Computer Lab 2 Covid

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Introduction

In this computer lab you will be practicing the following

- Creating time series plots with ggplot
- Performing hypothesis tests to test the equality of means
- Estimate regressions
- Perform inference on regression coefficients

```
library(readxl)       # enable the read_excel function
library(tidyverse)    # for almost all data handling tasks
library(ggplot2)      # plotting toolbox
library(utils)        # for reading data into R # for reading data into R
library(httr)         # for downloading data from a URL
library(stargazer)    # for nice regression output
library(ISOweek)      # Weeks are provided in the ISO weeks format
library(countrycode)  # to translate country codes
```

Data Import

Import the data from the "StaticECDCdata_18Feb22.csv" file. Make sure the file is saved in your working directory, that you set the working directory correctly and that you set the the `na=` option in the `read.csv` function to the value in which missing values are coded in the csv file. To do this correctly you will have to open the csv file (with your spreadsheet software, e.g. Excel) and check for instance cell K2.

```
setwd("YOUR WORKING DIRECTORY")
data <- read.csv(XXXX,na="XXXX",stringsAsFactors = TRUE)
str(data)
```

```
## 'data.frame':    22679 obs. of  14 variables:
##  $ X                       : int  1 2 3 4 5 6 7 8 9 10 ...
##  $ country                 : Factor w/ 226 levels "Afghanistan",..: 1 1 1 1 1 1 1 1 1 1 ...
##  $ country_code            : Factor w/ 220 levels "ABW","AFG","AGO",..: 2 2 2 2 2 2 2 2 2 2 ...
##  $ continent               : Factor w/ 5 levels "Africa","America",..: 3 3 3 3 3 3 3 3 3 3 ...
##  $ popData2019             : num  38928341 38928341 38928341 38928341 38928341 ...
##  $ dates                   : Factor w/ 111 levels "2020-01","2020-02",..: 1 2 3 4 5 6 7 8 9 10 ...
##  $ cases_weekly            : int  0 0 0 0 0 0 0 0 1 3 ...
##  $ deaths_weekly           : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ cases_weekly_cumulative : int  0 0 0 0 0 0 0 0 1 4 ...
##  $ deaths_weekly_cumulative: int  0 0 0 0 0 0 0 0 0 0 ...
##  $ cases_14_day            : num  NA 0 0 0 0 ...
##  $ deaths_14_day           : num  NA 0 0 0 0 0 0 0 0 0 ...
##  $ source_cases            : Factor w/ 3 levels "Epidemic intelligence national data",..: 1 1 1 1 1
##  $ source_deaths           : Factor w/ 3 levels "Epidemic intelligence national data",..: 1 1 1 1 1
```

The addition of `stringsAsFactors = TRUE` ensures that character variables are automatically translated into categorical (factor) variables. This will save us some work.

You got it right if the output from `str(data)` looks like the above. Thje dataset also contains data on entire continents but we will remove these datalies.

```
# remove continent data
data <- data %>% filter(!is.na(country_code))
```

Let's also calculate the per-capita data to ensure that we can compare countries of different sizes.

```
data <- data %>%
          mutate(pc_cases = (cases_weekly/popData2019)*100000,
                 pc_deaths = (deaths_weekly/popData2019)*100000)
```

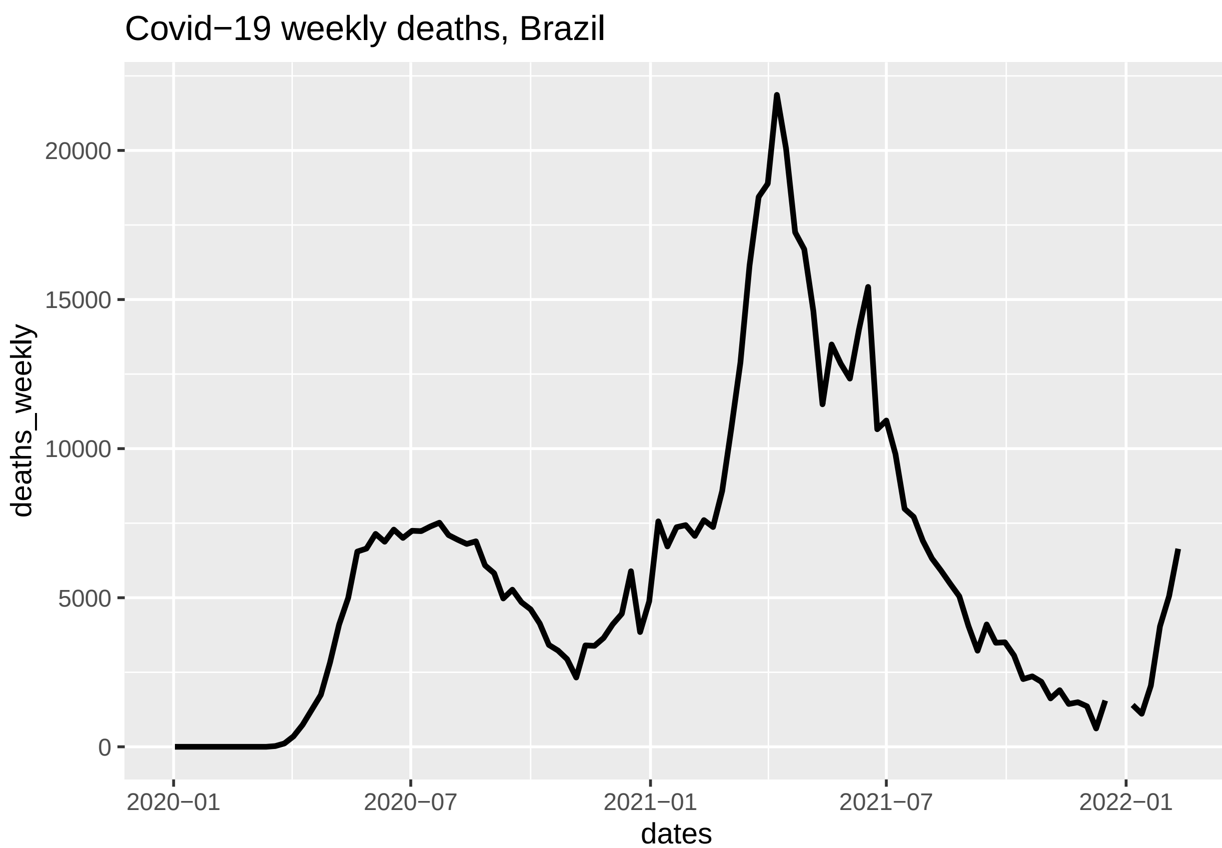
The date information is currently captured in the `dates` variable. Variable `dates` is currently a factor (`factor`) variable (originalla a `chr` but as we imported we converted these all to factor), but we want R to know that each string represents a date. What we do here was described in detail in the code to Lecture 2.

```
data <- data %>%
  separate(dates, c("year", "week"), "-") %>%
  mutate(dates = ISOweek2date(paste0(year,"-W",week,"-4")))
```

Plotting data as time-series

Here we will practice some time-series plotting. Let's start with a simple plot for Brazil.

```
g1 <- XXXX(subset(data, country == "XXXX"), aes(x=dates,y=deaths_weekly)) +
      geom_XXXX() +
      ggtitle("Covid-19 weekly cases, Brazil")
g1
```



Next we want to compare this development to the similar time line for the two countries which have population size close to Brazil. For that purpose we want to see a Table of Data with merely country names and populations ordered by population size. Then we pick the country with the next smaller and next larger population compared to Brazil.

```
temp <- data %>% select(country,popData2019) %>%
          unique() %>%
          arrange(desc(popData2019))
head(temp,14)
```

```
##                      country popData2019
## 1                      China  1439323774
## 2                      India  1380004385
## 3  United States Of America   331002647
## 4                  Indonesia   273523621
## 5                   Pakistan   220892331
## 6                     Brazil   212559409
## 7                    Nigeria   206139587
## 8                 Bangladesh   164689383
## 9                     Russia   145934460
## 10                    Mexico   128932753
## 11                     Japan   126476458
## 12                  Ethiopia   114963583
## 13               Philippines   109581085
## 14                     Egypt   102334403
```

Try and figure out what the above does. What do `select`, `unique` and `arrange` do? Could you change the order in which you call these actions?

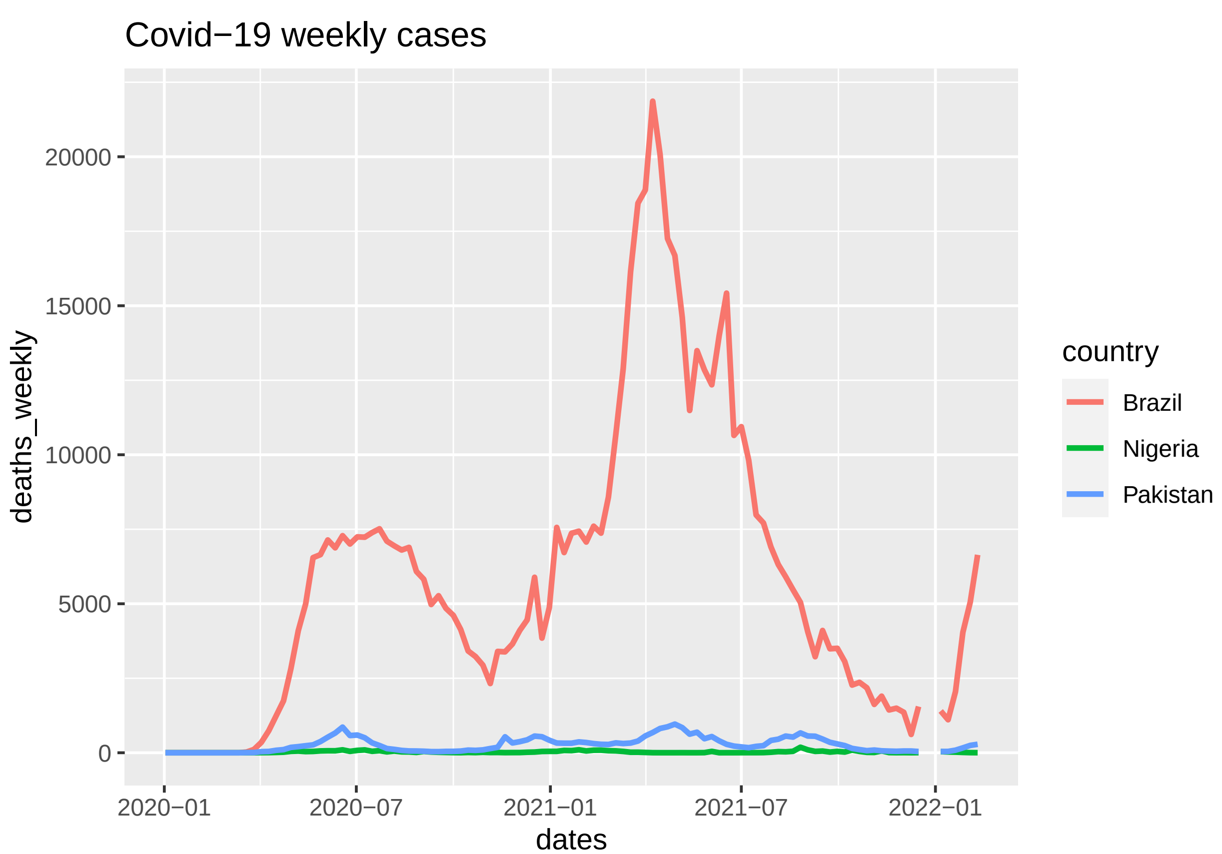
For instance, what does the following do?

```
temp2 <- data %>% arrange(desc(popData2019)) %>%
          unique() %>%
          select(country,popData2019)
```

You should find that table to be a lot less useful than `temp`.

From Table `temp` you should be able to identify that Pakistan and Nigeria are the next larger and next smaller country. Create a new variable `sel_countries` which you use to select data for these countries and then plot a line graph with weekly case numbers for these three countries. You may want to check out previous code (Week 2 Empirical Work Script) to see what needs doing.

```
sel_countries <- c("Brazil", "XXXX", "XXXX")
g2 <- ggplot(subset(XXXX, country %in% XXXX),
             XXXX(x=dates,XXXX=XXXX, color = XXXX)) +
      geom_line(XXXX=1) +
      XXXX("Covid-19 weekly cases")
g2
```



Import additional country indicators

The following three files will add the following variables to your dataframe

- Land_Area_sqkm
- HealthExp

- GDPpc
- Obese_Pcent
- Over_65s
- Diabetis

Make sure that these files are saved in your working directory. In our dataframe `data` we have 2-digit (`geoId`) and 3-digit (`country_code`) country codes. If at all possible you should merge data on the basis of such codes. Often different organisations name countries slightly differently (e.g. Ivory Coast or Cote d'Ivoire) and only the slightest difference will prevent any matching.

```
countryInd <- read_csv("CountryIndicators.csv",na = "#N/A")
countryInd <- countryInd %>% select(-country)
obesity <- read_csv("Obesity.csv")   # Adds obesity and diabetis country
obesity <- obesity %>% select(-country)
over65p <- read_excel("Over 65s 2.xlsx")
```

In "CountryIndicators.csv" and "Obesity.csv" we can find a 2-digit `geoID` and hence we will match on the basis of this variable. As both these files also contain a variable `country` (with potentially different spellings to those in `data`) we remove these variables before we merge. We use country codes to match the data precisely to avoid any problems from slightly different spellings.

The data coming from "Over 65s 2.xlsx" contain a three digit country code, as does the `data` file at this stage. For instance the 3 digit code for Afghanistan is AFG and the two digit code is AF. So, we have a mixture of codes and we need something that translates one into the other so that we can merge these data all into one dataframe.

As discussed in the Week 2 empirical workscript there is a tool just for that job, the `countrycode` library. We add a two digit country code to `data` and call it `geoID`.

```
data$geoID <- countrycode(data$country_code, origin = "iso3c", destination = "iso2c")
```

Now we are in a position to merge the datasets.

```
# by.x and by.y specify the matching variables of x (data) and y (countryInd)
data<- merge(data,countryInd,by.x="geoID", by.y="geoID",all.x=TRUE)
data <- merge(data,obesity,by.x="geoID", by.y="geoID",all.x=TRUE)
```

In "Over 65s 2.xlsx" you will find a 3-digit country code (`country_code`). This is spelled exactly as in `data` and hence we do not need to specify `by.x` and `by.y`. The merge function will, if not advised otherwise by `by.x` and `by.y` match on variables which have the same name in both dataframes.

```
data <- merge(data,over65p,by.x="country_code", by.y="countryCode",all.x=TRUE)
```

Check whether `data` indeed contains these variables. Which of the following commands is useful for this?

```
view(data)
str(data)
```

```
## 'data.frame':    22017 obs. of  25 variables:
##  $ country_code           : Factor w/ 220 levels "ABW","AFG","AGO",..: 1 1 1 1 1 1 1 1 1 1 ...
##  $ geoID                  : chr  "AW" "AW" "AW" "AW" ...
##  $ X                      : int  1245 1246 1263 1261 1262 1244 1264 1186 1242 1256 ...
##  $ country                : Factor w/ 226 levels "Afghanistan",..: 13 13 13 13 13 13 13 13 13 13 ..
##  $ continent              : Factor w/ 5 levels "Africa","America",..: 2 2 2 2 2 2 2 2 2 2 ...
##  $ popData2019            : num  106766 106766 106766 106766 106766 ...
##  $ year                   : chr  "2021" "2021" "2022" "2021" ...
##  $ week                   : chr  "35" "36" "02" "52" ...
##  $ cases_weekly           : int  353 231 3285 NA 5372 448 1728 8 877 121 ...
##  $ deaths_weekly          : int  12 4 2 NA 1 11 9 0 10 1 ...
```

```
##  $ cases_weekly_cumulative : int  14861 15092 30677 22020 27392 14508 32405 113 13406 16210 ...
##  $ deaths_weekly_cumulative: int  151 155 184 181 182 139 193 3 121 173 ...
##  $ cases_14_day           : num  750 547 8108 4844 NA ...
##  $ deaths_14_day          : num  215.42 149.86 28.1 9.37 NA ...
##  $ source_cases           : Factor w/ 3 levels "Epidemic intelligence national data",..: 1 1 1 1 1 
##  $ source_deaths          : Factor w/ 3 levels "Epidemic intelligence national data",..: 1 1 1 1 1 
##  $ pc_cases               : num  331 216 3077 NA 5032 ...
##  $ pc_deaths              : num  11.24 3.747 1.873 NA 0.937 ...
##  $ dates                  : Date, format: "2021-09-02" "2021-09-09" ...
##  $ Land_Area_sqkm         : num  NA NA NA NA NA NA NA NA NA NA ...
##  $ HealthExp              : num  NA NA NA NA NA NA NA NA NA NA ...
##  $ GDPpc                  : num  NA NA NA NA NA NA NA NA NA NA ...
##  $ Obese_Pcent            : num  NA NA NA NA NA NA NA NA NA NA ...
##  $ Over_65s               : num  14.1 14.1 14.1 14.1 14.1 ...
##  $ Diabetis               : num  11.6 11.6 11.6 11.6 11.6 11.6 11.6 11.6 11.6 11.6 ...
```

```
summary(data)
```

```
##   country_code      geoID                X             country    
##  AUT    :  111   Length:22017       Min.   :    1   Austria :  111  
##  BEL    :  111   Class :character   1st Qu.: 5835   Belgium :  111  
##  BGR    :  111   Mode  :character   Median :11561   Bulgaria:  111  
##  CYP    :  111                      Mean   :11520   Croatia :  111  
##  CZE    :  111                      3rd Qu.:17175   Cyprus  :  111  
##  DEU    :  111                      Max.   :22679   Czechia :  111  
##  (Other):21351                                      (Other) :21351  
##    continent     popData2019            year               week          
##  Africa :5467   Min.   :8.090e+02   Length:22017       Length:22017      
##  America:4922   1st Qu.:8.880e+05   Class :character   Class :character  
##  Asia   :4433   Median :6.871e+06   Mode  :character   Mode  :character  
##  Europe :5928   Mean   :3.790e+07                                        
##  Oceania:1267   3rd Qu.:2.638e+07                                        
##                 Max.   :1.439e+09                                        
##                                                                          
##   cases_weekly     deaths_weekly     cases_weekly_cumulative
##  Min.   :  -3864   Min.   : -439.0   Min.   :       0       
##  1st Qu.:     30   1st Qu.:    0.0   1st Qu.:    1234       
##  Median :    489   Median :    6.0   Median :   16839       
##  Mean   :  18417   Mean   :  264.1   Mean   :  584670       
##  3rd Qu.:   5027   3rd Qu.:   69.0   3rd Qu.:  199083       
##  Max.   :6178670   Max.   :29330.0   Max.   :77739880       
##  NA's   :188       NA's   :188                              
##  deaths_weekly_cumulative  cases_14_day       deaths_14_day     
##  Min.   :     0           Min.   :   -1.056   Min.   : -67.135  
##  1st Qu.:    18           1st Qu.:    2.229   1st Qu.:   0.000  
##  Median :   255           Median :   24.120   Median :   2.431  
##  Mean   : 12193           Mean   :  212.259   Mean   :  20.852  
##  3rd Qu.:  3452           3rd Qu.:  161.606   3rd Qu.:  19.898  
##  Max.   :919696           Max.   :20394.966   Max.   :1395.031  
##                           NA's   :409         NA's   :409       
##                                                      source_cases  
##  Epidemic intelligence national data                       :19020  
##  Epidemic intelligence national data and TESSy COVID-19:    0  
##  TESSy COVID-19                                            : 2997  
##                                                                    
```

```
##
##
##
##                                                  source_deaths
##  Epidemic intelligence national data                   :19575
##  Epidemic intelligence national data and TESSy COVID-19:    0
##  TESSy COVID-19                                        : 2442
##
##
##
##
##     pc_cases           pc_deaths          dates             Land_Area_sqkm
##  Min.   :  -21.901   Min.   :-6.7288   Min.   :2020-01-02   Min.   :      60
##  1st Qu.:    0.918   1st Qu.: 0.0000   1st Qu.:2020-08-20   1st Qu.:   28100
##  Median :   11.317   Median : 0.0986   Median :2021-02-18   Median :  130000
##  Mean   :  109.218   Mean   : 1.0413   Mean   :2021-02-14   Mean   :  717185
##  3rd Qu.:   79.563   3rd Qu.: 0.9462   3rd Qu.:2021-08-12   3rd Qu.:  548000
##  Max.   :10353.013   Max.   :80.1401   Max.   :2022-02-10   Max.   :16400000
##  NA's   :188         NA's   :188                            NA's   :3272
##    HealthExp         GDPpc            Obese_Pcent       Over_65s
##  Min.   : 1.597   Min.   :   310.3   Min.   : 2.10    Min.   : 1.157
##  1st Qu.: 4.401   1st Qu.:  2201.6   1st Qu.: 8.90    1st Qu.: 3.509
##  Median : 6.301   Median :  6372.6   Median :20.60    Median : 7.273
##  Mean   : 6.478   Mean   : 16783.1   Mean   :18.81    Mean   : 9.319
##  3rd Qu.: 8.136   3rd Qu.: 19441.1   3rd Qu.:25.00    3rd Qu.:15.061
##  Max.   :17.553   Max.   :185835.0   Max.   :55.90    Max.   :28.002
##  NA's   :3865     NA's   :3865       NA's   :3384     NA's   :2890
##     Diabetis
##  Min.   : 0.000
##  1st Qu.: 5.100
##  Median : 6.800
##  Mean   : 7.917
##  3rd Qu.:10.200
##  Max.   :30.500
##  NA's   :963
```

```
names(data)
```

```
##  [1] "country_code"             "geoID"
##  [3] "X"                        "country"
##  [5] "continent"                "popData2019"
##  [7] "year"                     "week"
##  [9] "cases_weekly"             "deaths_weekly"
## [11] "cases_weekly_cumulative"  "deaths_weekly_cumulative"
## [13] "cases_14_day"             "deaths_14_day"
## [15] "source_cases"             "source_deaths"
## [17] "pc_cases"                 "pc_deaths"
## [19] "dates"                    "Land_Area_sqkm"
## [21] "HealthExp"                "GDPpc"
## [23] "Obese_Pcent"              "Over_65s"
## [25] "Diabetis"
```

Now we need to calculate the Population density.

```
# calculate population density
data <- data %>% XXXX(popdens = XXXX/XXXX)
```

Confirm that the average population density in your dataset is 219.1622949.

```
##     Min.  1st Qu.   Median     Mean  3rd Qu.     Max.     NA's
##    2.115   36.175   86.756  219.162  213.783 8251.542     3272
```

Average data over the sample period

What we now do is to aggregate the weekly cases and deaths data. In the Lecture and the Review and Q&A session we did this over the entire available sample period. Could there be reasons why we may not want to do this over the entire period?

It is in the nature of such a pandemic that it starts in one location and then, initially slowly, spreads through different geographies. The initial spread may well be determined by travel patterns emanating from the country initial effected (here China). In order to reduce the influence of this initial geographic pattern we now decide to aggregate only for data from June 2021 onwards ("2020-06-01" and later).

This was the code we used in the Week2 material to calculate these averages (including all available data).

```
table3 <- data %>% group_by(country) %>% # groups by Country
            summarise(Avg_cases = mean(pc_cases,na.rm = TRUE),
                      Avg_deaths = mean(pc_deaths,na.rm = TRUE),
                      PopDen = mean(popdens))
```

Find a way to adjust this bit of code such that the average calculations are only based on data from "2020-06-01" onwards. What operation should you use in place of `XXXX`? Here is a link to a one page tidyverse cheat sheet. There are 4 major type of operations you can perform in a pipe (`%>%`), `filter`, `arrange`, `mutate`, `summarise\summarize` and (although not on the cheat sheet) `select`. Which one is the one to use?

Also note the following. The `summarise` function is designed to summarise information, e.g. for a particular country, which varies in the country specific sample. However, we not only want to summarise the number of weekly cases and deaths, we also want to have the country information for population density, obesity, diabetis, Over 65s, GDPpc, HealthExp and the countries continent. Below you see, inside the summarise function terms like `PopDen = first(popdens)`. This selects the first `popdens` observation for a particular country. As all these variables do not vary through our sample this little trick delivers exactly what we want.

```
table3 <- data %>% XXXX %>%
            group_by(country) %>% # groups by Country
            summarise(Avg_cases = mean(pc_cases,na.rm = TRUE),
                      Avg_deaths = mean(pc_deaths,na.rm = TRUE),
                      PopDen = first(popdens),
                      Obese = first(Obese_Pcent),
                      Diabetis = first(Diabetis),
                      Over_65s = first(Over_65s),
                      GDPpc = first(GDPpc)/1000,  # calculate GDPpc in $1000s
                      HealthExp = first(HealthExp),
                      Continent = first(continentExp))
```

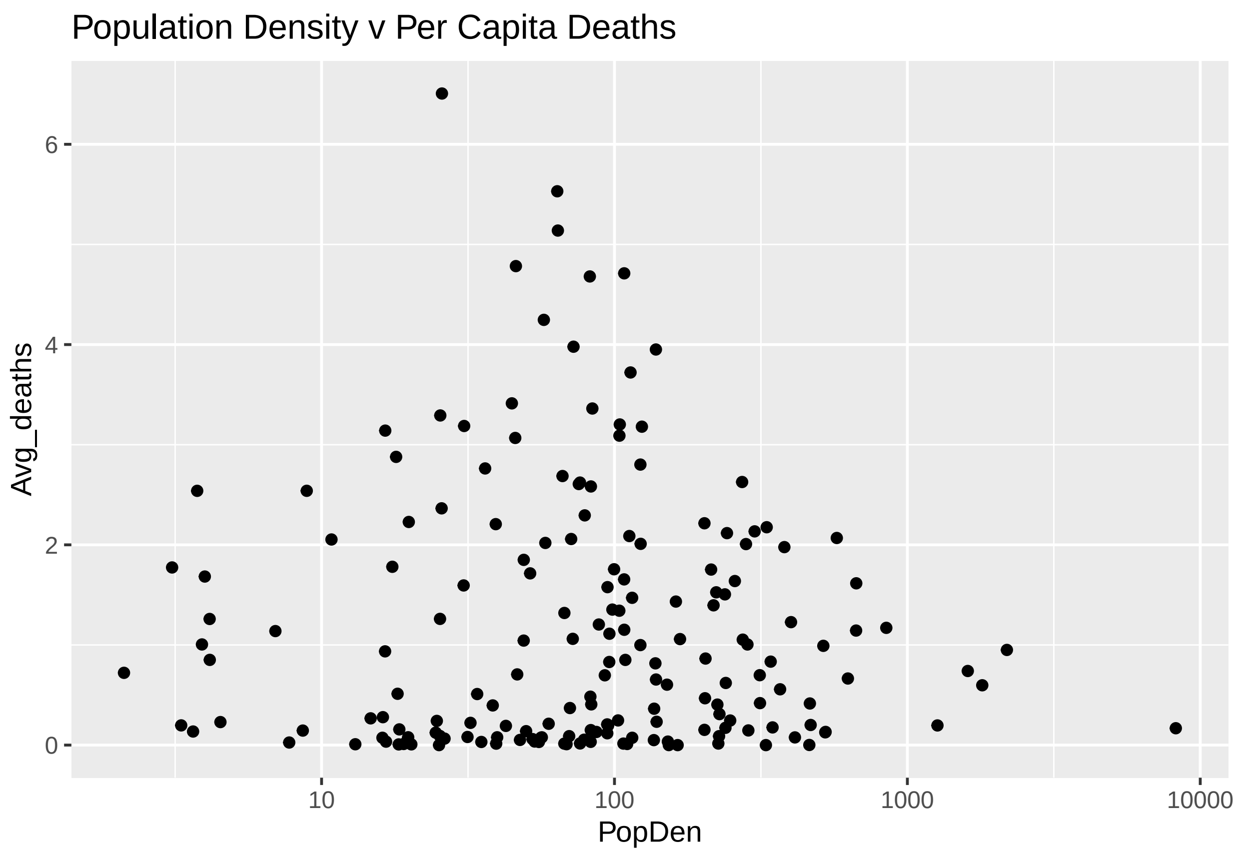
After you selected, check `head(table3)` to confirm that you got the same result.

```
## # A tibble: 6 x 10
##   country   Avg_cases Avg_deaths PopDen Obese Diabetis Over_65s  GDPpc HealthExp
##   <fct>         <dbl>      <dbl>  <dbl> <dbl>    <dbl>    <dbl>  <dbl>     <dbl>
## 1 Afghanis~      4.59      0.213   59.6   5.5      9.2     2.62  0.530      9.40
## 2 Albania      106.        1.34   104.   21.7      9      14.2   5.22       5.26
## 3 Algeria        6.52      0.157   18.4  27.4      6.7     6.55  4.11       6.22
## 4 American~      5.07      0        NA    NA       0      NA    NA         NA
## 5 Andorra      499.        1.43   162.   25.6      7.7    NA    42.1        6.71
```

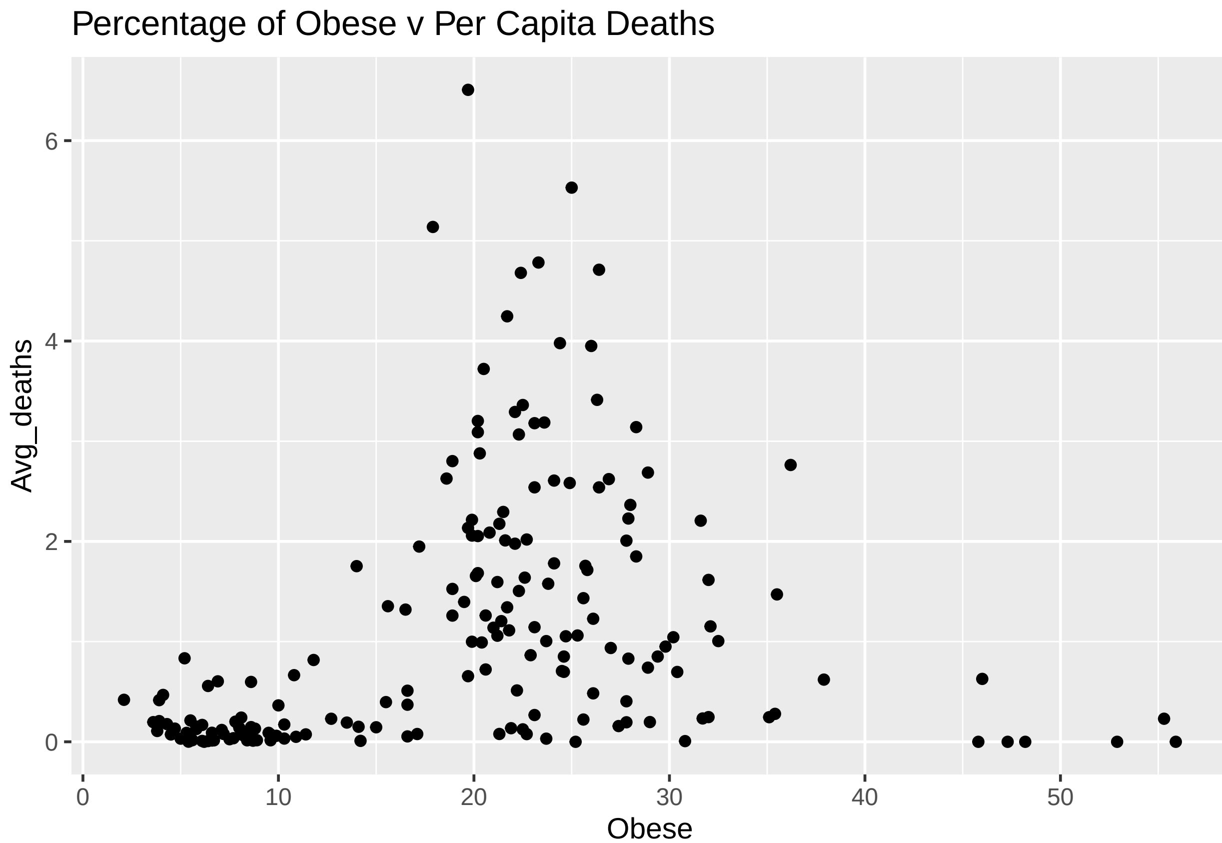
```
## 6 Angola         2.85     0.0650   26.3   8.2      4.5      2.20  3.44       2.55
## # ... with 1 more variable: Continent <fct>
```

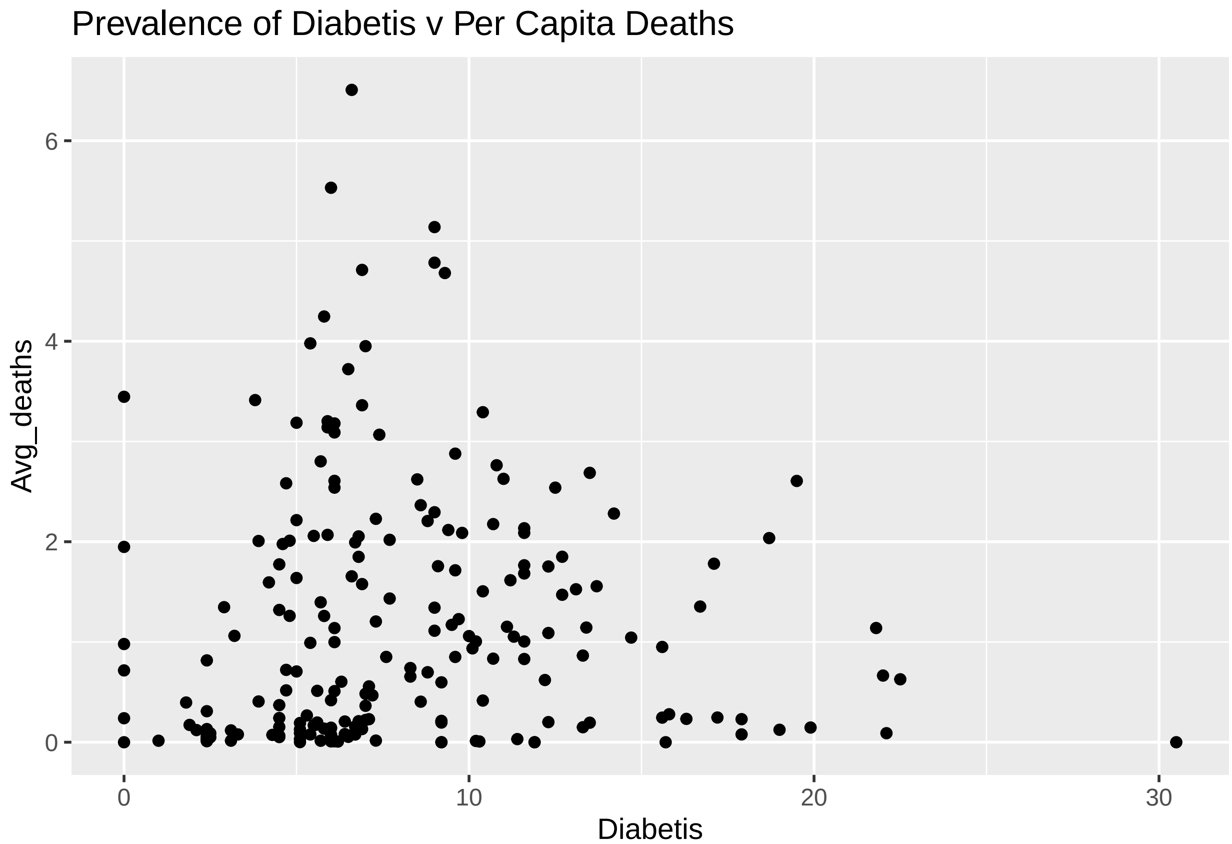
Let's create a few plots which show the average death numbers against some of our country specific information.

```
ggplot(table3,aes(PopDen,Avg_deaths)) +
  geom_point() +
  scale_x_log10() +
  ggtitle("Population Density v Per Capita Deaths")
```



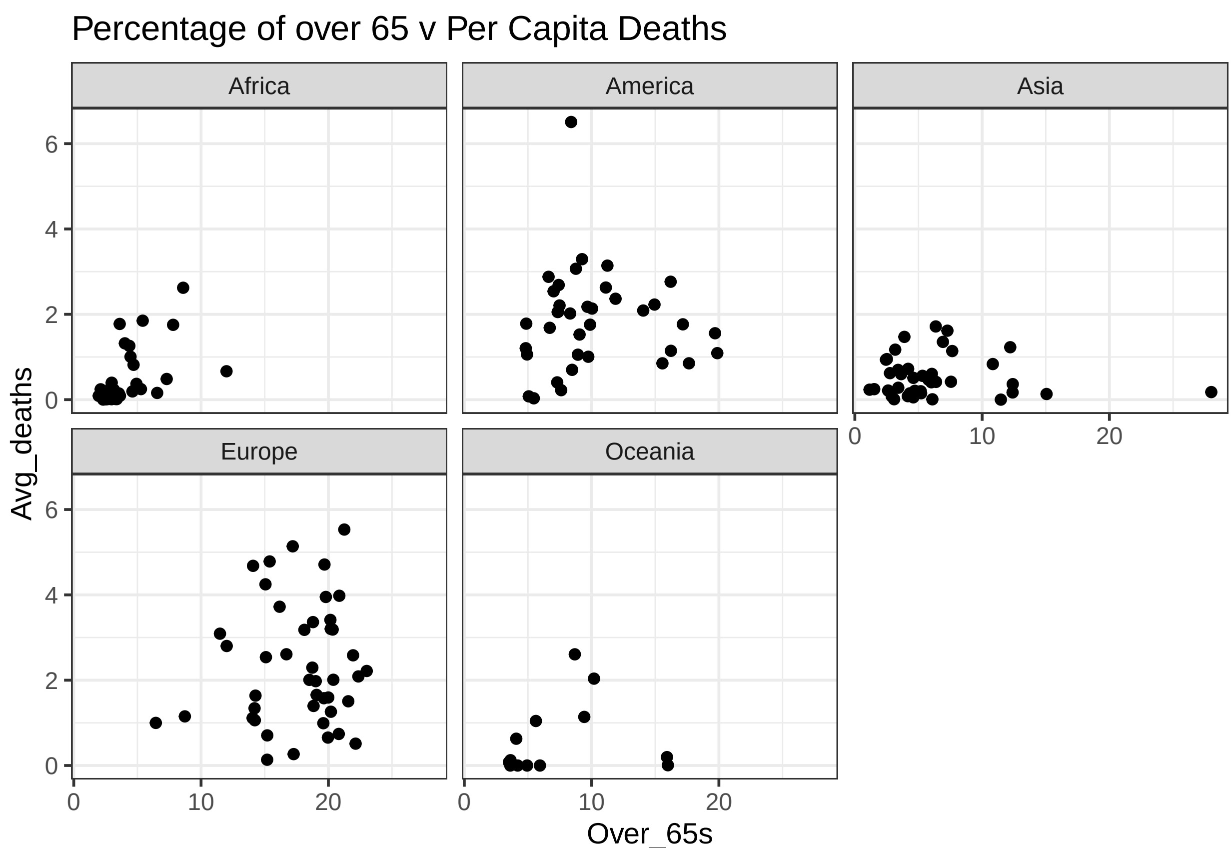
Now replicate the following graphs.


Percentage of Obese v Per Capita Deaths
Avg_deaths
Obese
0
2
4
6
0
10
20
30
40
50



Let’s also create plots of deaths against the proportion of over 65s, but this time we want to split the graph according to continents.

```
ggplot(table3,aes(Over_65s,Avg_deaths)) +
  geom_point() +
  facet_wrap(~ Continent) +  # this is where the magic happens!
  theme_bw() +
  ggtitle("Percentage of over 65 v Per Capita Deaths")
```



Nice, right?! Check out the GGplot cheat sheet for more tricks and illustrations of this packages' capabilities.

Testing for equality of means

Let's perform some hypothesis tests to check whether there are significant differences between the average rates of cases and deaths since June 2020 between continents.

We therefore continue to work with the data in `table3`. In `table4` we calculate continental averages.

```
table4 <- table3 %>%
              group_by(Continent) %>%
              summarise(CAvg_cases = mean(Avg_cases, na.rm = TRUE),
                        CAvg_deaths = mean(Avg_deaths, na.rm = TRUE),
                        n = n()) %>% print()
```

```
## # A tibble: 5 x 4
##   Continent CAvg_cases CAvg_deaths     n
##   <fct>          <dbl>       <dbl> <int>
## 1 Africa          25.2       0.329    55
## 2 America        133.        1.63     49
## 3 Asia            77.3       0.512    42
## 4 Europe         263.        2.15     55
## 5 Oceania        122.        0.487    19
```

Let's see whether we find the continental averages to be statistically significantly different. Say we compare the `avg_deaths` in America and Asia. So test the null hypothesis that $H_0 : \mu_{AS} = \mu_{AM}$ (or $H_0 : \mu_{AS} - \mu_{AM} = 0$) against the alternative hypothesis that $H_A : \mu_{AS} \neq \mu_{AM}$, where μ represents the average death rate of countries in the respective continent over the sample period (here June onwards).

```
test_data_AS <- table3 %>%
  filter(Continent == "Asia")      # pick Asian data

test_data_AM <- table3 %>%
  filter(Continent == "America")      # pick European data

t.test(test_data_AS$Avg_deaths,test_data_AM$Avg_deaths, mu=0)  # testing that mu = 0
```

```
##
##  Welch Two Sample t-test
##
## data:  test_data_AS$Avg_deaths and test_data_AM$Avg_deaths
## t = -6.1998, df = 65.827, p-value = 4.202e-08
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -1.4778610 -0.7578499
## sample estimates:
## mean of x mean of y
## 0.5122709 1.6301263
```

The difference in the averages is 0.5122709 - 1.6301263 = -1.1179 (a bit more than 1 in 100,000 population). We get a t-test statistic of around -6. If in truth the two means were the same then we should expect the test statistic to be around 0. Is -6 far enough away from 0 for us to conclude that we should stop supporting the null hypothesis? The value of the t-test is approximately -6.2. Is that big. If H_0 was correct (same average death rates in America and Asia) then we should on average expect the t-test to come out around a value of 0. So -6.2 is clearly not 0, but is it so far away from 0 that we should reject H_0?

The answer is yes and the p-value does tell us that it is. The p-value is 4.202e-08 or 0.00000004202 or 0.000004%. This means that if the H_0 was correct, the probability of getting a difference of -1.1179 (per 100,000 population) or a more extreme difference is 0.000004%. We judge this probability to be too small for us to continue to support the H_0 and we reject the H_0. We do so as the p-value is smaller than any of the usual significance levels (10%, 5% or 1%).

We are not restricted to testing whether two population means are the same. You could also test whether the difference in the population is anything different but 0. Say a politician claims that evidently the case rate in Europe is larger by more than 100 per 100,000 population than the case rate in America.

Here our H_0 is $H_0: \mu_{EU} = \mu_{AM} + 100$ (or $\mu_{EU} - \mu_{AM} = 50$) and we would test this against an alternative hypothesis of $H_A: \mu_{EU} > \mu_{AM} + 100$ (or $H_A: \mu_{EU} - \mu_{AM} > 100$). Here the statement of the politician is represented in the H_A.

```
test_data_EU <- table3 %>%
  filter(Continent == "Europe")      # pick European data

test_data_AM <- table3 %>%
  filter(Continent == "America")      # pick American data

t.test(test_data_EU$Avg_cases,test_data_AM$Avg_cases, mu=100, alternative = "greater")
```

```
##
##  Welch Two Sample t-test
##
## data:  test_data_EU$Avg_cases and test_data_AM$Avg_cases
## t = 1.4819, df = 93.809, p-value = 0.07086
## alternative hypothesis: true difference in means is greater than 100
```

```
## 95 percent confidence interval:
##  96.37232      Inf
## sample estimates:
## mean of x mean of y
##  263.1109  133.1460
```

Note the following. The parameter `mu` now takes the value 100 as we are hypothesising that the difference in the means in 100 (or larger than that in the H_A). Also, in contrast to the previous test we now care whether the deviation is less or greater than 100. In this case we wonder whether it is really greater. Hence we use the additional input into the test function, `alternative = "greater"`. (The default for this input is `alternative = "two.sided"` and that is what is used, as in the previous case, if you don't add it to the `t.test` function). Also check `?t.test` for an explanation of these optional input parameters.

Again we find ourselves asking whether the sample difference we obtained (263.1109-133.1460=129.9649) is consistent with the null hypothesis (of the population difference being 100 - or smaller). Here the answer is subtle. The p-value is 0.07086, so the probability of obtaining a sample difference as big as 129.9649 (or bigger) is just a little over 5%, if in truth H_0 was true. Say we set out to perform a test at a 10% significance level, then we would judge a probability of just above 5% to be too small and hence we would reject the null hypothesis. If however we set out to perform a test at a 1% significance level then we would not reject the null hypothesis.

So let's perform another test. An European opposition politician is lamenting that the European case rate is more than 200 (per 100,000 population) larger than that in Asia. Perform the appropriate hypothesis test.

```
t.test(test_data_XXXX$Avg_cases,test_data_XXXX$Avg_cases, mu=XXXX, alternative = XXXX)
```

```
##
##  Welch Two Sample t-test
##
## data:  test_data_EU$Avg_cases and test_data_AS$Avg_cases
## t = -0.62074, df = 94.421, p-value = 0.7319
## alternative hypothesis: true difference in means is greater than 200
## 95 percent confidence interval:
##  147.836     Inf
## sample estimates:
## mean of x mean of y
## 263.11095  77.30111
```

The p-value is certainly larger than any of the usual significance levels and we fail to reject H_0. This means that the opposition politician's statement is not supported by the data.

Regression and inference

To perform inference in the context of regressions it pays to use an additional package, the `car` package. So please load this package. (If you are working on your own computer you will first have to install this package. On university computers it should be pre-installed.)

```
library(car)
```

If you get an error message it is likely that you first have to install that package.

In the lecture we talked about a base case regression

$Avg\_deaths_i = \alpha + \beta_1 \ GDPpc_i + \beta_2 \ HealthExp_i + u_i$

Let us estimate this again using the average rates calculated on data from June 2020 onwards only (hence the results here will be somewhat different to those in the lecture).

```r
mod3 <- lm(Avg_deaths~GDPpc+HealthExp,data=table3)
stargazer(mod3,type = "text")
```

```
##
## ===============================================
##                         Dependent variable:
##                     ---------------------------
##                             Avg_deaths
## -----------------------------------------------
## GDPpc                         0.004
##                              (0.004)
##
## HealthExp                    0.086**
##                              (0.036)
##
## Constant                     0.579**
##                              (0.247)
##
## -----------------------------------------------
## Observations                   176
## R2                            0.044
## Adjusted R2                   0.032
## Residual Std. Error      1.280 (df = 173)
## F Statistic            3.938** (df = 2; 173)
## ===============================================
## Note:               *p<0.1; **p<0.05; ***p<0.01
```

We see that, for these data, the `HealthExp` variable remains statistically significant although the `GDPpc` variable is not statistically significant.

Now add the `Obese`, `Diabetis` and `Over_65s` variables to the regression in order to evaluate whether their inclusion change the implausible negative sign on `HealthExp`.

```r
mod4 <- lm(Avg_deaths~GDPpc+XXXX,data=table3)
stargazer(mod3,mod4,type = "text")
```

```
##
## =================================================================
##                                  Dependent variable:
##                     ---------------------------------------------
##                                      Avg_deaths
##                               (1)                     (2)
## -----------------------------------------------------------------
## GDPpc                        0.004                 -0.024***
##                             (0.004)                 (0.005)
##
## HealthExp                   0.086**                 -0.040
##                             (0.036)                 (0.035)
##
## Obese                                              0.051***
##                                                     (0.011)
##
## Over_65s                                           0.138***
##                                                     (0.016)
##
```

```
## Diabetis                                       -0.011
##                                                (0.022)
##
## Constant                   0.579**             -0.315
##                            (0.247)             (0.273)
##
## ----------------------------------------------------------------
## Observations                 176                  166
## R2                          0.044                0.458
## Adjusted R2                 0.032                0.441
## Residual Std. Error   1.280 (df = 173)      0.992 (df = 160)
## F Statistic         3.938** (df = 2; 173) 27.000*** (df = 5; 160)
## ================================================================
## Note:                                *p<0.1; **p<0.05; ***p<0.01
```

If you want to perform a hypothesis test say on β_3 (the coefficient on the `Obese` variable), then the usual hypothesis to pose is $H_0 : \beta_3 = 0$ versus $H_A : \beta_3 \neq 0$. It is the p-value to that hypothesis test which is represented by the asteriks next to the estimated coefficient. Let's confirm that. The estimated coefficient to the `Obese` variable is 0.051 and the (***) indicate that the p-value to that test should be less than 0.01.

Here is how you can perform this test manually using the `lht` (stands for Linear Hypothesis Test) function which is written to use regression output (here saved in `mod4`) for hypothesis testing.

```
lht(mod4,"Obese=0")
```

```
## Linear hypothesis test
##
## Hypothesis:
## Obese = 0
##
## Model 1: restricted model
## Model 2: Avg_deaths ~ GDPpc + HealthExp + Obese + Over_65s + Diabetis
##
##   Res.Df    RSS Df Sum of Sq      F    Pr(>F)
## 1    161 180.41
## 2    160 157.55  1    22.863 23.219 3.333e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

There is a lot of information, but the important one is the value displayed under ("Pr(>F)"), that is the p-value. Here it is very small, 0.00000333 (=3.333e-06), and as predicted < 0.01. In fact it is even smaller than 0.001.

Confirm that p-value for $H_0 : \beta_2 = 0$ versus $H_A : \beta_2 \neq 0$ (coefficient on `HealthExp`) is larger than 0.1.

```
## Linear hypothesis test
##
## Hypothesis:
## HealthExp = 0
##
## Model 1: restricted model
## Model 2: Avg_deaths ~ GDPpc + HealthExp + Obese + Over_65s + Diabetis
##
##   Res.Df    RSS Df Sum of Sq    F Pr(>F)
## 1    161 158.86
## 2    160 157.55  1    1.3096 1.33 0.2505
```

The use of the `lht` function is that you can test different hypothesis. Say $H_0 : \beta_4 = 0.1$ versus $H_A : \beta_4 \neq 0.1$

(coefficient on `Over_65s`).

```
lht(mod4,"Over_65s=0.1")
```

```
## Linear hypothesis test
##
## Hypothesis:
## Over_65s = 0.1
##
## Model 1: restricted model
## Model 2: Avg_deaths ~ GDPpc + HealthExp + Obese + Over_65s + Diabetis
##
##   Res.Df    RSS Df Sum of Sq      F  Pr(>F)
## 1    161 163.46
## 2    160 157.55  1    5.9163 6.0084 0.01531 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

So, that null hypothesis can be rejected at a 5% but not at a 1% level.

Even more so, you can use this function to test multiple hypotheses. Say you want to test whether the inclusion of the additional three variables (in `mod4` as opposed to `mod3`) is relevant. If it wasn't then the following null hypothesis should be correct: $H_0 : \beta_3 = \beta_4 = \beta_5 = 0$. We call this a multiple hypothesis.

Use the help function (`?lht`) or search for advice on how to use the `lht` function to test this hypothesis.

```
## Linear hypothesis test
##
## Hypothesis:
## Obese = 0
## Diabetis = 0
## Over_65s = 0
##
## Model 1: restricted model
## Model 2: Avg_deaths ~ GDPpc + HealthExp + Obese + Over_65s + Diabetis
##
##   Res.Df    RSS Df Sum of Sq     F    Pr(>F)
## 1    163 275.47
## 2    160 157.55  3    117.92 39.92 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The hypothesis that none of the three variables is relevant is clearly rejected.

The techniques you covered in this computer lab are absolutely fundamental to the remainder of this unit, so please ensure that you have not rushed over the material.