

MATHEMATICAL MODELS AND LOCKDOWN

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<http://hdl.handle.net/2268/246583>

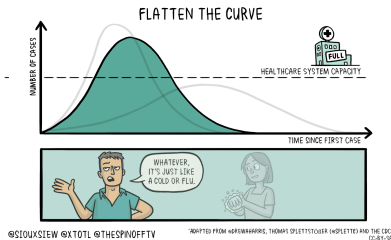
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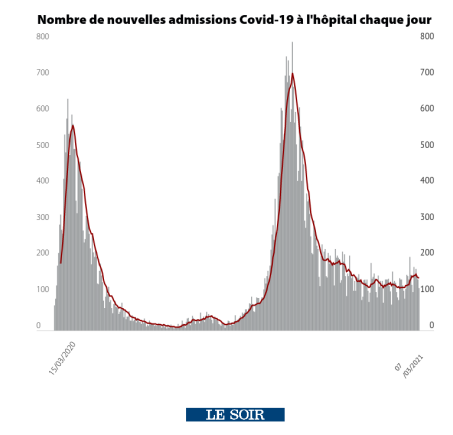


Belgian Biophysical Society Webinar — 11th March 2021

Disclaimer :

- ▶ I'm **not at all** a specialist of mathematical models, I'm **not** a statistician ; I do **not** manipulate data ; but (hopefully) I'm still a mathematician.
- ▶ In March 2020, I wanted to understand the sentence *"we have to flatten the curve"*.
- ▶ Based on available data, we want to predict how the situation will evolve.

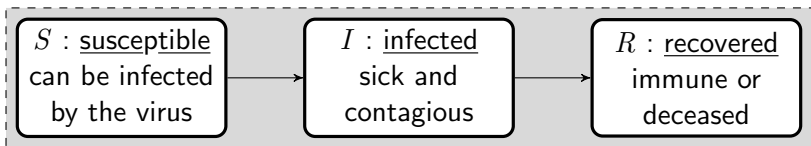




I found the following source useful (easy to Google it) :

- ▶ David Smith and Lang Moore, *The SIR Model for Spread of Disease*, Math. Assoc. Amer. 2001.

A “simple” model presented by Kermack and McKendrick in 1927



A *recovered* person can still suffer from several long term problems and might even die later on from subsequent complications.

Limitations of the SIR model :

- ▶ the incubation period is zero ;
- ▶ the period during which a person is contagious coincides with the period during which he or she is ill :

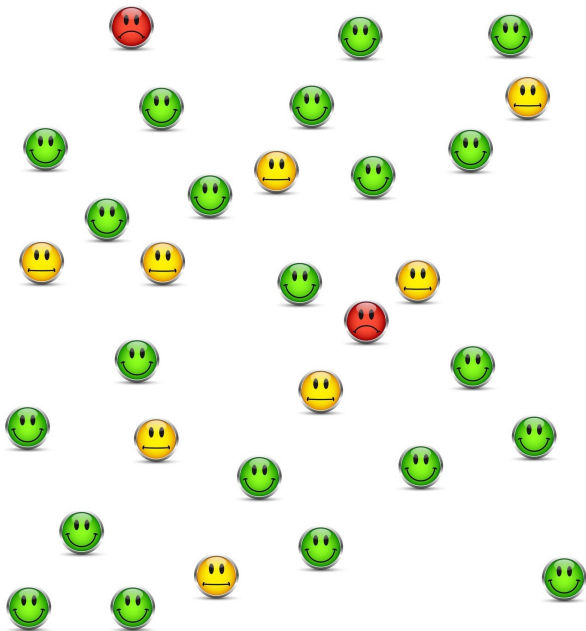
$$\text{infected} = \text{sick} = \text{contagious} = \text{infectious}$$

Remarks :

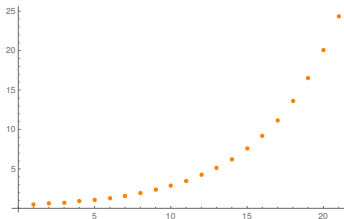
- ▶ The category R contains recovered and deceased persons.
- ▶ A recovered person cannot get sick again.

$$S \longrightarrow I \longrightarrow R$$

Population : uniform mix of individuals S , I and R



We would like to estimate the evolution $S(t)$, $I(t)$ and $R(t)$ along the time



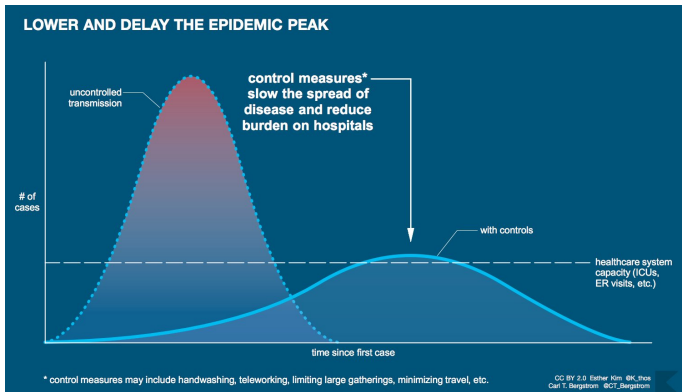
- ▶ Not all patients are seriously ill; in the case of COVID-19 there are also asymptomatic patients.
- ▶ A stable proportion of patients will require hospitalization.
- ▶ Amongst those, a stable proportion will require ICU.
- ▶ The maximum capacity of hospitals is known.
- ▶ We never know the “exact” value of $S(t)$, $I(t)$ and $R(t)$.

WHY SHOULD WE ESTIMATE $I(t)$?

We “know” what proportion will require care, e.g. 7%.

The goal of policy makers is therefore to maintain

$$0,07.I(t) < \text{capacity of hospitals.}$$

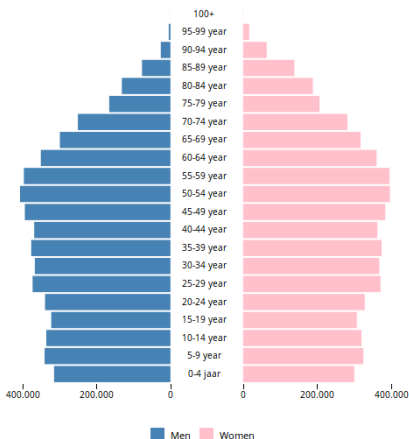


WHY SHOULD WE ESTIMATE $I(t)$?

population pyramid, cf. `statbel.fgov.be`

Belgium x ▼

Population pyramid of Belgium, the Regions and the Provinces



Belgium

11,431,406 inhabitants

50.8% women

49.2% men

Flemish

Region

6,589,069 (57.6%)

50.5% women

49.5% men

Walloon

Region

3,633,795 (31.8%)

51.1% women

48.9% men

Brussels-Capital Region

1,208,542 (10.6%)

51.1% women

48.9% men

WHY SHOULD WE ESTIMATE $I(t)$?

16 March 2020

Imperial College COVID-19 Response Team

Impact of non-pharmaceutical interventions (NPIs) to reduce COVID-19 mortality and healthcare demand

| Age-group (years) | % symptomatic cases requiring hospitalisation | % hospitalised cases requiring critical care | Infection Fatality Ratio |
|-------------------|---|--|--------------------------|
| 0 to 9 | 0.1% | 5.0% | 0.002% |
| 10 to 19 | 0.3% | 5.0% | 0.006% |
| 20 to 29 | 1.2% | 5.0% | 0.03% |
| 30 to 39 | 3.2% | 5.0% | 0.08% |
| 40 to 49 | 4.9% | 6.3% | 0.15% |
| 50 to 59 | 10.2% | 12.2% | 0.60% |
| 60 to 69 | 16.6% | 27.4% | 2.2% |
| 70 to 79 | 24.3% | 43.2% | 5.1% |
| 80+ | 27.3% | 70.9% | 9.3% |

DOI: <https://doi.org/10.25561/77482>

Counting or proportions :

| $S(t)$ | $I(t)$ | $R(t)$ | N |
|--------|--------|--------|-----|
| 160 | 2 | 38 | 200 |

$$S(t) + I(t) + R(t) = N$$

| $s(t)$ | $i(t)$ | $r(t)$ | |
|--------|--------|--------|------|
| 80% | 1% | 19% | 100% |

$$\textcolor{red}{s}(t) = \frac{S(t)}{N} \quad \textcolor{red}{i}(t) = \frac{I(t)}{N} \quad \textcolor{red}{r}(t) = \frac{R(t)}{N}$$

$$s(t) + i(t) + r(t) = 1.$$

EVOLUTION OF S

We place ourselves at the global level of the entire population ; it's a public health problem. We look at *average* not at individuals.

β **average transmission rate** of the disease (*daily and for each infectious person*)

$$\beta = m.p$$

This average transmission rate depends on two parameters

- ▶ m : average number of daily contacts
- ▶ p : probability to get sick when encountering an infectious person

local ZOOM :



$$m = 8$$

$$p = \frac{1}{2}$$

$$s(t) = \frac{3}{4}$$

An infectious person can only infect a “healthy” person (susceptible to get sick).

He/she will therefore contaminate on average

$$\underbrace{m \cdot p}_{\beta} \cdot s(t) \text{ susceptible persons}$$

$$\text{on the example : } 8 \cdot \frac{1}{2} \cdot \frac{3}{4} = 4 \cdot \frac{3}{4} = 3$$

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$$s(t) = \frac{1}{2}$$



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$\underbrace{m \cdot p}_{\beta} \cdot s(t)$ susceptible persons

on the example : $8 \cdot \frac{1}{2} \cdot \frac{1}{2} = 4 \cdot \frac{1}{2} = 2$

ZOOM local :

$$m = 8$$

$$p = \frac{1}{2}$$

$$s(t) = \frac{1}{2}$$



An infectious person can only infect a “healthy” person (susceptible to get sick).

He/she will therefore contaminate on average

$\underbrace{m \cdot p}_{\beta} \cdot s(t)$ susceptible persons

on the example : $8 \cdot \frac{1}{2} \cdot \frac{1}{2} = 4 \cdot \frac{1}{2} = 2$

Notation, first difference :

$$\Delta I(t) = I(t + 1) - I(t)$$

gives the *increment* to move from one day t to the next

Simplification of counting : it is assumed that infectious people meet different people. It's unlikely that someone healthy will meet several infectious persons on the same day.

The total number of contaminations on day t is equal to

$$\underbrace{\beta \cdot s(t)}_{\text{infected by 1}} \times \underbrace{I(t)}_{\text{number of infectious}}$$

First equation of the model :

$$S(t+1) = S(t) - \beta \cdot s(t) \cdot I(t)$$

$$\boxed{\underbrace{S(t+1) - S(t)}_{\Delta S(t)} = -\beta \cdot s(t) \cdot I(t)}$$

If we express the proportions (we divide by the total number of people)

$$\frac{S(t+1)}{N} = \frac{S(t)}{N} - \beta \cdot s(t) \cdot \frac{I(t)}{N}$$

$$\boxed{\Delta s(t) = -\beta \cdot s(t) \cdot i(t)}$$

As a reminder, the average transmission rate $\beta = m.p$

$m \downarrow$ with isolation, lock-down, prohibition of large gatherings, ...



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$$m = 3$$

As a reminder, the average transmission rate $\beta = m.p$

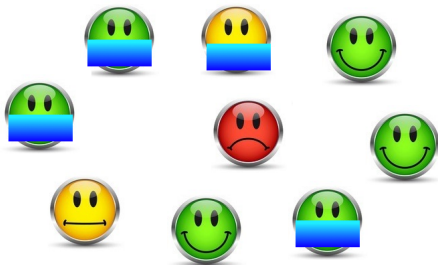
$p \downarrow$ with hygiene measures, wearing a mask, social distancing,
outdoor activities, ...



$$p = \frac{1}{2}$$

As a reminder, the average transmission rate $\beta = m.p$

$p \downarrow$ with hygiene measures, wearing a mask, social distancing,
outdoor activities, ...



$$p = \frac{1}{4}$$

EVOLUTION OF R

γ : *the proportion of contaminated people who recover during the course of a day*

Let us say, on average, 5 days are needed to recover.

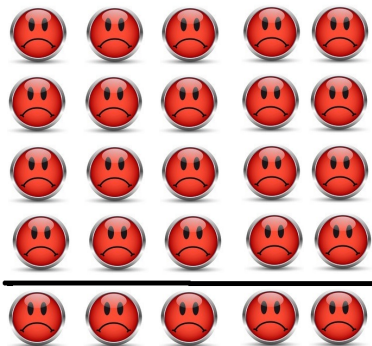


On average, $\gamma = 1/5$ of patients will recover during the day t

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EVOLUTION OF R

$$S(t+1) = S(t) - \beta \cdot s(t) \cdot I(t)$$

Second equation of the model :

$$R(t+1) = R(t) + \gamma \cdot I(t)$$

$$\boxed{\underbrace{R(t+1) - R(t)}_{\Delta R(t)} = \gamma \cdot I(t)}$$

If we express the proportions (we divide by the total number of people)

$$\boxed{\Delta r(t) = \gamma \cdot i(t)}$$

THE FULL MODEL

$$\Delta s(t) = -\beta.s(t).i(t)$$

$$\Delta r(t) = \gamma.i(t)$$

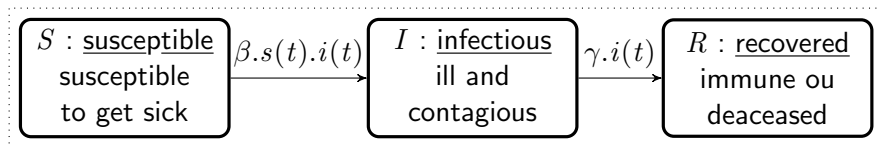


FIGURE – Win and loss within the three categories.

$$\Delta i(t) = i(t+1) - i(t) = \beta.s(t).i(t) - \gamma.i(t)$$

THE FULL MODEL

$$\Delta s(t) = -\beta.s(t).i(t)$$

$$\Delta r(t) = \gamma.i(t)$$

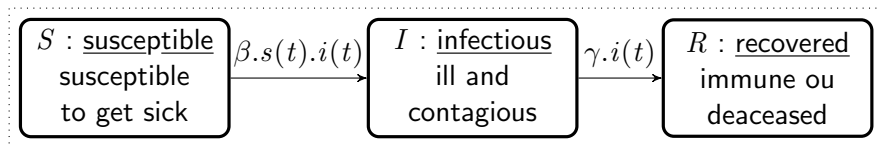


FIGURE – Win and loss within the three categories.

$$\Delta i(t) = i(t+1) - i(t) = \beta.s(t).i(t) - \gamma.i(t)$$

THE FULL MODEL

We therefore have a system of equations

$$\begin{cases} \Delta s(t) &= s(t+1) - s(t) &= -\beta \cdot s(t) \cdot i(t) \\ \Delta i(t) &= i(t+1) - i(t) &= \beta \cdot s(t) \cdot i(t) - \gamma \cdot i(t) \\ \Delta r(t) &= r(t+1) - r(t) &= \gamma \cdot i(t) \end{cases}$$

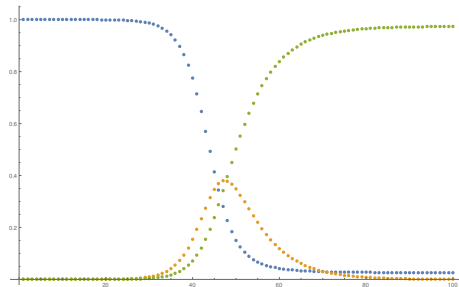
whose solution depends on initial conditions

If the time interval (instead of a day) tends towards 0, the model is often presented as a system of differential equations

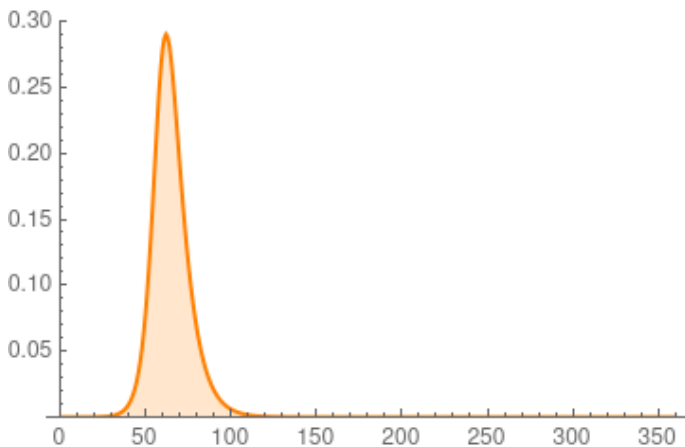
$$\begin{cases} s'(t) &= -\beta \cdot s(t) \cdot i(t) \\ i'(t) &= \beta \cdot s(t) \cdot i(t) - \gamma \cdot i(t) \\ r'(t) &= \gamma \cdot i(t) \end{cases}$$

THE FULL MODEL

```
s[0] = 1 - 0.000001;  
i[0] = 0.000001;  
r[0] = 0;  
 $\beta = 1/2$ ;  
 $\gamma = 1/7$ ;  
s[t_] := s[t] = s[t - 1] -  $\beta$  s[t - 1]  $\times$  i[t - 1];  
i[t_] := i[t] = i[t - 1] +  $\beta$  s[t - 1]  $\times$  i[t - 1] -  $\gamma$  i[t - 1];  
r[t_] := r[t] = r[t - 1] +  $\gamma$  i[t - 1];  
  
ListPlot[{Table[s[t], {t, 1, 100}], Table[i[t], {t, 1, 100}], Table[r[t], {t, 1, 100}]}]
```

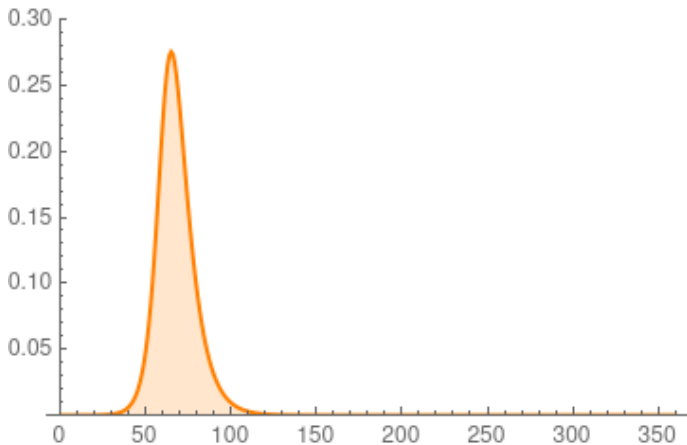


If β evolves? For instance, between 0,4 and 0,2 ($\gamma = 1/7$)



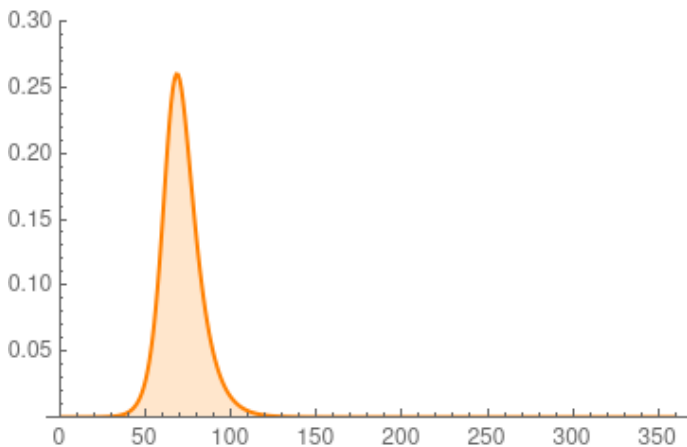
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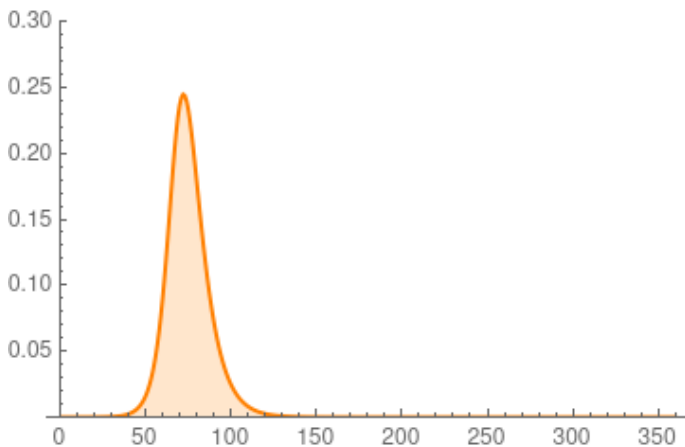
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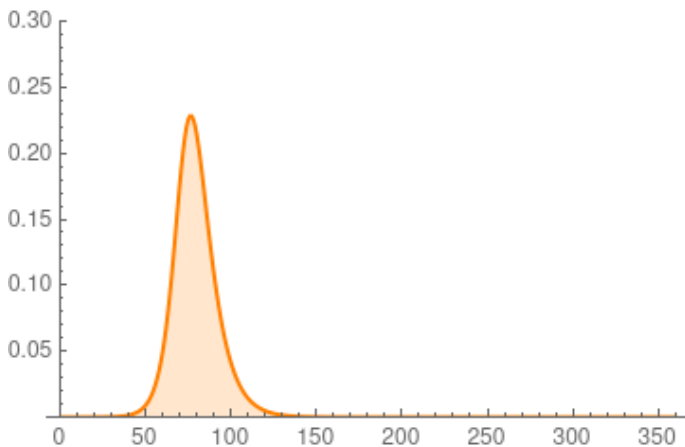
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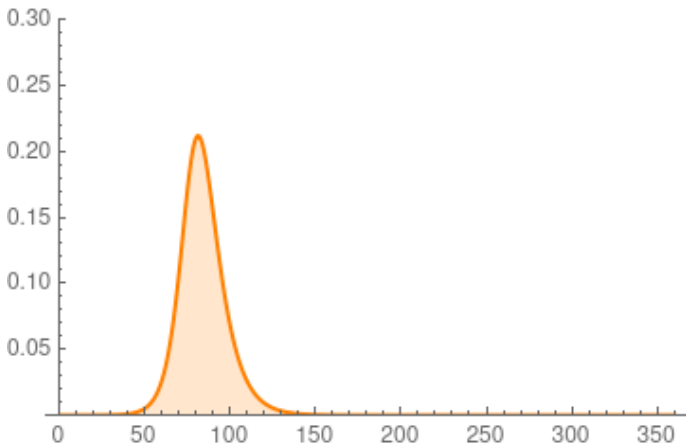
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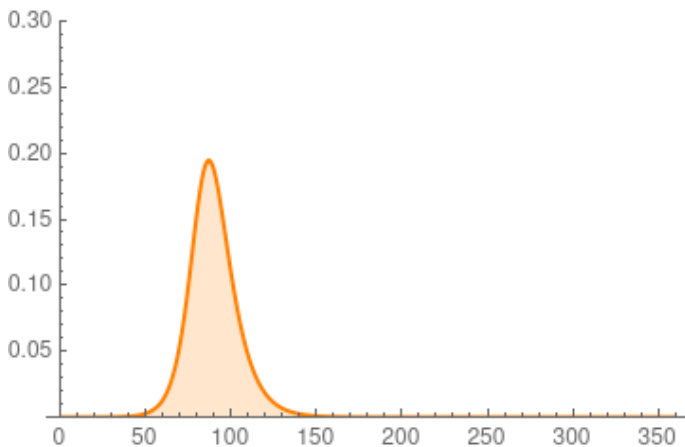
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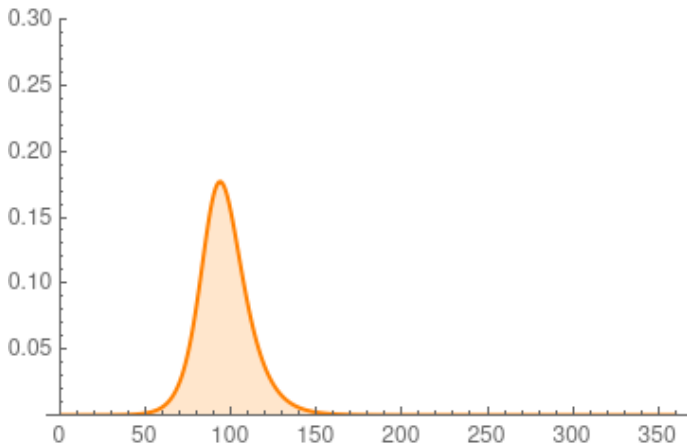
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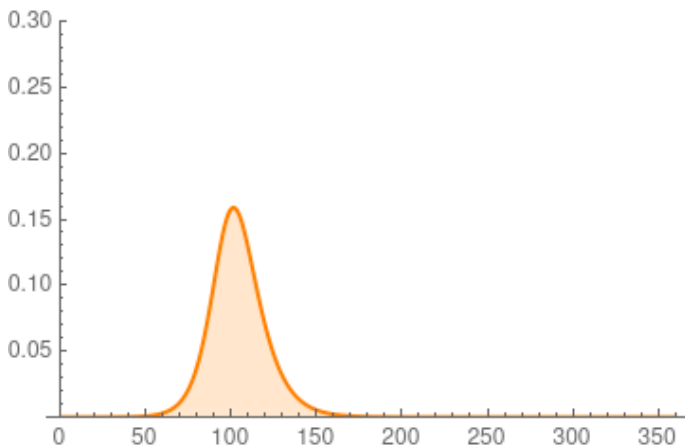
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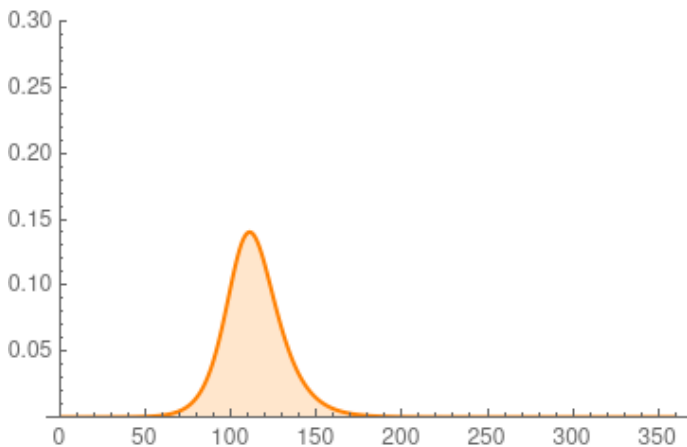
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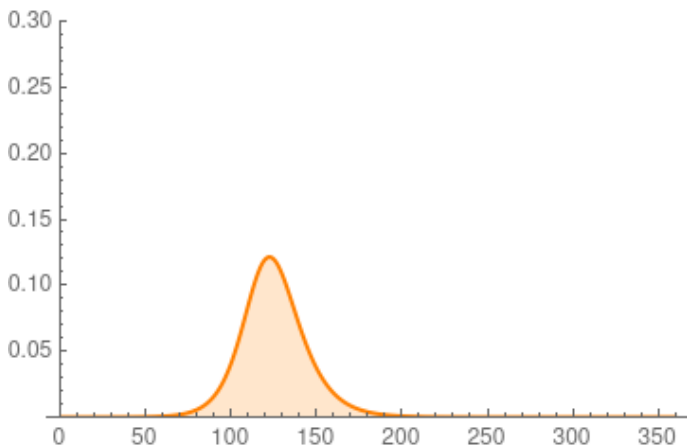
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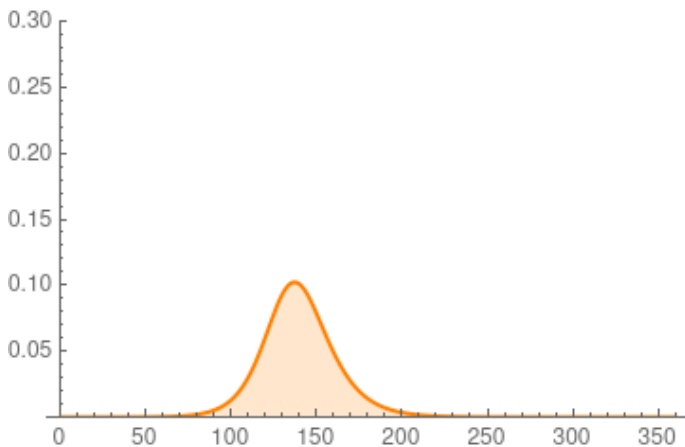
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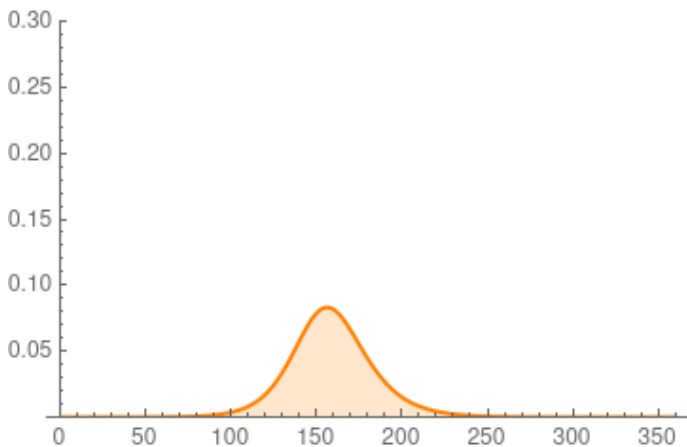
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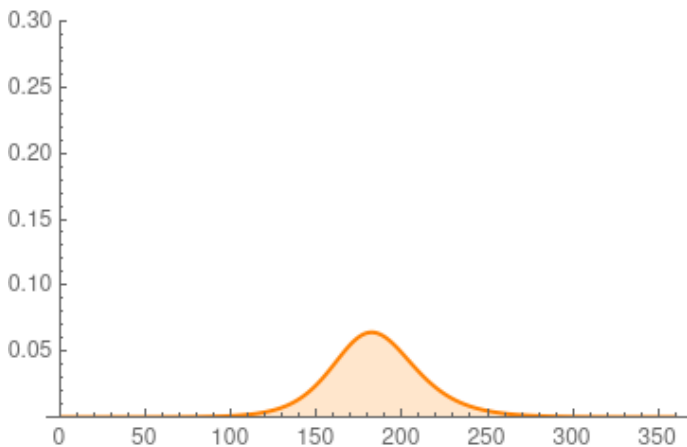
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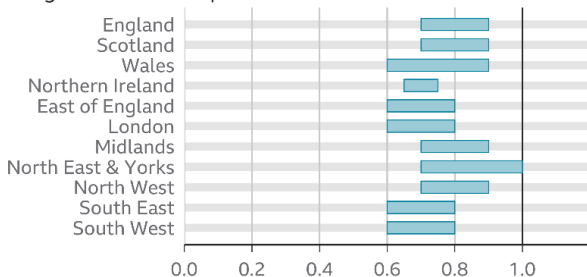


Second (and last) part :

Reproduction rate (or R_0 number)
and vaccination

R number estimates in the nations & regions

Range of Covid-19 reproduction numbers



Figures for England published on 5 Mar, Scotland on 4 Mar, Wales on 26 Feb and Northern Ireland on 2 Mar

Source: DHSC, Scottish Government, NI Dept. of Health, Wales TAC

BBC

- ▶ β average transmission rate (daily, for each infectious person)
- ▶ $1/\gamma$ average number of days needed to recover

Reproduction number

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

average number of transmissions **throughout the infectious period** for each infectious person

for COVID-19, $R_0 \simeq 2.4$, new British variant 'raises by up to 0.7'.
In Belgium, on 9th March 2021, $R_0 \simeq 0.99$.

As we did earlier, if it is multiplied by the proportion of people susceptible to get sick, then we will have the average number

$$\frac{\beta \cdot s(t)}{\gamma}$$

of persons infected by a single infectious person
(over the entire period of time he or she is ill/infectious).

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of persons infected by a single infectious person
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Recall the third equation

$$\Delta i(t) = \beta \cdot s(t) \cdot i(t) - \gamma \cdot i(t)$$

and manipulate

$$\Delta i(t) = \left(\frac{\beta \cdot s(t)}{\gamma} - 1 \right) \cdot \underbrace{\gamma \cdot i(t)}_{\geq 0}.$$

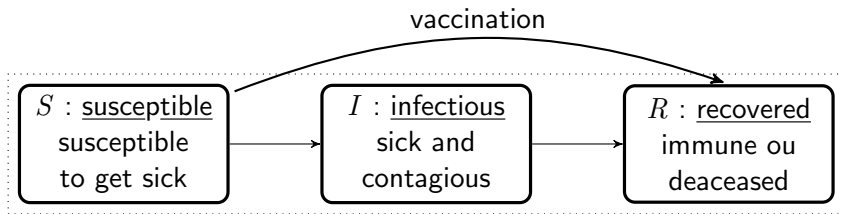
- ▶ If $\Delta i(t) > 0$, increase in the proportion of sick people
- ▶ If $\Delta i(t) < 0$, decrease in the proportion of sick people

We want that

$$\frac{\beta \cdot s(t)}{\gamma} - 1 < 0$$

Assume that the population is divided into S/R only, we want

$$s(t) < \frac{\gamma}{\beta}, \quad \text{thus, } r(t) > 1 - \frac{\gamma}{\beta} = 1 - \frac{1}{R_0}$$



If $\beta/\gamma \simeq 2.4$, at least $1 - (1/2.4) \simeq 58\%$ vaccination coverage is required

The more contagious a disease is, the greater the vaccination coverage needs to be :

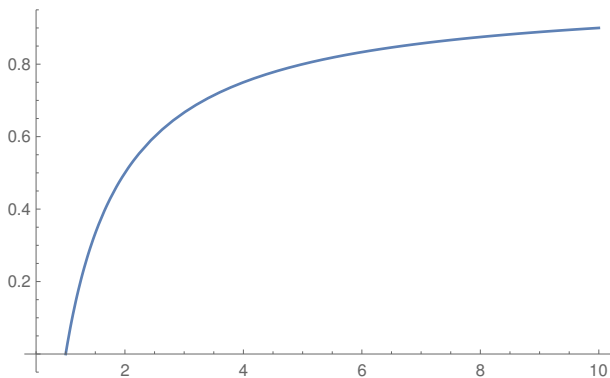


FIGURE – Evolution of vaccination coverage $1 - \gamma/\beta$ depending on the reproduction rate β/γ .

- ▶ Much more sophisticated models exist :
 - ▶ SEIR, a class of *exposed* individuals in incubation period (infected, but not yet infectious) ;

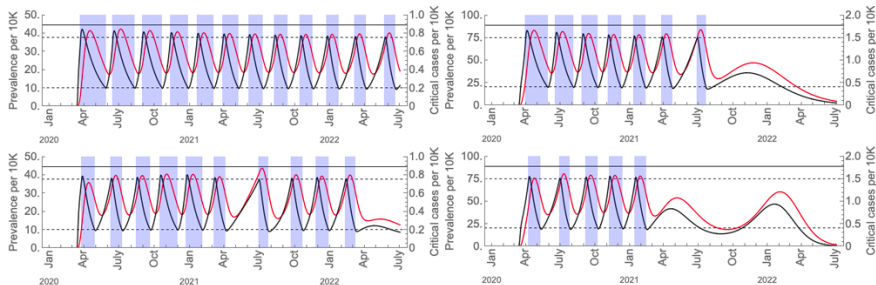
$$S \longrightarrow E \longrightarrow I \longrightarrow R$$

- ▶ MSEIR, an initial passive immunity exists ;

$$M \longrightarrow S \longrightarrow E \longrightarrow I \longrightarrow R$$

- ▶ MSEIRS, immunity within class R is temporary, return to class S after a certain period of time.
- ▶ Taking into account the spatial distribution.
- ▶ Having accurate data helps refine predictions ; in particular, estimating $S(t)$ is important but difficult.

What I discovered a year ago — What could be expected ?



intermittent periods of social distancing (Social distancing strategies for curbing the COVID-19 epidemic, Kissler *et al.*)



28



Agent-Based Network Models for COVID-19

Christopher Wolfram, WOLFRAM

Posted 1 month ago

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