

# Covid19-TN

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19/03/2020

This is a strange year! In Tunisia since the beginning of March, and the appearance of the first case of COVID-19, we are more than ever worried. Here are some simulations following an SIR model. Data are missing, since for this model to be relevant it would require at least 10 more days of data's evolution.

I will use the same model already used in *Epidemiology: How contagious is Novel Coronavirus (2019-nCoV)?*; <https://blog.ehorie.de/epidemiology-how-contagious-is-novel-coronavirus-2019-ncov>

```
library(magrittr)# pipe operations
library(lubridate)# date operations

##
## Attaching package: 'lubridate'

## The following object is masked from 'package:base':
##
##   date

library(tidyverse)# ggplot2, tidyr, dplyr...

## -- Attaching packages ----- tidyverse 1.2.1 --
## v ggplot2 3.2.1    v purrr  0.3.3
## v tibble  2.1.3    v dplyr  0.8.3
## v tidyr   1.0.0    v stringr 1.4.0
## v readr   1.3.1    v forcats 0.4.0

## -- Conflicts ----- tidyverse_conflicts() --
## x lubridate::as_datetime() masks base::as_datetime()
## x lubridate::date()        masks base::date()
## x tidyr::extract()         masks magrittr::extract()
## x dplyr::filter()          masks stats::filter()
## x lubridate::intersect()   masks base::intersect()
## x dplyr::lag()             masks stats::lag()
## x purrr::set_names()       masks magrittr::set_names()
## x lubridate::setdiff()     masks base::setdiff()
## x lubridate::union()       masks base::union()

library(gridExtra)# multiple grid-based plots on a page

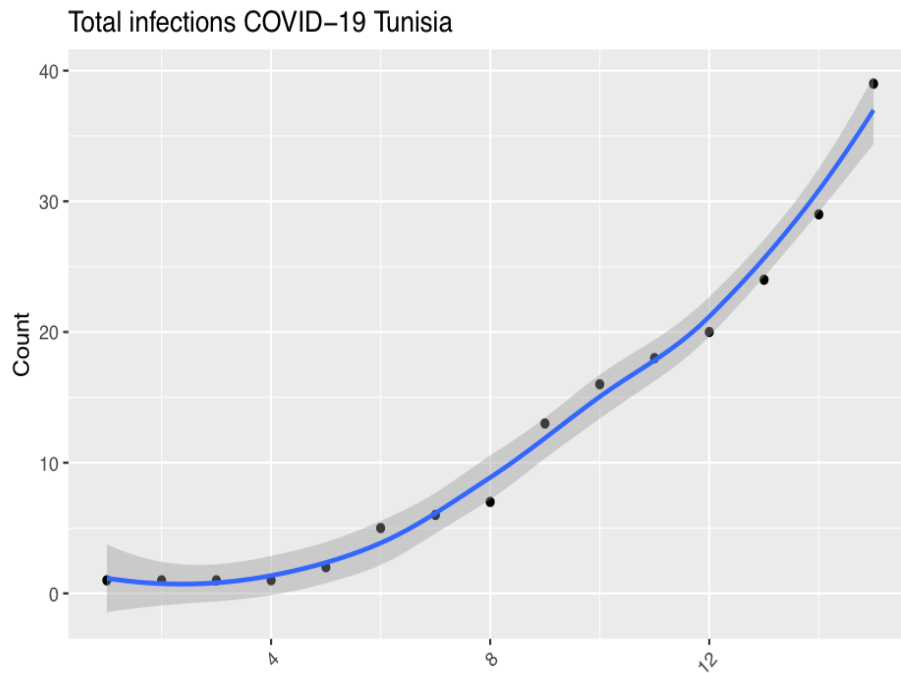
##
## Attaching package: 'gridExtra'

## The following object is masked from 'package:dplyr':
##
##   combine

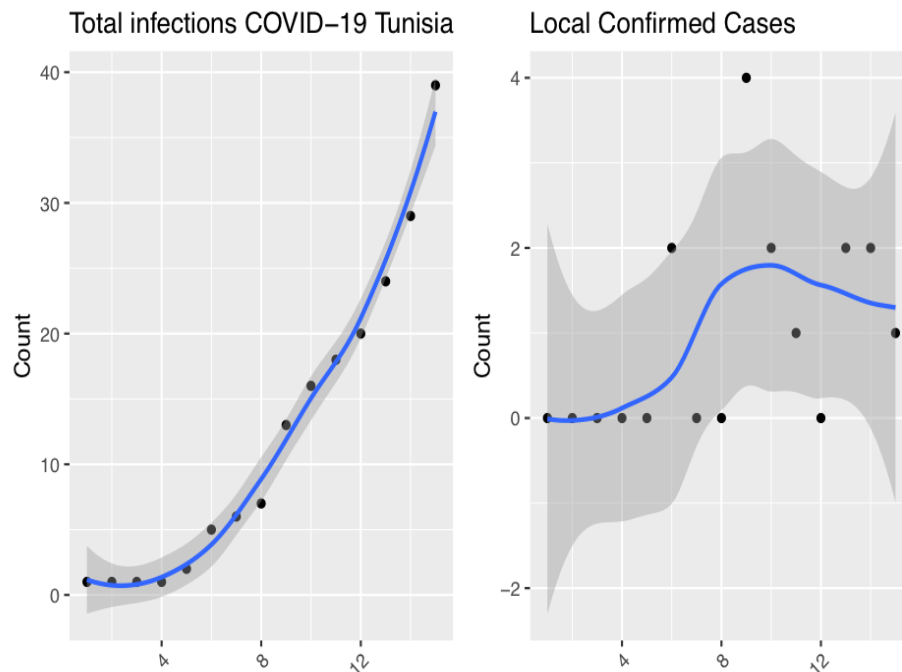
library(ggforce)# accelerating ggplot2
library(kableExtra)# complex tables

##
## Attaching package: 'kableExtra'
```

```
## The following object is masked from 'package:dplyr':
##
##   group_rows
data <- data.frame(Day,Infected)
plot1 <-ggplot(data = data, aes(x=Day, y=Infected))+geom_point()+ geom_smooth(method="loess",formula=y~x)
plot1
```



```
plot2 <-ggplot(data,aes(x=Day, y=Local.Infected))+geom_point()+ geom_smooth(method='loess',formula=y~x,
## show two plots side by side
grid.arrange(plot1, plot2, ncol=2)
```



```
library(deSolve)
# I followed the SIR used in https://www.r-bloggers.com/covid-19-the-case-of-germany/
SIR <- function(time, state, parameters) {
  par <- as.list(c(state, parameters))
  with(par, {
    dS <- -beta/N * I * S
    dI <- beta/N * I * S - gamma * I
    dR <- gamma * I
    list(c(dS, dI, dR))
  })
}

init <- c(S = N-Infected[1], I = Infected[1], R = 0)
RSS <- function(parameters) {
  names(parameters) <- c("beta", "gamma")
  out <- ode(y = init, times = Day, func = SIR, parms = parameters)
  fit <- out[, 3]
  sum((Infected - fit)^2)
}

Opt <- optim(c(0.5, 0.5), RSS, method = "L-BFGS-B", lower = c(0, 0), upper = c(1, 1)) # optimize with s
Opt$message

## [1] "CONVERGENCE: REL_REDUCTION_OF_F <= FACTR*EPSMCH"
## [1] "CONVERGENCE: REL_REDUCTION_OF_F <= FACTR*EPSMCH"

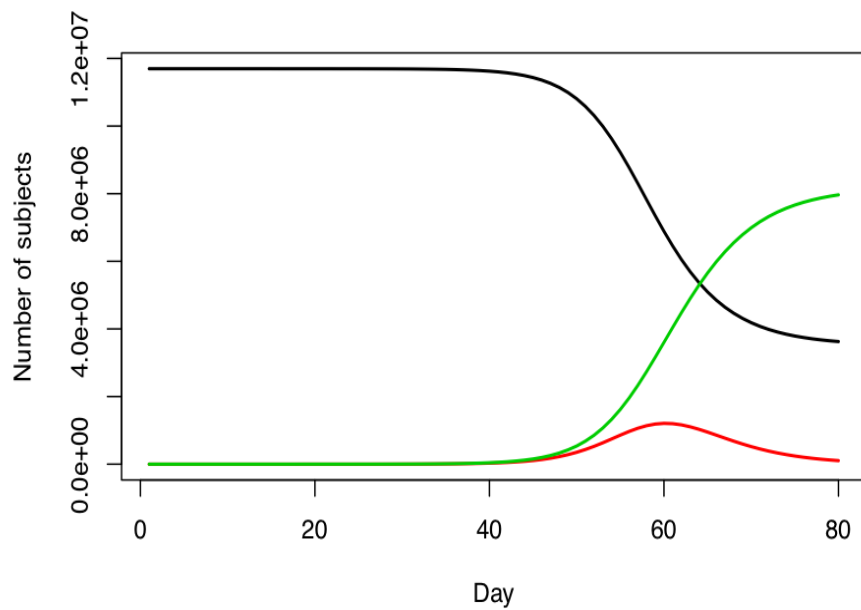
Opt_par <- setNames(Opt$par, c("beta", "gamma"))
Opt_par
```

```
##      beta      gamma
## 0.6322778 0.3677222

##      beta      gamma
## 0.6322778 0.3677222

t <- 1:80 # time in days
fit <- data.frame(ode(y = init, times = t, func = SIR, parms = Opt_par))
col <- 1:3 # colour

matplot(fit$time, fit[, 2:4], type = "l", xlab = "Day", ylab = "Number of subjects", lwd = 2, lty = 1,
```



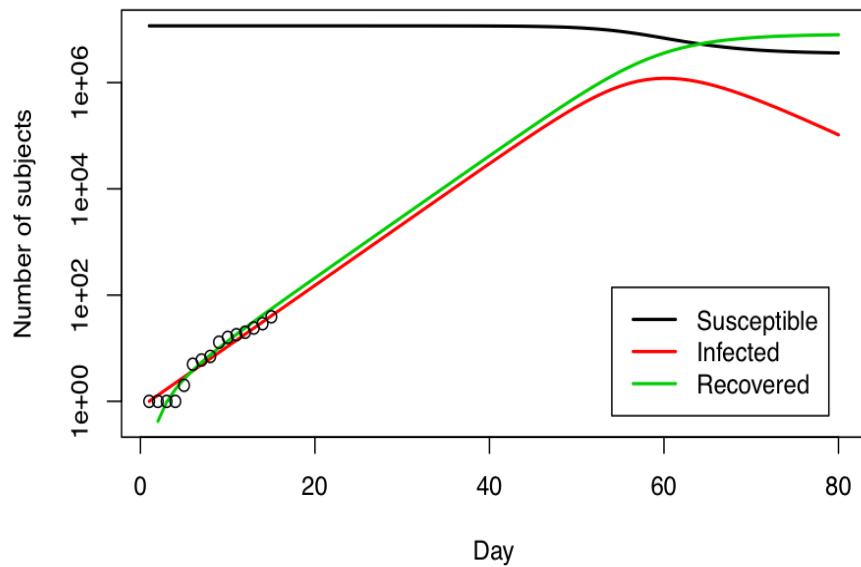
```
matplot(fit$time, fit[, 2:4], type = "l", xlab = "Day", ylab = "Number of subjects", lwd = 2, lty = 1,

## Warning in xy.coords(x, y, xlabel, ylabel, log = log): 1 y value <= 0
## omitted from logarithmic plot

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## omitted from logarithmic plot

points(Day, Infected)
legend("bottomright", c("Susceptible", "Infected", "Recovered"), lty = 1, lwd = 2, col = col, inset = 0
title("SIR model Covid-19 Tunisia", outer = TRUE, line = -2)
```

## SIR model Covid-19 Tunisia



```
R0 <- setNames(Opt_par["beta"] / Opt_par["gamma"], "R0")
print(R0)
```

```
##      R0
## 1.719444
```

```
fit[fit$I == max(fit$I), "I", drop = FALSE] # height of pandemic
```

```
##      I
## 60 1206340
##      I
## 60 1206340
```

```
max_infected <- max(fit$I)
max_infected / 5 # severe cases
```

```
## [1] 241267.9
## [1] 241267.9
```

```
max_infected * 0.06 # cases with need for intensive care
```

```
## [1] 72380.37
## [1] 72380.37
```

```
# https://www.newscientist.com/article/mg24532733-700-why-is-it-so-hard-to-calculate-how-many-people-wi
max_infected * 0.007 # deaths with supposed 0.7% fatality rate
```

```
## [1] 8444.377
```

```
## [1] 8444.377
```

So, according to this model, the height of the pandemic will be reached by the end of May, beginning of June. About 1.2 million people would be infected by then, which translates to about 240000 severe cases, about 72000 cases in need of intensive care and up to 8500 deaths.

Those are the numbers this model produces and nobody knows whether they are correct while everybody hopes they are not. One thing has to be kept in mind though: the numbers used in the model are from before the shutdown. So hopefully those measures will prove effective and the actual numbers will turn out to be much, much lower.

I wish you all the best and stay healthy!