	20.93	-0.12	1.63
polio	82.64	25.40	-2.17	6.60
total.expenditure	6.18	2.48	0.21	2.72
diphtheria	84.53	22.58	-2.51	8.70
hiv.aids	1.08	2.15	2.83	11.13
gdp	7460.10	12333.66	2.90	11.53
population	13580015.34	35183192.47	4.32	23.81
thinness.10.19.years	4.76	4.57	1.92	7.77
thinness.5.9.years	4.74	4.46	1.96	8.48
income.composition.of.resources	0.66	0.15	-0.25	2.04
schooling	12.54	2.73	-0.07	2.89

FIGURE 2 – table of moments (mean, standard deviation, skewness, kurtosis) for the quantitative variables

The **life expectancy** has a mean of roughly 70 years with a standard deviation of 8.6. It is slightly negatively skewed which indicates that some countries have low life expectancy. The kurtosis is less than 3 so the distribution is a little bit flattened.

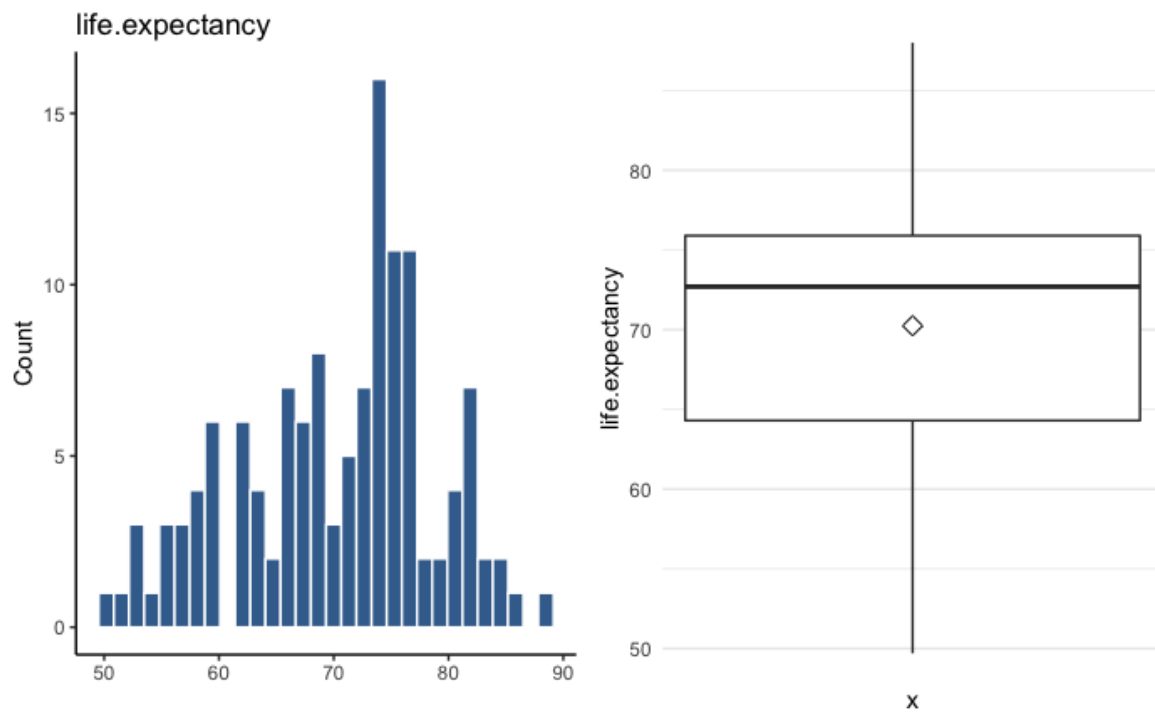


FIGURE 3 – Histogram and boxplot of the target variable (life expectancy)

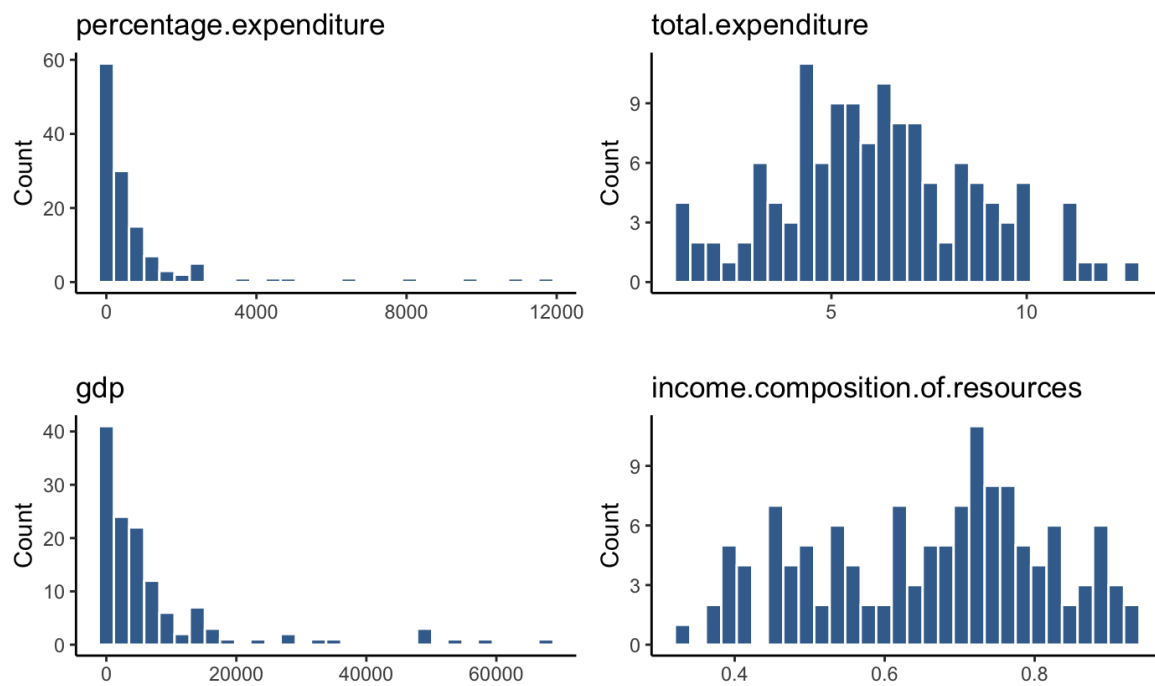


FIGURE 4 – Histogram of economic features

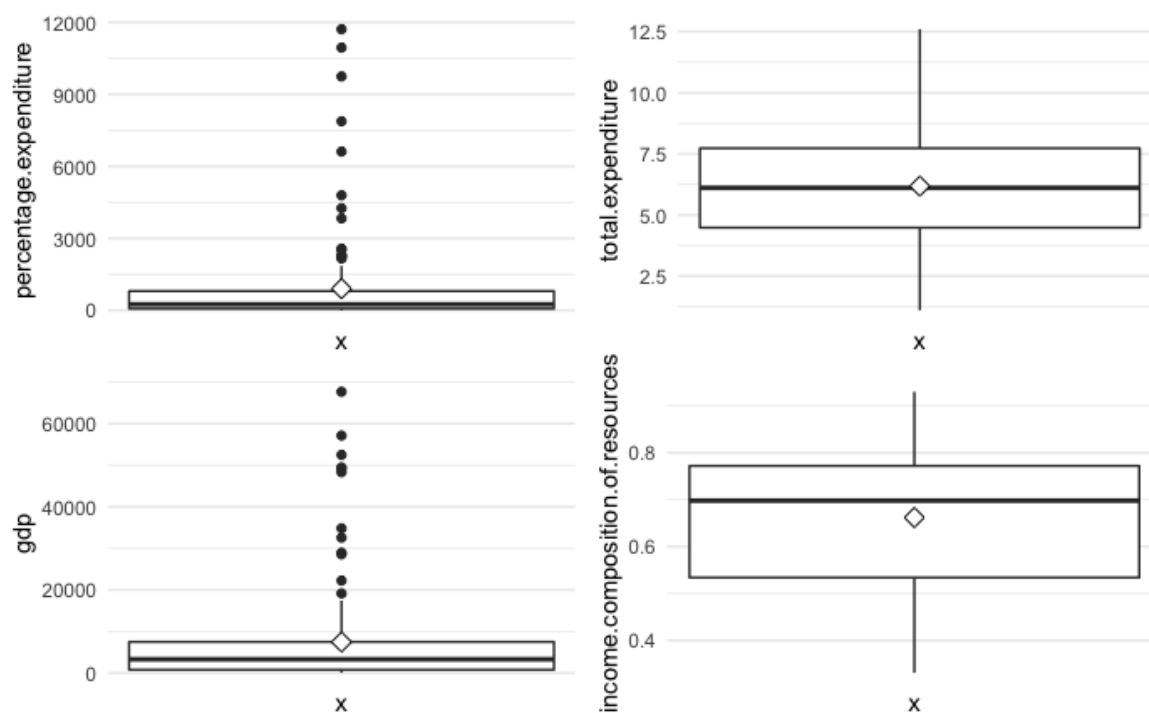


FIGURE 5 – Boxplot of economic features

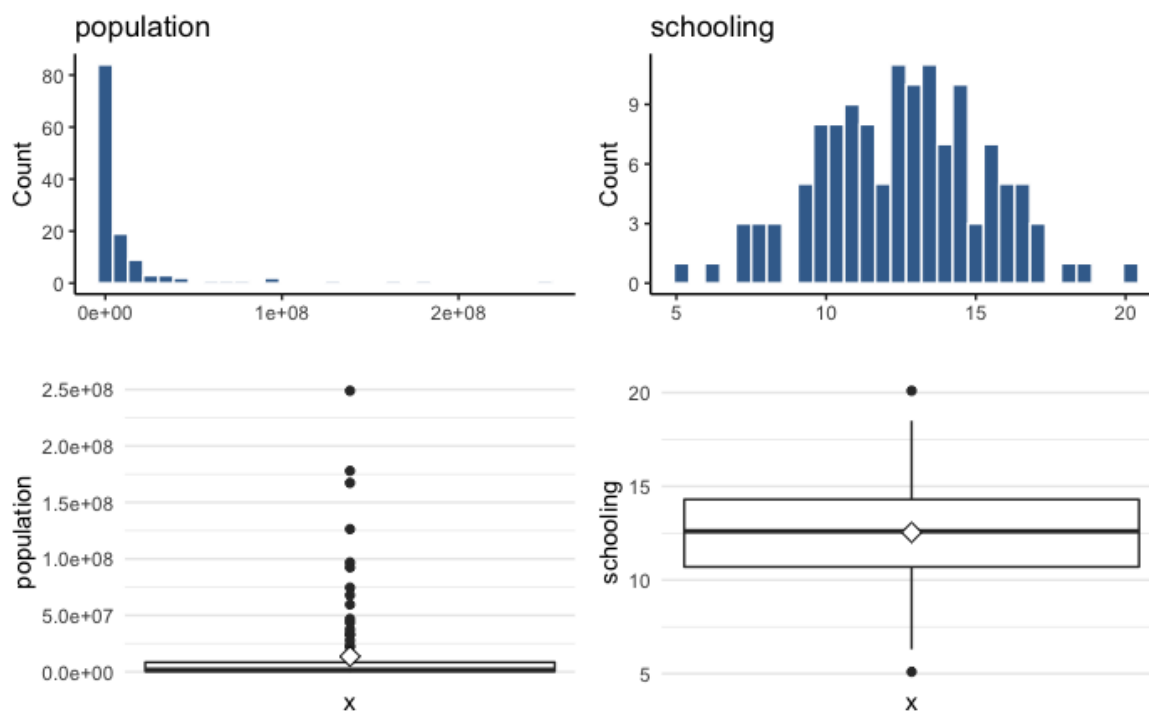


FIGURE 6 – Histogram and boxplot of social features

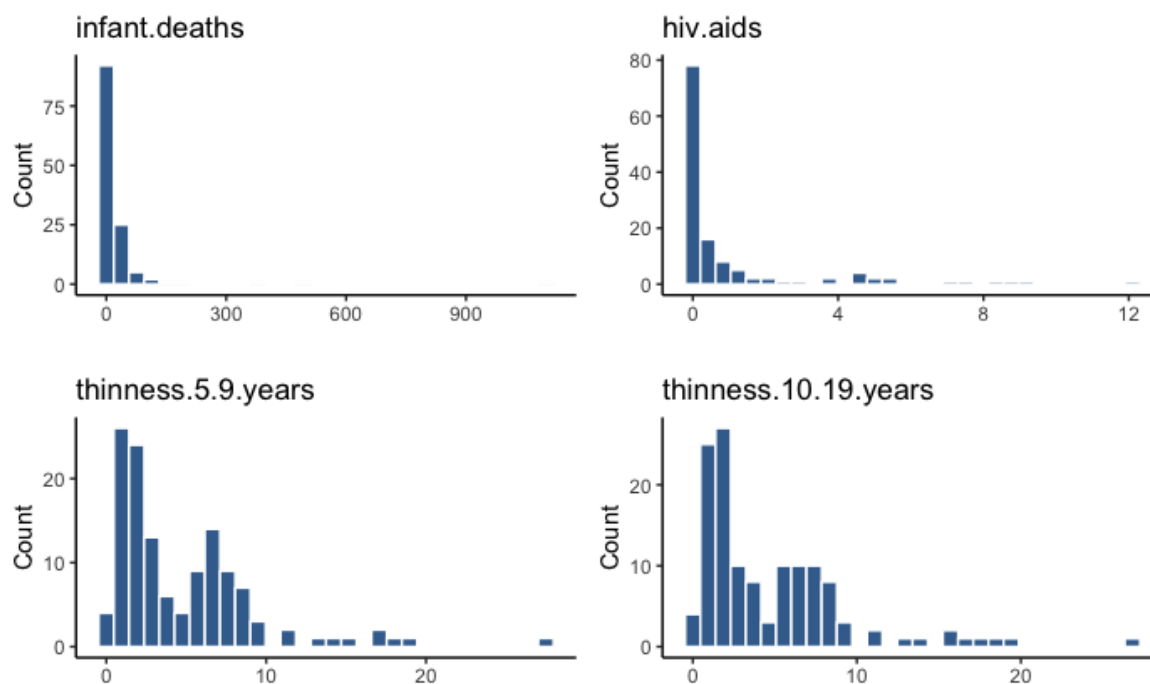


FIGURE 7 – Histogram of mortality features

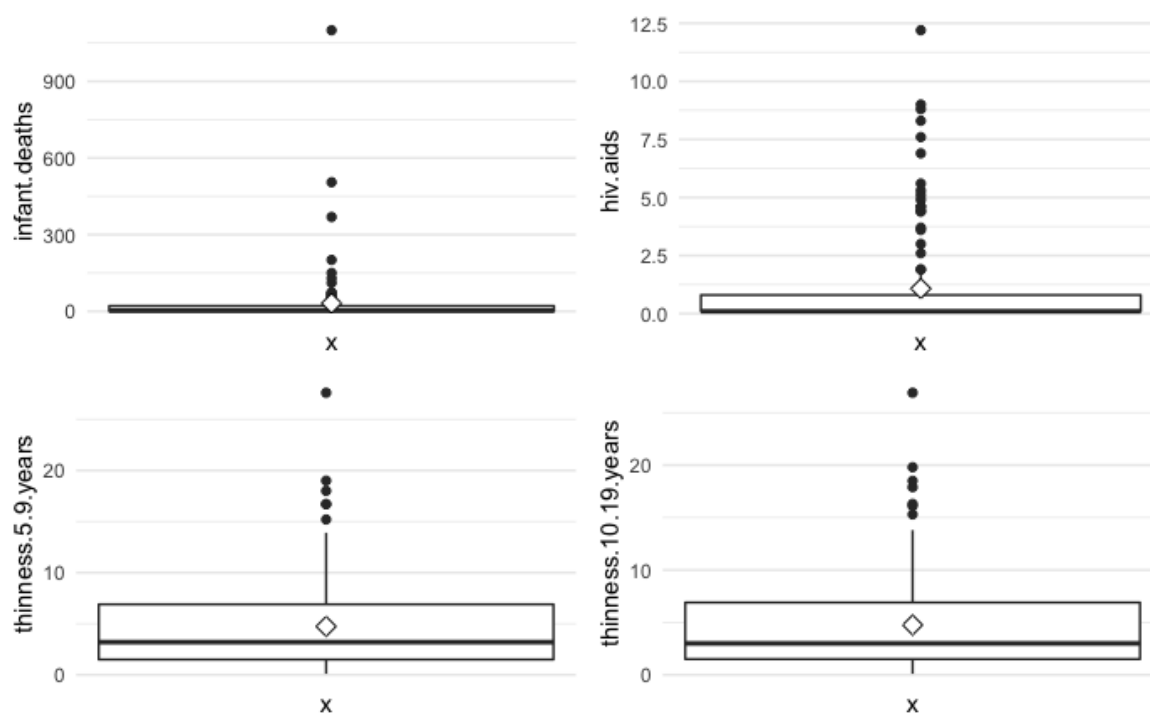


FIGURE 8 – Boxplot of mortality features

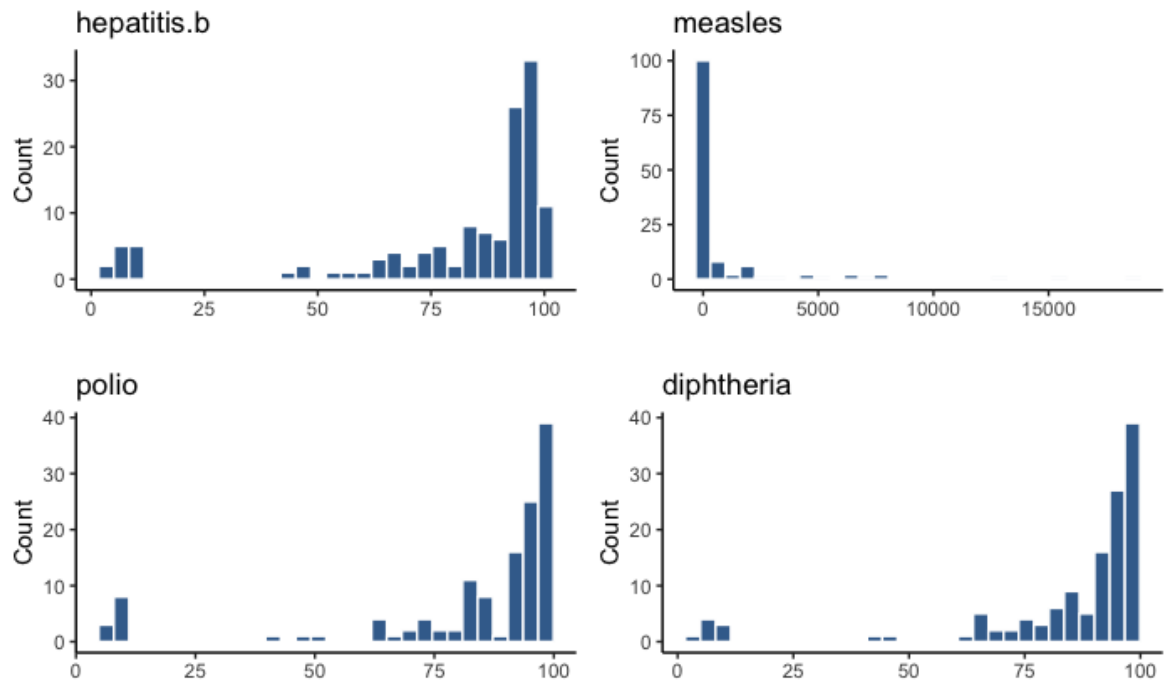


FIGURE 9 – Histogram of health features

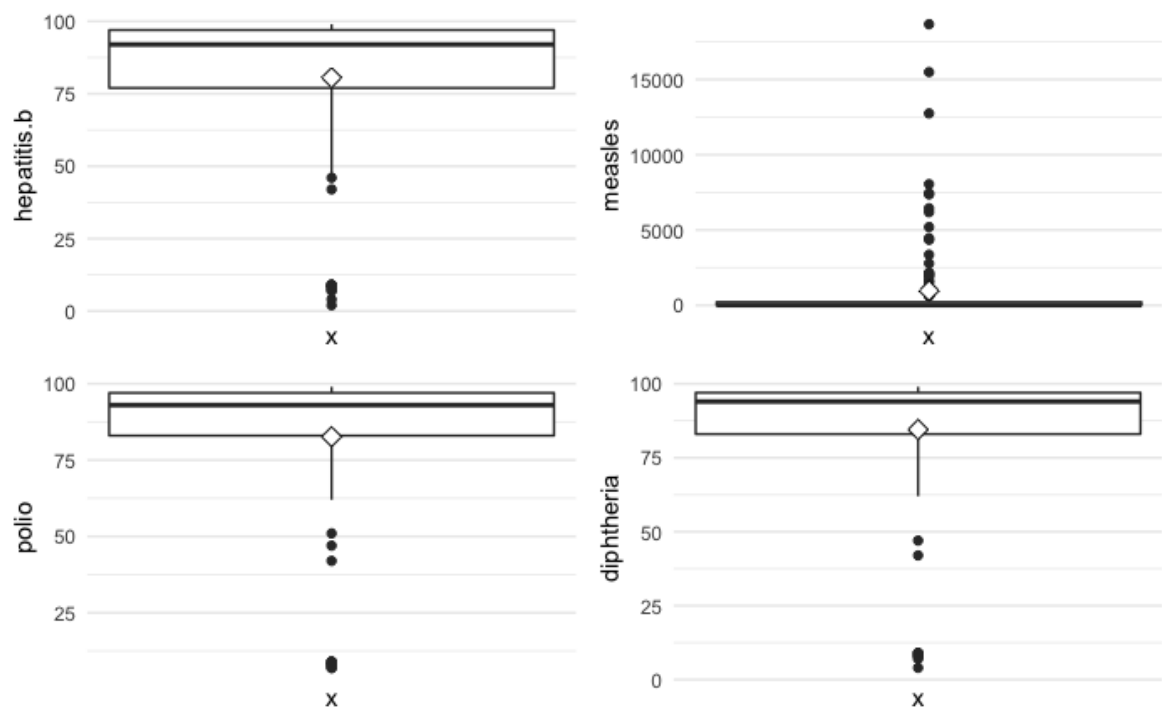


FIGURE 10 – Boxplot of health features

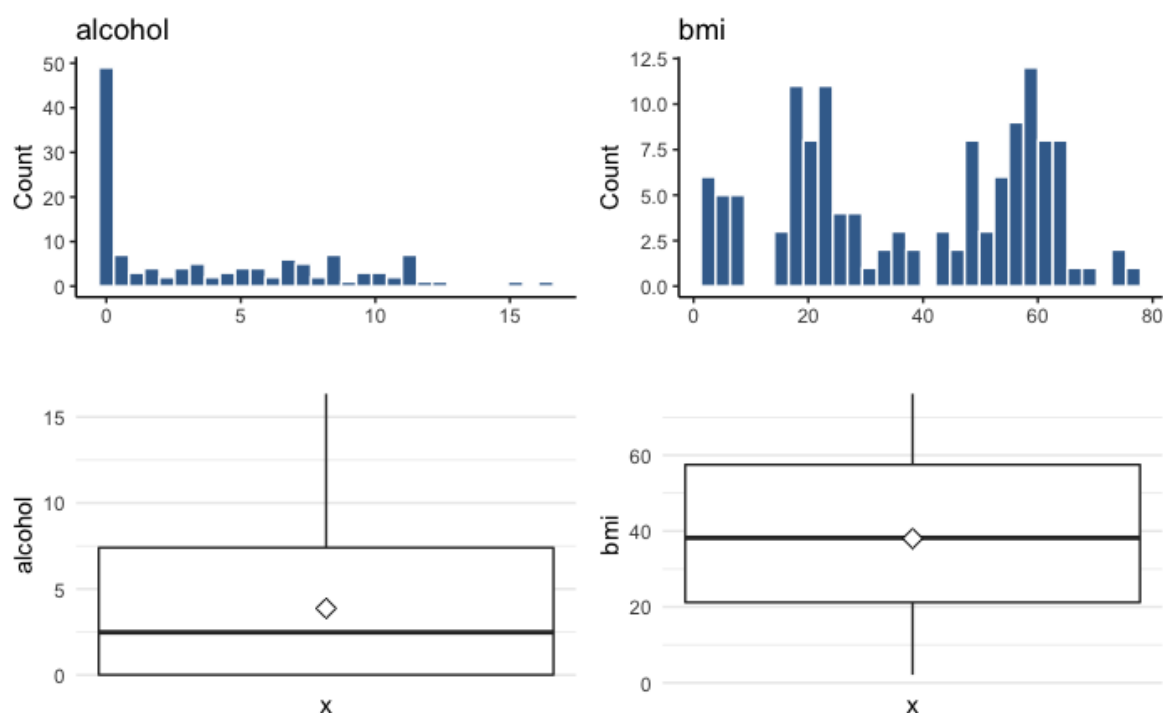


FIGURE 11 – Histogram and boxplot of misc features

The **infant death** has a mean of 31/1000 but has a huge standard deviation (112.6). We see that heavily tailed with a kurtosis of 66.9. The same kind of conclusion can be made for the **deaths under five year old**.

In average, countries spend 9 times the GDP¹ per capita on health services but the standard deviation is huge (1931.8) which indicates the presence of outliers far away from the mean. Therefore, we expect that some countries spend much less than that on health services.

Furthermore, in average, countries spend 6% of their total budget on health services. The distribution of this variable seems to follow a normal distribution given the skewness and kurtosis.

3.3 Correlation matrix

We look at the correlation matrix in order to see if there are any highly correlated variables. Indeed, it could be a sign of multicollinearity

1. Gross Domestic Product

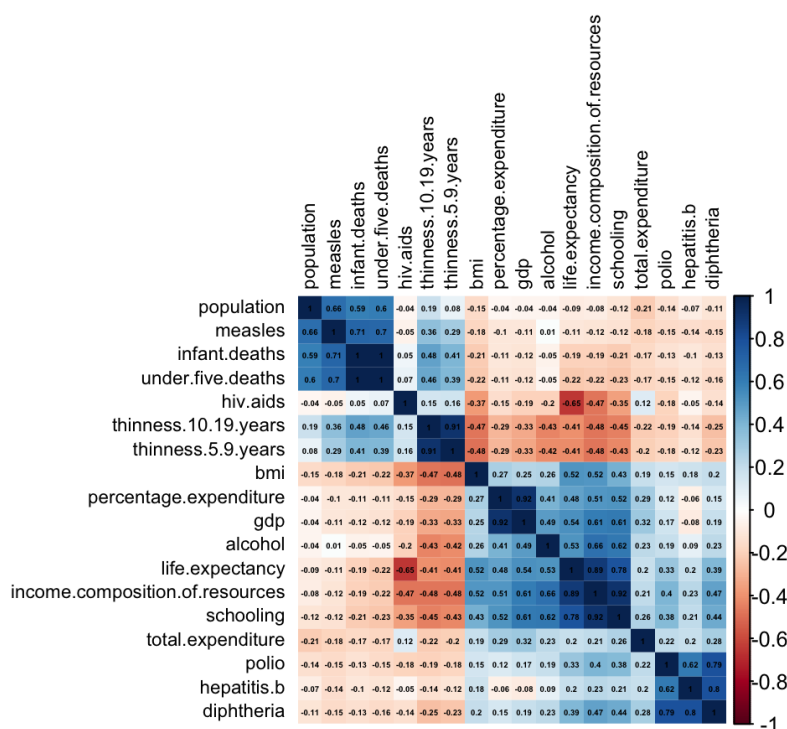


FIGURE 12 – correlation matrix of dataset

We see that several variables are highly correlated :

- The **infant death** is perfectly correlated with the **death under five year old** : these two features are redundant. As a consequence, we're gonna remove *under.five.death* feature from our dataset.
- The **thinness from 5 to 9 years old** with the **thinness from 10 to 19 years old** : we could suspect that extreme thinness comes from a problem of access to food which implies that thinness doesn't stop at 10 years old but continue throughout the teenage.
- The **number of measles cases per 1000 inhabitants** with the **infant death** : indeed, measles hits essentially children and youth and can (often) lead to death.
- The **percentage of expenditure made on health services** with the **GDP per capita**.
- The **hepatitis B** and **polio** with **diphtheria**.
- The **life expectancy** with the **HDI in terms of income composition of resources** and **schooling**.

4 Model selection

To maximize our model accuracy, we need to carefully select variables without adding too much to avoid overfitting. To do that, we will perform model selection using AIC , BIC and R_a^2 criterions. Since we have a lots a variables in our full model, we will only consider model selection of type II and III. Hence, we will not consider C_p Mallow criterion.

4.1 Type II : forward / backward stepwise selection

The goal of a forward/backward stepwise selection is to start from the full model and then gradually adding/removing variables one at a time. At each iteration, we add/remove the one that yields the

lowest accuracy in prediction when added the pool of selected variables. We can measure the accuracy using different criterions, for this project, we will focus on *p-value* and *AIC* criterions.

4.1.1 p-value

At each step, we chose the variable where,

$$r_{yk}^2 = \frac{\text{SSR}(X_k)}{\text{SST}}, \quad k = 1, \dots, p-1 \quad (1)$$

is maximum. As a rule of thumb, we include the variable X_k if its p-value is smaller than the SLE (significance level to enter) that we set to 0.15.

4.1.2 Akaike Information Criterion (AIC)

We want to minimize the AIC that is,

$$\text{AIC} = -2 \ln L(\hat{\beta}) + 2k \quad (2)$$

where $L(\hat{\beta})$ is the maximum of the likelihood function and p is the number of estimated parameters in the model.

4.2 Type III : LASSO

The LASSO estimator is similar to the OLS (it minimizes the SSR) but it adds a constraint on the L_1 norm (Manhattan) for β . The constraints is,

$$\sum_{j=1}^p |\beta_j| \leq t \quad (3)$$

where $t \in \mathbb{R}$ is a parameter to be determined.

This change allows some coefficients to be shrunk exactly to zero.

4.2.1 Models comparison

Comparison of models			
Model	Number_of_variables	AIC	Adj_R2
Full model	21	542.14	0.88
Forward p-value	7	520.79	0.89
Backward p-value	6	519.51	0.89
Forward AIC	7	520.79	0.89
Backward AIC	6	519.51	0.89
LASSO	9	522.94	0.89

FIGURE 13 – Comparison of the full model with models resulting of forward/backward selections using p-value and AIC criterion

We compared the full model with forward/backward selections using the p-value criterion and AIC criterion. Each selected model has a slightly better adjusted R^2 of 0.89 compared to the full model with the benefit of being much simpler. Therefore, we choose the model with the less variables. We noticed that the backward elimination select the same variable for the p-value criterion and the AIC criterion. We chose to go for the backward selected model using p-value.

4.3 Interactions between variables

We should then try to add interactions between variables to our chosen model. We decide to test the following interactions and compare the resulting models with our chosen one,

- *infant.deaths* with *measles*
- *adult.mortality.high* with *alcohol*
- *adult.mortality.very_high* with *alcohol*
- *total.expenditure* with *adult.mortality.low*
- *total.expenditure* with *infant.deaths*

Comparison of the chosen model with the adding of interaction term			
Model	Number_of_variables	AIC	Adjusted_R2
infant.deaths * measles	9	525.40	0.88
adult.mortality.high * alcohol	9	522.49	0.89
adult.mortality.very_high * alcohol	8	523.21	0.89
total.expenditure * adult.mortality.low	7	520.20	0.89
total.expenditure * infant.deaths	8	523.25	0.89
percentage.expenditure * diphtheria	9	523.71	0.89

FIGURE 14 – Comparison of the chosen model with the adding of an interaction term

Looking at the adjusted R^2 , we notice that the different interacting terms do not explain more our target variable (it's even lower for the first interacting term). Moreover, the AIC criterion is worse than the model without any interaction. Therefore, we choose to not add an interaction term.

Our final model is then,

$$\begin{aligned}
 \text{life.expectancy} = & \beta_0 + \beta_1 \cdot \text{total.expanditure} + \beta_2 \cdot \text{hiv.aids} + \beta_3 \cdot \text{income.composition.of.resources} \\
 & + \beta_4 \cdot \text{adult.mortality.low} + \beta_5 \cdot \text{adult.mortality.middle} \\
 & + \beta_6 \cdot \text{adult.mortality.very_high}
 \end{aligned}$$

4.4 Verifying underlying hypotheses

After selecting a model, we want to check the underlying hypothesis of the linear model. We will verify the 3 main hypothesis : homoskedasticity, independance of observations and normality of the residuals. we will also check for outliers, autocorrelation and nonlinearity.

4.4.1 Nonlinearity

We can check for nonlinearity by looking at the scatterplot of the residuals (e_i) versus the explanatory variables.

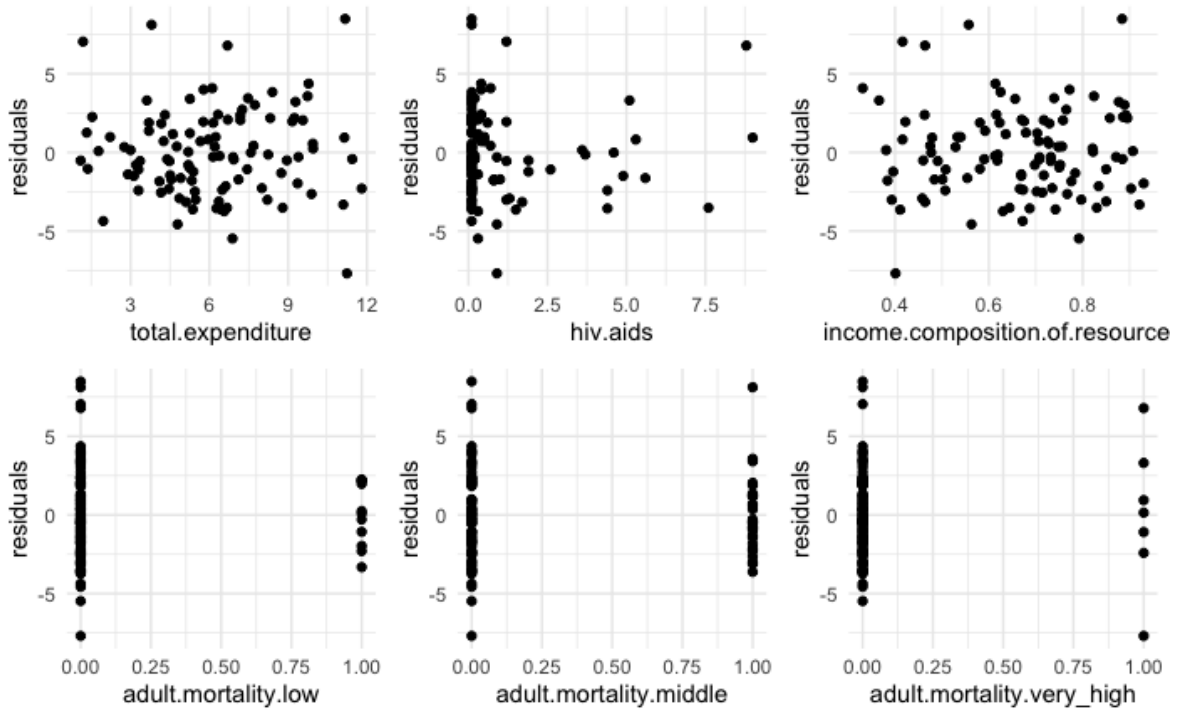


FIGURE 15 – scatterplots of residuals versus explanatory variables for the selected model

We do not see clear nonlinear patterns in the different plots above. Every variable has more or less a linear relation with its residuals. The continuous variable *hiv.aids* has a strange pattern but the nonlinear seems too complicated to infer and would add a lot of complexity to our model. Therefore, we do not take remedial actions.

4.4.2 Outliers and influential observations

a) outliers with respect to the explanatory variables

We first try to identify outliers with respect to the explanatory variables X_{ij} . They can be identified by studying the leverages that are the diagonal elements of the "hat matrix" $H := X(X^T X)^{-1} X^T$. X_i is an outlier if,

$$h_{ii} > \frac{2p}{n} \approx 0.116$$

We find **13** outliers that are the following rows of our dataset : 6, 9, 11, 23, 35, 40, 49, 58, 65, 82, 97, 99, 100.

We want then know if the outliers found are influential for the their fitted values. We use the DFFITS criterion for the i -th observation,

$$\text{DFFITS}_i = d_i^* \sqrt{\frac{h_{ii}}{1 - h_{ii}}} \quad (4)$$

where d_i^* are the standardized deleted residuals,

$$d_i^* = e_i \sqrt{\frac{n - p - 1}{\text{SSE}(1 - h_{ii}) - e_i^2}} \quad (5)$$

We have a criterion for DFFITS. For $n > 30$, the i -th observation is influential for its fitted value if,

$$|\text{DFFITS}_i| > 2\sqrt{\frac{p}{n}} \approx 0.52 \quad (6)$$

We find that 8 observations are influential for the fitted values : 2, 9, 23, 35, 49, 95, 96. Therefore, the observations 9, 23, 35, 49 are outliers and influential for the fitted values.

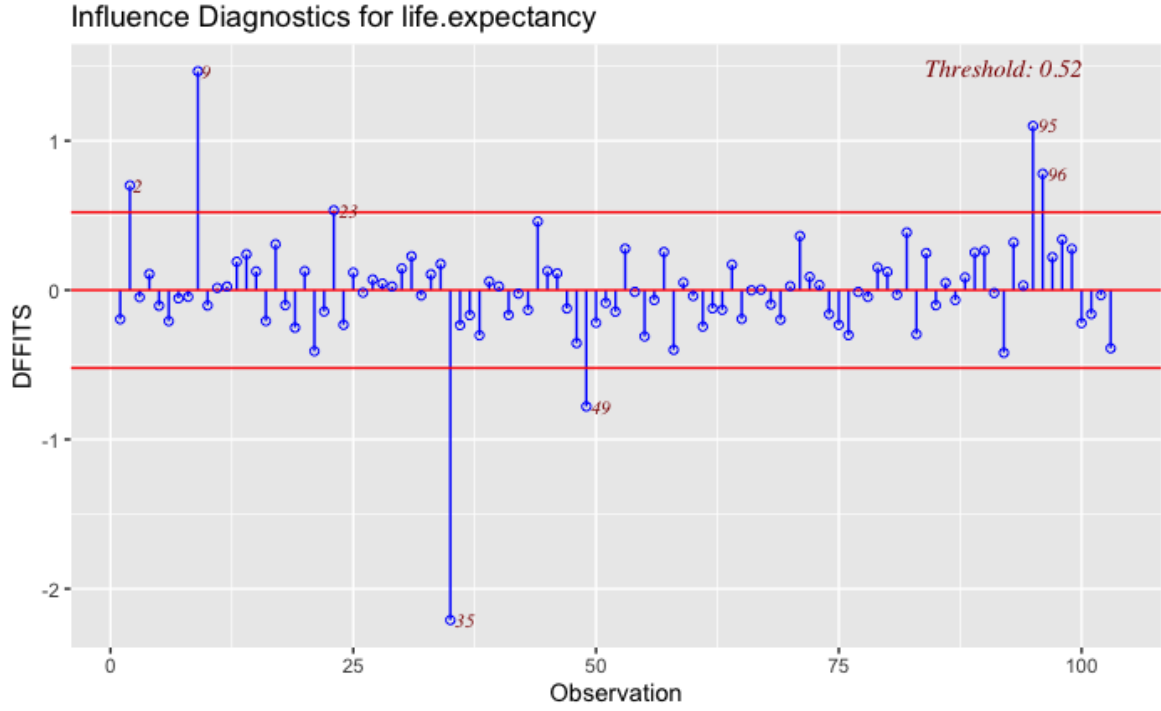


FIGURE 16 – Plot of DFFITS vs observations. Outside the two red lines are the outliers influential for their fitted values.

Now, are they also influential for the regression coefficients? We find that the same 8 observations influential for the fitted values are also influential for the regression coefficients. We use the DFBETAS criterion for the i -th observation and k -th coefficient $\hat{\beta}_k$,

$$|\text{DFBETAS}_{k,i}| = \frac{\hat{\beta}_k}{\hat{\beta}_{k,i}} \text{MSE}_i \cdot c_k, \quad c_k = (X^T X)_{kk}^{-1} \quad (7)$$

We have a criterion for DFBETAS. The i -th observation is influential for the k -th coefficient if,

$$\text{DFBETAS}_{k,i} > \frac{2}{\sqrt{n}} \approx 0.197 \quad (8)$$

In the following plots, you can have a look at the different outliers for each coefficient

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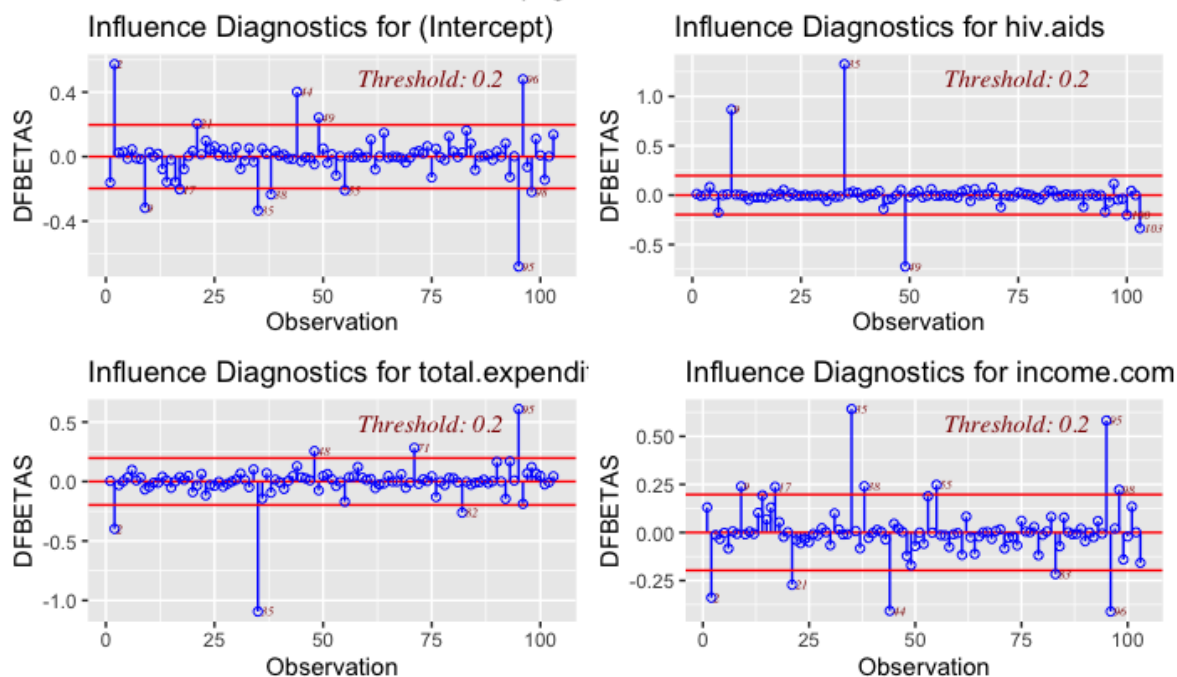


FIGURE 17 – Plot of DFFITS vs observations. Outside the two red lines are the outliers influential for the respective variable.

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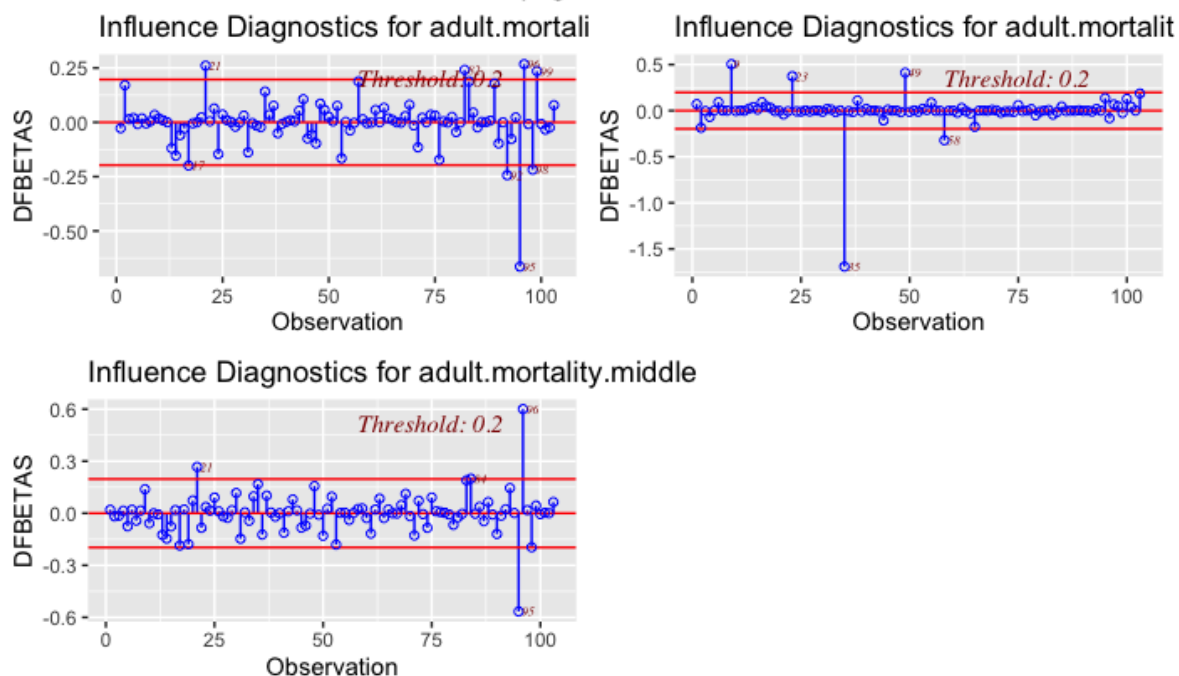


FIGURE 18

To summarize this, let's have a look at the Cook's distance D_i .

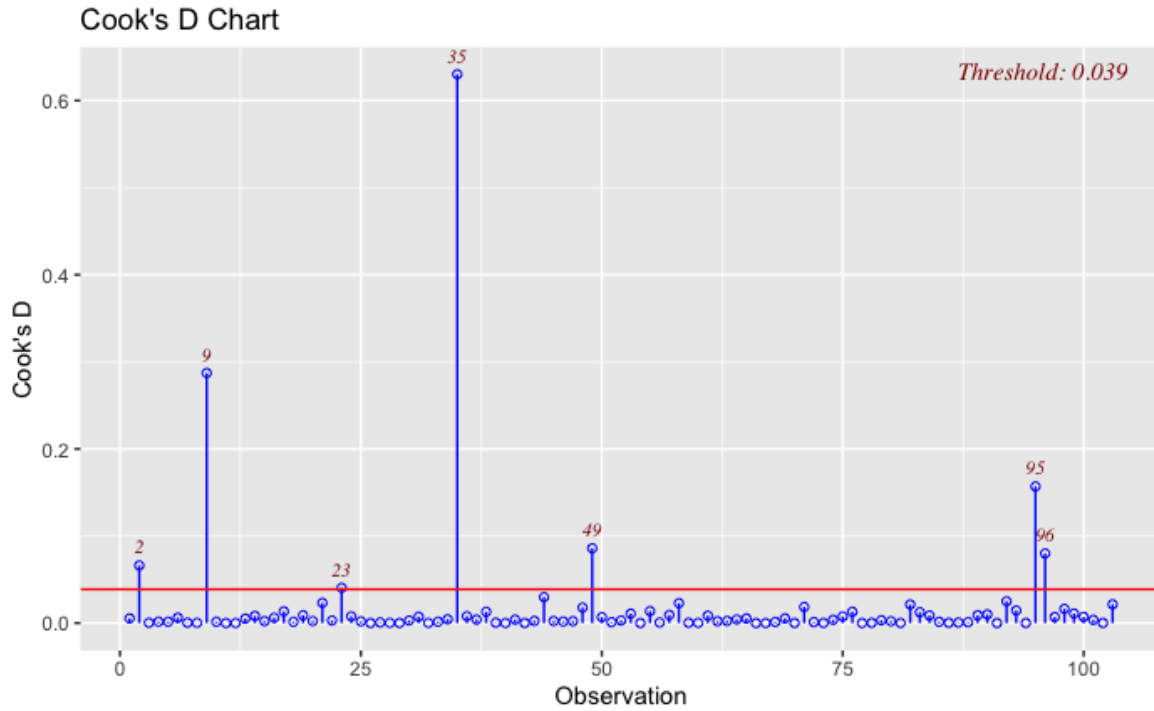


FIGURE 19 – Cook's distance. Outside the red lines are the outliers influentials for the regression coefficients.

b) outliers with respect to the response variable

We then identify outliers with respect to the response variable Y_i . Y_i is an outliers if $d_i^* > t_{n-p-1; 1-\frac{\alpha}{2}}$. For a level of significance of $\alpha = 0.05$, we have $t_{94; 0.975}$ and we find that the observations 2, 9, 95 and 96 are outliers for the response variable.

4.4.3 Multicollinearity

We verify now if we have any multicollinearity problem. We saw in the descriptive statistic section that some variables were highly correlated. These high pairwise correlations could lead to multicollinearity problem but it is not always the case.

Let the full model be,

$$Y = X\beta + \varepsilon \quad (9)$$

To check for multicollinearity, we can use the **Variance inflation factor (VIF)** that is defined by for the coefficient $\hat{\beta}_k$,

$$\text{VIF}_k = \frac{1}{1 - R_k^2}, \quad k = 1, \dots, p-1 \quad (10)$$

where R_k^2 is the coefficient of determination of a regression of X_k on $X_1, \dots, X_{k-1}, X_{k+1}, \dots, X_{p-1}$. Multicollinearity leads to an "ill-conditioned" matrix X . As a consequence, this matrix is numerically instable and becomes difficult to invert. Therefore, the OLS estimator $\hat{\beta}$ cannot be "correctly" computed. We have multicollinearity problem if the **VIF** is greater than 10 and if the **average VIF** is much greater than 1. We can also check the tolerance which is $1 - R_k^2$.

Variation inflation factor (VIF)		
final model		
Variables	Tolerance	VIF
total.expenditure	0.86	1.17
hiv.aids	0.56	1.78
income.composition.of.resources	0.51	1.96
adult.mortality.low	0.65	1.55
adult.mortality.middle	0.75	1.34
adult.mortality.very_high	0.64	1.55

FIGURE 20 – VIF for the selected model

We notice we do not have any variable with a **VIF** > 10 so we do not have multicollinearity problem.

4.4.4 Heteroskedasticity

We can try to check for heteroskedasticity by looking at the plot of the residuals versus the fitted response variable.



FIGURE 21 – scatterplots of residuals versus fitted response variable

However, it's not that clear with plot if there is heteroskedasticity problem or not. The best way to determinate if there is heteroskedasticity is to perform the **White test**. The hypothesis are,

H_0 : there is homoscedasticity

H_1 : there is heteroskedasticity

The result is,

studentized Breusch-Pagan test

```
data: final_lm
```

```
BP = 10.548, df = 6, p-value = 0.1034
```

FIGURE 22 – Result of White test for homoskedasticity

The p-value of the **White test** is 0.01729. At a significance level of $\alpha = 0.05$, we reject the null hypothesis and therefore we can conclude there is **heteroskedasticity**.

Although heteroskedasticity does not produce biased OLS estimators, it tends to make the variance-covariance matrix biased leading to standard error being untrustworthy. We first tried to fix the heteroskedasticity by making a Box-Cox transformation of the dependant variable but unfortunately, this did not work well. In order to rely on model testing methods such as F-tests or T-tests in the following sections, we will have to make **robust inference**.

4.4.5 Autocorrelation

We can check for autocorrelation by performing the **Breusch-Godfrey test**. The hypotheses are,

H_0 : there is no autocorrelation

H_1 : there is autocorrelation

Breusch-Godfrey test for serial correlation of order up to 8

```
data: final_lm
LM test = 10.783, df = 8, p-value = 0.2143
```

FIGURE 23 – Result of Breusch-Godfrey test for autocorrelation

The p-value of the **Breusch-Godfrey test** is 0.2143. At a significance level of $\alpha = 0.05$, we fail to reject the null hypothesis and therefore we can conclude there is **no autocorrelation**.

4.5 Normality of the residuals

Considering the Normal Q-Q plot of the residuals comparing the quantiles of the residuals versus the quantiles of a normal distribution. If the residuals are normal, the points on the following plot should follow the straight line,

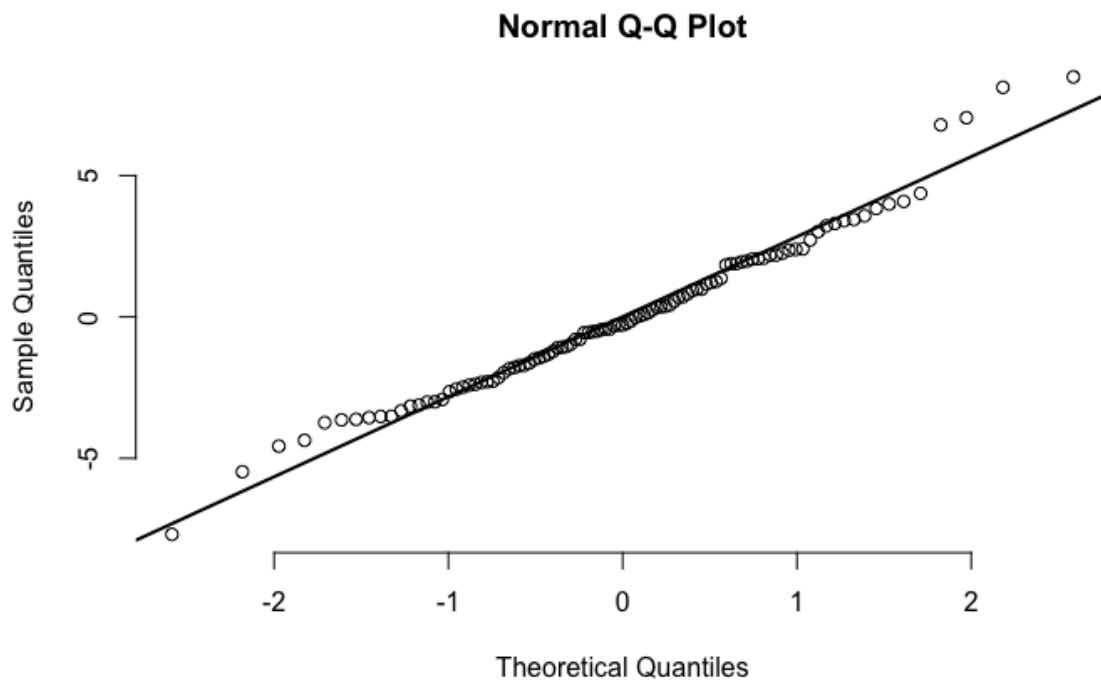


FIGURE 24 – Normal QQ-plot

Looking at this plot, we see that globally the points follow the straight line so the residuals are normals.

To ensure there is no a problem of normality for the residuals, we can perform a **Jarque Bera test**.

Let S be the skewness and κ of the residuals. The **Jarque Bera test** is given by,

$$JB = \frac{n}{6} \left(S^2 + \frac{(\kappa - 3)^2}{4} \right) \quad (11)$$

The hypothesis are,

$$H_0 : JB \sim X_2^2$$

H_1 : residuals are not normally distributed

Jarque Bera Test

```
data: final_lm$residuals
X-squared = 6.3201, df = 2, p-value = 0.04242
```

FIGURE 25 – Result of Jarque-Bera test

The p-value of the **Jarque Bera test** is 0.042. At a significance level of $\alpha = 0.05$, we fail to reject the null hypothesis and therefore we can conclude the **residuals are normaly distributed**.

5 Coefficients

Coefficients of the final model				
term	estimate	std.error	statistic	p.value
(Intercept)	46.9234057	1.6548829	28.354518	1.903320e-48
total.expenditure	0.2611431	0.1206013	2.165342	3.283970e-02
hiv.aids	-1.0780480	0.2061631	-5.229102	9.950743e-07
income.composition.of.resources	33.6849505	2.5773667	13.069522	4.956676e-23
adult.mortality.low	3.6805535	1.1469092	3.209106	1.810698e-03
adult.mortality.middle	2.3088195	0.7402049	3.119163	2.394658e-03
adult.mortality.very_high	-5.0068839	1.4094384	-3.552396	5.937956e-04

FIGURE 26 – Coefficients of the model

Looking at the p-values, all the coefficients β_k are statistically significant at a significance level of $\alpha = 0.05$.

We can interpret the different coefficients the following way,

- An increase of 1% in the government expenditure on health (as a percentage of total expenditure) leads to an increase of 0.26% of life expectancy.
- An increase of 1 death caused by HIV/AIDS for people under 5 years old per 1000 births leads to a decrease of 1.07/1000 of life expectancy.
- An increase of ...
- Having a low adult mortality leads to an increase of 3.6 years of life expectancy.
- Having a middle adult mortality leads to an increase of 2.3 years of life expectancy.
- Having a very high adult mortality leads to a decrease of 5 years of life expectancy.

6 Significance of estimated coefficients

We perform t-tests of estimated coefficients in order to test their significance. For t-tests, we use the following null and alternative hypotheses for each regression coefficient :

$$H_0 : \beta_i = 0$$

$$H_1 : \beta_i \neq 0$$

t test of coefficients:

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	46.92341	2.08377	22.5185	< 2.2e-16	***
Total.expenditure	0.26114	0.14365	1.8179	0.0721908	.
HIV.AIDS	-1.07805	0.27553	-3.9126	0.0001705	***
Income.composition.of.resources	33.68495	3.11526	10.8129	< 2.2e-16	***
Adult.Mortality_low	3.68055	1.14964	3.2015	0.0018545	**
Adult.Mortality_middle	2.30882	0.79029	2.9215	0.0043427	**
Adult.Mortality_very.high	-5.00688	1.92222	-2.6047	0.0106559	*

 Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

FIGURE 27 – *Output of t-test of coefficients*

On the basis of the p-values, we can reject the null hypothesis for all the coefficients. We can conclude that all the coefficients are statistically significant at a level of significance of 10%. At a significance level of 5%, the “total expenditure” coefficient is no longer statistically significant.

On the basis of the estimates, we can say that the effect of low and middle adult mortality rates on life expectancy are positive while the effect of a very high adult mortality rate on life expectancy is negative and stronger. From the regression output, we see that the estimate of the regression coefficient for “Adult mortality very high” is -5.007. This signifies that on average, a country with a very high adult mortality rate has a life expectancy of 5 years less. On the contrary, a country with a low adult mortality rate has a life expectancy higher of 3 years on average and 2 years for a country with a moderate adult mortality rate.

7 Linear combination of coefficients

We want to test the hypothesis that there exists a linear combination between two regression coefficients :

$$\beta_4 = \beta_5$$

With this, we want to test if these two coefficients are equal. We can also write it as follow :

$$\beta_4 - \beta_5 = 0$$

We formulate the null and alternative hypotheses :

$$H_0 : \beta_4 - \beta_5 = 0$$

$$H_1 : \beta_4 - \beta_5 \neq 0$$

Simultaneous Tests for General Linear Hypotheses

```
Fit: lm(formula = Life.expectancy ~ Total.expenditure + HIV.AIDS +  
      Income.composition.of.resources + Adult.Mortality_low + Adult.Mortality_middle +  
      Adult.Mortality_very.high, data = df_train)
```

Linear Hypotheses:

	Estimate	Std. Error	t value
Adult.Mortality_low - Adult.Mortality_middle == 0	1.3717	0.8286	1.655
	Pr(> t)		
Adult.Mortality_low - Adult.Mortality_middle == 0			0.101

(Adjusted p values reported -- single-step method)

FIGURE 28 – Output of linear combination test

Since the p-value (0.101) is larger than the significance level of 0.05, we fail to reject the null hypothesis that these two regression coefficients are equal. This signifies that a country with a low adult mortality rate and a country with a moderate adult mortality rate could have the same reduction in years of life expectancy if all the other effects remain constant.

8 Coefficients equal to zero

We test a subset of coefficients equal to zero. In this case, we test the coefficients corresponding to all qualitative variables equal to zero. Hence, the null and alternative hypotheses are the following :

$$H_0 : \beta_4 = \beta_5 = \beta_6 = 0$$

$$H_1 : \text{at least one of these is not equal to zero}$$

```
wald test

Model 1: Life expectancy ~ Total.expenditure + HIV.AIDS + Income.composition.of.resources +
  Adult.Mortality_low + Adult.Mortality_middle + Adult.Mortality_very.high
Model 2: Life expectancy ~ Total.expenditure + HIV.AIDS + Income.composition.of.resources
  Res.Df Df      F    Pr(>F)
1      96
2      99 -3 5.1282 0.002474 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

FIGURE 29 – *Output of Wald test*

The p-value is 0.0025 which is below the significance level of 0.05. We can thus reject the null hypothesis. We can conclude that there is sufficient statistical evidence that the different categorical variables corresponding to adult mortality rates explain life expectancy.

9 Prediction interval

We calculate a 95% prediction interval for the 26 observations excluded from the dataset in the beginning. We conclude that almost all the intervals cover the excluded observations. The last observation of the test dataset is the only one not covered by the corresponding 95% prediction interval. However, if we take the 99% prediction interval, this observation is contained in the prediction interval.

Appendix

The **response variable** is *life.expectancy*.

The **explanatory variables** are the following :

Economic factors :

- *status* : is the country **developping** or **developped**.
- *percentage.expenditure* : expenditure on health as percentage of gross domestic product (PIB in french) per capita (%).
- *total.expenditure* : general government expenditure on health as a percentage of total government expenditure (%).
- *gdp* : gross domestic product per capita (\$).
- *income.composition.of.resources* : human development index (HDI) in terms of income composition of resources ($\in [0, 1]$).

Social factors

- *population* : total population of the country.
- *schooling* : number of years of schooling

Mortality factors :

- *adult.mortality* : probability of dying between 15 and 60 years old (**very low, low, middle, high, very high**).
- *under.five.deaths* : number of under five deaths per 1000 population.
- *infant.deaths* : number of infant deaths per 1000 population.
- *hiv.aids* : death per 1000 live births HIV/AIDS (between 0 and 4 years old).
- *thinness.5.9.years* : prevalence of thinness among children for age 5 to 9 years old.
- *thinness.10.19.years* : prevalence of thinness among children and adolescents for age 10 to 19 years old.

Immunization factors

- *hepatitis.b* : Hepatitis B immunization coverage among 1 year olds (%).
- *measles* : number of reported cases of measles per 1000 population.
- *polio* : Polio immunization coverage among 1 year olds (%).
- *diphtheria* : Diphtheria tetanus toxoid and pertussis (DPT3) immunization coverage among 1 year olds (%)

Other factors

- *alcohol* : consumption of alcohol (15 years old or more) per capita (**in litres of pure alcohol**).
- *bmi* : average BMI of entire population.