How can we predict the evolution of COVID-19 in Belgium?

Antoine Soetewey

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SIR model

- A classic epidemiological model
- Applicable to many disease outbreaks
- 3 groups of individuals:
  1. **S**usceptible: healthy individuals but susceptible to the disease. At t_0, $S =$ entire population since no one is immune to the virus
  2. **I**nfectious
  3. **R**ecovered (or removed): contaminated individuals but who have either recovered or died. They are not infectious anymore

SIR model

As the virus progresses in the population:

- S decreases when individuals are contaminated and move to I
- As people recover or die, they go from I to R

SIR model

To model the outbreak we need to describe the change in each group, parameterised by:

- β (infection rate) which controls $S \to I$
- γ (removal rate) which controls $I \to R$

SIR model

$$\frac{dS}{dt} = -\frac{\beta IS}{N}$$

$$\frac{dI}{dt} = \frac{\beta IS}{N} - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

- Eq. 1: S decreases with newly infected individuals
- Eq. 2: I increases with newly infected individuals, minus infected people who recovered
- Eq. 3: R increases with the number of individuals who were infectious and who either recovered or died

SIR model

In R:

```
SIR <- function(time, state, parameters) {
  par <- as.list(c(state, parameters))
  with(par, {
    dS <- -beta * I * S / N
    dI <- beta * I * S / N - gamma * I
    dR <- gamma * I
    list(c(dS, dI, dR))
  })
}
```

Fitting a *SIR* model

To fit the model to the data we need to find the optimal values of our parameters that minimise the sum of the squared differences between $I(t)$ and the corresponding number of cases as predicted by our model $\hat{I}(t)$:

$$RSS(\beta, \gamma) = \sum_t \left(I(t) - \hat{I}(t)\right)^2$$

Fitting a *SIR* model

In R, with ode() (for ordinary differential equations) and optim():

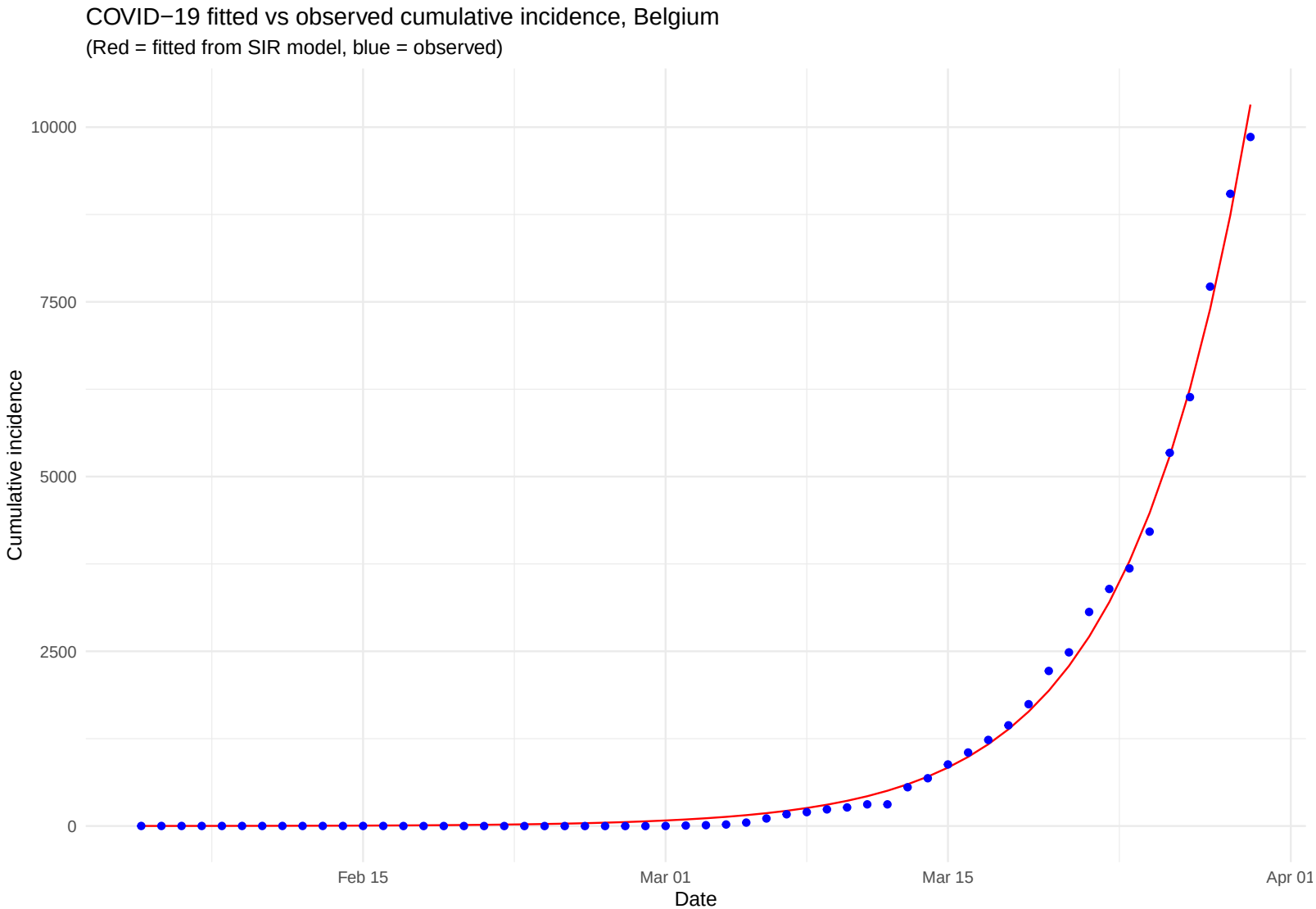
```
library(deSolve)

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), # find the optimal values
  RSS,                    # that give the smallest RSS
  method = "L-BFGS-B",    # start with values of 0.5
  lower = c(0, 0),        # and constrain them to
  upper = c(1, 1)         # the interval 0 to 1.0
)
```

Data

- Dataset of John Hopkins (collection of 12 resources), via `{coronavirus} R` package
- Data from Feb. 4 (1^{st} confirmed case) until March 30 because:
  - What is needed are currently infected persons (cumulative infected minus the removed, i.e. recovered or dead)
  - But numbers of recovered persons are hard to obtain and probably underestimated (underreporting bias)
  - We thus consider the cumulative number of infected people until the number of recovered individuals becomes non-negligible
  - Which I assumed was ± 14 days[1] after lockdown
- Analyses done here are still valuable to see how the virus would have evolved

[1] Average duration after which COVID-19 patients are considered as cured.

Application to Belgium



Reproduction number R_0

- Model fits well to the observed data, so we can compute the *reproduction number* R_0 as

$$R_0 = \frac{\beta}{\gamma}$$

- Gives the average number of healthy people that get infected per number of sick (infectious) people

- The larger the R_0, the harder it is to control the epidemic and the higher the probability of a pandemic

Reproduction number R_0

In R:

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

```
##      beta     gamma
## 0.5841185 0.4158816
```

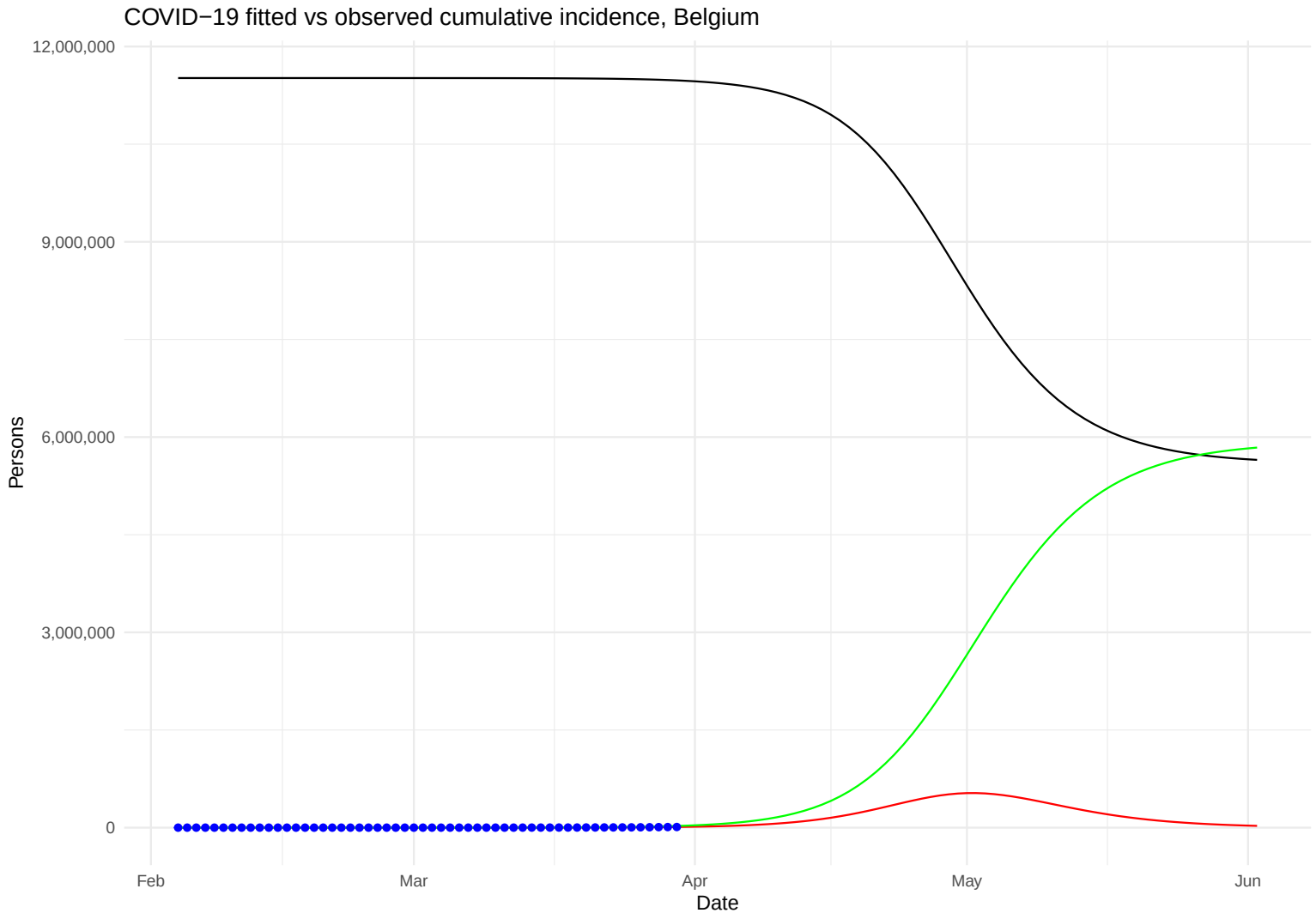
```
R0 <- as.numeric(Opt_par[1] / Opt_par[2])
R0
```

```
## [1] 1.404531
```

- On average in Belgium, 1.4 persons were contaminated for each infected person for the period considered

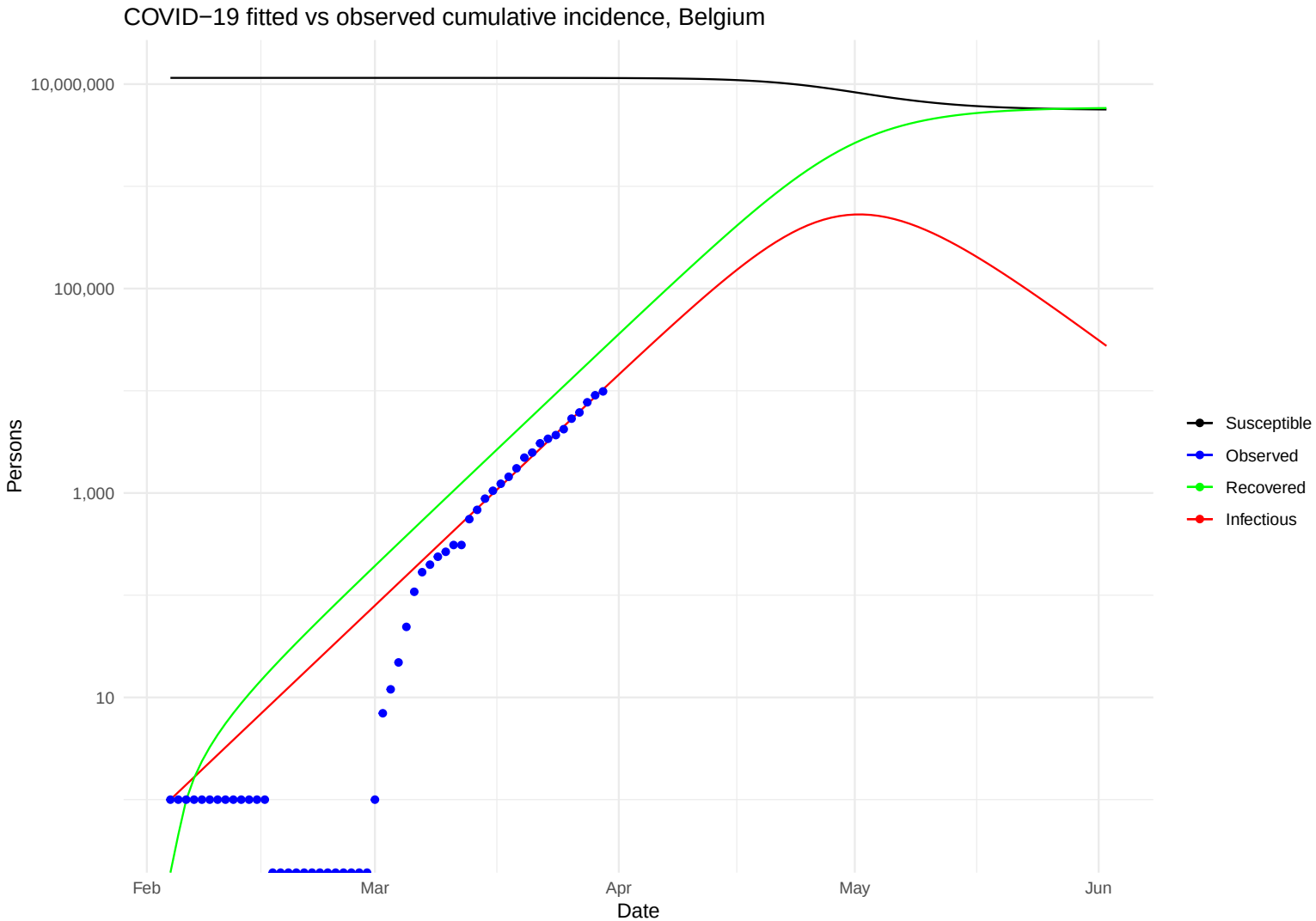
Predictions

- No health intervention and fixed R_0:



Predictions

- In log scale:



More summary statistics

```
# peak of pandemic
fit[fit$I == max(fit$I), c("Date", "I")]
```

```
##           Date         I
## 89 2020-05-02 531000.4
```

```
# severe cases
max(fit$I) * 0.2
```

```
## [1] 106200.1
```

```
# cases with need for intensive care
max(fit$I) * 0.06
```

```
## [1] 31860.03
```

```
# deaths with supposed 4.5% fatality rate
max(fit$I) * 0.045
```

```
## [1] 23895.02
```

Additional considerations

- Previous figures must be taken with extreme caution:
  - Based on rather unrealistic assumptions:
    - no public health interventions
    - fixed reproduction number R_0
  - Other assumptions (more realistic?) for severe cases, ICU and fatality rates
  - Data quality
- BUT previous pandemics (e.g., Spanish & swine flu) showed that high number are not impossible...

Improvements

- *SEIR* model: $\approx$ *SIR* but infected people *I* are divided into:
  1. *E* for *E*xposed/infected but asymptomatic
  2. *I* for *I*nfected and symptomatic
- Modelling the epidemic trajectory using 2 log-linear models:[2]
  1. one to the growth phase (before the peak)
  2. one to the decay phase (after the peak)

  allowing to estimate doubling and halving times
- Estimate the current effective reproduction number R_e on a day-by-day basis[3]
- More sophisticated projections[4]

[2] See `{incidence} R` package.
[3] See `{EpiEstim} R` package.
[4] See `{projections} R` package.

This talk is based on & complements:

- LIDAM Report (link)
- Blog (link)

Thanks!

Questions?